Improving the crown rot resistance and tolerance of wheat using marker-assisted recurrent selection

BY

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Statement of Originality

I certify to the best of my knowledge, the content of this thesis has not been submitted elsewhere for the purposes of obtaining the award of any other degree or diploma in any University.

I also certify that it contains no material previously published or written by any other person, except where due references are made in the text.

Md. Mahbubur Rahman

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Abstract

Wheat (*Triticum aestivum* L.), the most important food crop globally, is one of the most traded agricultural commodities and is a major source of calories for large numbers of people. Wheat is an annual crop and production is limited by a wide range of biotic and abiotic stresses. Among the diseases, crown rot of wheat and barley is a serious disease caused by the fungus *Fusarium pseudograminearum*; a stubble-borne pathogen common in no-till farming systems in water-limited grain growing regions. Symptoms include honey-brown discoloration on the crown and lower stem. Premature ripening of developing heads caused by disruption of vascular tissue results in white head formation, directly leading to grain yield loss. Symptoms are exacerbated under post-anthesis drought stress. The genetic control of crown rot resistance and tolerance in wheat is generally complex, with many minor genes and quantitative trait loci (QTLs) implicated. Attempts to combine these factors using traditional breeding strategies, such as backcrossing, have generally proven ineffective. Therefore, a different strategy is required to more efficiently transfer crown rot resistance and tolerance into adapted backgrounds.

This study examined Marker Assisted Recurrent Selection (MARS) as a strategy to more effectively pyramid the many minor genes controlling plant response to crown rot. Three different resistant sources were utilized to develop each of the three MARS populations to (i) establishment the degree of resistance in each population by comparing field and pot-based phenotyping, (ii) confirm the relationship, if any, between resistance and tolerance, (iii) identify QTLs that explain crown rot resistance and tolerance, (iv) pyramid these QTLs using MARS and (v) confirm response to selection by evaluating parents and recombinants under crown rot pressure.

Although three MARS populations were developed, a total of 475 genotypes (250 derived from population 1; 225 derived from population 2) were evaluated in pot and field conditions to asses stem disease severity in adult plants. Transgressive segregation was observed for crown rot resistance in both populations. Disease severity in pot tests (established in the greenhouse with added inoculum) was generally too severe and inconsistent, hence field screening using managed inoculum was considered more reliable and representative of actual genotype responses to crown rot (Chapter 4).

The 475 lines of both populations were also genotyped using a 9K SNP platform. The genotypes and phenotypes thus generated were used to perform genome wide association mapping as more than two parents were recombined in each population. Following two cycles of recombination, up to 22 markers of a possible 23 were recombined. Two-hundred and ninety-seven doubled haploid derived lines representing both cycles of recombination, the original parents, parents selected from the base population and local cultivars were evaluated for crown rot resistance and tolerance in 2016 and 2017 in the field under crown rot pressure. A significant and positive response to selection was observed. Some recombinants showed significantly higher resistance compared to their parents and local cultivars, combined with high grain yield (Chapter 7).

Population 3 was developed to examine both tolerance, defined as reduced yield loss under crown rot inoculum, and resistance. The yield loss of 196 derived lines was determined in replicated, inoculated and un-inoculated paired-plots in 2014 and 2015. Some genotypes expressed consistent tolerance to crown rot infection across years and were subsequently recombined using the MARS approach to develop materials with enhanced tolerance. A weak relationship was observed between tolerance and basal stem browning defined as resistance (Chapter 5). Population 3 was genotyped using a high-density 90K SNP genotyping array and a genome wide association analysis conducted to identify QTLs for both tolerance and resistance based on multi-year, multi-environment data (Chapter 5). Forty-eight QTLs were associated with resistance and tolerance traits and 9 previously reported QTLs were confirmed. Resistance associated with basal stem browning was always independent of tolerance (Chapter 6). These results are now being used to combine multiple trait alleles into a single genotype using MARS.

MARS was identified as an effective breeding strategy to combine many QTL of minor effect in wheat. The strategy can clearly be used to improve complex, polygenic traits in self-pollinated crops. The genotypes identified in this study combine multiple sources of resistance and tolerance. These materials and their associated markers can be used by the Australian wheat industry to improve wheat yield in the presence of crown rot.

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Abbreviations/Acronyms

BLUEs	Best Linear Unbiased Estimators
CIMMYT	International Maize and Wheat Improvement Centre
CR	Crown rot
cM	centiMorgan
DArT	Diversity arrays technology
DH	Doubled haploid
DNA	Deoxyribonucleic acid
FCR	Fusarium crown rot
F	F statistic
FAO	Food and Agricultural Organization of the United Nations
GA	Genetic advance
GBS	Genotyping-by-Sequencing
GWAS	Genome wide association study
GRDC	Grains Research and Development Corporation
GS	Genomic selection
Ha	Hectare
LD	Linkage disequilibrium
TKW	Thousand kernel weight (g)
MAS	Marker-assisted selection
MABC	Marker-assisted back crossing
Mb	Megabyte
MARS	Marker-assisted recurrent selection
MAF	Minor allele frequency
Mpa	Megapascals
MTA	Marker trait association
NDVI	Normalized difference vegetation index

NGS	Next-generation sequencing
NSW	New South Wales
PBIN	Plant Breeding Institute, Narrabri
QTL	Quantitative trait locus
REML	Restricted Maximum Likelihood
% Screenings	Percentage of screenings
SNPs	Single nucleotide polymorphisms
USDA	United States Department of Agriculture
% WH	Percentage of white heads
Wald	Wald statistic
WSB	Weighted stem browning
GY	Grain yield (kg ha^{-1})
% Yield loss	Percentage of yield loss

CHAPTER 1

Introduction

Wheat (*Triticum aestivum* L.) is one of the most important food crops globally and is the most traded agricultural commodity (Curtis and Halford, 2014). Wheat as a staple food is second only to rice but has higher grain protein (8-14%) and nutritive value; providing more than 20% of the calories and protein requirements of 35% of the world's population (Hawkesford *et al.*, 2013; Kumar *et al.*, 2011a; Tyagi *et al.*, 2014). Wheat is the most economically important food crop in Australia (Fischer *et al.*, 2014); however production is limited by crown rot disease which causes annual losses of $79 million. These losses are even greater when barley is included (estimated at $97 million annually) (Murray and Brennan, 2009b; Murray and Brennan, 2010). The primary causal fungal pathogen of crown rot in wheat and barley is *Fusarium pseudograminearum*; a stubble-borne pathogen commonly found in no-till farming systems in semi-arid grain growing regions (Burgess *et al.*, 2012). The disease results in significant yield loss (Smiley *et al.*, 2005), particularly under post-anthesis drought stress (Simpfendorfer, 2012b). Crown rot was first reported in Australia in 1951 (McKnight and Hart, 1966) and was subsequently found across the wheat growing belt of New South Wales (Burgess *et al.*, 1975; Backhouse *et al.*, 2004); South Australia (FEDEL-MOEN and Harris, 1987; Wallwork *et al.*, 2004), Western Australia (Khangura *et al.*, 2013) and Queensland (Purss, 1969; Wildermuth *et al.*, 1997). The disease is also found in New Zealand (Monds *et al.*, 2005), the Pacific Northwest of the USA (Smiley *et al.*, 2005; Paulitz *et al.*, 2002; Cook, 2007), the Canadian Prairies (Fernandez *et al.*, 2007), the upper coastal plains of the Mississippi (Gonzalez and Trevathan, 2000), South America (Burgess *et al.*, 2001), Europe (Rossi *et al.*, 1995), South Africa (Lamprecht *et al.*, 2006), East Asia (Zhang *et al.*, 2015), West Asia (Tunali *et al.*, 2008) and North Africa (Nicol *et al.*, 2007).

The most typical symptom of crown rot is light honey-brown to dark-brown discoloration of the base of infected tillers (Chapter 2, Figure 2.5) (Mudge *et al.*, 2006; Klein *et al.*, 1988; Simpfendorfer *et al.*, 2006). The pathogen invades seedlings early in crop development through direct hyphal penetration and the infection is stimulated by surface soil moisture (Swan *et al.*, 2000). The most pronounced symptoms develop when plants are subjected to post-anthesis drought. Hyphae proliferate within stem tissue, causing premature ripening of developing heads and the eventual expression of characteristic white heads (Milgate, 2013). The conservation agricultural practices used in water-limited environments reduce tillage (in some cases eliminate all tillage) and retain crop residues. These residues serve as harbours to build-up inoculum for increasing the incidence of the disease in newly sown crops (Wildermuth *et al.*, 1997; Chakraborty *et al.*, 2006). Moreover, the crown rot pathogen can survive up to three years on stubble (Burgess, 2014; Summerell *et al.*, 1990). Rotation to non-host crops, including pulses, oilseed crops and summer cereals can reduce inoculum by facilitating breakdown of infested stubble (Golkari *et al.*, 2008; MacLeod, 2008). This strategy must remain the cornerstone of any integrated disease management (IDM) strategy for crown rot. However, a number of other control measures have been demonstrated to be at least partially effective, including repeated cultivation and stubble burning, although these are not compatible with the objectives of conservation agriculture. No fungicides have proven to be effective at controlling this disease (GRDC, 2009). Therefore the development of resistant and/or tolerant cultivars, deployed in combination with optimized crop rotation, remains the most effective and sustainable control strategy.

Partial resistance or tolerance to crown rot was identified in a wide range of wheat germplasm (Burgess *et al.*, 2012). However, incorporation of these sources into cultivars has proven challenging due to quantitative inheritance, ineffective phenotyping and the poor agronomic characteristics of resistant germplasm including low yield potential, tall plant stature, poor grain quality and undesirable maturity. The genetic control of the resistance and tolerance is complex and many minor genes and QTLs are implicated (Collard *et al.*, 2005; Bovill *et al.*, 2006; Liu and Ogbonnaya, 2015; Martin *et al.*, 2015).

Genome wide association studies (GWAS) have been used to identify marker-trait associations and QTLs linked to important traits in cereals (Crossa *et al.*, 2007; Pasam *et al.*, 2012; Huang and Han, 2014; Mwadzingeni *et al.*, 2017). Once validated, the marker-trait associations or QTLs can be used in marker assisted selection (MAS) to develop new cultivars (Zhang *et al.*, 2013). GWAS has been used to identify marker trait associations for globally important diseases including stripe rust (*Puccinia striiformis* f. sp. *tritici*), leaf rust (*Puccinia triticina*) and stem rust (*Puccinia graminis* f. sp. *tritici*) (Crossa *et al.*, 2007; Neumann *et al.*, 2011; Yu *et al.*, 2012). Many marker-trait associations have also been reported for yield and yield contributing traits (Dodig *et al.*, 2012; Zhang *et al.*, 2013; Thudi *et al.*, 2014).

Most of the QTLs reported for crown rot resistance are of minor effect and represent only a small portion of the available phenotypic variability in the trait (Liu and Ogbonnaya, 2015). Attempting to combine major and minor effects or QTL using traditional breeding strategies has largely proven ineffective. Hence a new approach is required. Marker assisted recurrent selection (MARS) is a possible strategy that can be used to pyramid many QTL (Bernardo and Charcosset, 2006). This technique was successfully applied to sunflower, soybean and maize to bring desirable alleles into single elite lines (Todorovska *et al.*, 2010). The improvement of complex traits via phenotypic recurrent selection is generally possible, however long recurrent selection cycles and the difficulty of identifying unique genes or alleles imposes restrictions on the practicability of this breeding method. This is particularly the case with crown rot as a strong interaction between disease expression and the environment makes phenotyping challenging. However, MARS overcomes the problem of identifying and combining unique alleles. Fewer more targeted crosses are required in the recombination phase compared to traditional recurrent selection. This is critical when applying the method to self-pollinated crops.

This study evaluated diverse wheat lines derived from complex crosses of polymorphic parents carrying different sources of resistance for crown rot. Materials were phenotyped using managed inoculum in pots and in the field. GWAS was used to determine markers linked to genes controlling resistance and tolerance. Offspring were subsequently recombined across two cycles of recurrent selection with the aid of genetic markers. Doubled haploids were made from selected plants and these were compared to their constituents and local cultivars to determine response to selection. The primary aims of this study were to:

1. Evaluate parents and their offspring for resistance and tolerance to crown rot and identify marker-trait associations.
2. Develop progeny with enhanced crown rot resistance and tolerance using MARS.

3. Demonstrate the practicalities of using of MARS to accumulate minor QTLs for crown rot resistance and tolerance.

4. Establish a response to selection by evaluating parents, the base population, and recombined materials under crown rot pressure.

5. Generate a database of SNP markers linked to crown rot resistance and tolerance that can be used for wheat breeding.

CHAPTER 2

Literature and review

2.1. Wheat

Wheat (*Triticum aestivum*) is one of the most important food crops globally and is the most traded agricultural commodity (Curtis and Halford, 2014). Wheat is second only to rice as a staple food and is the primary source of protein (8-14%) and nutritive value for many people. Wheat provides over 20% of the calories and 25% of the protein requirements of more than one-third of the world's population (Kumar *et al.*, 2011a; FAO, 2012). Wheat is the world's most important crop because of the acreage it occupies, high productivity, wide adaptation and prominent position in international food grain trade (Lagudah *et al.*, 2001; Khan *et al.*, 2015).

Wheat (*Triticum spp.*) originated some 55-70 million years ago. It is a monocot belonging to the class *Liliopsida*, tribe *Triticeae* (*Hordeae*), family *Poaceae* (grasses) and sub-family Pooideae (Kellogg, 2001; Huang *et al.*, 2002). According to archeological records, wheat was domesticated in the Fertile Crescent region of the Near East (the Karacadag Mountains in south-eastern Turkey) as early as 17,000 BC (Zohary *et al.*, 2012; Sharma, 2012; Clay, 2013), and evolved through several spontaneous hybridisation events as described in Figure 2.1 (Huang *et al.*, 2002). These hybridization events led to the accumulation of three different but closely related diploid genomes, designated AA, BB and DD. Thus allopolyploid or hexaploid (2n=6x=42, AABBDD) bread wheat (*T. aestivum*) evolved. This species accounts for 95% of global wheat production. The balance of production is comprised of tetraploid durum wheat or *T. durum* (2n=4x=28 AABB) (Peng *et al.*, 2011).

Studies on the genetic relationships between wild and domesticated einkorn wheat (*T. monococcum,*2n=2x=14; AA) and emmer wheat (*T. turgidum,* 2n=4x=28; AABB) at the molecular level suggest that the Middle-East is the most likely site of origin and domestication (Kilian *et al.*, 2007; Dubcovsky and Dvorak, 2007). The first cultivated landraces were diploid (einkorn) and tetraploid (emmer). The hexaploid form was later cultivated in the near east by 5000 BC (Kilian *et al.*, 2007). It is the consensus of researchers that modern wheat cultivars were derived from einkorn (*T. monococcum* ssp. *urartu*) and emmer wheat (*T. turgidum*) (Feldman, 1976).

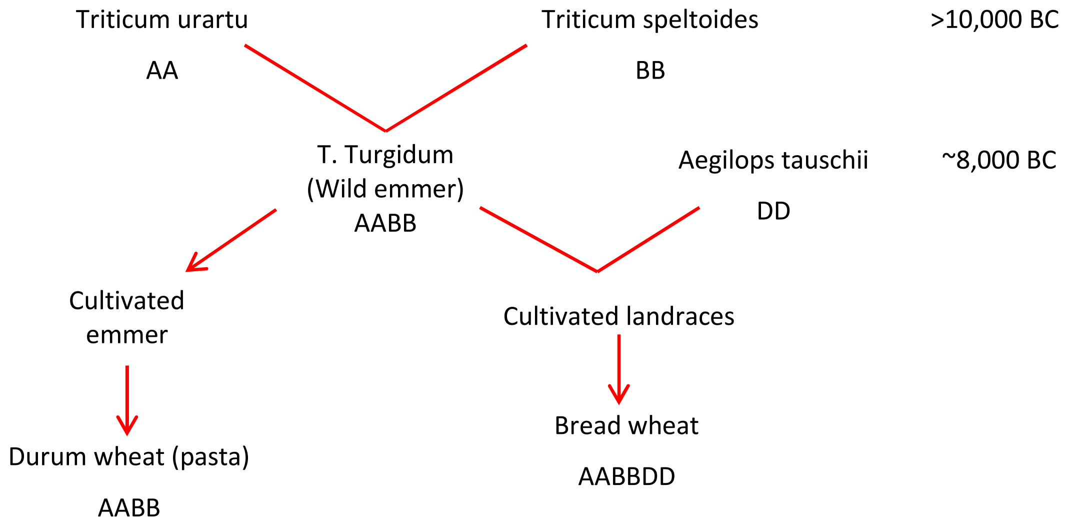


Fig. 2.1: Hexaploid and tetraploid wheat evolution

The hexaploid bread wheat genome is both large and highly complex compared to many other living organisms. It is estimated at 16,000 Mb which is large compared to rice (400 Mb), *Arabidopsis thaliana* of (130-140 Mb) (Bennett and Leitch, 2010), maize (2300 Mb) (Schnable *et al.*, 2009) and humans (3,000 Mb) (NIH, 2015).

2.1.1 Biogeography of wheat cultivation

Wheat covers 22% of the total cultivated area sown to crops globally (Leff *et al.*, 2004), with more than 33,000 known varieties produced (Stodart *et al.*, 2005). Production extends from its centre of origin through Iran into central Asia, China, Africa, Europe, America and was eventually introduced to Australia following European settlement. Forty-acre farm of wheat at paramatta, Sydney was established in 1788 (Anonymous, 2006). The most intensive wheat cultivation occurs in the temperate latitudes of both hemispheres. Wheat is grown from sea level to over 3000 m above sea level. While found in tropical and subtropical regions and is most successfully cultivated between the latitudes of 30°N and 60°N and 27°S and 45°S (Lantican *et al.*, 2005; Briggle and Curtis, 1987). Wheat is a cool season crop and its cultivation is feasible within a temperature range of 3 - 32°C (optimal growth occurring around 25°C) and annual precipitation between 250 and 1750 mm (Saunders and Hettel, 1994; Briggle and Curtis, 1987).

2.1.2 Significance of wheat

Global food security strongly depends on the cultivation of three major cereals - wheat, maize (*Zea mays L.)* and rice (*Oryza sativa L.).* Wheat is used to make chapati, biscuits, bread, cakes, noodles and pasta as human food. It is also used by industry to prepare paper and cosmetics, alcohol and bio-fuel and to supply feed for animals (Tyagi *et al.*, 2014; Kumar *et al.*, 2011b; Zhang *et al.*, 2012b). Global population is expected to grow to 8.3 billion in 2030 and 9.3 billion in 2050 (Bruinsma, 2003; Alexandratos and Bruinsma, 2012). Increasing wheat yield is therefore crucial to food security and reducing poverty. However, to meet the predicted global demand for wheat, yield will need to increase at 2% per annum. The current rate of increase is only 0.6% (Sukumaran *et al.*, 2015).

2.1.3 World wheat production

Average global wheat yield is more than 3 ton ha^{-1} with substantial variation between countries, influenced by region specific factors. Global wheat production is dominated by a few countries (Table 2.1), with China, India, United States of America, Russian Federation, France, Germany, Pakistan, Canada, Australia and Turkey accounting for more than 70% of the global production of more than 700 million tons (USDA, 2016). Wheat is produced on 17% of the world's arable land (Gooding and Davies, 1997), and is the staple carbohydrate source for 35% of the world's population (Ogbonnaya *et al.*, 2013).

Table 2.1: Wheat production of countries producing more than five million tons of wheat in different production years.

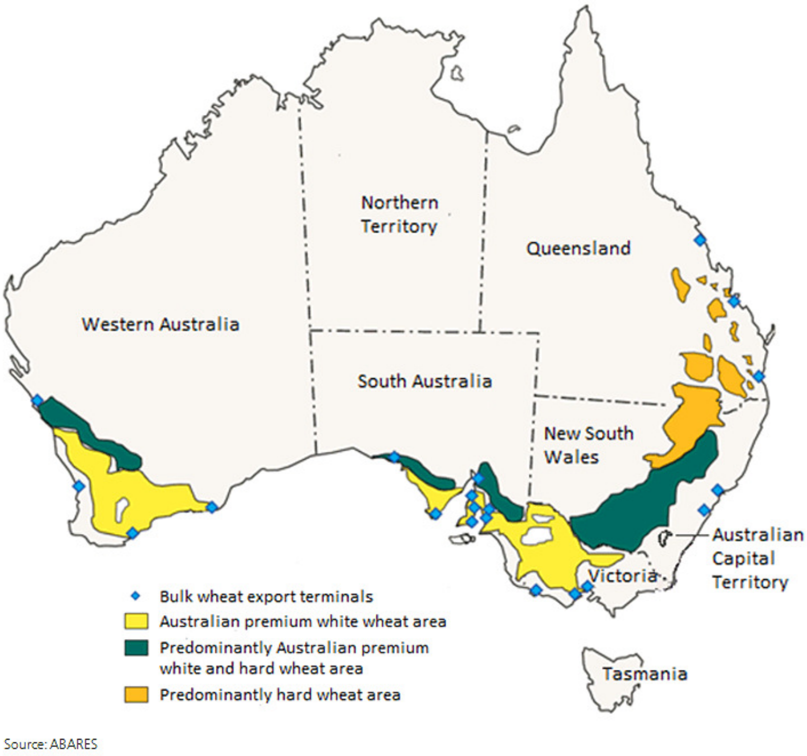
Country/Region	Production (million tons)		
	2013-2014	2014-2015	2015-2016
European Union	144.42	156.45	160.01
China	121.93	126.17	130.19
India	93.51	95.85	86.53
Russia	52.09	59.08	61.04
United States	58.11	55.13	55.84
Canada	37.53	29.42	27.60
Pakistan	24.00	25.98	25.10
Ukraine	22.28	24.75	27.27
Australia	26.93	23.91	24.50
Turkey	18.75	15.25	19.50
Kazakhstan	13.94	13.00	13.75
Iran	14.50	13.00	15.00

Argentina	10.50	13.93	11.30
Egypt	8.25	8.30	8.10
Morocco	7.00	5.10	8.00
World Total	716.82	727.87	734.8

2.2.1 Wheat production in Australia

Wheat was first grown in a small plot of 8 acres at Farm Cove (currently Sydney Royal Botanic Gardens) under Governor Phillip in Australia in 1788 at the time of European settlement. William Farrer (1845-1906) developed the first early maturing wheat varieties adapted to Australian conditions in the early 20th century (OGTR, 2008; Simmonds, 1989). Yields were initially very low due to lack of adaptability and high rust susceptibly. The early wheat breeders improved adaptation and resistance and formed the basis for a successful wheat industry.

Wheat is produced in all states except the Northern Territory, but primarily on the mainland in a narrow crescent known as the 'grain belt' (Figure 2.2). The eastern grain belt is separated into two agro-climatic zones; the northern region, characterised by summer dominant rainfall, and the southern region, with a Mediterranean winter dominant rainfall pattern. Much of the northern grain region supports both summer and winter cropping, with winter crops grown on stored soil moisture. Wheat production in Australia is limited by phosphate-deficient soils with low water holding capacity. However, intermittent rainfall is the critical factor that mostly influence yields (Figure 2.3)(Curtis and Halford, 2014). National average yield has reduced due to changing climatic conditions and the movement of wheat to more marginal environments (Anwar *et al.*, 2007). Australia is not a large wheat producing country, accounting for only 3.3% of annual global production. However, more than 73% of production is exported equating to 11% of world wheat trade, making Australia the fifth largest exporter after the European Union, Canada, United States and Russia (Figure 2.4).



Source: ABARES

Fig. 2.2: Wheat growing regions of the Australian wheat belt (ABARES, 2012).

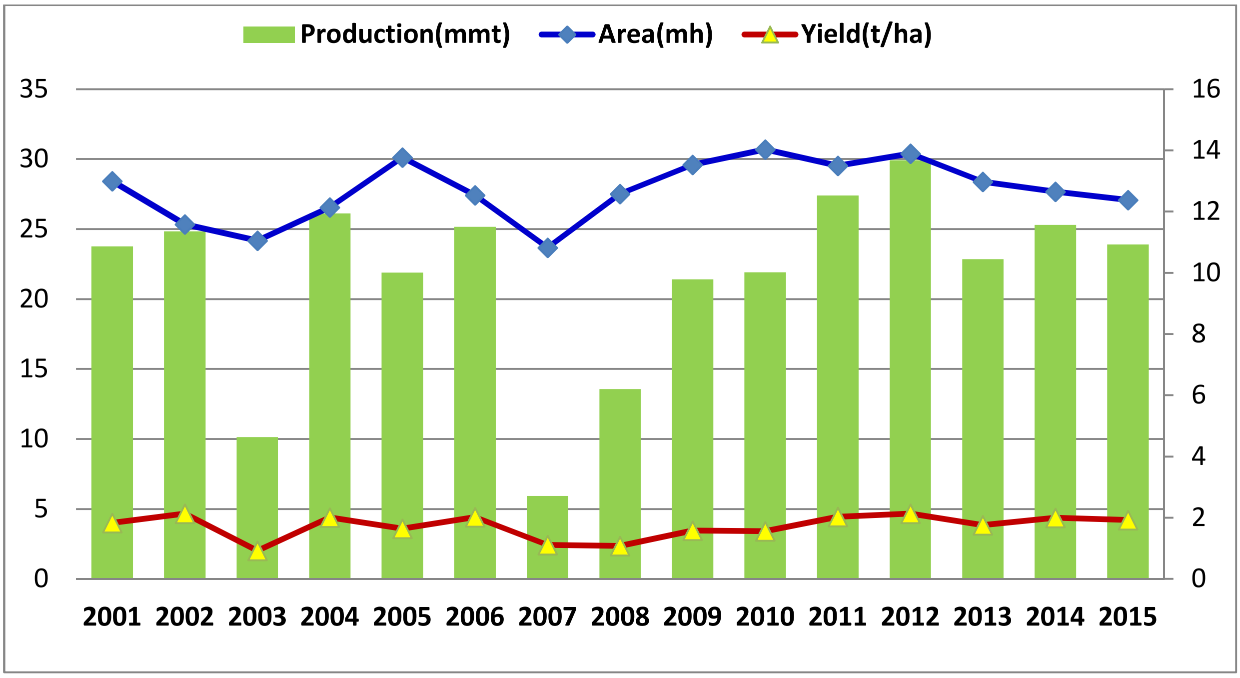


Fig. 2.3: Australian wheat production (m/tons; y-axis 2), area (m/ha; y-axis 1) and yield (t/ha; y-axis 2), 2001 to 2015. Source: The United States Department of Agriculture (2016)

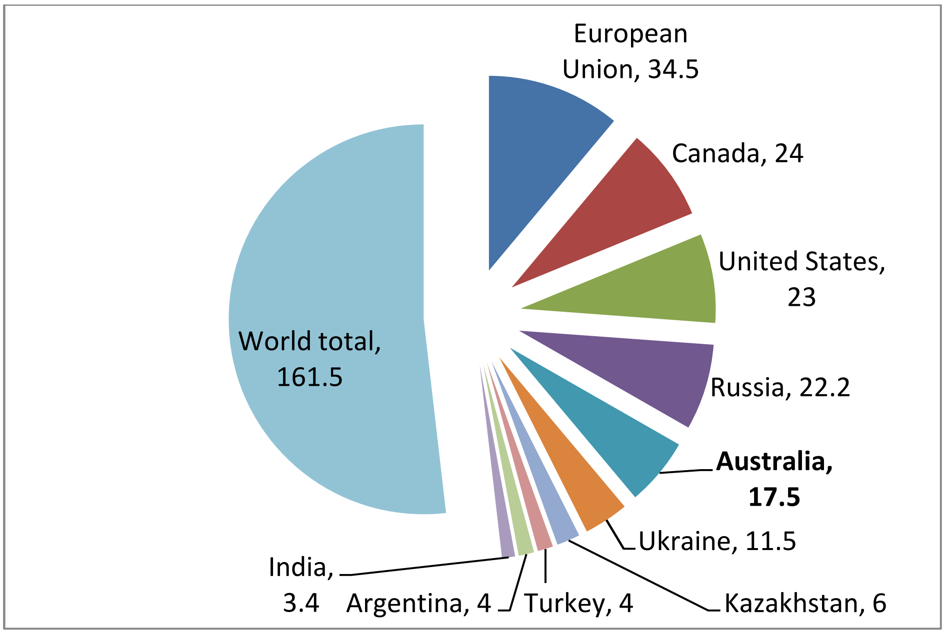


Fig. 2.4: World top 10 wheat exporters in 2015 (USDA, 2016)

2.2 Factors affecting wheat production in Australia

2.2.1 Drought and low rainfall

More than 237 million ha under wheat cultivation globally experiences periodic water stress (Rajaram, 2001; Ala *et al.*, 1994) which reduces grain yield by an average of 20% (Daryanto *et al.*, 2016). Increasing urbanization and shrinking water resources are expected to worsen the effects of drought (Hu and Xiong, 2014). Different root diseases, especially *Fusarium* species, reduce the functional root and crown tissue in wheat, particularly under moisture-restricted conditions (Cook, 1981; Burgess *et al.*, 2001; Paulitz *et al.*, 2002). Wheat is grown mostly as a dry land crop in Australia, although a small proportion is cultivated under irrigation (Turner, 2004). Water accessibility has become one of the biggest challenges to wheat production in Australia and variable rainfall is the most critical factor (Simmonds, 1989). Drought reduces wheat yield (Semenov and Shewry, 2011; Lott N *et al.*, 2011) and affects all stage of growth (Daryanto *et al.*, 2016). It reduces leaf area, number of leaves per plant, leaf size and leaf longevity (Klepper *et al.*, 1982; Ji *et al.*, 2010), spike size, grain number per spike (Innes and Blackwell, 1981; Ji *et al.*, 2010), grain size and weight and grain filling rate and duration (Wardlaw and Willenbrink, 2000; Ji *et al.*, 2010).

2.2.2 Conservation agriculture and diseases

Conservation agricultural practices can mitigate the impacts of low rainfall and drought stress by improving moisture management (Alliaume *et al.*, 2014; Thomas *et al.*, 2008; Hobbs, 2007; Reicosky, 2003). Conservation agricultural practices, including the maintenance of crop residues, has increased wheat yields (Thomas *et al.*, 2007). However, there are drawbacks as the incidence of stubble-borne pathogens such as crown rot (*Fusarium pseudograminearum*), common root rot (*Bipolaris sorokiniana*) , yellow spot of wheat (*Pyrenophora tritici-repentis*) and Fusarium head blight (*F. graminearum* and *F. pseudograminearum*) (Smiley, 1996; Wildermuth *et al.*, 1997; Rees and Platz, 1979; Backhouse *et al.*, 2004) have increased. Furthermore, conservation practices can favour nematodes and bacterial root diseases (Watt *et al.*, 2006). Wheat diseases, including stubble borne pathogens, currently cost the Australian wheat industry $913 million annum (Murray and Brennan, 2009a).

On the basis of Murray and Brennan (2009b), five major diseases dominate national wheat yield losses: yellow spot ($ 17.82 per hectare), strip rust ($ 10.62 per hectare), *Septoria nodorum* blotch ($ 9.07 per hectare), crown rot ($ 6.63 per hectare) and *Pratylenchus neglectus* ($ 6.13 per hectare). The losses would be higher without current control measures. Crown rot losses, for instance, could reach $ 434 million ($ 36.44 per hectare) without control. Crown rot has become widespread in the northern grains region (Wallwork *et al.*, 2004) due to residue retention from conservation tillage practices, limited crop rotation, extended dry periods that impede residue breakdown, and a lack of resistant or tolerant genotypes. In addition, increasing cultivation of highly susceptible durum wheat has increased the available inoculum (Williams *et al.*, 2002).

2.3 Crown rot disease: History and consequence for agriculture

2.3.1 Australian and global crown rot history

Crown rot was first reported in Queensland, Australia, in 1951 but the cause at the time was unknown. It was described as the main disease causing wheat yield loss and could have been observed as early as 1941 (McKnight and Hart, 1966). The disease was subsequently reported across the wheat growing belt of Australia including New South Wales

(Burgess *et al.*, 1975; Backhouse *et al.*, 2004); South Australia (FEDEL-MOEN and Harris, 1987; Wallwork *et al.*, 2004), Western Australia (Khangura *et al.*, 2013) and Queensland (Purss, 1969; Wildermuth *et al.*, 1997). Fusarium crown rot was first reported in the USA in 1966 (Cook, 2007). It has also been reported in New Zealand (Monds *et al.*, 2005), the Pacific Northwest of the USA (Smiley *et al.*, 2005; Paulitz *et al.*, 2002; Cook, 2007), the Canadian Prairies (Fernandez *et al.*, 2007), the upper coastal plain area of Mississippi (Gonzalez and Trevathan, 2000), South America (Burgess *et al.*, 2001), Europe (Rossi *et al.*, 1995), South Africa (Lamprecht *et al.*, 2006), East Asia (Zhang *et al.*, 2015), West Asia (Tunali *et al.*, 2008) and North Africa (Nicol *et al.*, 2007). Crown rot is therefore a global disease of wheat and barley.

2.3.2 Crown Rot Pathogens

The generic name of crown rot disease is Fusarium crown rot (FCR) which refers to the disease caused by *Fusarium* (genera) species. The causal agent of crown rot was first recorded as *Fusarium graminearum* Schwabe during the 1960s (Purss, 1969). Two morphologically and culturally inseparable populations within *Fusarium graminearum* Schwabe were later designated as Group 1 and Group 2 by Burgess *et al.* (1975). The Group 1 strains were characterized as not forming perithecia in culture and were presumably heterothallic, while the Group 2 strains were associated with Gibberella stalk and cob rot of maize and Fusarium head blight of wheat and were characterized as forming homothallic perithecia (Francis and Burgess, 1977; Burgess *et al.*, 1988). Groups 1 and 2 were delineated as *F. pseudograminearum* and *Fusarium graminearum* respectively, using phylogenetic analysis of deoxyribonucleic acid (DNA) sequences from the β-tubulin gene (Schilling *et al.*, 1996; Aoki and O'Donnell, 1999; Williams *et al.*, 2002; Akinsanmi *et al.*, 2004), restriction fragment length polymorphisms (Benyon *et al.*, 2000) and isozymes (Laday *et al.*, 2000). Aoki and O'Donnell (1999) separated the groups on the basis of phenotypic characters including colony growth rates, regions of conidia with greatest width, different reactions to near-ultraviolet black-light-blue light and heterothallic production of perithecia. Based on Group 1 isolates collected from fields in Queensland and New South Wales, Scott and Chakraborty (2006) later reported that *F. pseudograminearum* is a single phylogenetic species.

While *F. pseudograminearum* is the most commonly associated and widespread causal agent of crown rot of wheat (Klein *et al.*, 1990), several other pathogens have been implicated in different geographical regions. This list includes *F. acuminatum, F. avenaceum, F. crookwellense, F. equiseti* and *F. graminearum* (Akinsanmi *et al.*, 2004; Hogg *et al.*, 2010). Whilst these species can readily be isolated from wheat stems, evidence to support yield loss is scarce and environmentally and geographically limited (Cook, 2010). Burgess *et al.* (2001) argue that these species should be referred to as secondary pathogens, capable of infecting wheat crowns and stems in semi-arid conditions. *Fusarium culmorum* also causes a crown rot like disease in southern Australia and other parts of the world, often referred to both as crown rot and perhaps more correctly as foot rot (Burgess *et al.*, 2001).

2.3.3 Pathogen Distribution

Fusarium pseudograminearum is epidemiologically the most important crown rot pathogen. Slightly warmer and drier conditions favour *F. pseudograminearum* and *F. graminearum* whereas *F. culmorum* is associated with cooler semiarid wheat growing regions (Cook, 1981). Increases in *F. pseudograminearum* in wheat plants was reported with increased post-anthesis temperature (Moya-Elizondo *et al.*, 2011). Burgess *et al.* (2001) reported that crown rot severity is higher when the crop matures under hot and dry conditions. In northern New South Wales and Queensland, *F. pseudograminearum* is the dominant crown rot pathogen (Summerell *et al.*, 1989) (Williams *et al.*, 2002). Crown rot aetiology is presumably more complex in other parts of Australia because both *F. culmorum* causing foot rot and *F. pseudograminearum* can be recovered from the same infected tissue (Williams *et al.*, 2002). While its influence on host resistance is not clear, a high level of genetic diversity in *F. pseudograminearum* populations collected throughout the Australian grain belt has been reported (Bentley *et al.*, 2008; Akinsanmi *et al.*, 2006). In Australia, 128 distinct genotypes were identified using simple sequence repeats applied to 163 *F. pseudograminearum* isolates collected from three field sites in NSW. Scott and Chakraborty (2010) further observed a high degree of genetic diversity within fields and low genetic variation between fields.

2.3.4 Symptoms

The crown rot pathogen infects and colonizes in the host plant endophytically (Burgess *et al.*, 2012). The pathogen can cause pre-emergence rot and seedling blight under high inoculum loads (McKnight and Hart, 1966). The most characteristic symptom of crown rot is the development of light honey-brown to dark-brown discoloration of the base of infected tillers (Figure 2.5A) (Mudge *et al.*, 2006; Klein *et al.*, 1988; Simpfendorfer *et al.*, 2006). This stem browning becomes more distinct from mid to late grain filling until harvest (GRDC, 2009). The symptom can spread up the stem in susceptible genotypes (Mudge *et al.*, 2006) and can be observed at any growth stage (Summerell *et al.*, 1989). Secondary symptom development occurs when plants are subjected to post-anthesis water stress and temperatures are high (Paulitz *et al.*, 2002), causing hyphae to proliferate within stem tissue. This results in the disruption of both xylem and phloem tissues causing premature ripening of developing heads and the expression of characteristic white heads, containing shrivelled grain or no grain at all (Figure 2.5B)(Burgess *et al.*, 2001).

Fig. 2.5: Crown rot symptom: A. Honey-brown to dark-brown discoloration of the base of infected tillers. B. White heads

Crown rot symptoms were reported to be directly related to crop yield loss (Milgate, 2013; Klein *et al.*, 1990). Scattered white heads and plant death occurs when infected plants are water stressed and the translocation process is hindered by fungal stem colonisation, with the mycotoxin, deoxynivalenol, causing necrosis (Burgess *et al.*, 2001; Nyvall, 1979; Obanor and Chakraborty, 2014). Early maturity and crop lodging are also symptomatic of high levels of crown rot infection.

2.3.5 Host Ranges

Fusarium pseudograminearum has a wide range of hosts. Hosts include wheat, barley, oats, rye and triticale and the residues of native and naturalised grasses. Many of these grasses, including canary grass/phalaris, wheat grass, brome grass, barley grass, winter grass and ryegrass (*Lolium perenne*) (Aoki and O'Donnell, 1999; Bentley *et al.*, 2008; Burgess *et al.*, 2001; DEPI, 2013) are common weeds of cereal farming systems. Importantly, many of these hosts, including both cultivated and wild oats are symptomless, with the pathogen able to infect the hosts endophytically (Burgess *et al.*, 2012). The importance of native and naturalised grasses as hosts of the pathogen should not be underestimated, particularly in fields with uncontrolled grassy weed burdens or in rotational fields with grassy pastures (Hogg *et al.*, 2010; Chakraborty *et al.*, 2006; Burgess, 2005). Survival of the crown rot pathogen on infected crown and stem residues for two or more seasons has been reported, with the potential to contaminate subsequent wheat crops. The incidence of the disease has increased in recent years because of the retention of residues in conservation agricultural practices and the increased acreage of highly susceptible durum wheat (Burgess *et al.*, 2001). Moreover, the cessation of stubble burning and cultivation has built-up of inoculum levels and increased the frequency of the disease (Summerell *et al.*, 1989; Wildermuth *et al.*, 1997). Crown rot has therefore become a significant problem across much of the northern wheat belt where conservation agriculture is practiced (Wallwork *et al.*, 2004).

2.3.6 Fungus colonisation and infection

The colonisation of the wheat stem base is an important crown rot pathogen survival mechanism. *F. pseudograminearum* produces a toxin, trichothecene mycotoxin deoxynivalenol (DON), which suppresses the production of host defence enzymes and other compounds and plays an important role in colonization of the wheat stem base (Mudge *et al.*, 2006). Small (<1mm) and large stubble fragments carrying *F. pseudograminearum* hyphae survive as saprobes and provide the principal source of inoculum for initiating infection through the scutellum, sub-crown internode and lower crown regions of the wheat plant at any growth stage between seedling emergence and maturity (Burgess *et al.*, 1993; Burgess *et al.*, 2001; Summerell *et al.*, 1990). Infected stubble residues carry asexual hyphe and conidia which are the primary cause of infection, as the sexual stage or teleomorph is rarely observed in the field (Paulitz *et al.*, 2002). A field study conducted by Swan *et al.* (2000) revealed that infection is favoured by surface soil moisture, particularly in the first 6-8 weeks of plant growth. After infection, the pathogen proceeds to parasitically colonise the plant crown and stem tissue and can reach the third or fourth internode and the leaf sheath (Wildermuth *et al.*, 1997; Klein *et al.*, 1988). Stephens *et al.* (2008) used real-time quantitative polymerase chain reaction (qPCR) to indirectly assess fungal biomass during infection and concluded that infection occurred in three phases: i) after inoculation, the spore germinates and develops a superficial hyphal mat, ii) colonies are established from the adaxial epidermis of the outer leaf sheath and mycelial growth occurs from the inoculation point to the crown, concomitant with a drop in fungal biomass, and iii) successful colonization of the crown tissue.

F. pseudograminearum is a monocyclic pathogen and does not produce secondary infection during growing season (Backhouse, 2006). The pathogen saprophytically survives as mycelia in crop stem residues, including the crown, which were colonized parasitically by the fungus during the growing season. This residue provides inoculum for the following season as described by Kazan and Gardiner (2017) (Figure 2.6).

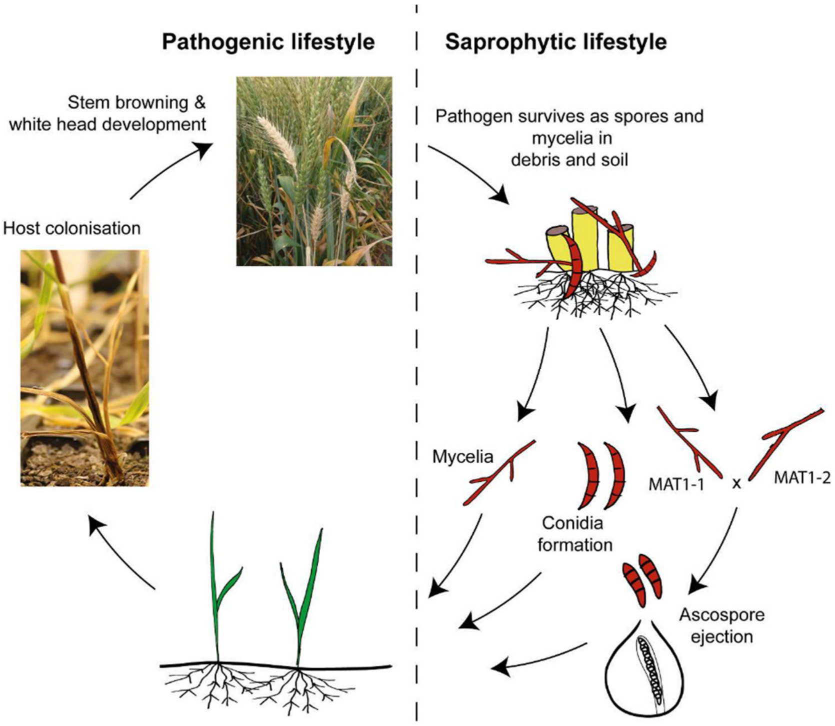


Fig. 2.6: Life cycle of the crown rot pathogen (*Fusarium pseudograminearum*) in wheat, reproduced from Kazan and Gardiner (2017).

2.4 Factors affecting on crown rot disease development:

Environmental conditions are well known to influence the Fusarium crown rot (Klein *et al.*, 1989). Considerable research has investigated the role of environmental factors on the incidence and severity of disease development. It was reported that a number of environmental and other distinct factors account for the development of crown rot disease. These include the following factors:

2.4.1 Temperature

Temperature influences the growth and development of *F. pseudograminearum* causing crown rot necrosis on seedlings and adult plants. The maximum temperature in areas where *F. pseudograminearum* was found were in excess of 31°C (Backhouse and Burgess, 2002). However, *F. pseudograminearum* does not seem to infect seedlings at temperatures less than 12°C (Dickson, 1923), although this needs to be confirmed. Smiley (2009) found that crown rot was highly and positively correlated with mean soil temperature and concluded that high soil temperature favoured infection of wheat by *F. pseudograminearum.* A laboratory study suggested that *F. pseudograminearum* grows best under a broad range of temperatures (10–30°C) in dry conditions (1 Mpa and lower) but does not grow in temperatures of < 5 or >35°C (Singh *et al.*, 2009). The influence of increasing temperature and elevated CO_2 on Fusarium crown rot susceptibility of wheat at different growth stages were examined in three glasshouse environments (Melloy *et al.*, 2014). The proportion of crown rot infected tillers (incidence), length of stem browning (severity) and biomass of *F. pseudograminearum* was observed to be greater with higher CO_2 at ambient temperature. In contrast, when wheat lines with different levels of crown rot resistance were evaluated at four diurnal temperatures, it was concluded that pathogen overall fitness (the ability of a pathogen to survive and reproduce) was greater at 15/15°C, and reduced with increasing temperature (Sabburg *et al.*, 2015).

2.4.2 Soil moisture

Soil moisture is important for initiating infection and increasing crown rot severity in the field (Swan *et al.*, 2000). High water potential (Mpa) favours infection by the crown rot pathogen and the optimum water potential (Mpa) in soil for infection of the seedling is between -0.3 and -0.7 and a little infection occurs when the water potential is less than -1.5 MPa (Liddell and Burgess, 1988). The relationship between surface soil water potential and seedling infection was examined (Beddis and Burgess, 1992) and it was observed that moisture stress or low water potential can reduce plant resistance and help the pathogen to colonize seedlings. Hare and Parry (1996) noticed that during the water stress, wheat plants became less able to resist pathogen infection and colonization.

2.4.3 Nutrients

Verrell *et al.* (2003) investigated the effects of varied nitrogen (N) concentrations and watering regimes on the incidence and severity of crown rot in wheat. They found that higher N led to higher crown rot incidence and severity. Higher levels of soil nitrogen have been reported to directly increase the incidence of infection and colonization by crown rot pathogen (Felton *et al.*, 1998). Higher nitrogen enhances vegetative growth and rapid water use which increases late season moisture stress and crown rot intensity (Burgess *et al.*, 2001). Furthermore, nitrogenous fertilizers increase soil acidity which is related to increased crown rot incidence (Smiley *et al.*, 1996). Others reported that crown rot is more severe in zinc deficient plants (Sparrow and Graham, 1988) and that basal stem browning was substantially lower in zinc efficient cultivars (Grewal *et al.*, 1996). Kirkegaard *et al.* (2004) also observed that the previous crop residue increased the intensity of crown rot disease, in part because of higher soil nitrogen.

2.4.4 Farming practice

Fusarium pseudograminearum is a necrotroph that most commonly survives as mycelium on non-decayed plant residue. The level of pathogen inoculum and its distribution in the paddock is intensified by earlier cropping sequences and agronomic approaches (Burgess *et al.*, 2001). Thus, environmentally sustainable farming practices such as minimum tillage have increased the incidence of crown rot (Wildermuth *et al.*, 1997). Late sowing subjects the crop to higher temperature and drought stress during grain filling and this increases disease severity and crown rot incidence in wheat (Simpfendorfer, 2012c). Timely sowing, non-host rotation and high-yielding crown rot resistant and or tolerant cultivars could significantly decrease disease incidence and severity (Cook, 2010).

2.4.5 Plant height

There is no linear relationship between plant stature and crown rot disease susceptibility in wheat. Tall genotypes are generally more susceptible to crown rot (*F. pseudograminearum*) compared to semi-dwarf genotypes due to differences in cell density and other physiological and structural differences (Bai and Liu, 2014). However, when the semi-dwarfing gene *Rht-B1b* was removed others reported that taller genotypes gave better resistance (Collard *et al.*, 2005; Wallwork *et al.*, 2004). A significant positive interaction between plant height and crown rot resistance was also detected in a genetic study of the bread wheat variety EGA Wylie (Zheng *et al.*, 2014), while others found no association (Poole *et al.*, 2012) or a negative association between plant height and crown rot resistance (Li *et al.*, 2010). Another report in barley also found that there is a significant effect of plant height on crown rot resistance and that shorter plants increased resistance (Li *et al.*, 2009). They concluded that slow growth provides higher resistance which is in accordance with the findings of (Liu *et al.*, 2010) who found that higher cell density in short plants improved resistance.

2.5 Economic importance of crown rot disease

The economic importance of wheat crown rot varies by country and region (Moya-Elizondo and Jacobsen, 2016). However, crown rot causes a greater impact on wheat and barley yield than any other soil-borne disease (Smiley *et al.*, 2005; Burgess *et al.*, 2001; Paulitz *et al.*, 2002). Crown rot is the second most important disease (economically) in Australia (Chakraborty *et al.*, 2006) and causes significant yield and quality losses (Murray and Brown, 1987; Klein *et al.*, 1990). The total annual estimated yield loss due to crown rot in wheat was reported at $79 million, this increases to $97 million when barley is included (Murray and Brennan, 2009b; Murray and Brennan, 2010). Yield losses up to 50 % in bread wheat and 90% in durum wheat are not uncommon (GRDC, 2009) under climatic conditions that favour the pathogen. Crown rot can cause up to 100% crop losses (Stephens *et al.*, 2008) and others reported an 89% reduction in average yield in Australia (Klein *et al.*, 1991).

2.6 Disease management

Crown rot is a stubble-borne disease with a wide host range among cereals and grasses. Initially, the disease was managed by conventional tillage and stubble burning to decrease the inoculum level by destroying hyphae in crop residues in the field (Klein *et al.*, 1988). Farmers currently use a number of control strategies to manage crown rot disease of wheat ranging from stubble burning, fallow, rotation, grass weed control and the cultivation of partially resistant and/or tolerant cultivars. Repeated cultivation and stubble burning are not compatible with sustainable conservation agriculture (Burgess *et al.*, 1996) and have been largely discontinued as primary control methods.

2.6.1 Stubble management

The Australian cropping system has moved from stubble burning to stubble retention to reduce soil erosion and conserve soil moisture. Several authors reported higher incidence of crown rot in field retained stubble compared to stubble that was removed (Hollaway *et al.*, 2012; Burgess *et al.*, 1993; Summerell *et al.*, 1989). While stubble burning significantly reduced crown rot incidence (Hollaway *et al.*, 2012; Simpfendorfer *et al.*, 2005; Wildermuth *et al.*, 1997) it had no effect on the survival of the crown rot fungus in the crowns below ground (Simpfendorfer *et al.*, 2012b). Hence, burning infested stubble is not a viable long-term control method, notwithstanding environmental concerns such as air pollution. Simpfendorfer *et al.* (2012b) reported that stubble burning reduced soil carbon, and affected soil water storage and the activity of soil biota. Wheat grain protein was also reduced after burning stubble due to reduced soil nitrogen sequestered from biomass (Summerell *et al.*, 1989). Rapid decomposition of crop residue can help reduce the incidence of disease in the following crop (Swan *et al.*, 2000). However, stubble decomposition is highly dependent on soil moisture and seasonal rainfall.

2.6.2 Crop rotation

Rotation with non-host crops remains the cornerstone of crown rot control (Burgess *et al.*, 2012). Crop rotation can reduce crown rot infection by 3.4 - 41.3% thus reducing inoculum in the field (Kirkegaard *et al.*, 2004). Crop rotation, reduced levels of infested stubble and increased wheat yield and has been encouraged for controlling crown rot infestation (Lamprecht *et al.*, 2006; Wildermuth *et al.*, 1997). However, a minimum of two years are required for breaking down crop residues and fungal hyphae (MacLeod, 2008; Burgess, 2005; Summerell *et al.*, 1989; Hogg *et al.*, 2010), and this may not be feasible under dry conditions. Winter crops such as faba beans (*Vicia faba*), chickpeas (*Cicer arientinum*), canola (*Brassica napus*), field peas (*Pisum arvense*) and mustard (*Brassica juncea*) and Summer crops like sorghum (*Sorghum bicolor*), cotton (*Gossypium hirsutum*) and mungbeans (*Vigna radiate*) are all effective non-host options for rotation with wheat and barley (Simpfendorfer, 2012a; Kirkegaard *et al.*, 2004; Burgess *et al.*, 2001; Felton *et al.*, 1998). Since the intensity of crown rot is generally high in wheat-wheat rotations, Hollaway *et al.* (2012) suggested that crown rot inoculum could be decreased by rotating with field pea. Simpfendorfer *et al.* (2012a) further suggested that canola, mustard and chickpea were effective rotation crops for controlling crown rot disease. The bio-fumigation properties of brassica associated with isothiocyanates (ITCs) may also contribute to reduced crown rot incidence and severity in wheat (Rapp, 2018). Chickpea were less effective at decomposing cereal stubble due to their reduced canopy growth, particularly when grown on wider row spacing to manage Aschcochyta blight, and *F. pseudograminearum* severity may also have been enhanced after chickpea due to higher available soil nitrogen.

2.6.3 Inter-row sowing

Inter-row sowing or sowing between the rows of the previous crop may reduce the incidence and severity of crown rot. Inter-row sowing was shown to decrease crown rot severity and increase yield in winter cereals (Simpfendorfer, 2012d; Verrell *et al.*, 2006). Simpfendorfer (2012d) observed that inter-row sowing reduced the incidence and severity of crown rot by an average of 34% in barley and 43% in bread wheat and 52% in the durum wheat. However, inter-row sowing will not control crown rot on its own, but rather should be used as part of an integrated disease management strategy along with stubble management, crop rotation and resistant cultivars.

2.6.4 Biological-control

There are few studies on the bio-control of crown rot in wheat; however some research focussed on bio-agents to reduce disease severity. (Huang and Wong, 1998)) observed that the bacteria *Burkholderia (Pseudomonas) cepacia* (A3R) reduced crown rot symptoms significantly both in glasshouse and field experiments in three soil types. It was concluded that antibiotics produced by *B. cepacia* were highly inhibitory to *F. pseudograminearum*. In contrast, the crown rot pathogen was completely eradicated from buried straw in the presence of *Trichoderma* spp, while 40% stubble was infected in the absence of *Tricoderma* (WONG *et al.*, 1999). Singh *et al.* (2009) found that *Fusarium equiseti* living in stubble is the most effective antagonist to *F. pseudograminearum* under cool and dry conditions and may reduce the severity of crown rot in the field.

2.6.5 Chemical control

There is no commercially available fungicide registered for treatment of crown rot. Early studies investigated the use of mercurial seed treatments ‘Ceresan” and ‘Agrosan’, copper carbonate and hexachlorbenzene to control the disease in north-eastern Australia (McKnight and Hart, 1966). These authors argued that the treatment had no effect on yield. More recent reports have suggested that coating seed with the fungicides thiabendazole and

Difenoconazole-mefenoxam do produce a significant reduction in crown rot disease development (Pariyar *et al.*, 2014). However, these chemicals are not commercially available, nor is their interaction with the environment understood.

2.6.6 Genetic control of crown rot disease

Resistant or tolerant wheat genotypes are the most environmentally friendly, effective and efficient control strategy to reduce the impact of crown rot disease (Stephens *et al.*, 2008). Breeding for resistance to crown rot requires access to diverse and effective sources of resistance or tolerance (Ma *et al.*, 2012). However, cultivars with a high level of resistance have yet to be identified in wheat (Burgess *et al.*, 2001).

The first report of *Fusarium* crown rot resistance in bread wheat was published in 1966 (Purss, 1966). Resistance to crown rot disease of wheat is generally categorized into two types: partial resistance detected in adult plants and seedling resistance (Wallwork *et al.*, 2004). Partial resistance is incomplete resistance, characterized by a reduced rate of epidemic development (Parlevliet, 1978). Partial resistance is considered to be mostly race-nonspecific and controlled by many minor genes (Parlevliet, 1985). Partial resistance to crown rot in wheat is highly complex and controlled by multiple loci (Bovill *et al.*, 2006; Collard *et al.*, 2005; Wallwork *et al.*, 2004). However, partial resistance cannot prevent disease outbreaks during favourable environmental conditions for the pathogen (Strausbaugh *et al.*, 2005). In the absence of complete or highly resistant wheat varieties, the cultivar EGA Wylie was considered to be the most crown rot resistant variety in Australia for many years (Queensland, 2014; Zheng *et al.*, 2014). Moreover, partial resistance was also found in other materials including the wheat cultivars Sunco, Gala and Kukri and the lines 2-49, IRN497 and CPI133817 (Smiley and Yan, 2009; Wallwork *et al.*, 2004; Martin *et al.*, 2015). Wildermuth *et al.* (2001) also reported that partial resistance was related to crown depth in adult plants and seedlings. They concluded that resistant plants had shallower crowns.

2.6.6.1 Assays of crown rot resistance

High levels of crown rot resistance are not yet available in wheat. A major limitation is the lack of a reliable and high throughput bioassay for crown rot resistance. Several diseases phenotyping methods have been developed, including seedling, terrace and field assays (Poole *et al.*, 2012). These procedures can be classified as glasshouse-based or field-based assays. The reactions of adult plants are routinely assessed in field based assays (Dodman and Wildermuth, 1987) and the cost of these screens is relatively low once established and large numbers of lines can be assessed (Wallwork *et al.*, 2004). However, field assays are often highly variable due to uneven disease severity, environmental fluctuations and variable pathogen populations (Mitter *et al.*, 2006). Field-based assays are difficult to repeat and no report describing significant QTL from field based crown rot assays have been published (Martin *et al.*, 2015). Reliable and reproducible data is the main constraint for the researchers and breeders.

Several glasshouse assays and screenings methods have been used in wheat and barley for determining crown rot resistance (Yang *et al.*, 2010; Smiley and Yan, 2009; Li *et al.*, 2008; Mitter *et al.*, 2006; Wallwork *et al.*, 2004; Wildermuth *et al.*, 2001; Wildermuth and McNamara, 1994; Dodman and Wildermuth, 1987). Two of these assays, developed by Wildermuth and McNamara (1994) and Li *et al.* (2008), were successfully used in several QTL mapping studies (Bovill *et al.*, 2010; Collard *et al.*, 2005; Martin *et al.*, 2015) to identify QTL. Seedling resistance is most commonly assessed using glasshouse-based analyses. Adult plant resistance determined in the field may or may not be correlated with seedling resistance (Klein *et al.*, 1985; Wildermuth and McNamara, 1994; Mitter *et al.*, 2006; Li *et al.*, 2008), is likely to be QTL specific. The glasshouse based assays results tend to be more reproducible because it is easier to control the environment. Glasshouse assays can be used to test large numbers of genotypes and highly susceptible genotypes can be identified and eliminated in breeding programs. However, seedlings are required to grow in soil or potting mixture for up to six weeks prior to assessment. It can be difficult to get same level of soil compactness due to variation in the shape and size of containers. Differences in soil compactness will influence water-holding capacity and hence the expression of crown rot resistance (Li *et al.*, 2008). Multiple replications are also required to improve the accuracy of these assays (Mitter *et al.*, 2006; Li *et al.*, 2008). Therefore, screening large numbers of breeding lines requires space, labour and time. To complicate matters, different resistance genes can express at different stages of development or differ with environment (Yang *et al.*, 2010; Martin *et al.*, 2015). A new soil-less assay with enhanced capacity and reproducibility has been developed to screen larger numbers of genotypes in 10 days (Yang *et al.*, 2010). However, QTLs detected in soil-based assays are not detected in soil-less assays. A part form field-based or glasshouse-based assays, a terrace method was used to screen for resistance (Wallwork *et al.*, 2004). Seeds are sown in open ended plastic tubes with potting mixture and *F. pseudograminearum* inoculum. The tubes are subsequently placed outdoors on sand-based terraces and grown to adult plants for assessment of crown rot resistance. While, the method does not generate the disease severity observed on highly susceptible durum wheat cultivars in the field, it does provide an adult plant method that more closely mimics field conditions.

2.6.6.2 Real-time qPCR and crown rot resistance

Pathogen population dynamics has been investigated in wheat tissue through isolation and culture of specific pathogen species. However, this technique was inefficient and laborious and the results inaccurate (Hogg *et al.*, 2010). As an alternative, real-time quantitative polymerase chain reaction (qPCR) can be used to quantify the biomass of pathogens in plant tissues (Pettitt *et al.*, 2003; Stephens *et al.*, 2008; Knight *et al.*, 2012). This technique has been used to determine crown rot and common root rot pathogen population levels within fields in Montana and the Pacific Northwest (Moya-Elizondo *et al.*, 2011). Hogg *et al.* (2007), conducted a study to determine the utility of qPCR for accessing crown rot disease severity on wheat in field experiments and concluded that qPCR was effective in determining crown rot severity in mature wheat stems. However, they suggested that qPCR was not more effective than traditional methods when pathogen populations are low to moderate and plants are not under stress.

2.6.6.2.1 Identification of sources of crown rot resistance

Although complete resistance to crown rot has not been observed in wheat, partially resistant wheat germplasm (both seedling and adult plant) has been identified from various studies including the genotypes 2-49, Sunco, W21MMT70 (Bovill *et al.*, 2010), EGA Wylie (Zheng *et al.*, 2014), AUS29529 (Nicol *et al.*, 2012), Gluyas Early, Janz (Collard *et al.*, 2006), Macon, Gala, Otis, Kukri (Poole *et al.*, 2012), CSCR6 (Ma *et al.*, 2010), IRN497 and CPI133817 (Martin *et al.*, 2015). Earlier reports described screening germplasm for FCR resistance in wheat based on seedling assays in glasshouses (Mitter *et al.*, 2006; Wildermuth and McNamara, 1994). Additional methods such as screenings, based on the percentage of small or shrivelled grains, are required. However, very little attention has been given to selection of new sources of crown rot resistance using screenings. This is probably due to the difficulty of assessing screenings on large numbers of genotypes.

2.6.6.3 Genes and QTLs conferring crown rot resistance

Several sources of partial and/or seedling resistance to crown rot disease were identified and these are summarised in Table 2.2. However, most QTL studies have been conducted on either adult plants or seedlings but not on both. Stem browning of the seedlings or adult plant has been used to identify QTLs conferring crown rot resistance in all previous studies. The first resistance locus was detected on the long arm of chromosome 4B near the semi-dwarfing gene *Rht1* in the variety 'Kukri' based on the outdoor 'terrace' assay in a doubled haploid population derived from the cross 'Kukri/Janz' (Wallwork *et al.*, 2004). In a glasshouse seedling experiment, six QTLs explained 40.6% of the phenotypic variance for resistance in the population '2-49/Janz' (Collard *et al.*, 2005). Two of these QTLs, contributed by '2-49' were located on chromosomes 1DL and 1AL and explained 21% and 10% of the phenotypic variance, respectively. Later, a QTL was found on chromosome 1DL that explained 10-20% of the phenotypic variance in the population 'Gluyas Early x Janz' (Collard *et al.*, 2006). Three QTLs were reported on chromosomes 2D and 5D inherited from the genotype 'W21MMT70' and a further QTL on 2B inherited from 'Mendos' were identified from a seedling assay (Wildermuth and McNamara, 1994; Bovill *et al.*, 2006). However, another investigation failed to identify the QTLs on chromosomes 2D and 5D in the RIL population 2-49/ W21MMT70 (Bovill *et al.*, 2010). Instead a new QTL with a large effect that explained up to 40.5% of the phenotypic variance was observed. These inconsistencies are not surprising because precise assessment of crown rot resistance is very difficult (Collard *et al.*, 2005). Glasshouse-based assays also identified three QTLs on chromosome 2B from the adult plant resistant variety Sunco (Bovill *et al.*, 2010). The QTL on chromosome 2BS contributed by Sunco was also detected in both seedling and field trials (Martin *et al.*, 2015). A QTL located on chromosome 3BL identified from a *T. spelta* accession CSCR6 in the population 'CSCR6/Lang' explained 49% of the phenotypic variance (Ma *et al.*, 2010). This QTL was also identified at a similar position in five different backgrounds; Ernie, Macon, W21MMT70, IRN497 and Otis (Poole *et al.*, 2012; Bovill *et al.*, 2010; Martin *et al.*, 2015; Li *et al.*, 2010). Four QTL linked to crown rot resistance were detected by Zheng *et al.*

(2014) in EGA Wylie, the most resistant bread wheat variety in Australia, in the population EGA Wylie/Sumai3. One of these loci explained up to 31.1% of the phenotypic variance and was located on chromosome 5DS. The second locus was positioned on 2DL and explained 20.2% of the phenotypic variance. The remaining two QTLs located on 4Bs each explained up to 18% of phenotypic variance. However, when these data were adjusted for differences in plant height the QTL effects became non-significant. Crown rot resistance QTL are present at similar locations across studies for loci on chromosomes 3BL, 2DL and 5DS (Zheng *et al.*, 2014; Poole *et al.*, 2012; Bovill *et al.*, 2010; Ma *et al.*, 2010; Li *et al.*, 2010). However, it is essential that QTL and associated markers be validated in different backgrounds before they are used in marker-assisted selection or gene pyramiding.

Table 2.2: QTL linked to crown rot resistance in wheat.

Source of resistance	QTL on Chromosome location	Significant phenotypic variance (%)	Population	Phenotyping	Reference
2-49	1AS	12.8	153 DHs of 2-49/ Janz	Glasshouse	Martin *et al.* (2015)
2-49	1AS	16.4	153 DHs of 2-49/ Janz	Field	
2-49	1AS	8.5	134 DHs of Sunco/2-49	Field	
2-49	1AL	10	100 DHs of 2-49/Janz	Glasshouse	Collard *et al.* (2005)
2-49	1BS	7.2	134 DHs of Sunco/2-49	Glasshouse	(Martin *et al.*, 2015)
2-49	1BS	12.6	153 DHs of 2-49/ Janz	Field	
2-49	1DL	12.6	134 DHs of Sunco/2-49	Glasshouse	
2-49	1DL	21	100 DHs of 2-49/Janz	Glasshouse	Collard *et al.* (2005)
2-49	1DL	17.4	153 DHs of 2-49/ Janz	Glasshouse	Martin *et al.* (2015)
2-49	1D	10	208 DHs of 2-49/ W21MMT70	Glasshouse	Bovill *et al.* (2010)
Gluyas Early	1DL	21	90 DHs of Gluyas Early/Janz	Glasshouse	Collard *et al.* (2006)
IRN497	2AL	19.7	122 DHs of IRN497/Janz	Field	Martin *et al.* (2015)
Sunco	2B	8	151 Rils of Sunco/Otis	Terrace	Poole *et al.* (2012)
Sunco	2BS	7.3	134 DHs of Sunco/2-49	Glasshouse	Martin *et al.* (2015)
Janz	2BS	8.8	153 DHs of 2-49/ Janz	Glasshouse	
Janz	2DS	12.1	110 DHs of CPI133814/Janz	Field	
CPI133814	3AL	11.9	110 DHs of CPI133814/Janz	Glasshouse	
2-49	3BS	11.1	134 DHs of Sunco/2-49	Field	
IRN497	3BL	18.8	122 DHs of IRN497/Janz	Glasshouse	
CPI133814	3BL	12.1	110 DHs of CPI133814/Janz	Glasshouse	
W21MMT70	3B	41	208 DHs of 2-49/ W21MMT70	Glasshouse	Bovill *et al.* (2010)
CSCR6	3B	49	92 RIL of Lang/CSVR6	Glasshouse	Ma *et al.* (2010)
Ernie (US)	3BL	35	153 DHs of Batavia/ Ernie	Glasshouse	(Li *et al.*, 2010)
Macon (US)	3BL	34	92 RIL of Sunco/Macon	Growth room Terrace	Poole *et al.* (2012)
Sunco	3BS	8	151 Rils of Sunco/Otis	Terrace	
	3BL	12		Field	
Otis (US)	3BL	22	151 Rils of Sunco/Otis	Growth room	
EGA Wylie	3BL	20.2	120 Rils of EGA Wylie/Sumai3	Glasshouse	Zheng *et al.* (2014)
2-49	4BS	18.3	153 DHs of 2-49/ Janz	Field	Martin *et al.* (2015)
IRN497	4BS	8.6	122 DHs of IRN497/Janz	Field	
Sunco	4B	7	151 Rils of Sunco/Otis	Terrace Field	
2-49	4BS	20.4	134 DHs of Sunco/2-49	Glasshouse	

Kukri	4B	48	100 DHs of Kukri/Janz	Terrace	Wallwork *et al.* (2004)
Macon (US)	4D	7	92 RIL of Sunco/Macon	Growth room Terrace	Poole *et al.* (2012)
W21MMT70	5D	28	100 DHs of 21MMT70/Mendos	Glasshouse	Bovill *et al.* (2006)
EGA Wylie	5DS	31.1	120 Rils of EGA Wylie/Sumai3	Glasshouse	Zheng *et al.* (2014)
CPI133814	6DL	18.6	110 DHs of CPI133814/Janz	Field	Martin *et al.* (2015)
Sunco	7A	20	151 Rils of Sunco/Otis	Terrace	Poole *et al.* (2012)

2.7 Crown rot tolerance

Tolerance is the ability of a genotype to yield well in the presence of pathogen inoculum. Reduced yield loss of some genotypes under crown rot pressure has been observed in wheat (Kramer *et al.*, 1980). Genetic improvement of tolerance could be an attractive strategy as it exerts little or no selection pressure on the pathogen and could be a useful component of durable disease management (Bingham *et al.*, 2009). As tolerance ratings of wheat genotypes in traditional breeding and yield testing nurseries was not successful, paired inoculated and un-inoculated plots were used to identify tolerant genotypes in spring wheat (Smiley and Yan, 2009). Tolerant lines exhibited reduced yield loss in the presence of the pathogen (Liu and Ogbonnaya, 2015).

2.8 Molecular markers and marker assisted selection

Molecular markers supplement the phenotypic selection of both simple and complex traits (Gupta *et al.*, 1999b; Lande and Thompson, 1990). Molecular markers are generally classified into three groups based on their method of detection: (1) polymerase chain reaction (PCR)-based or simple sequence repeats (SSRs); (2) Hybridization-based such as restriction fragment length polymorphisms (RFLPs) or (3) DNA sequence-based such single-nucleotide polymorphisms (SNPs) (Gupta *et al.*, 1999b; Jones *et al.*, 1997; Joshi *et al.*, 1999).

SNPs are the most commonly used DNA sequence based marker. Each and every nucleotide may vary in the genomic DNA of individuals in a population facilitating selection using SNPs (Brookes, 1999; Deschamps and Campbell, 2010). Since SNPs are gene specific markers gel electrophoresis is not required (Gupta *et al.*, 1999b) and SNP detection is rapid as it is based on biallelic molecular hybridization (Gupta *et al.*, 1999a). The hexaploid wheat genome is large (16Gb) compared with rice (~400Mb) and maize (~3Gb) (Ware and Stein, 2003). Therefore, direct cloning of candidate genes is difficult and it is easier to map QTLs using SNP technology (Varshney *et al.*, 2000; Wang *et al.*, 2009; Zhang *et al.*, 2010; Zhang *et al.*, 2012a; Cui *et al.*, 2014; Liu *et al.*, 2015). SNPs have been used for marker assisted selection, to study ancestral relationships among individuals in populations and to evaluate marker-trait associations among diverse materials (Wang *et al.*, 2014).

2.8.1 Marker assisted selection (MAS)

Molecular markers or DNA markers are used for marker-assisted selection (MAS), marker-assisted back-crossing (MABC), marker-assisted recurrent selection (MARS) and genomic selection (GS) (Ribaut and Ragot, 2006; Beyene *et al.*, 2016). The term "marker-assisted selection" was first used in literature about three decades ago (Beckmann and Soller, 1986). Molecular marker use for plant breeding applications was first popularized in the early 1980s when isozyme markers were used to introgress traits from exotic germplasm into cultivars (Tanksley and Rick, 1980; Tanksley, 1983). The essential requirement for MAS is that markers should either co-segregate or be closely linked to the target genes. MAS can save time and money and undesirable genotypes can be rapidly eliminated. Moreover, MAS can be implemented at any stage of plant growth. Therefore, it will save times, resources and efforts from the field trials and undesirable genotypes can be quickly eliminated. While MAS is effective for simply inherited traits, recent studies show that MAS has been much less successful for polygenic traits (Bernardo, 2008). The identification of genetic markers that are tightly linked to crown rot resistance loci would be valuable tools for the development of resistant cultivars MAS. However, resistance appears to be controlled by many QTLs of minor effect and highly background and assay method specific. Even MABC is of limited value for polygenic traits such as crown rot resistance, although there are plenty of examples of successful MABC for simply inherited traits (Miklas *et al.*, 2006; Ribaut and Ragot, 2007).

2.8.2 Marker assisted recurrent selection (MARS)

Recurrent selection is a cyclical population improvement strategy that can uses multiple parents in the crossing program to accumulate desirable alleles and allele combinations for one or more quantitatively inherited traits. Recurrent selection is utilised widely in maize (Bolaños and Edmeades, 1993; Hallauer, 1992; Moll *et al.*, 1994), and subsequently extended to other crops like rice (Châtel and Guimarães, 1997; Veillet *et al.*, 1996); soybean (Lewers and Palmer, 1997); pearl millet (Dutt and Bainiwal, 2005); oat (Diaz-Lago *et al.*, 2002) and barley (Foroughi-Wehr and Wenzel, 1990). In wheat, recurrent selection strategy has successfully been applied to improve grain protein percentage (Löffler *et al.*, 1983; Delzer *et al.*, 1995); grain yield (Olmedo-Arcega *et al.*, 1995); seed weight (Wiersma *et al.*, 2001) and early vigour (Zhang *et al.*, 2014). In a more recent report, Ramya *et al.* (2016) studied the effects of recurrent selection on drought tolerance and related morpho-physiological traits in bread wheat and revealed that the recurrent selection identified lines with significant (17.5%) yield increases under water stress conditions. Recurrent selection for resistance to Fusarium head blight (*Gibberella zeae*) in wheat and tolerance to barley yellow dwarf virus in oat was reported as an effective and feasible breeding method (Jiang *et al.*, 1993).

The improvement of complex traits using phenotypic recurrent selection is generally possible, but the long selection cycles and difficulty in identifying unique genes or alleles imposes restriction on the practicability of this breeding method. In the same way, most QTLs for biotic and abiotic stress tolerance provide only a small portion of the total expression of the trait (Trethowan and Mahmood, 2011). This is particularly the case with crown rot, where disease expression x environment interaction makes phenotyping more challenging. FCR is a complex quantitative trait with involving many minor genes influenced by genotype by environment interaction at many genomic regions (Martin *et al.*, 2015). To overcome these problems MARS could be an alternative strategy, where progeny are recombined on the basis of their estimated gene effects through several cycles (Monds *et al.*, 2005; Bernardo and Charcosset, 2006). MARS for complex traits could increase the gain per unit time and gain per unit cost in breeding programs, particularly when phenotyping is time-consuming, expensive, and erratic (Bernardo, 2008). Eathington *et al.* (2007) reported that MARS-derived soybean lines were better performing compared to conventionally selected lines for grain yield and maturity. In wheat, Jain *et al.* (2014) has successfully used MARS to improve complex quantitative traits such as drought and heat tolerance by conducting multi-locational phenotyping followed QTL detection and progeny recombination. The best homozygous lines carrying 4-8 QTLs were superior to the parents and check variety under heat and drought stress.

2.9 Association analysis

DNA based molecular marker studies were traditionally based on linkage analysis in mapping populations including backcross progeny, doubled haploids, recombinant inbred lines and near isogenic lines; consequently the genetic variation of any trait studied was relatively narrow (Gupta *et al.*, 2005). Moreover, mapping populations used to identify QTL often lack relevance to breeding programs (Beavis, 1998). GWAS has been successfully used to study complex traits (including diseases) in humans (Hirschhorn and Daly, 2005; Slatkin, 2008; Altshuler *et al.*, 2008) and various plant species including wheat (Neumann *et al.*, 2011), maize (Kump *et al.*, 2011), barley (Mohammadi *et al.*, 2015), rice (Huang *et al.*, 2010), sorghum (Morris *et al.*, 2013), soybean (Hwang *et al.*, 2014), sugarcane (Gouy *et al.*, 2015), fruit trees (Khan and Korban, 2012), potato (Rosyara *et al.*, 2016) and forage grasses (Jonavičienė *et al.*, 2018). Genome wide association study is an analysis of a large and diverse population of individuals. These materials are genotyped using high throughput genotyping technologies such as Diversity Arrays Technology (DArT), SNP and genotyping-by-sequencing (GBS). GWAS has advantages over traditional QTL mapping as it does not require the development of mapping populations and the multi environment evaluation of these populations to produce robust phenotypic data (Gupta *et al.*, 2005; Hansen *et al.*, 2001; Stella and Boettcher, 2004). GWA analysis permits a survey of a wide range of alleles at each locus, detection of marker-trait associations at the whole genome level, and identification of elite alleles for significantly associated loci (Zhang *et al.*, 2013). The International Maize and Wheat Improvement Centre (CIMMYT) used GWAS to identify marker-trait associations for grain yield, disease resistance and a number of other traits in wheat using multi-environment trials (Crossa *et al.*, 2007). Others have used GWAS to identify significant marker association for thousand kernel weight (TKW), yield and several drought-adaptive traits (Dodig *et al.*, 2012; Zhang *et al.*, 2013).

2.10 Doubled haploid production in wheat

The fixation of target markers using traditional breeding techniques typically requires multiple generations of inbreeding to stabilize desired yield, quality, disease resistance and agronomic traits. Doubled haploids allow wheat breeders to stabilize desired traits in a single generation, delivering lines with 100% homozygosity in nine months (personal communication; Dr Nizam, PBI, Cobbitty, The University of Sydney) thus reducing the time required for variety development by up to five years (Barkley and Chumley, 2012). There are several techniques for producing double haploids including interspecific hybridization and microspore culture. However, the most feasible doubled haploid producing technique is crossing wheat x maize with subsequent embryo rescue once the maize chromosomes have been eliminated and chromosome doubling using colchicine (Sadasivaiah *et al.*, 1999; Ushiyama *et al.*, 2007). Doubled haploids have been extensively used in genetic studies, including gene/QTL mapping and GWAS (Collard *et al.*, 2005; Czembor *et al.*, 2003; Trkulja *et al.*, 2012; Zhang *et al.*, 2008; Choo, 1981).

2.11 Justification of the current research

Crown rot resistant and/or tolerant are required by wheat growers as part of an integrated crown rot control program. Traditional breeding methods, including phenotypic selection, MAS and MABC have not produced cultivars with levels of resistance/tolerance equivalent to source materials. The MARS strategy has not been used in wheat to improve crown rot resistance and in fact, has been used only once before in wheat to the authors knowledge. Given the difficulty of phenotyping for crown rot resistance, the complexity of the trait and the significant influence of genetic background on crown rot expression, the MARS strategy provides a way to potentially accumulate QTLs of minor effect rapidly in the same population. Little is known about crown rot tolerance in wheat and the relationship between tolerance and resistance. This study also examines the relationship between resistance and tolerance and the genetic control of both traits.

CHAPTER 3

General Materials and Methods

3.1 Outline of marker-assisted recurrent selection (MARS)

The MARS approach used in this study comprised of two recombination cycles for populations 1 and 2 (Figures 3.1 and 3.2) and one recombination cycle for population 3 (Figure 3.3). The process is described below.

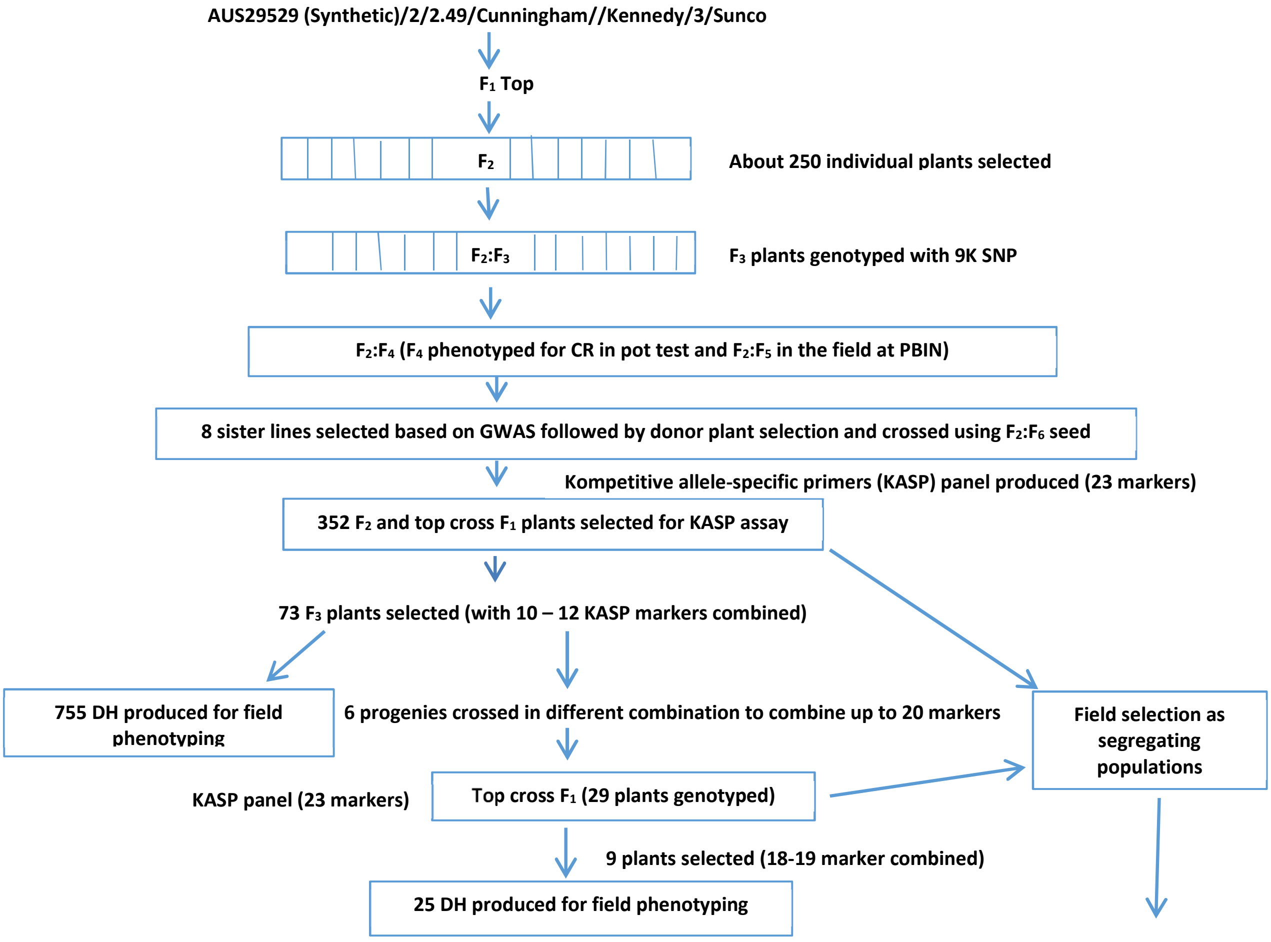


Fig. 3.1: Schematic representation of MARS for population 1

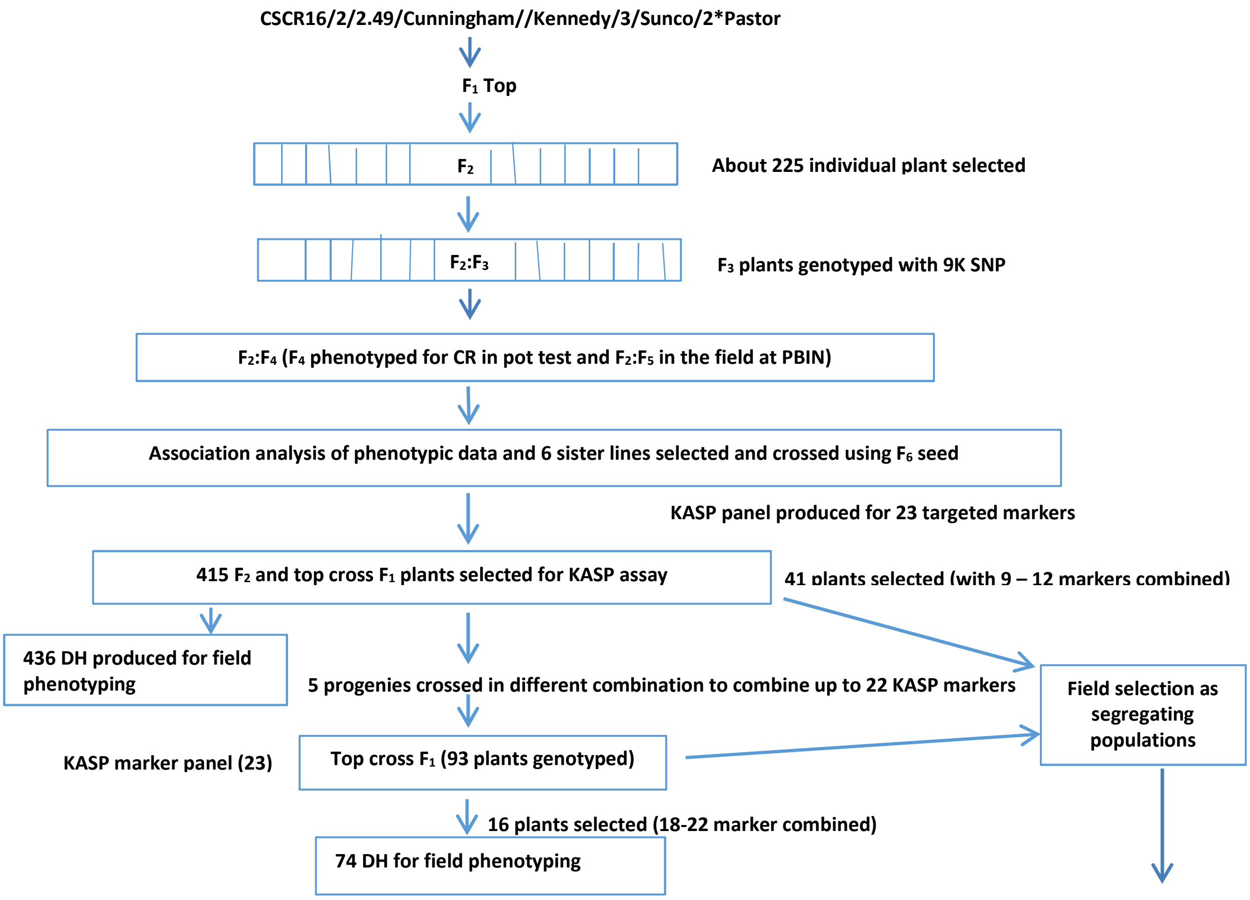


Fig. 3.2: Schematic representation of MARS for population 2

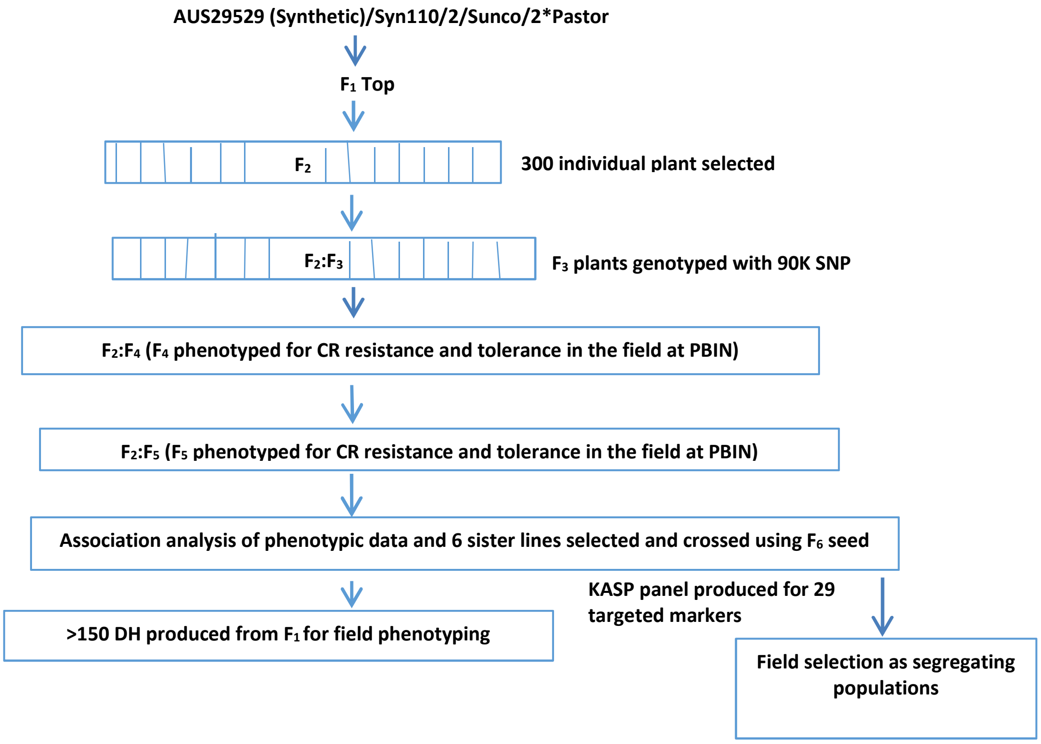


Fig. 3.3: Schematic representation of MARS for population 3

3.2 Population development

Three MARS populations were developed by making top-crosses among three sources of resistance. The pedigrees of population 1 was AUS29529/2/2-49/Cunningham//Kennedy/3/Sunco, population 2 CSCR16/2/2-49/Cunningham//Kennedy/3/Sunco/2*Pastor and population 3 AUS29529/Syn110/2/Sunco/2*Pastor. All parental materials combined in crosses were polymorphic and represented different sources of crown rot resistance (Table 3.1).

Table 3.1: Parental lines used to generate MARS populations.

Name	**Pedigree**	**Origin**	**Evidence**
AUS29529 (Synthetic)	SABUF/7/ALTAR 84/AE.SQUARROSA(224)//YACO/6/ CROC_1/AE.SQUARROSA(205)/5/BR12*3 /4/IAS55*4/CI14123/3/IAS55*4/EG,AUS/IAS55*4/ALD	CIMMYT	Partial resistance (Nicol *et al.*, 2012)
2-49/Cunningham//Kennedy	Same	CIMMYT	Partial resistance
2-49	(Gluyas Early/Gala)	Australia	Partial resistance (Wildermuth *et al.*, 2001)
CSCR16		Australia	Partial resistance
Sunco/2*Pastor	Same	CIMMYT	Partial resistance (Wallwork *et al.*, 2004)
Sunco	Cook*3/WW15/4SUN9E-27/3Ag14	Sydney Uni. (1986)	Partial resistance (Wildermuth *et al.*, 2001)
Syn110 (Primary synthetic)	Altar84 /Ae squarrosa (J Bangor)	CIMMYT	Partial resistance (The University of Sydney)

AUS29529 was a synthetic derivative from CIMMYT and resistance was validated by several crown rot ring tests in Australia. Genotype 2-49/Cunningham//Kennedy was a CIMMYT advanced line with crown rot resistance derived from 2-49, a breeding line recognized as one of the best partial resistance sources to crown rot in Australian environments. Cultivar Sunco was released by the University of Sydney in 1988 and was subsequently reselected in Turkey. This reselection has stable partial adult plant resistance. CSCR16 is a landrace selected for crown rot resistance by CSIRO, Australia. SUNCO/2*PASTOR is a CIMMYT advanced line which was screened for crown rot resistance in Turkey and confirmed at SARDI, Adelaide (Wallwork *et al.*, 2004) and in the field at Narrabri by the University of Sydney.

A total of 250 and 225 F_2 single plants were selected from population 1 and population 2 respectively, and 300 F_2 plants from population 3. These lines, referred to as the base populations, were selected in first segregating generation (F_2) based on uniform plant height and maturity and stripe rust resistance. DNA was extracted from the $F_{2:3}$ (populations 1-2) and $F_{2:3}$ (population 3) lines, parents and check cultivars using the protocol described below. The DNA was genotyped using the 9K SNP platform for populations 1 and 2, and the 90K SNP platform for population 3, at the Bioscience Research Division of the Department of Economic Development, Jobs Transport and Resources, Bundorra, Victoria, Australia. The 90K SNP platform was not available at the time populations 1 and 2 were genotyped.

3.3 Genotyping

3.3.1 DNA extraction

Four pieces of leaves of 2 cm length were collected in 2 ml labelled Eppendorf tubes from two weeks old plants raised in pots. The leaf tissue was dried on silica gel and two ball bearings were added to each tube. The leaf tissue was crushed in matrix mill for 2 min at 20 rpm. Ball bearings were removed before adding CTAB buffer (750 µl). Samples were then incubated at 65°C for 30 min with occasional shaking. Tubes were taken out of water bath and kept at room temperature for 5 min. Six hundred µl of Chloroform: phenol (24:1 v: v) was added and mixed gently by inversion for 2 min until the two layers mixed together. Tubes were then centrifuged at 3600 rpm at room temperature for 20 min. A wide bore pipette was used to transfer 600-650 µl of supernatant to 1.5 ml Eppendorf tube and 600 µl of cold isopropanol was added to precipitate nucleic acids. Tubes were placed at -20°C for 20 min and then centrifuged at 10,000 rpm for 10 min. The supernatant was discarded and the DNA pallet was washed with 70% ethanol. The tube was again centrifuged after adding 500 µl of 70 % ethanol at 10,000 rpm for 10 min and supernatant was discarded and pellet was left for drying overnight. Finally, 100 µl of TE (pH-8) with RNAs (1 µl per 100 µl of TE) was added to each tube and the samples were kept at 37°C in the incubator for 3 hours. The DNA was quantified using a Nanodrop ND-100 spectrophotometer and dilutions of genomic DNAs (ng/µl) were made using deionized water.

3.3.2 SNPs genotyping

Populations 1 and 2 were genotyped using the 9K Infinium SNP genotyping assay according to the manufacturer's protocols (Illumina) to identify polymorphic markers with high calling rates (Cavanagh *et al.*, 2013). Those SNP with >90% call rate were included in further analyses resulting in 7285 SNPs of which 5,895 (or 80.9%) were polymorphic. In the genotyping assay, a clustering algorithm produced three distinct clusters corresponding to the AA, AB, and BB alleles where AA and BB indicates homozygosity and AB heterozygosity for the bi-allelic SNPs. Genotyping of population 3 was carried out using the Illumina iSelect 90K Infinium SNP genotyping array (Wang *et al.*, 2014).

3.4 Phenotyping

The $F_{2:4}$ and $F_{2:5}$ of populations 1 and 2 and the parents and check cultivars were screened for crown rot resistance using pot tests in the glasshouse in summer and winter, and in the field at Narrabri in 2012 (procedures are described below). Two years of yield loss trials of population, including checks and parents, were conducted using paired plots of inoculated and un-inoculated materials with two replications to evaluate important agronomic traits at the I.A. Watson Grains Research Centre, Narrabri, NSW (30 ° 20´S, 149° 45´E) in 2014 and 2015. A description of the phenotypic data assessed in the yield loss trials is found in Chapter 5, section 5.2.10.

3.4.1 Artificial inoculum production

Isolates of F. pseudograminearum were collected in north-western NSW in 2011 and 2012 from the crown region of bread wheat plants expressing crown rot symptoms. These were stored as mycelial and conidial suspensions in 15% glycerol solution at -80°C, from which scrapings were taken for sub-culturing. These remained in storage until used. Artificial crown rot inoculum was produced by colonising durum screenings (grains less than 2 mm in diameter) with *F. pseudograminearum*. A total of 500 kg of durum grain screenings was soaked in water at 10°C for 24 hours (h), after which the grain was rinsed for 15 min to remove any tannins. The grain was allowed to drain to remove excess water, then approximately 1 kg (dry weight) of grain was placed into each of 500 (30 cm x 40 cm) autoclave bags, then frozen to stop the germination process. The grain was then autoclaved at 121°C for 20 min to kill the developing embryo and any fungi or bacteria.

A total of five isolates of *F. pseudograminearum*, all field tested for crown rot aggressiveness, were grown on each of 100 x 90 mm SNA (Spezieller Nahrstoffarmer agar) plates, incubated at standard culturing conditions (14 h light 10 h dark at 23°C and 18°C, respectively). A combination of spore, mycelial and agar suspension was produced by blending agar from 10 plates with litre (L) of sterile water, such that each 1 L suspension contained only one isolate.

A 100 ml aliquot of spore, mycelial and agar suspension was added to each cooled autoclaved bag to produce infected seed for inoculation. The bag was sealed using a rubber band, and shaken to mix the suspension through the grain. The bags were then transferred to a glasshouse, with the temperature set to achieve an ambient temperature of 22°C. After 3-5 days when colonisation of the grain had commenced, the bags were opened, and a cotton stopper was installed. This cotton stopper consisted of a sterilised 50 mm length of 25 mm poly pipe placed in the top of the bag and secured with a rubber band. A piece of cotton wool was then placed in the pipe to allow the bag to breathe. The bags were left in the glasshouse for 2-4 weeks to allow the grain to be fully colonised. The grain was then dried in a dehydrator at 35°C for 4 days. The contents of all the bags were then mixed thoroughly, then stored in poly bags at 10°C prior to use.

3.4.2 Adult Plant Pot Test

An adult plant pot test was carried out for populations 1 and 2. This pot test was developed to provide repeatable glasshouse based screening for crown rot. A single *F. pseudograminearum* isolate was grown on PDA (potato dextrose agar) media for 10 days under standard culturing conditions (14 h light 10 h dark at 23°C and 18°C respectively). Four wheat seedlings were grown in each 150 mm pot containing standard commercial potting mix with slow release fertiliser (Searle potting mixture with the slow release fertiliser Osmocote N:P:K 19.4:1.6:5) and two pots were sown per genotype. A single 5 mm disc of PDA agar colonised by *F. pseudograminearum* was transferred to the soil surface next to a wheat seedling 15 days after sowing, when the seedling was at the 3rd leaf stage. The soil surface was then covered with wheat bran and lightly misted for 7 days to allow mycelial growth across the surface of the pot. The plants were irrigated using a pressure compensated dripper, with each pot receiving 0.5 L per day. This was reduced to 0.2 L per day post anthesis to induce stress in the wheat plants (Figure 3.4). At maturity, the plants were harvested and scored using the 0 to 4 scale as described in Table 3.2.

Table 3.2: The crown rot 0-4 stem browning scoring system.

Score	**Description**
0	No visible symptoms
1	Visible lesions on the 1st internode
2	Visible lesions on the 1st and 2nd internodes
3	Visible lesions on the 1st, 2nd and 3rd internodes
4	Visible lesions on the at least the 2nd two internodes and the development of a white head or aborted tiller

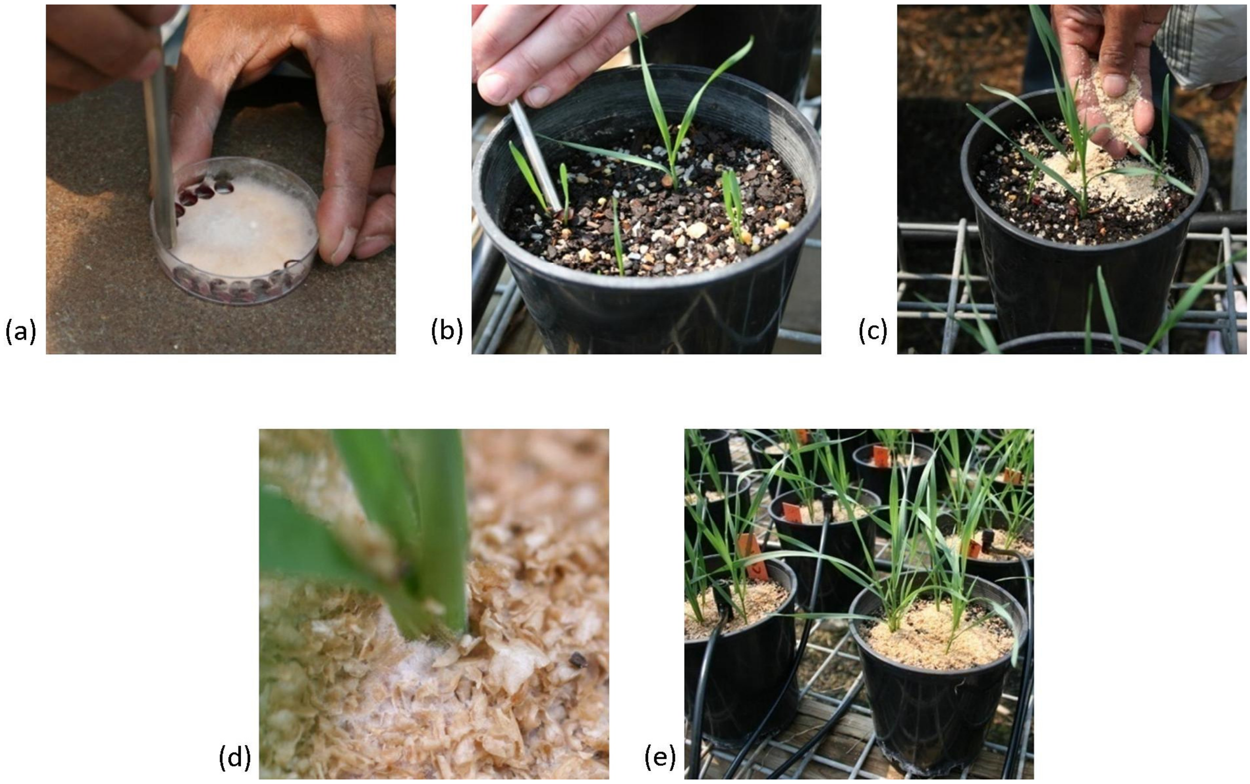


Fig. 3.4: The adult plant pot test. The inoculum is cut from an agar plate (a), the disc is placed on the pot surface (b), the soil surface then covered in bran (c), the pathogen then colonises the bran causing infection (d) and the plant grown to maturity for evaluation.

3.4.3 Field resistance screening

Field resistance screening was conducted on the crown rot nursery block at the IA Watson Grains Research Centre, Narrabri. This field was managed to create a high level of *F. pseudograminearum* inoculum by regular rotation to durum wheat over many years. Experiments were planted into durum residue, with artificial inoculum added to ensure a uniform high level of inoculum pressure. Experiments were planted at a row spacing of 50 cm and row lengths of 130 cm. The experimental layout is described in Chapter 4. Each 130 cm row had 2 g of artificial inoculum added to 5 g of seed at planting.

The lower parts of the stems of each plant from each plot were collected from the field before harvest ripeness and subsequently stored at room temperature until rating. The leaf sheaths were removed from individual plants and the main tiller and 4 randomly sampled secondary tillers were rated for the degree of discoloration on the stem internodes. The stems were rated based on the extent of stem browning on a 0-4 scale as described in Table 3.2. The stem browning was then weighted towards the primary tiller using the following equation:

$$Weighted\ Stem\ Browning = (2 * primary\ tiller\ score + (seccondary\ and\ tertiary\ tiller\ scores)$$

$$Number\ of\ tillers + 1$$

The resistance in population 3 (F_2:F_5) in 2015 was estimated by the extent of stem browning along the entire stem, measured in mm from the base of each stem. This newly adopted method addressed the limitations of the discrete 0-4 scale used in 2014. The 0-4 method resulted in poor discrimination of genotypes with moderate levels of resistance or susceptibility due to a lack of scale. While the earlier method was effective at discriminating highly resistant or highly susceptible lines, it did not provide a good spread of genotypes with moderate levels of resistance. The use of a continuous measure of resistance using the extent of stem browning in mm provided better discrimination.

3.5 Genome-wide association analysis and KASP marker development

The genotypic and phenotypic data was used in genome-wide association mapping (GWAS) to identify significant marker-trait associations for crown rot resistance and tolerance in all populations. Linear mixed models with kinship matrix and principal components to account for population relatedness were used for GWA analysis. The analyses were conducted using the R-package GAPIT. The significant marker-trait associations (MTAs) (identified at $p<0.001$) identified in populations 1 and 2 are summarized in Appendix I, Tables 1 and 2. Eighty-eight SNPs that were significant across both populations 1 and 2 were selected from Appendix I, Tables 1 and 2 and their primer sequences identified. A KASP (Kompetitive allele-specific primers) panel of 78 markers then produced and these are presented in Appendix I, Table 3. Twenty-three polymorphic KASP markers were eventually retained from the panel for genotyping once monomorphic markers were removed (Table 3.3). The incidence of monomorphic markers was perplexing as these SNPs differentiated in the population. This may have been an artefact of primer design and or progeny numbers. The KASP panel was then used to genotype the parents and progeny of the first and second rounds of recombination. In population 3, 29 SNP markers were selected from GWAS (Table 3.6). These are currently being converted into KASP markers for future selection.

Table 3.3: Selected markers used for KASP panel development and their primer sequences; populations 1 and 2.

Marker (SNP ID)[1]	Chromosome	[2]Position cM	[3]Allele 1 primer	[4]Allele 2 primer	Common/reverse primer
BobWhite_c1027_1127(IWB38)	1A	149.82	CGATGGTCGACTCCGACCG	GCGATGGTCGACTCCGACCA	CTGAGCGTATCTTTGCCTTCTAGTCTA
CAP7_c821_239(IWB14279)	1A	130.09	AGGATGGGAACACACCAGCTG	CAGGATGGGAACACACCAGCTA	GCAGAAGAAAGGAATTTGCGGTGGAA
IAAV2694(IWB34600)	1A	93.61	GTCACGACCGTAGCTCATATCG	AGTCACGACCGTAGCTCATATCT	GAAACGTGGCAGCCGAGCTGAA
wsnp_Ku_c183_358844(IWA6649)	1A	27.071	GCGGAGTTGCAATCACACCGAA	CGGAGTTGCAATCACACCGAG	TACCATGCCAAAGCCATAAACGTCAATT
BS00070139_51(IWB10444)	1B	68.037	GACGACCTACATTATTCAGTACCTG	GACGACCTACATTATTCAGTACCTT	CGCTCTTGTTTGGATGTAGTCCGTT
Excalibur_c21898_1423(IWB23711)	1B	8.3607	CAAGATCATCCTTCTGAAGGAAGCA	AAGATCATCCTTCTGAAGGAAGCG	TAGTAGCCCTGTCGTCCGCCTT
Ra_c16069_1820(IWB51198)	1B	64.099	AAGCTACTCCCCGTGTCCAAC	CAAGCTACTCCCCGTGTCCAAT	CGGCAAGGCAGACAAATGAGTGTAT
Tdurum_contig13117_1316(IWB67865)	1B	86.073	TTACTTATTTGTATGTTAAATCTTCCTAGTCT	ACTTATTTGTATGTTAAATCTTCCTAGTCC	ATAGACAAGCTGAAAGATGCAGCCATATA
wsnp_Ex_c3372_6195001(IWA3446)	1D	75.036	GTCGGTCAACGTCTGCATCTGT	CGGTCAACGTCTGCATCTGG	GAACAATCATTTGTCAGGCAAGATACCTA
BS00062567_51(IWB8864)	2Dx	82.821	CGGAGAATAGCCCATTGGTCGA	GGAGAATAGCCCATTGGTCGG	GCATGCCGGCGCACGCGTT
BS00072994_51(IWB10632)	3B	85.517	GTGGTACTTGGTAGTGGACATTGAT	GGTACTTGGTAGTGGACATTGAC	TAGTTCTGGTGTACAATAGTTGCGAGAA
BS00079029_51(IWB11049)	3B	140.51	ATTCACACAAGGCAATTTGTCAGCG	ATTCACACAAGGCAATTTGTCAGCA	CCTCTTCCATAACTTGCTTATCCAGAAT
IACX11310(IWB35687)	3B	72.018	GTGCCTGTTGGATATTTACCTAGTTC	AGTGCCTGTTGGATATTTACCTAGTTT	GTTCTGGCATCTGAAGAAAACGCGAT
BS00035307_51(IWB8008)	4A	11.598	CGCGCACGCTAAATGAACTACG	GCGCGCACGCTAAATGAACTACA	CGGTGATGCATCAGGATCCAACAAA
Ku_c3385_521(IWB39213)	4B	71.914	TCTGCATATCCCATGACCTTTCG	CTTCTGCATATCCCATGACCTTTCA	GTCAACACGGGAGCACTTCCATTAA
BS00032003_51(IWB7864)	5B	0.4281	CCGACCCGTCTGGCCT	CTCCGACCCGTCTGGCCC	TTCAGGTTAGACAGCCCTCTCTCTT
BobWhite_c6094_447(IWB4087)	5B	69.191	GCATACATGATGCAAGACCCGAT	GCATACATGATGCAAGACCCGAC	TGATCTTGGCCTCTGGCAACAAGTT
RAC875_c60007_199 (IWB59482)	6B	78.991	GCTGGTCACCAATGGGTTGGCTCAT	GTCACCAATGGGTTGGCTCAC	CCCATGAGCTTCCGGCAGAGTT
BS00097659_51(IWB12011)	7A	113.3	GAAGTCTGAACTAGTACACCTTTGGT	AAGTCTGAACTAGTACACCTTTGGC	TGAATTCTGATGGAGCTGGATTGTTCAA
BobWhite_c33300_159(IWB2616)	7A	45.245	CGCAGTTGAGCCAAACTTGATTA	CGCAGTTGAGCCAAACTTGATTG	CAATGAGGAGCTGCAGGTGTGTAAA
Kukri_rep_c70199_506(IWB49992.1)	7A	213.2	ATGAAGGCCGTGTGGCTTCGT	GAAGGCCGTGTGGCTTCGC	TTTGCATACTCTTCTTCAGTAACCTCCTT
wsnp_JD_c1219_1766041(IWA5797)	7A	241.4	TCATGAGATAACCTAATTCTGGAGGA	CATGAGATAACCTAATTCTGGAGGG	GGGACAACCAACTCTTTGGACGTAT
wsnp_be352570B_Ta_2_1(IWA4)	7B	67.473	GTAACTGTTTTTATAAACTATCCAAGATCCA	AACTGTTTTTATAAACTATCCAAGATCCG	GCAACTGAATGCACTGAAAATTGGAATCAT

[1] (SNP ID)

[2] Genetic map position reported in Wang *et al.* (2014)

[3] A1 Primer labelled with FAM: GAAGGTGACCAAGTTCATGCT

[4] A2 Primer labelled with HEX: GAAGGTCGGAGTCAACGGATT

The KASP primers were designed from a 101 bp Infinium sequence carrying the SNP of interest. Two allele specific A1 and A2 primers corresponding to the SNP and a common reverse (C) primer were designed. An example is given below for the marker BobWhite_c33300_159 (*IWB2616*)

TCGATATCTGGAATGTACACAGCATGCTCGCAGTTGAGCCAAACTTGATT[A/G]CAAATTTACACACCTGCAGCTCCTCATTGTTAGCCCGAACTACGTACAGA

KASP_2616A1 5′ GAAGGTGACCAAGTTCATGCTCGCAGTTGAGCCAAACTTGATTA 3′
KASP_2616A2 5′ GAAGGTCGGAGTCAACGGATTCGCAGTTGAGCCAAACTTGATTG 3′
KASP_2616C 5′ CAATGAGGAGCTGCAGGTGTGTAAA 3′

The fluorescent dyes FAM (gaaggtgaccaagttcatgct) and HEX (gaaggtcggagtcaacggatt) were added at the 5′ end of A1 and A2 primers, respectively. A negative control (water) and positive control (parental DNA) were included in the KASP assay for allelic discrimination. The final volume of the PCR reaction was 8 µl, containing 4 µl of 2×KASP mix (KBioscience), 0.11 µl primer mix (mixture of 12 µM each allele-specific A1 and A2 primers and 30 µM of common reverse primer), 3 µl of genomic DNA (30 ng/µl) and 0.89 µl of autoclaved ddH_2O. Universal FRET (fluorescence resonance energy transfer) cassettes for FAM and HEX, ROXTM passive reference dye, Taq polymerase, free nucleotides and MgCl2 in optimized buffer were present in KASP mix.

The PCR reactions were carried out following, 15 min at 94°C; 10 touchdown (TD) cycles of 20 s at 94°C, 60 s at 65-57°C (dropping 0.8 °C per cycle); and 35-38 cycles of 20 s at 94°C, 60 s at 57°C, using 96-well PCR microplates. The reactions were carried out in T100™ thermal cycler (BioRad, USA).

3.6 Recombination cycles

F_5 sister lines were selected from the base populations (Appendix I, Tables 1 and 2). The progeny identified parents from the base population for the 1st recombination are presented in Table 3.4. Based on marker effects, progeny were recombined in simple and three-way crosses (top-crosses) to combine complementary alleles. The inter-crossed F_1 seed from simple crosses were planted in the pots in summer to produce top-cross F_1 and F_2. The F_2 and F_1-top seeds were sown in the birdcage at the Plant Breeding Institute, IA Watson Grains Research Centre, Narrabri during the 2014 cropping season. When plants were six weeks old, a total of 767 plants (representing 352 and 415 from populations 1 and 2, respectively) were selected and tagged on the basis of good agronomic type. Two pieces of 2cm long leaves were collected from every selected plant and DNA was extracted using the procedure described in section 3.4.1. This DNA was used to genotype 23 KASP markers. Finally, seventy-three and 41 plants from populations 1 and 2, respectively, were selected based on marker information. Approximately 10 doubled haploid plants were then made on each selected plant using the methods described in section 3.7.

Table 3.4: Parents selected from the base populations of population 1 and 2 for crossing in the first round of recombination (see Appendix1, Tables 1 and 2)

Genotype/line (population 1)	Genotype/line (population 2)

MARS 1 - #3	MARS 2 - #5
MARS 1 - #68	MARS 2 - #16
MARS 1 - # 125	MARS 2 - #33
MARS 1 - # 131	MARS 2 - #36
MARS 1 - #149	MARS 2 - #50
MARS 1 - #157	MARS 2 - #100
MARS 1 - # 168	
MARS 1 - # 206	

Table 3.5: Selected genotypes from populations 1 and 2 with complementary target alleles in the 2nd recombination cycle.

Population 1			
Genotype/line	No. of significant markers	Hybridization	Markers combined
MARS4-702	12	702/673//558	18-19
MARS4-673	11		
MARS4-558	11		
MARS4-542	11	542/128//730	18-19
MARS4-128	10		
MARS4-702	11		
Population 2			
MARS5-68	11	68/86//90	18-20
MARS5-86	10		
MARS5-90	12		
MARS5-277	10	90/452//277	21-22
MARS5-452	10		

Following the 1st recombination, 11 plants were selected from populations 1 and 2 based on the complementary of their target markers. These were crossed and top-crossed to produce the 2nd recombination cycle (Table 3.5). Thus up to 22 markers could potentially be recombined. These selected genotypes were hybridized in a three-way cross amongst selected progeny at Cobbitty in 2015. Eighty-five top-cross F_1 plants were then genotyped using the KASP panel of 23 markers. Six plants with 18-19 combined markers and 14 plants with 18-22 with combined markers subsequently selected from populations 1 and 2, respectively. Approximately 10 doubled haploids were then produced from each of the selected plants for phenotyping. Six F_5 progeny were selected from the base population of population 3. These were hybridized to combine complementary genomic regions identified from GWAS (Table 3.6). Approximately 10 – 20 doubled haploids were subsequently produced from each $F_{1.}$

Table 3.5: Selected genotypes from populations 1 and 2 with complementary target alleles in the 2nd recombination cycle.

Genotype/line	No. of significant markers	Hybridization	Markers combined
Population 1			
MARS4-702	12	702/673//558	18-19
MARS4-673	11		
MARS4-558	11		
MARS4-542	11	542/128//730	18-19
MARS4-128	10		
MARS4-702	11		
Population 2			
MARS5-68	11	68/86//90	18-20
MARS5-86	10		
MARS5-90	12		
MARS5-277	10	90/452//277	21-22
MARS5-452	10		

Table 3.6: Selected markers linked to target traits from population 3 for hybridization in the 1st recombination cycle.

Traits	Markers
Yield Nil and Plus	BS00000929_51
	BS00037002_51
	BS00037003_51
	BS00067024_51
	RAC875_c35672_136
	RFL_Contig727_736
	Tdurum_contig19852_242

Stem Browning	Excalibur_c65830_82
	Tdurum_contig14544_1550
	Tdurum_contig83066_276
Yield Nil	BobWhite_rep_c48966_570
	IAAV7856
	Kukri_c3507_158
	Kukri_c5252_107
	RAC875_rep_c72517_1215
	Tdurum_contig10466_87
	wsnp_Ex_c2277_4267788
	wsnp_Ku_rep_c103274_90057407
Yield Plus	BS00063589_51
	D_contig17313_245
	Excalibur_c40068_522
	RAC875_rep_c72984_1417
	Tdurum_contig56157_1595
	wsnp_Ex_c35910_43971560
White head	BS00034147_51
	Excalibur_c18966_1008
	IACX9217
	RAC875_c12879_176
	RAC875_c1035_65
	wsnp_Ex_c4484_8065800
	Total

3.7 The production of doubled haploids

The emasculation of wheat spikes in the wheat x maize wide cross was slightly different from the normal emasculation procedure. After heading, plants were observed every day to assess the exact stage of emasculation by the colour of the spikes, maturity of flowers and experience. Ideal spikes of the plants were medium hard, and anther colour was green to light yellow. This was judged by opening a floret in the middle of the spike. Middle florets of the spikelets were removed with the help of forceps, leaving the primary and secondary florets. Five to eight spikelets from the middle portion of a spike were used for the emasculation. Awns were cut at the base keeping the lemma and palea intact and the anthers were removed without damaging the stigma from the florets of each of the spikelet of both sides. The emasculated spike was then covered with a glassine bag. Two to three days after emasculation, the spikelets were pollinated using fresh maize pollen between 8.30 am 12 noon in the morning and 2.00 pm to 3.30 pm in the afternoon. After pollination, the spike was covered again with a glassine paper bag.

A solution of 150 ppm 2, 4-D (Sigma D-7299, Granule form) was prepared and one drop applied using a plastic pasture pipette with a slanting cut at the tip to middle portion of two florets (where the middle floret had been removed). The 2, 4-D solution was applied 24 hours after pollination. The spikes were not covered after application of 2, 4-D to avoid fungal growth. Spikes and peduncles were collected 17 – 19 days after pollination and collected in a flask with water. The caryopses were collected using forceps and placed in a 30 ml tube. The caryopses were sterilized and cultured on the same day.

The caryopses were sterilized using commercial bleach (full strength-Milton antibacterial soln. 0.95% w/w Sodium Hypochlorite equivalent to 1.00% w/w available chlorine, www.miltonpharma.com) followed by rinsing 3 times in autoclaved distilled water. The caryopses were dissected under a stereo microscope and cultured on B5 medium (Sigma) in a vial (30 ml) on a slant position. The tubes were placed in a fridge for two days at 4°C and then kept for two days in the complete dark at 20-22°C. The tubes were then transferred to a growth chamber at 19-22°C under a 16 h light cycle. The tubes were then transferred into the growth chamber and kept at 19-22°C under a 16 h light cycle for three weeks. The media for embryo culture was prepared by adding 2.4 g of B5 salts (Appendix I, Table 4) to 500 ml of distilled water and mixed according the manufacturers recommendations.

After three weeks, the haploid plantlets were gently taken out of the tubes and transferred into 4 cm diameter pots, containing soil (90% of crushed bark and 10% of sand) without fertilizer. Before planting, the roots of haploid plantlets were cut down by 3-4 cm for easy transplanting. After 3-4 days the plants were transferred to a net house and allowed to produce 3-4 tillers. Prior to colchicine treatment, the soil was gently taken out and the roots of the plants were trimmed to a length of 3-4 cm. The roots were thoroughly washed and all the soil particles were removed.

The roots were wrapped in a towel and treated in 0.15% colchicine solution. For colchicine treatment 100-150 plants were put in beakers with 300 ml of colchicine solution for 3 h. Eight to 10 ml of DMSO was then added to the 300 ml solution. Roots were immersed in the solution up to the crown level and then placed in a fume hood at 20-21°C. An air pump was put into the solution to facilitate the absorption of colchicine. After three hours, plants were taken out of colchicine solution and the roots were washed thoroughly under tap water.

The colchicine treated plants were then transplanted in 5 cm diameter pots filled with soil (90% of crushed bark and 10% of sand). The top portion of leaves was cut 10 cm from the crown to reduce evaporation and pots were watered before transplanting. After 2 weeks, plants were shifted to a net house and grown at 22-30°C for seed production. Plants were fertilized with Aquasol, a balanced soluble fertilizer containing nine essential nutrient elements at the rate of 30 g per 10 L every fifteen days. The mature seeds were harvested and multiplied for crown rot phenotyping.

CHAPTER 4

Expression of crown rot resistance in MARS materials in the field and glasshouse

4.1 Introduction

The deployment of crown rot resistant varieties is the most effective, environment-friendly and efficient way to reduce the effects of crown rot disease in wheat (Stephens *et al.*, 2008). However, the inheritance of crown rot resistance, determined as a reduction in basal stem-browning, is complex and the heritability of most disease phenotyping methods is low. Clearly, effective crown rot resistance will require the accumulation of multiple genes of minor but additive effect (Ma *et al.*, 2012). Although high priority has been given to crown rot resistance breeding in Australia, a high level of resistance in modern wheat cultivars has yet to be achieved (Burgess *et al.*, 2001).

Further complicating phenotyping of this disease, the expression of the crown rot disease is strongly influenced by environmental factors and effective phenotyping is time-consuming, technically laborious and expensive when a large number of genotypes are screened, as is required in wheat breeding programs (Yang *et al.*, 2010; Li *et al.*, 2010). Complete resistance to crown rot disease has yet to be reported in any wheat genotype and several methods have been used to differentiate susceptible and partially resistance infection types. The most common method is basal stem browning of mature plants following infection in the field. This field based assessment of adult plant resistance is more representative of genotype response than glasshouse-based assays of seedling resistance or partial resistance (Wildermuth and McNamara, 1994; Liu and Ogbonnaya, 2015). A compromise method is the assessment of adult plant resistance in pots in the greenhouse (Raju *et al.*, 2012). In this method, genotypes are sown in pots and the germinating seedling grows through a layer of crown rot inoculum. Adult plants are then assessed for basal stem browning.

In this chapter, adult plant resistance was assessed on genotypes evaluated in a pot test and under field conditions. The aim was to (i) establish the degree of resistance in MARS populations and (ii) assess the reliability of pot based testing for resistance to crown rot.

4.2 Materials and Methods

4.2.1 Experimental site

The field study was conducted at the IA Watson Grains Research Centre at Narrabri, NSW (30° 20′S latitude and 149° 45′E longitude; elevation of 212 m. above sea level) during 2012. The pot test experiments were conducted at the Plant Breeding Institute (PBI), University of Sydney, Cobbitty, NSW 2570 during the summer of 2011/12 and winter of 2012.

4.2.2 Germplasm evaluated

Populations 1 and 2, and their parents were evaluated for both pot and field adult plant resistance. The parents of these populations, and their development, were described in Chapter 3 section 3.2. A number of industry standards were also included in the study: Sunco and Batavia for the pot experiments, and Batavia, Bellaroi, Janz, Wylie and 2-49 for the field experiments.

4.2.3 Irrigation practices

The field based experiments were grown on stored soil moisture and two irrigations were applied during tillering. The aim was to provide sufficient moisture for crown rot infection early in the season and a grain-filling period moisture stress to promote the expression of the disease. Similar moisture regimes were generated in the two pot experiments using hand-watering in the greenhouse.

4.2.4 Weather conditions

The meteorological data were recorded for 2012 at the Narrabri Airport Automatic Weather Station (AWS) which was located near the experimental field. The link used to access these data was:

Narrabri Airport AWS NSW (054038) http://www.bom.gov.au/climate/data/

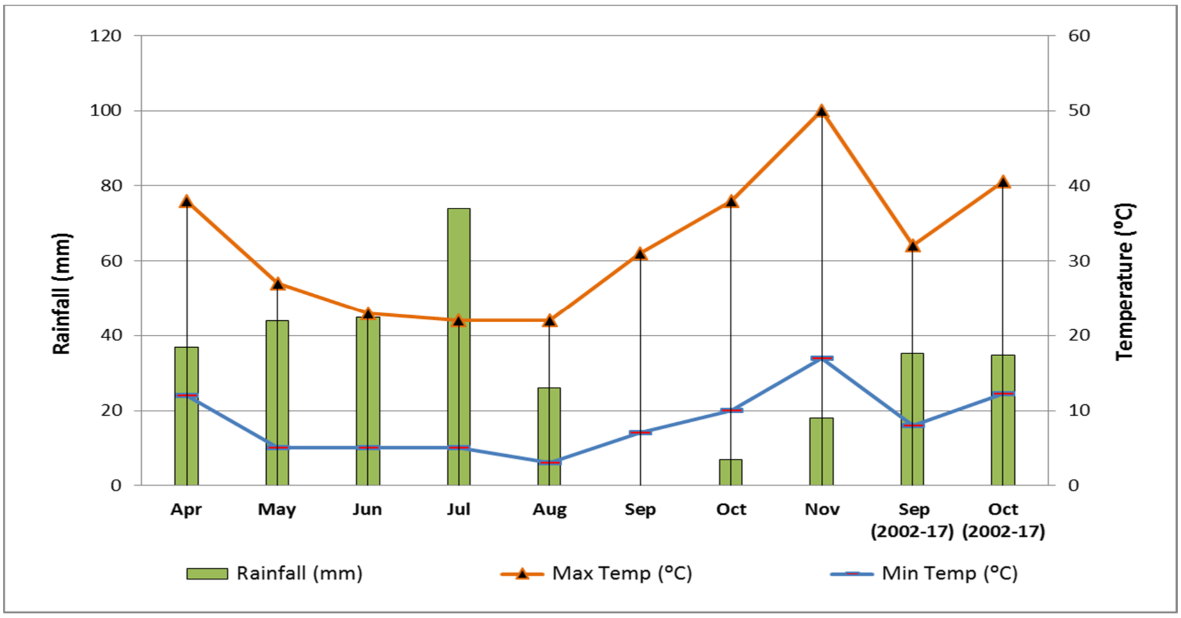


Fig. 4.1: Monthly rainfall and maximum and minimum temperature during the cropping season in 2012 and the long-term (2002-2017) mean average rainfall and maximum and minimum temperature of September and October.

4.2.5 Screening for adult plant resistance

The experimental protocols for both the field and pot experiments, including sowing, inoculum production and inoculation, and disease assessment on the basal stem browning scoring system (0-4 scale) are described in Chapter 3, Sections 3.4.1, 3.4.2 and 3.4.3.

In these experiments, resistance to crown rot was determined by the extent of invasion of *F. pseudograminearum* through the infected wheat stem. Stem browning in plants with little resistance to crown rot extended through several internodes, while plants with partial resistance had restricted stem browning. In the pot-test, a single plant from each pot was selected at maturity and the main stem was rated for disease intensity. In the field experiment, 7-10 plants were randomly selected at maturity stage and 5 plants and up to a maximum of 5 tillers per plant, based on the available tillers, were assessed from each plot.

4.2.6 Experimental design and data analysis

In summer and winter 2012, two pot test experiments of populations 1 and 2 were laid out in completely randomized designs in the greenhouse with two replications. Three seeds of each genotype were sown per pot per replicate. The two populations were arranged in a randomized complete block design in the field with two replications. Twenty seeds of each genotype were sown in 1 m rows per replicate.

The GenStat statistical software package (18th edition, www.vsin.co.uk) was used to analyse all experimental data. A linear mixed model (LMM) in the Residual Maximum Likelihood (REML) function of GenStat was used to estimate components of variance in the field experiment. Genotypes were considered fixed effects and plants within replicates as random terms in the model. A general analysis of variance was used to estimate components of variance in the pot test. Genotypes were considered as a fixed effects and plants within replicates as random effects. Means were calculated and compared using Fisher's protected least significant difference (LSD) test at P < 0.05. A summary statistical analysis was conducted to determine the minimum and maximum trait values and ranges for both years.

4.3 Results

4.3.1 Components of variance in the field and pot experiments

Significant differences among genotypes for stem browning (p<0.05) were observed in the field test and winter pot test of population 1, while no significant genotypic differences were observed in the summer pot test (Table 4.1). A wide range of variation was observed for stem browning response under field conditions; this ranged from 0.0001-2.9568. However, a much narrower range of variation was observed in the pot tests, particularly in the summer where the range was very small (3.0 - 4.0).

Table 4.1: Components of variation for basal stem browning in the population 1

Components	Field test	Pot test (Summer 2012)	Pot test (Winter 2012)
d.f.	197	251	250
Mean square /Wald statistic (Entry)	654.44**	0.0544 ^{ns}	1.1812 **
Mean	0.934	3.896	2.45
Max.	2.9568	4	4
Min.	0.0001	3	0.447
Standard error	0.0343	0.2374	0.9382
%CV	45.03	5.34	36.9
LSD(0.05)	1.29	0.612	1.840
Heritability	0.05	0.39	0.24

** indicates significance level at p= 0.01, ns = non-significant

In population 2, significant differences among genotypes (p<0.01) were also observed in the field trial and winter pot test. However, no significant genotypic differences were observed in the summer pot test (Table 4.2). A wide range of variation was observed for disease severity in both the field experiment and winter pot test. This ranged from 0.006-2.732 and 0.5 - 4, respectively. In contrast, a much narrower range of variation was observed in the summer pot test.

Table 4.2: Components of variation for basal stem browning in the population 2

Components	Field test	Pot test (Summer 2012)	Pot test (Winter 2012)
d.f.	197	226	227
Mean square/Wald statistic	474.17**	0.05281^{ns}	1.0308 **
Mean	1.008	3.9563	3.205
Max.	2.732	4	4
Min.	0.006	2.75	0.5
Standard error	0.0148	0.1382	1.3092
%CV	49.95	7.41	23.25
LSD(0.05)	1.42	0.29	2.037
Heritability	0.03	0.64	0.64

** indicates significance level at p= 0.01, ns = non-significant

4.3.2 Comparison of basal stem browning screenings methods

The correlation between crown rot severities obtained from the field and pot tests for population 1 are presented in Figure 4.2, 4.3 and 4.4. Non-significant relationships were observed between the field experiment and the two pot tests. Similarly, no significant relationship was observed between the summer and winter pot tests.

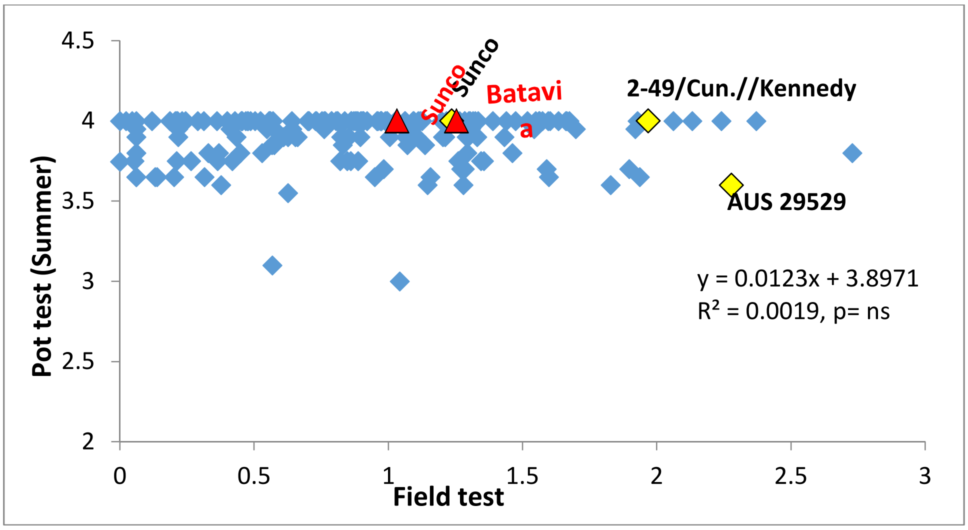


Fig. 4.2: The relationship between the field test and pot test (summer) for population 1. The red triangles and yellow squares indicate checks and parents, respectively.

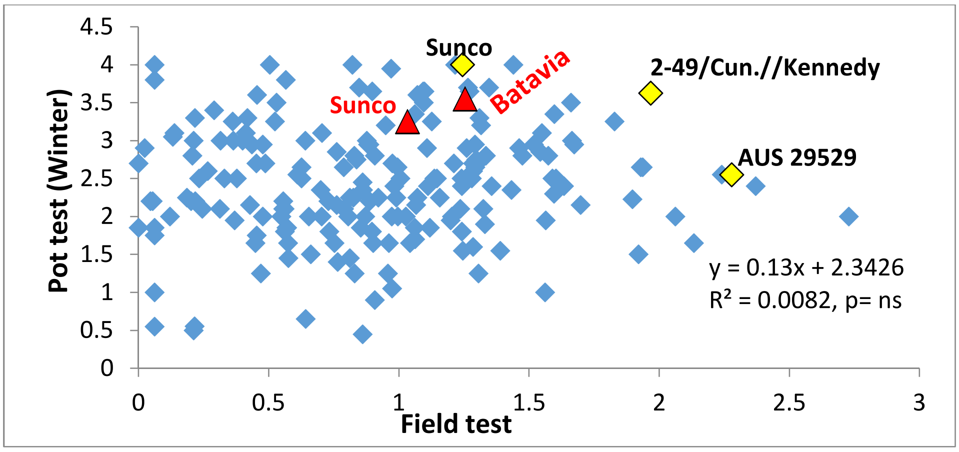


Fig. 4.3: The relationship between the field test and pot test (winter) for population 1. The red triangles and yellow squares indicate checks and parents, respectively.

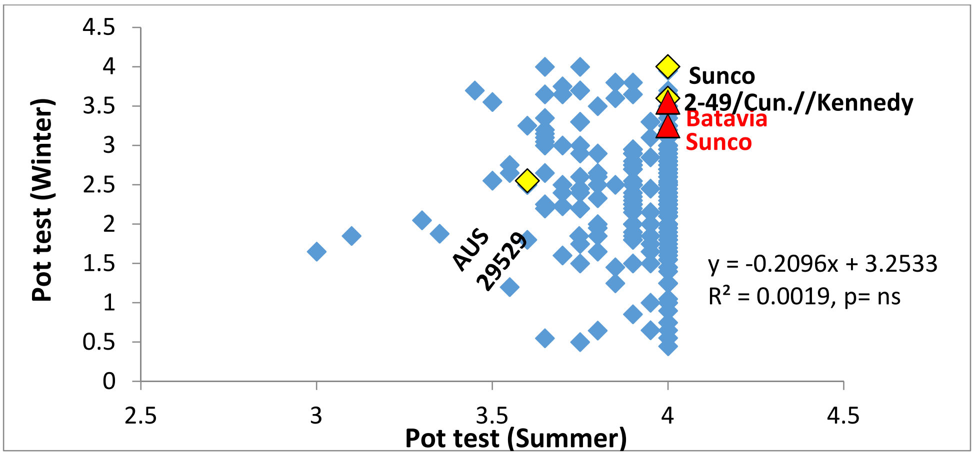


Fig. 4.4: The relationship between the winter and summer pot tests for population 1. The red triangles and yellow squares indicate checks and parents, respectively.

A total of 114 (0.0001-1.026), 137 (0.0001-1.245) and 187 (0.0001-1.93) genotypes from population 1 showed lower crown rot severity in the field experiment than the checks, Sunco (1.032), the Sunco-parent (1.245) and the susceptible check Batavia (1.254), respectively (Appendix II, Table 1). The Sunco-parent was simply the seed source used to make the crosses. While only 10 genotypes (scores ranging from 3.0-3.55) had lower severity than the parent AUS29529 (3.6) in the summer pot test, in the winter pot test, 144 genotypes out of 250 showed lower crown rot severity (0.447-2.529) than AUS29529. A further 212 genotypes (0.447-3.20) were more resistant than the Sunco-check (3.25). Interestingly, the susceptible bread wheat check, Batavia (3.55), appeared to be more resistant than the partially resistant parents Sunco (4.0) and 2-49/Cunningham//Kennedy (3.63) in the winter pot test. Importantly, the genotypes 6, 25, 62, 122, 204 and 168 all showed consistently lower disease severity than checks and parents across all three tests (Appendix II, Table 1).

The relationships between crown rot severities obtained from the field experiment and the two pot tests for the population 2 are presented in Figures 4.5, 4.6 and 4.7. No significant correlation was observed between the summer and winter pot tests and the field experiment.

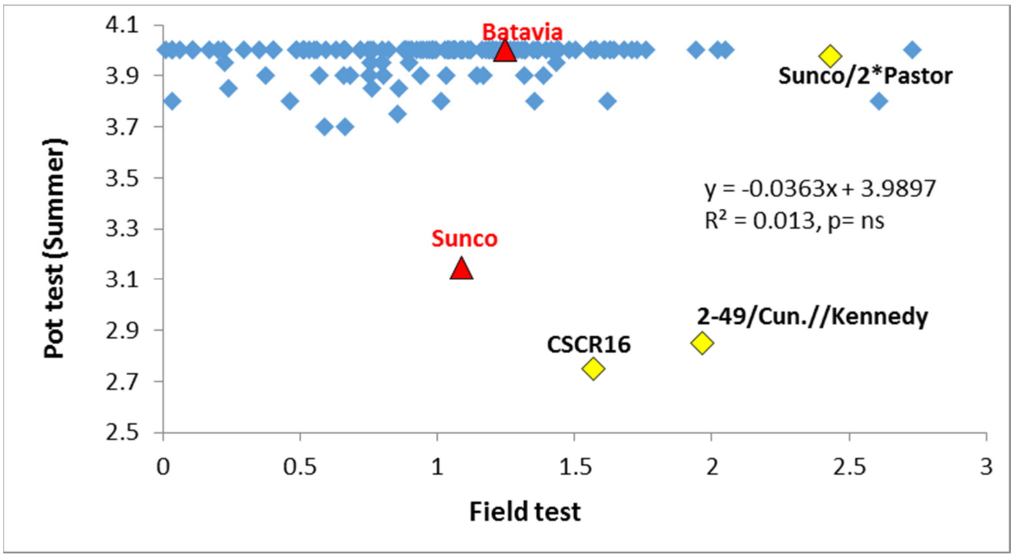


Fig. 4.5: The relationship between the field test and pot test (summer) for population 2. The red triangles and yellow squares indicate checks and parents, respectively.

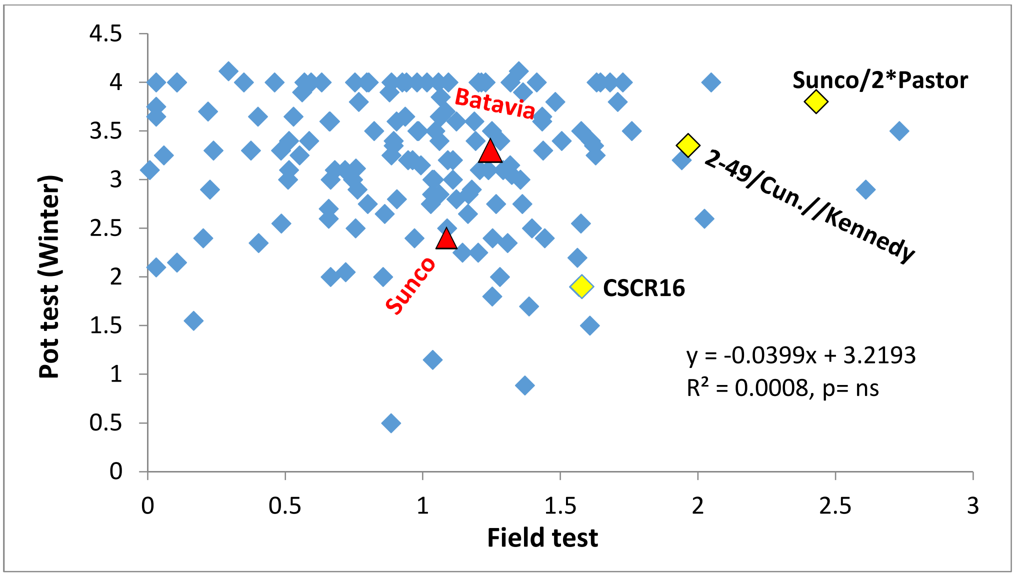


Fig. 4.6: The relationship between the field test and pot test (winter) for population 2. The red triangles and yellow squares indicate checks and parents.

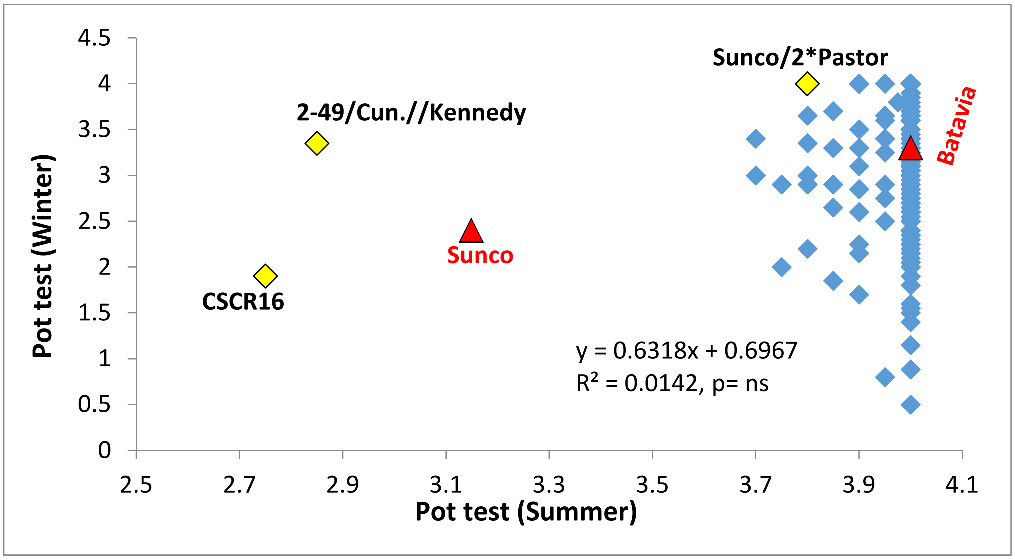


Fig. 4.7: The relationship between the winter and summer pot tests for population 2. The red triangles and yellow squares indicate checks and parents, respectively.

A total of 85 (scores ranging from 0.006-1.08), 104 (0.006-1.23), 130 (0.006-1.561), 144 (0.006-1.941) and 146 genotypes (0.006-2.43) from population 2 showed lower crown rot severity in the field test than the checks and the parents Sunco (1.086), Batavia (1.245), CSCR16 (1.567), 2-49/Cunningham//Kennedy (1.964) and Sunco/*2Pastor (2.43), respectively. Although not statistically significant, two parents (CSCR16 and 2-49/Cunningham//Kennedy) and the check Sunco showed the lowest severities (2.75-3.149) in the summer pot test (Appendix II, Table 1). However, only 41 genotypes had lower severity (3.7-3.95) than the susceptible check Batavia in the summer pot test. A total 11 (0.5-1.85), 30 (0.5-2.35) and 107 (0.5-3.3) genotypes had lower crown rot severity in the winter pot test than CSCR16 (1.9), Sunco- check (2.4) and Batavia (3.3). Moreover, 113 genotypes including 2-49/Cunningham//Kennedy and Sunco/*2Pastor showed very high (3.35-4) susceptibility. The genotype 71 (0.007) was the most resistant followed by 29, 37, 120, 224 (0.031) and 77 (0.059) respectively while line 138 (2.732) was found to be the most susceptible in the field test. The genotype 38 (0.5) had the lowest disease severity followed by 111 (0.885), 39 (1.15) and 69 (1.5) in the winter pot test. Several genotypes (29, 37, 120 and 224) showed consistently lower disease severity across all three tests (Appendix II, Table 2).

4.4 Discussion

Large numbers of genotypes need to be routinely assessed for crown rot response if resistance to crown rot in wheat is to be improved through breeding (Yang *et al.*, 2010). However, it is difficult to control conditions in the field (Mitter *et al.*, 2006), particularly moisture and temperature, and crown rot infection and disease expression is not always reliable and obtainable each year. Thus, the rate of genetic advance can be reduced. In contrast, temperature and moisture can be controlled in the greenhouse as can the placement of inoculum. This chapter evaluated an adult plant pot test against field screenings to validate pot screening as an effective and reliable method for assessing resistance. Generally, neither post-test was effective in producing a range of crown rot responses. The disease severity was too high to discriminate among genotypes for partial resistance, particularly in the summer. In contrast, the field screening method produced significant results and differentiated the check cultivars based on known resistance responses. Thus the assessment of genotype disease resistance can be considered reliable. The disease severity assessed in populations 1 and 2 indicated transgressive segregations for crown rot (Fig 4.2 to 4.7 and Appendix II, Table 1). While the winter pot test did show significance variation among genotypes, the range in responses was generally too low to adequately select partial resistance. For example, only 12 genotypes were observed to have lower disease severity scores than the parent, CSCR16 in population 2. The level of correlation between all methods, especially the summer and winter pot tests, was generally very poor reflecting a general lack of range in these tests. This lack of range is likely due to the high level of inoculum and artificial conditions which promoted disease infection. Li *et al.* (2008) reported that crown rot development is affected by the difference in water availability due to soil competence in pots.

As crown rot resistance is highly complex and controlled by multiple loci (Bovill *et al.*, 2006; Collard *et al.*, 2005; Wallwork *et al.*, 2004), the pot test method did not provide adequate differentiation. However, in population 1, the genotypes 25 (0.55) and 122 (0.50) in the winter pot test also produced lower disease severity in the field test (while the summer pot test rating was poor). While the pot tests were less able to differentiate partial resistance than the field method, the winter pot test did produce significant results and was superior to the summer test where higher temperatures probably exacerbated infection and symptom expression.

There is only one published report on the assessment of adult plant response to crown rot disease using the pot test (Raju *et al.*, 2012). Pot tests have historically been used to assess seedling resistance only and little correlation between seedling resistance thus measured and adult plant resistance has been reported Purss (1966). Another method of assessing adult plant resistance (the Terrace method) was closely related to the adult plant pot test when used to screen durum wheat for crown rot resistance (Wallwork *et al.*, 2004). However, this method also failed to correlate with crown rot resistance under field conditions.

4.5 Conclusion

This chapter showed that transgressive segregation exists for crown rot resistance in both populations. However, disease severity in the pot tests (both summer and winter) was too severe and inconsistent to be considered a reliable method. This may have been a result of lack of control over spore concentration in the development of the inoculum and finer control may have reduced the intensity of the disease expression. Nevertheless, field screening was considered more reliable and representative of actual genotype responses to crown rot. All further screening of materials in this thesis therefore used the field-based method.

CHAPTER 5

Expression of tolerance to crown rot in MARS materials and the relationship between tolerance and resistance

5.1 Introduction

Plants have various defence mechanisms such as resistance, tolerance and avoidance to protect against pathogen infection (Parlevliet, 1981).

Resistance is the ability of a genotype to stop (complete) or restrict (partial) the ability of a pathogen to colonise a plant, to reduce the severity of the disease (Agrios, 2005). Partial resistance to crown rot has been widely reported, and discussed previously in this thesis. Crown rot resistant genotypes can be identified by assessing the degree of symptom development, including the extent of basal stem browning (Liu and Ogbonnaya, 2015). The degree of stem browning and subsequent white head formation on adult plants is however greatly affected by the environmental conditions, resulting in enormous variation year to year, paddock to paddock and even within paddocks in the same year (Smiley *et al.*, 2005).

The development of whiteheads is also used to study resistance to crown rot (Liu and Ogbonnaya, 2015). However whitehead development is both highly influenced by variable environmental conditions, and is likely a response of both resistance and tolerance, as it is not directly linked to the amount of fungus in the plant. Its role in phenotyping crown rot therefore needs to be clarified.

Tolerance is defined by Bingham *et al.* (2009) as a reduction in yield loss in the presence of a pathogen. It is the ability of a plant to yield, despite infection. Although not widely investigated, tolerance to crown rot in under varying levels of disease severity has been reported in wheat (Kramer *et al.*, 1980). Improving tolerance to crown rot may be an alternative method for improving of wheat under crown rot, particularly given a lack of high levels of genetic resistance to crown rot in commercially cultivated varieties (Yang *et al.*, 2010). The ability however to accurately measure tolerance to crown rot, particularly independently of resistance is crucial if improved genotypes are to be developed (Davies, 2016).

A combination of resistance and tolerance may provide more durable and economically effective protection against disease (Kramer *et al.*, 1980).

The objectives of this chapter were to: i) confirm the expression of resistance and tolerance to crown rot in the progeny of population 3, ii) establish the relationship, if any, between resistance and tolerance and iii) assess the relationship between stem browning and white head formation as measures of resistance.

5.2 Materials and Methods

5.2.1 Experimental site and the duration of experiments

The crown rot yield loss experiments were conducted at the I.A. Watson Grains Research Centre, The University of Sydney, Narrabri (30° 20ʹS latitude and 149° 45ʹE longitude; elevation of 212 m above sea level) during two consecutive growing seasons; 2014 and 2015 (May-October). The experiments were sown between the third and last week of May and harvested in the first week of November in both years. This period represented the optimum growing conditions for the establishment of crown rot on wheat.

5.2.2 Climate and Soil

The experimental site at Narrabri is considered to be a variable summer dominant rainfall location with an annual average rainfall of 572 mm (2001-2015). Forty percent of rainfall occurs in the winter cropping season and 60% in the summer (November-April). In the two years of experiments, 2014 and 2015, the recorded annual rainfall was 373 mm and 603.9 mm, respectively. The dominant soil type at this location was a self-mulching, grey vertosol (Isbell, 2016). The soil is a high smectite, dark plains soil with pH 7.4 in a 1:5 soil suspension in 0.01 M $CaCl_{2,}$ 51.1% clay, 12.6% silt, 19.6% fine sand, 16.0% coarse sand and 1-1.6 g cm^{-3} bulk density (Uchiyama and Shioya, 1999; Liddell *et al.*, 1986).

5.2.3 Experimental material

The experimental material consisted of 196 F4 (2014) and F5 (2015) progeny derived from the top cross AUS29529 (Synthetic)/2/Syn110/3/Sunco/2*Pastor, the parental lines AUS29529, Sunco/Pastor and Syn110, and the check cultivars Suntop, Sunguard, Sunco, Gregory, Bellaroi, Batavia, Wylie and Spitfire. The check cultivars were chosen on the basis of their differential reactions to crown rot. Details of the parental lines are given in Chapter 3, Section 3.2.

5.2.4 Land preparation and fertilization

The experimental field was prepared using offset discs to provide good tilth prior to sowing. Recommended fertilizer practice for this region of NSW was adopted following a pre-sowing soil nutrient analysis (Table 5.1).

Table 5.1: Fertilizer applied to the experimental site in 2014 and 2015.

Year	Product	Kg/ha	Time of application
2014	Nitrogen (Urea)	220	15th April
		100	28 July
	Gold Phos 10 (P: S: Zn=18.3: 10.3: 1)	100	Banded with the seed at sowing
2015	Nitrogen (Urea)	220	25th March
		100	1 August
	Granulock cotton sustain (P:N:K:Zn=10:5:21:1)	100	Banded with the seed at sowing

5.2.5 Field layout

The experiments were established as plots of 12 m^2 sown as paired plots with and without crown rot inoculum in both seasons. The experiments comprised 616 plots in 2014 and 832 plots in 2015, arranged in augmented partially replicated designs. The awnless variety Sunlin was used as a buffer around the experiment.

5.2.6 Seeding, harvest and plot size

Seeds of each genotype were sown in 6m plots of 6 rows with a 33 cm row spacing, giving a total plot area of 12 m^2. Experiments were sown on the 19 and 27th of May in 2014 and 2015, respectively. The plots were machine sown at a seeding rate of 50 kg ha^{-1} to establish a plant population of approximately 100 seed m^{-2}. One meter at the head and tail of each plot was removed before harvest giving a harvested plot area of 8 m^2. Plots were mechanically harvested.

5.2.7 Inoculum preparation and field inoculation

The trial was planted into fields with low to nil levels of crown rot, into field pea residue in 2014 and faba bean residue in 2015. The genotypes were sown in paired plots with and without inoculum of *F. pseudograminearum.* The production of inoculum is described in Chapter 3, Section 3.4.1. The inoculum was delivered to each furrow at the rate of 2 g per m of row (72 g/plot) just above the seed during seeding.

5.2.8 Agronomic practices

Agronomic practices followed standard recommendations for wheat in north-western NSW. In season herbicides were applied as required. These included Hotshot and MCPA LVE @ 750 ml ha^{-1} during tillering to control weeds such as milk thistle, wild turnip, volunteer field pea and wild mustard as required. Fungicide was sprayed to control rust in the late grain filling stage (Zadok, Z-77) in 2014 only.

5.2.9 Irrigation regimes and weather conditions

Genotypes were sown on stored soil moisture and two irrigations were applied, depending on in season rainfall, up to flowering with an overhead irrigator at the rate of 35 mm per irrigation. The aim was to generate moisture stress conditions across the experiments from late anthesis throughout the grain-filling period to provide a favourable environment for disease development. The first irrigation was applied 40 DAS (days after sowing) in 2014 and 35 DAS in 2015. Metrological data for 2014 and 2015 was accessed from http://ozforecast.com.au/cgi-bin/aws_export.cgi?aws=11250

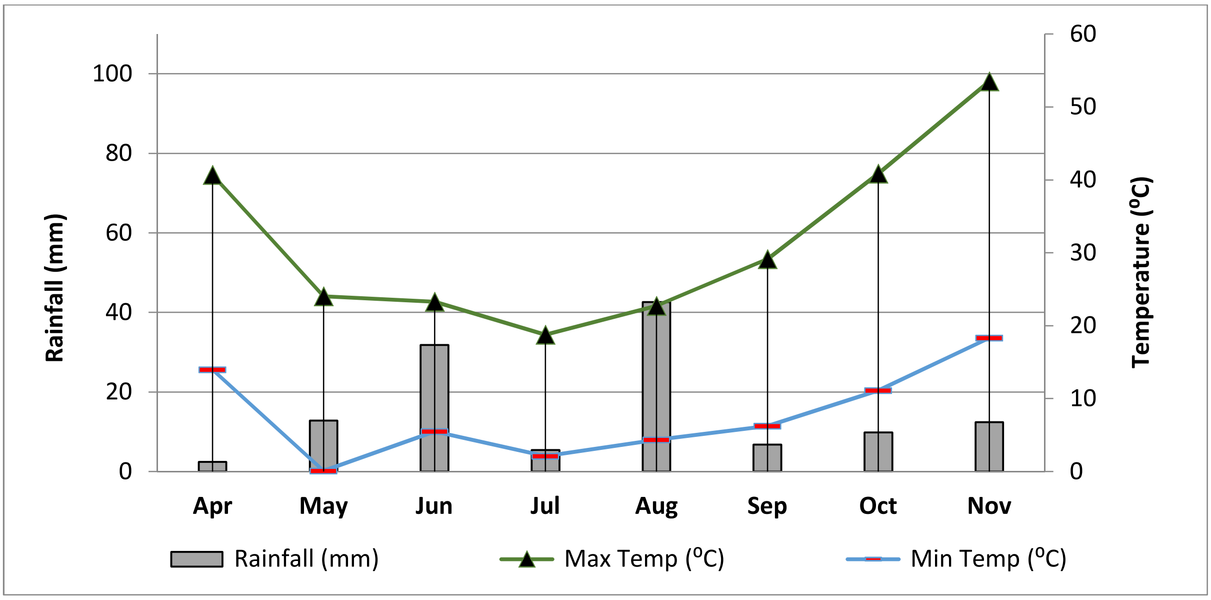


Fig. 5.1: Rainfall and minimum and maximum temperature at Narrabri during the 2014 cropping season.

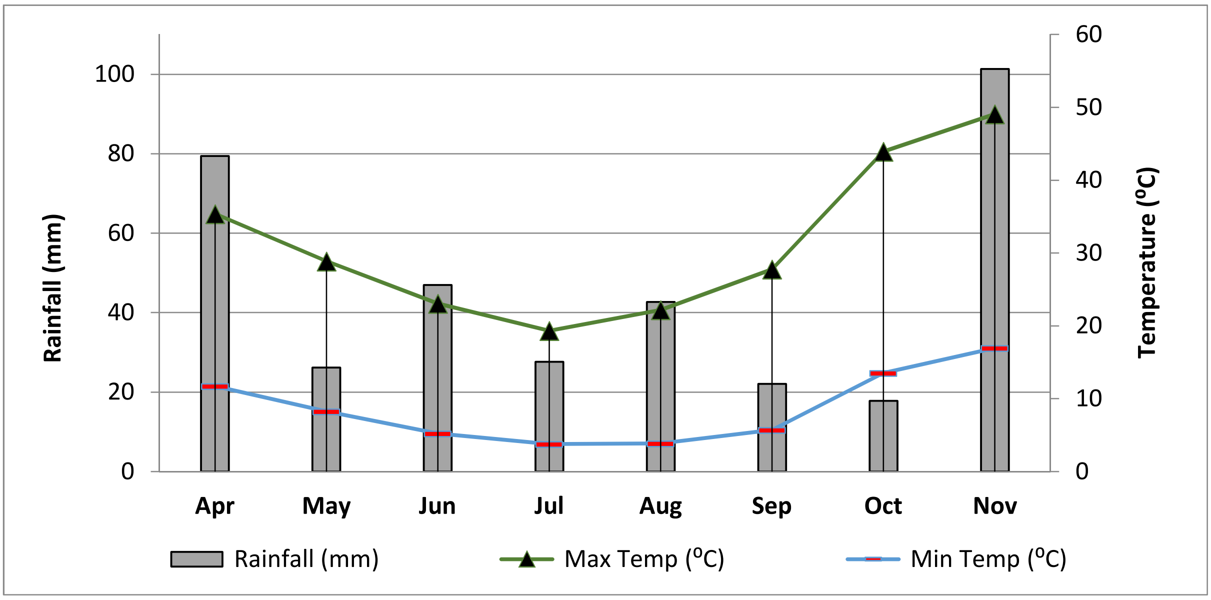


Fig. 5.2: Rainfall and minimum and maximum temperature at Narrabri during the cropping season 2015.

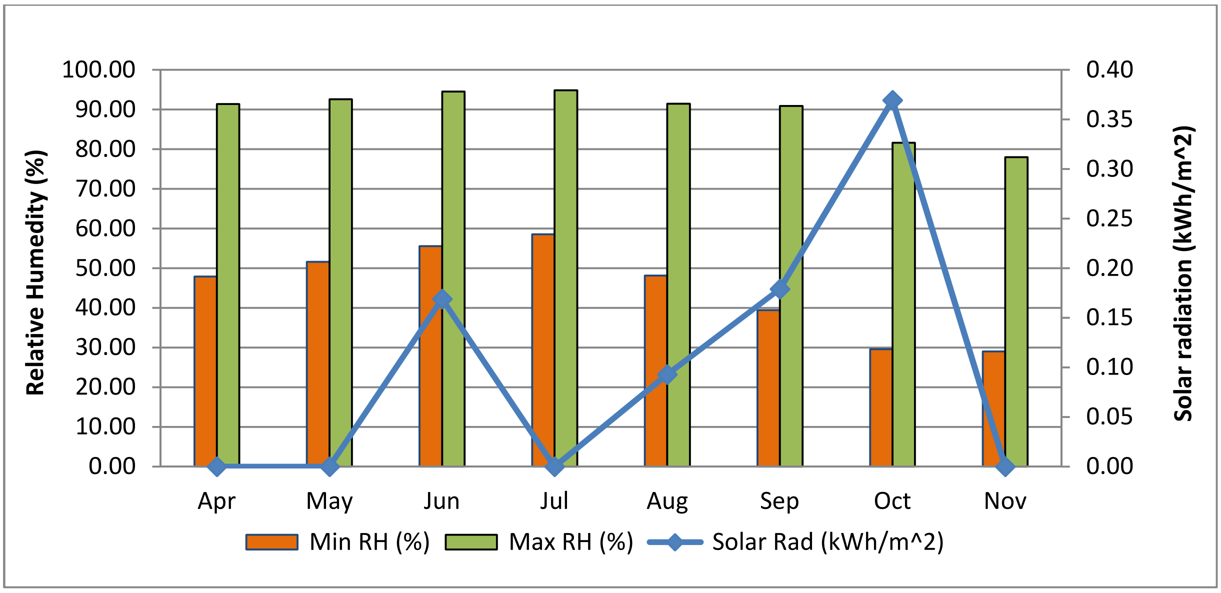


Fig. 5.3: In-season relative humidity and solar radiation at Narrabri during the cropping 2015 season.

5.2.10 Physiological and agronomic trait assessments

Plant height (PH) was measured at physiological maturity using a meter scale and expressed in cm. Five random main tillers were selected from each plot and the distance from ground level to the top of the spike excluding awns was assessed and averaged for each plot. The number of days to heading (HD) per plot was recorded as the difference between the date of seeding and the date at which 50% of the spikes were fully extended from the leaf sheath. The number of days to physiological maturity (PMD) was recorded as the difference between sowing date and the date at which 80% of the plants of each plot had lost green colour in their spikes and 10 cm of the peduncle. Normalised difference vegetative index (NDVI) is an index of the amount of light in the near-infrared spectra, which plants strongly reflect, and the red spectra, which plant strongly absorb. It is calculated by the equation below.

$$ndvi = \frac{NIR - red}{NIR + red}$$

Differences among genotypes in canopy structure, crop establishment and vegetative greenness were assessed using NDVI was measured at tillering (Zadock scale 33), heading (Zadock scale 55-59) and anthesis (Zadock 61-69) in both years. NDVI was measured using a

Hand Held Green Seeker^R (NTech Industries, Canada) by holding the sensor at a horizontal angle with consistent alignment over the plot at a distance of 60-120 cm above the canopy. NDVI readings were taken from the middle rows between 10 am and 2 pm.

Weighted basal stem browning was assessed from 10 plants per plot were randomly collected and plants subsequently stored at 10°C for assessment. Leaf sheaths were removed from individual plants and individual tillers were assessed for stem discoloration as described in Chapter 3, sections 3.4.3. The percentage of white head (%WH) development per plot was recorded visually on three occasions just before physiological maturity. Two hundred cleaned grains from each plot were randomly counted using a CONTADOR seed counter (Pfeuffer, Germany) and subsequently weighed using a digital balance. The weight was then multiplied by five to record thousand kernel weight (TKW) in grams. Percentage screenings was assessed from 400 g of seed was taken from each plot and poured into a 2.0 mm seed sieve. The percentage of shrivelled grains or screenings was assessed by shaking the sample 40 times over a 2.0 mm sieve with elongated slots (Agtator). All shrivelled seeds were weighed and expressed as a percentage of the total. Percent yield loss was calculated as:

$$Percent\ (\%)\ yield\ loss = \frac{Yield\ of\ un-inoculated\ plot\ -\ Yield\ of\ inoculated\ plot}{Yield\ of\ un-inoculated\ plot} \times\ 100$$

Grain yield was generally lower in inoculated plots than un-inoculated plots. However, in some instances the reverse was noted. In these cases the percent yield loss was adjusted to zero. Grain yield was assessed at maturity at 12% moisture content. The first and last meter of each plot was removed and an area of 8m^2 was harvested at maturity using a combine harvester. Grain yield per plot was measured in gram (g) and subsequently converted to Kg ha^{-1}.

5.2.11 Statistical analysis

Analyses of the individual yield loss trials were performed to assess differences between genotypes and treatments (inoculated and un-inoculated) and their interactions. A combined analysis of all genotypes in both years was also conducted excluding Spitfire as it was not used as a check in 2014. The GenStat 18th Edition (www.vsin.co.uk) statistical software package was used to analyse all experimental data. The Residual Maximum Likelihood (REML) function of GenStat was used to spatially analyze all data and to test differences among genotypes and between years and treatments. Years, Genotypes and Treatments (inoculum) were considered fixed terms and plots within treatments and treatments within replications as random terms in the model. Means were separated using Fisher's protected least significant difference test at $P < 0.05$. Relationships among traits within and across years were then tested using the Pearson's simple correlation test in GenStat. The predicted means (genotype x inoculum) were used for subsequent correlation analysis. Simple linear and multiple regressions were conducted using GenStat statistical software.

Broad sense heritability (H^2) was estimated for different traits by modifying the equation of Piepho and Möhring (2007). Heritability was estimated for each trait individually on a mean basis across years according to the following equation:

$$H^2 = \frac{\sigma^2 g}{\sigma^2 g + (\sigma^2 gy/y + \sigma^2 e/r)}$$

Where r = number of replications y = year, $\sigma^2 e$= error variance, $\sigma^2 g$ = genotypic variance, and $\sigma^2 gy$ = variance due to genotype by year interaction. The heritability was categorized as low, moderate and high as suggested by Johnson *et al.* (1951); low 0-30%, moderate 30-60% and high >60%.

The expected genetic advance (GA) for different characters under selection and percent genetic gain was estimated using the formula suggested by Allard (1960):

$$\text{Genetic advance (GA)} = H^2 b \times i \times \sigma_p$$

Where, $H^2 b$ = Heritability in the broad sense; i = Selection differential set at 1.76 at the 10% level of selection intensity; σ_p = Standard deviation of phenotypic variance for a trait. Genetic gain was then estimated as:

$$\text{Genetic gain\%} = \frac{GA}{\mu} \times 100.$$

Where, GA = Genetic advance and μ= Mean of a trait. Genetic advance as percentage of the mean was categorized as low (0-10%), moderate (10-20%) and high (>20%) as suggested by Johnson *et al.* (1951). The observed selection response (R_o) for each trait was also calculated using the following formula (Fehr, 1987):

$$R_0 = S \times H^2$$

Where, S = the selection differential (Xs – X), Xs = mean of the top 10% of progeny and X = the mean of all progeny in the experiment.

5.3 Results

5.3.1 Data adjustment

Following trait analysis with and without inoculum, the genotype means for white heads, screenings and stem browning with negative values were classified as zero (0). This adjustment was made to avoid the confounding effects of negative mean values and to assess relationships among traits more accurately. NDVI was assessed at different growth stages. However, only NDVI at stem elongation (Zadock scale 33)(Zadoks *et al.*, 1974) was retained as no differences between inoculated and un-inoculated plots were observed at heading and anthesis.

5.3.2 Impact of crown rot inoculation: 2014

Genotypic effects were highly significant (p<0.001) for all the traits studied (Appendix III, Table 1). Grain yield (kg ha^{-1}), percent screenings (% screenings), NDVI, plant height (PH), percent white heads (% WH) and disease severity/weighted stem browning (WSB) were significantly influenced by crown rot inoculation (Appendix III, Table 1). However, the genotype (G) x treatment (T) interaction while significant for most traits, was non-significant for TKW, NDVI, PH and days to heading (HD) (Appendix III, Table 1). Means for grain yield (4229 ± 38.11), TKW (33.18 ± 0.35), NDVI (0.814 ± 0.001) and PH (97.9 ± 0.64) were higher in un-inoculated treatments compared to the inoculated treatments. Higher % screenings and % WH were observed under inoculation. Days to heading, days to physiological maturity (PMD) and TKW were not influenced by crown rot inoculum. Days to heading, PMD, PH, %

screenings, TKW and grain yield had high to moderate heritability (in the range 0.58- 0.97) while the heritability of white heads was low in both treatments. A low heritability was estimated for WSB and NDVI under both treatments (Appendix III, Table 1). However, under inoculated conditions, TKW, NDVI and % WH showed higher heritability. Although of a smaller magnitude compared to the control, TKW, NDVI, HD and the % WH under crown rot pressure produced a higher GA. This indicates that some genotypes either performed better under crown rot conditions or that there was a greater range in the data.

Correlation coefficients among all traits evaluated in 2014 are presented in the appendix (Appendix III, Table 3). Significant positive correlations were observed between PMD-plus and PMD-nil and grain yield, HD, NDVI and % screenings, and a significant negative association with TKW and PH. NDVI-nil and NDVI-plus revealed a significant positive correlation with grain yield-plus and % screenings, but a strong negative association with TKW and PH. HD and % screenings in both treatments showed a strong negative correlation with TKW and PH was strongly positively correlated with TKW. Screenings in both treatments were weakly negatively correlated with grain yield-plus. A highly significant and positive correlation was observed between both treatments for NDVI, PH, HD, PMD, TKW, grain yield and % screenings.

5.3.3 Impact of crown rot inoculation: 2015

Significant genotypic effects ($p<0.001$) were observed for all traits in 2015 (Appendix III, Table 2). Environmental effects were also highly significant ($p<0.001$) for all traits except TKW, PMD and HD. Genotype x treatment interactions were significant for grain yield, TKW, % screenings, NDVI and % WH and non-significant for HD, PMD and PH (Appendix III, Table 2). Average grain yield (3409 ± 30.81), TKW (29.53 ± 0.26), NDVI (0.8218 ± 0.00058) and PH (98.43 ± 0.70) were higher in the un-inoculated treatment (Appendix III Table 2). However, as expected, mean % screenings (12.0 ± 0.40) and % WH (25.35 ± 0.98) were higher in the inoculated treatment (Appendix III, Table 2). No treatment effect was observed for HD and PMD (Appendix III, Table 2) indicating that phenology was not influenced by the disease. Higher NDVI, grain yield and TKW and fewer screenings and % WH were observed in the un-inoculated treatment. High heritability was observed for TKW, % screenings, HD, PMD and PH in both treatments and for WSB in the presence of inoculum. Low to medium heritability were estimated for NDVI, % WH and grain yield. The expected selection response (GA) for traits such as grain yield, % screenings, PH and % WH tended to be higher in un-inoculated treatments, and this probably reflects the lower observed error variance under reduced disease pressure.

Correlation coefficients among all traits are presented in the appendix (Appendix III, Table 4). Grain yield in both treatments showed a strong positive correlation with TKW and PH. Significant negative correlations were observed between yield and traits such as % screenings, HD and PMD. TKW in both treatments was strongly positively associated with PH and negatively correlated with % screenings, HD, PMD and NDVI. % screenings was negatively correlated with PH in both treatments. However, % screenings was strongly positively correlated with NDVI, HD and PMD in both treatments.

5.3.4 The impact of crown rot inoculation: combined across years

Grain yield under crown rot pressure is the overriding trait sought by breeders and farmers. The combined analysis of 2014 and 2015 showed that season (year), genotype, inoculum treatment, year x genotype and year x treatment interactions had a significant ($p<0.001$) impact on grain yield (Table 5.2). Clearly, the grain yield of genotypes differed between years and inoculation treatments. The incidence of % WH is an important trait for measuring crown rot resistance. This trait varied significantly by genotype and treatment and year x genotype, year x treatment and genotype x treatment interaction effects were observed. However, no significant year effects were observed for % screenings, NDVI and PH. Genotypic and year/season effects were significant for all traits (Table 5.2). Mean grain yield (3851±34.48), TKW (31.29±0.29), NDVI (0.818±0.0009) and PH (98.23±0.23) were higher in the un-inoculated treatment (Appendix III, Table 2). In contrast, mean screenings (10.12±0.33) and % WH (15.15±0.61) were observed to be higher under inoculation. HD and PMD were similar under both treatments. Overall, inoculation reduced grain yield and TKW by 11% and 4%, respectively. Furthermore, inoculation increased screenings and white head formation by 27% and 87%, respectively (Appendix III, Tables 5, 6, 7 and 12). Mean grain yield (4531 kg ha^{-1} and 4146 kg ha^{-1}), TKW (40 g and 38.4 g) and NDVI (0.83 and 0.80) of the top 10% ranking lines were higher than the mean grain yield (3931 kg ha^{-1} and 3547 kg ha^{-1}), TKW (31 g and

28.6 g) and NDVI (0.82 and 0.78) of the three parents in their respective un-inoculated and inoculated treatments (Table 5.3).

Table 5.2: Wald statistics, means and summary statistics of traits in inoculated (Plus) and un-inoculated (Nil) treatments across the 2014 and 2015 growing seasons.

					Wald statistics				
Source of variation	**d.f**	**GY**	**TKW**	**% screenings**	**NDVI**	**HD**	**PMD**	**PH**	**% WH**
Year (Y)	1	8.99**	16.20*	2.00^{ns}	13.60^{ns}	23.57***	63.30*	0.01^{ns}	29.60*
Genotype (G)	205	2015.74***	4515.20***	2322.50***	1202.50***	18105.57***	2771.20***	6791.67***	717.70***
Inoculum (I)	1	1094.13***	441.40***	322.50***	333.10***	0.75^{ns}	1.92^{ns}	13.02***	1280.20***
Y x G	205	1184.95***	654.50***	451.40***	591.10***	1405.83***	600.0***	579.48***	264.20*
Y x I	1	109.12***	183.40***	87.90***	57.90***	2.75^{ns}	1.30^{ns}	2.65^{ns}	551.30***
G x I	205	183.83^{ns}	181.40^{ns}	147.00^{ns}	227.50^{ns}	38.7^{ns}	148.50^{ns}	22.03^{ns}	288.30**
Y x G x I	205	98.94^{ns}	168.10^{ns}	103.40^{ns}	183.50^{ns}	37.93^{ns}	89.90^{ns}	17.74^{ns}	151.60^{ns}
					Treatment means				
Nil		3851a	31.29a	7.41a	0.82a	112.30a	148.80a	98.23a	1.98a
Plus		3448b	30.03b	10.11b	0.77b	112.30a	148.70a	97.51b	15.15b
SED		10.67	0.08	0.17	0.002	0.07	0.08	0.22	0.43
LSD		20.91	0.16	0.33	0.004	0.14	0.16	0.44	0.86
					Year means				
2014		4188.00a	32.94a	7.67a	0.78a	113.70a	152.80a	97.71a	3.24a
2015		3110.00b	28.38b	9.87a	0.80a	110.90b	144.70b	98.04a	13.89b
SED		389.40	1.19	1.80	0.007	0.53	1.02	0.91	1.99
LSD		424.89	3.89	5.88	0.24	2.21	3.59	6.75	3.91

Note: *** indicates significance level at p= ≤0.001, ** indicates significance level p= ≤0.01, * indicates significance level at p= ≤0.05 and ns = non-significant. h^2 = Heritability; LSD = Least significant difference; SED = Standard error of differences; GA = Genetic advance (5%); GG = Genetic gain (Genetic advance % of mean); NDVI = Normalized difference vegetation index; PH = Plant height (cm); HD = Heading days; PMD = Physiological maturity days; TKW = Thousand kernel weight (g); GY = Grain yield (Kg ha^{-1}); % screenings = Percent screenings, % WH = Percent white heads. Treatment mean followed by different letters indicates significance at ≤ 0.05.

Table 5.3: Means of the top 10% of lines (Xs), parents (Xp), all 196 lines (X), and estimated genetic gain (GA), selection differential (S), broad sense heritability (h^2) and observed selection response (Ro) in inoculated (plus) and un-inoculated (nil) treatments across years (except WSB which is presented by year).

Traits	**Environments**	**GA**	**Xs**	**Xp**	**X**	**S**	**h^2**	**R_0**
GY	**Nil**	639.20	4531.00	3931.00	3842.59	688.41	0.51	350.09
	Plus	589.62	4176.00	3547.00	3447.71	728.29	0.46	335.01
TKW	**Nil**	8.26	40.00	31.00	31.38	8.62	0.82	7.04
	Plus	7.65	38.36	28.64	30.10	8.26	0.79	6.53
% screenings	**Nil**	6.96	1.50	5.87	7.45	-5.95	0.68	-4.08
	Plus	8.88	2.57	8.00	10.11	-7.54	0.75	-5.66
NDVI	**Nil**	0.01	0.83	0.82	0.82	0.01	0.18	0.00
	Plus	0.02	0.80	0.78	0.77	0.03	0.32	0.01
HD	**Nil**	10.42	105.00	111.00	112.31	-7.31	0.92	-6.72
	Plus	10.15	105.00	111.00	112.35	-7.35	0.90	-6.62
PMD	**Nil**	6.12	143.00	149.00	148.70	-5.70	0.81	-4.60
	Plus	5.93	143.00	149.00	148.62	-5.62	0.80	-4.50
PH	**Nil**	19.44	80.00	98.00	98.36	-18.36	0.89	-16.35
	Plus	18.88	79.00	97.00	97.62	-18.62	0.88	-16.39
% WH	**Nil**	3.41	0.00	1.90	1.84	-1.84	0.48	-0.88
	Plus	12.06	4.36	14.00	14.81	-10.45	0.49	-5.12
WSB (2014)	**Nil**	0.39	0.18	0.65	0.93	-0.75	0.31	-0.23
	Plus	0.36	1.00	2.00	1.75	-0.75	0.29	-0.22
2015	**Plus**	77.57	16.74	71.88	44.94	-28.20	0.68	-19.18

Note: NDVI = Normalized difference vegetation index; PH = Plant height (cm); HD = Heading days; PMD = Physiological maturity days; TKW = Thousand kernel weight (g); GY = Grain yield (Kg ha^{-1}); % screenings = Percent screenings, % WH= Percent white heads; WSB= Weighted stem browning.

The GA response was greater for all traits than the observed selection response (R_0). Percentage screenings (2.57%), HD (105 days), PMD (143 days), PH (79 cm) and % WH incidence (4.36%) of the top 10% of lines based on rank were lower than the mean % screenings (8%), days to heading (111 days), days to physiological maturity (149 days), plant height (97 cm) and incidence of % WH (14%) of their parents under crown rot inoculum. Mean disease severity (i.e., the incidence of % WH) of the top 10% of lines was also lower than the mean of the three parents in the inoculated treatment in 2014 and 2015 (Table 5.3).

The high estimated heritability for TKW, % screenings, HD, PMD and PH under both treatments (Table 5.4), indicated that these variables were less affected by inoculation treatment. Moderate to low heritability was observed for grain yield, % WH, NDVI and disease severity (2014). However, a high heritability was estimated for disease severity (basal stem browning) under inoculum in 2015. In a general sense, the heritability estimated in this population does not necessarily reflect the heritability of the trait itself. The experimental site at Narrabri was carefully managed and irrigation was used to reduce the impacts of the season as needed and thus a higher heritability can be expected in some seasons at this site. Moreover, while heritability can be overestimated in certain populations of distantly or unrelated individuals in wheat, this is unlikely in the current study as most of the lines were progeny derived from the same cross.

Correlation coefficients were calculated on the combined data (Table 5.4) to compare the relationships among the traits and the degree of variation between treatments and years. Significant negative correlations were observed between grain yield and HD and % screenings and % WH in both treatments. Grain yield was not correlated with NDVI and PMD in either treatment. However, TKW in the inoculated treatment was observed to be significantly positively associated with grain yield in both treatments (Table 5.4).

Table 5.4: Phenotypic correlation of 8 agronomic and yield contributing traits evaluated under inoculated (Plus) and un-inoculated (Nil) treatments (combined across 2014 and 2015).

	NDVI Nil	***NDVI Plus***	***HD Nil***	***HD Plus***	***PMD Nil***	***PMD Plus***	***PH Nil***	***PH Plus***	***TKW Nil***	***TKW Plus***	***GY Nil***	***GY Plus***	***% screenings Nil***	***% screenings Plus***	***% WH Nil***	***% WH Plus***
NDVI Nil	1															
NDVI Plus	0.74***	1														
HD Nil	0.47***	0.54***	1													
HD Plus	0.47***	0.54***	1.00***	1												
PMD Nil	0.48***	0.56***	0.88***	0.88***	1											
PMD Plus	0.46***	0.53***	0.83***	0.83***	0.93***	1										
PH Nil	-0.22**	-0.29***	-0.30***	-0.31***	-0.33***	-0.32***	1									
PH Plus	-0.22**	-0.29***	-0.32***	-0.32***	-0.34***	-0.33***	0.99***	1								
TKW Nil	-0.35***	-0.47***	-0.64***	-0.64***	-0.66***	-0.65***	0.37***	0.38***	1							
TKW Plus	-0.36***	-0.47***	-0.67***	-0.67***	-0.67***	-0.65***	0.38***	0.39***	0.93***	1						
GY Nil	0.05	0.03	-0.24***	-0.25***	0.04	0.08	-0.14*	-0.14*	0.10	0.14*	1					
GY Plus	0.06	0.04	-0.28***	-0.29***	-0.03	0.02	-0.10	-0.09	0.11	0.20***	0.89***	1				
% screenings Nil	0.32***	0.42***	0.57***	0.57***	0.56***	0.57***	-0.36***	-0.36***	-0.79***	-0.74***	-0.15*	-0.20**	1			
% screenings Plus	0.33***	0.44***	0.62***	0.63***	0.61***	0.61***	-0.34***	-0.35***	-0.81***	-0.82***	-0.17*	-0.29***	0.90***	1		
% WH Nil	0.01	0.01	0.19**	0.19**	0.17*	0.16*	-0.13	-0.13	-0.24***	-0.25***	-0.31***	-0.44***	0.33***	0.40***	1	
% WH Plus	0.14*	0.16*	0.34***	0.34***	0.29***	0.27***	-0.06	-0.08	-0.36***	-0.40***	-0.27***	-0.48***	0.41***	0.53***	0.75***	1
%Yield loss	-0.03	-0.02	0.17*	0.18**	0.17*	0.13	-0.08	-0.10	-0.08	-0.19**	-0.03	-0.49***	0.17*	0.31***	0.40***	0.54***

Note: *** indicates significance level at p= ≤0.001, ** indicates significance level p= ≤0.01 and * indicates significance level at p= ≤0.05. Correlation coefficients not highlighted are non-significant. NDVI = Normalized difference vegetation index; PH = Plant height (cm); HD = Heading days; PMD = Physiological maturity days; TKW = Thousand kernel weight (g); GY = Grain yield (Kg ha^{-1}); % screenings = Percent screenings, % WH = Percent white heads and WSB= Weighted stem browning.

The correlation between % yield loss and grain yield in un-inoculated treatments was non-significant. Significant negative associations were observed between grain yield and NDVI, HD, PMD, % WH and % screenings in all treatments. TKW also had a significant negative correlation with % yield loss in the inoculated treatment. % screenings was significantly positively correlated with % WH and % yield loss in both treatments. However, a significant positive correlation was obtained between % WH and % yield loss in both treatments.

5.3.5 Multiple regression analysis

Multiple regression analysis was performed using the means of two years (2014 and 2015) to identify key traits linked to the economically important traits of GY, TKW, % yield loss and % screenings (Table 5.5). Grain yield was observed to be significantly influenced by % WH, HD, PH, PMD and NDVI at the stem elongation stage under inoculation. These traits explained 47.2% of the yield variation under inoculation. The same traits (except NDVI) explained 43.3% of total yield variation in the un-inoculated treatment. Percentage WH, HD, PH and PMD accounted for 53.1% of the variation in TKW in the presence of inoculum. In the un-inoculated treatment, 45.4% of the variation in TKW was explained by PH and PMD. Thousand kernel weight, % WH and PMD explained 73% of the variation in % screenings, and TKW alone explained 62% of the variation in the same trait in the un-inoculated treatment. Percentage WH and GY accounted for 45.2% of the variation in % yield loss. Grain yield was not significantly influenced by stem browning in 2014 under crown rot inoculum, however stem browning in the inoculated treatment explained 5.5% of total yield variation in 2015 (Table 5.5).

Table 5.5: Summary of multiple regression analysis of the response variables grain yield, TKW, % screenings and % yield loss for inoculated (plus) and un-inoculated (nil) treatments across two seasons; 2014 and 2015.

Variables	**Grain yield**		**TKW**		**% Screenings**		**%Yield loss**	**Grain yield (2015)**
	Nil	**Plus**	**Nil**	**Plus**	**Nil**	**Plus**		
1	**% WH**	% WH	PH	% WH	TKW	% WH	% WH	WSB
2	**HD**	HD	PMD	HD	-	PMD	GY	
3	**PH**	NDVI	-	PH	-	TKW	-	
4	**PMD**	PH	-	PMD	-	-	-	
5	**-**	PMD	-	-	-	-	-	
Percentage variation	43.3	47.2	45.4	53.1	61.8	72.7	45.2	5.5

Note: GY = Grain yield (Kg ha^{-1}); TKW = Thousand kernel weight (g); % screenings = Percent screenings; NDVI = Normalized difference vegetation index; HD = Heading days; PMD = Physiological maturity days; PH = Plant height (cm); % WH= Percent white heads; WSB= Weighted stem browning.

5.3.6 Genetic variability for crown rot tolerance and resistance among genotypes

Percentage yield loss was strongly significantly negatively correlated ($p<0.001$, r= -0.49) with grain yield under crown rot inoculum (Table 5.4). Percentage yield loss also varied significantly among all the genotypes evaluated (Figure 5.4). Overall, crown rot inoculum influenced yield across years with yield ranging from 1525 to 4581 kg ha^{-1} (Appendix III, Table 5). Percentage yield loss due to crown rot varied from 1% to 36%, with an average 12.3 ± 0.38%. Percentage yield losses from crown rot were higher in 2015 than 2014 (43.9% ± 0.59 versus 29.6% ± 0.39) whereas the combined analysis showed an overall yield loss of 35.47% ± 0.39 (Appendix III, Table 14). Percentage screenings also varied significantly ($p<0.001$) across years ranging from 1.71% to 23.55%, with an average 10.16% ± 0.33 and overall mean screenings were higher in 2015 than 2014 (8.21 ± 0.31% versus 12.0 ± 0.40%) (Appendix III, Table 7). Comparisons among parents, checks and the top 10% of progeny selected for the lowest yield loss (and therefore tolerance to crown rot) are presented in Figure 5.5a. All 21-selected progeny produced significantly lower yield loss (<5.5%) compared to their parents [AUS29529 (15.7%) and Syn110 (13%)].

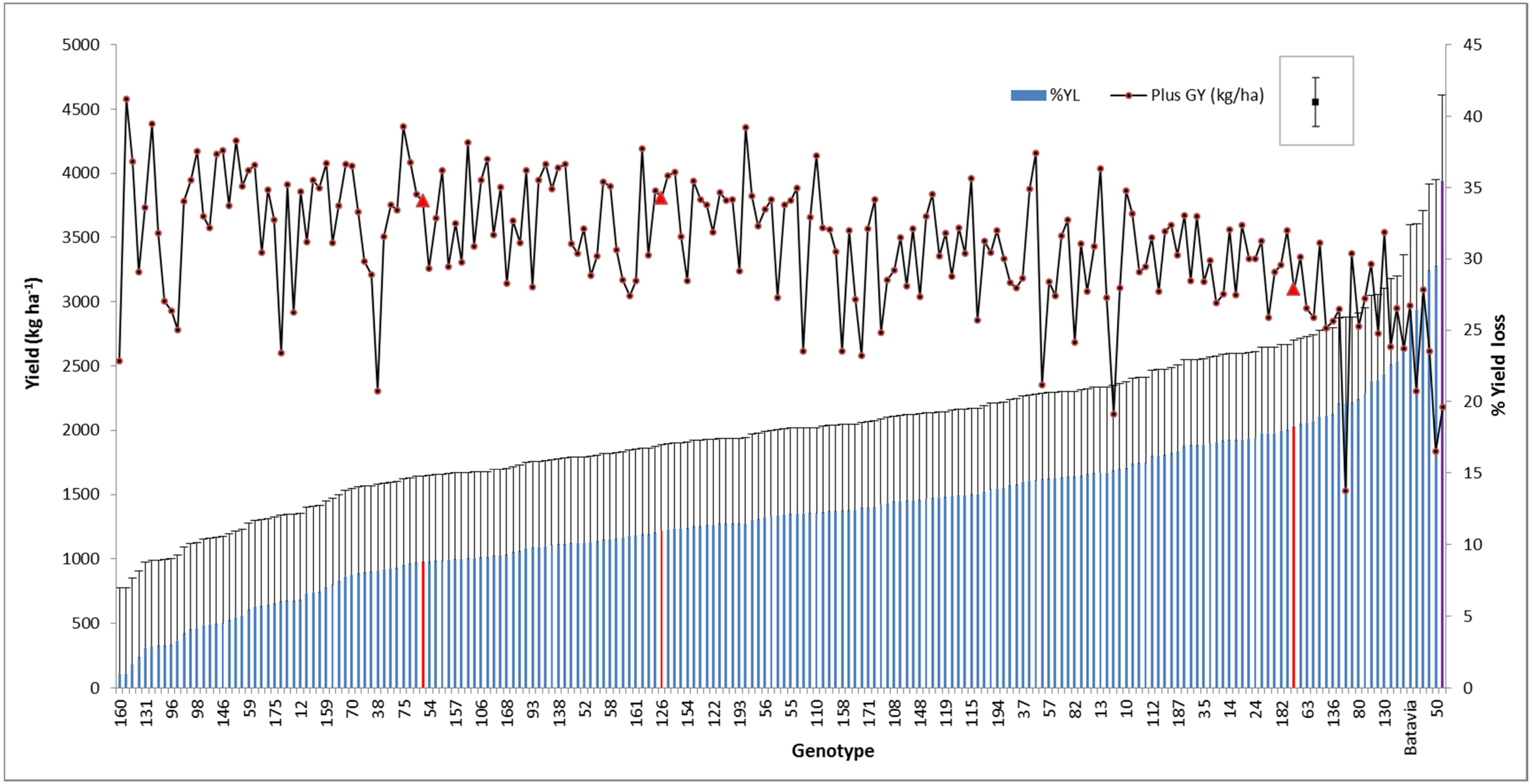


Fig. 5.4: Comparison of mean yield combined across 2014 and 2015 in the inoculated treatment with percentage yield loss among parents (represented as triangles and red bars) and their progeny. Note: The error bar for grain yield is shown in the top right-hand corner.

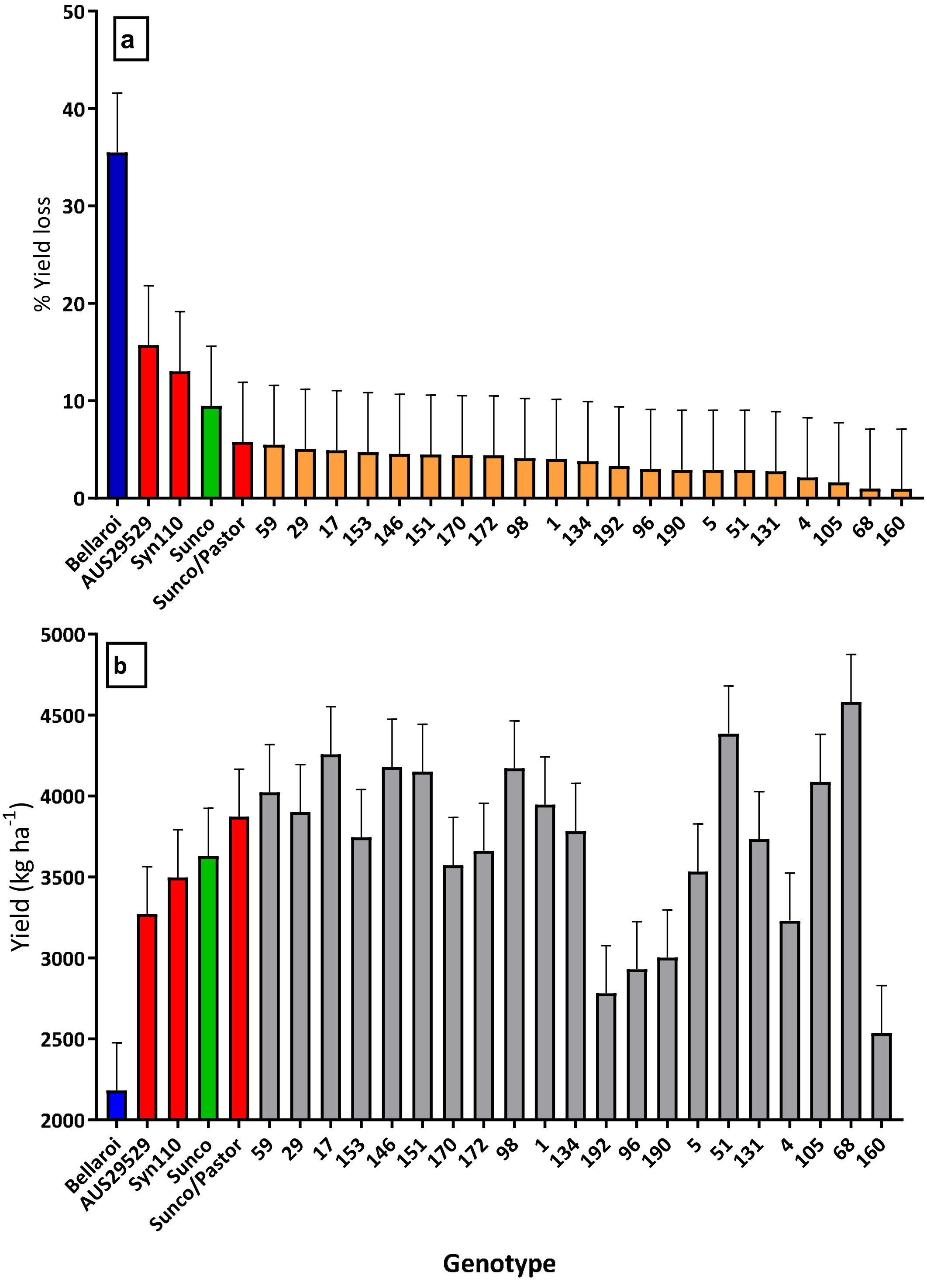


Fig. 5.5: Comparisons of parents (red colour) and their top 10% of progeny and checks (blue and green colour) for (a) % yield loss and (b) yield across years.

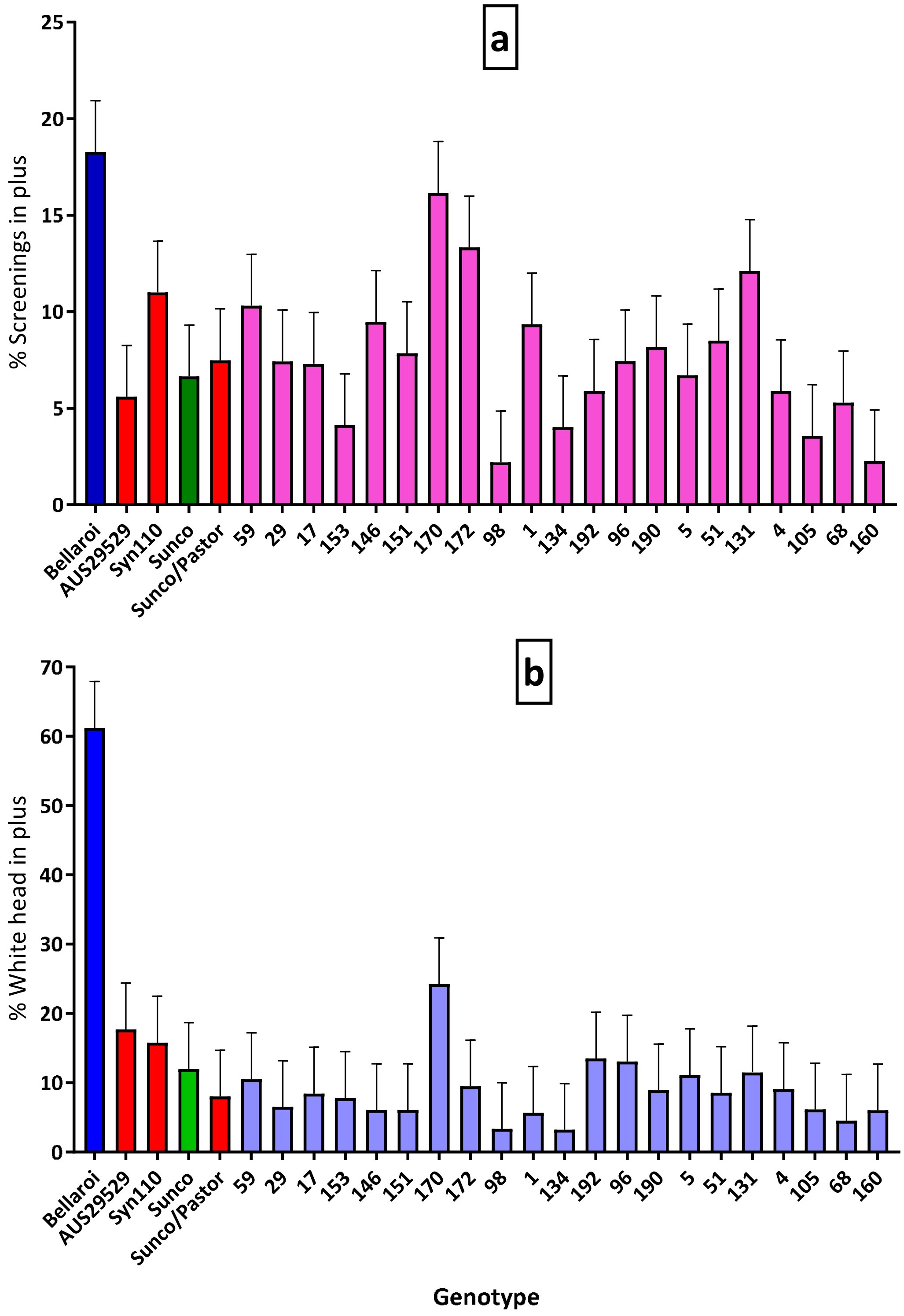


Fig. 5.6: Comparisons of parents and their top 10% of progeny and checks (blue and green colour) for (a) % screenings and (b) % white heads across years.

Ten selected progenies had significantly lower yield loss (ranging from 0.96% to 3.25%) compared to the Sunco (9.5%). However, none of the progeny showed a significant yield loss difference compared to the parent Sunco/Pastor (5.8%). Bellaroi, a susceptible durum wheat check, produced the highest grain yield loss (35.47%) in this study. In addition, the parents, checks and the selected progeny were compared for grain yield, % screenings and % WH across years. These comparisons are shown in Figures 5.5b, 5.6a and 5.6b. Ten progeny produced more yield than their parents and the best check Sunco under inoculation while others were either not different or lower yielding. The entries 68 (4581 kg ha^{-1}), 51 (4386 kg ha^{-1}), 17 (4258 kg ha^{-1}), 146 (4180 kg ha^{-1}) and 98 (4171 kg ha^{-1}) produced significantly higher grain yield than their highest yielding parent; Sunco/Pastor (3872 kg ha^{-1}). The susceptible check Bellaroi was the third-lowest yielding genotype (2181 kg ha^{-1}). Entries 98 (2.2%) and 160 (2.25%) had significantly lower % screenings compared to the best parent AUS29529 (5.6%) under crown rot, while other progeny had either equal or higher screenings than their parents (3.56 -16.15%) and/or the best check Sunco (6.65%). The susceptible check, Bellaroi had the highest % screenings (18.28%). There were no significant differences in % WH between the selected progeny (3.24-6.55%) and the best parent Sunco/Pastor (8.05%) under inoculation, while entries 134, 98, 68 and 1 produced a significantly lower % WH, ranging from 3.24 to 5.66%, compared to the check cultivar Sunco (12%). Seventeen progeny showed significantly lower % WH than two parents; Syn110 (15.83%) and AUS29529 (17.74%). Bellaroi, one of the susceptible checks, produced the highest white head incidence (61.21%) across the population. Entries 68, 98 and 105 had lower % yield loss, % screenings and % WH and higher grain yield than their parents and the best check cultivar, Sunco. Entry 146 had higher % screenings than its parents AUS29529 and Sunco/Pastor, but produced higher grain yield, lower yield loss and lower % WH (Figures 5.5a, b and 5.6a, 5.6b).

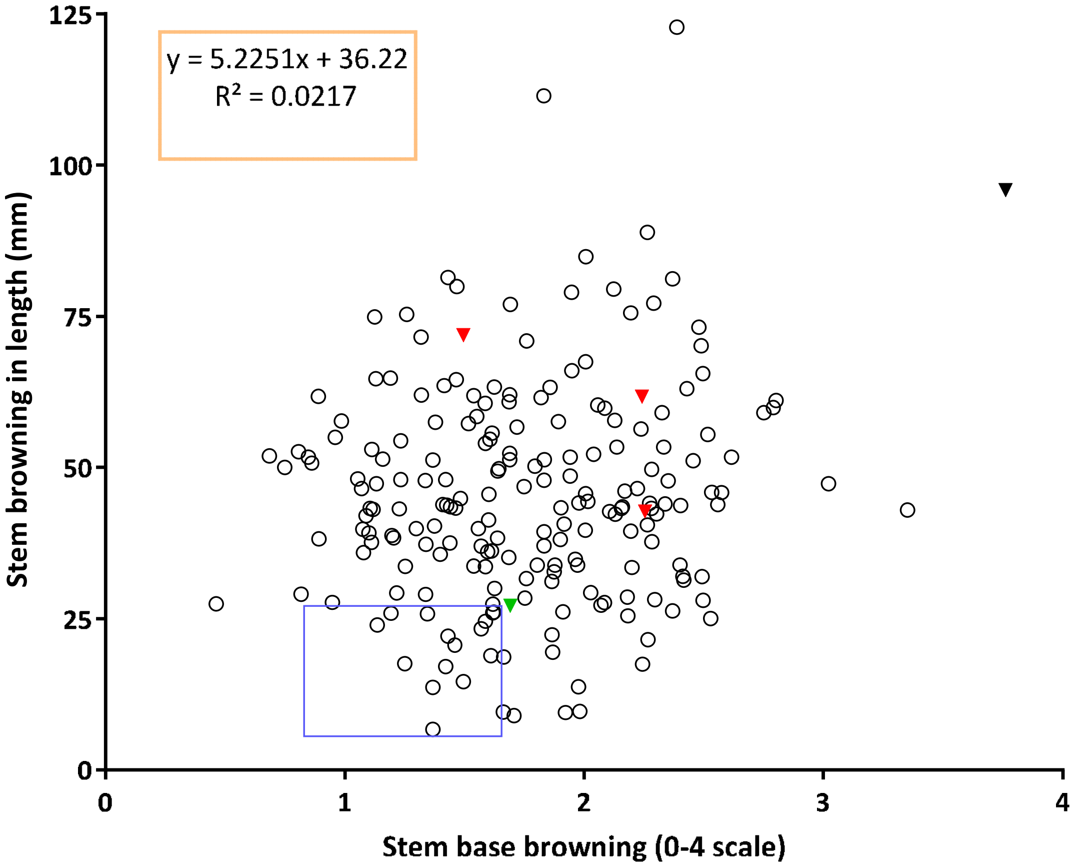


Fig 5.7: Association between weighted basal stem-browning (disease severity) in 2015 and 2014 field experiments on 206 genotypes. Checks are triangles (Red, green and black triangle indicate parents, the best check Sunco and the susceptible check Bellaroi, respectively). The blue rectangle indicates genotypes that had lower disease severity in both scoring methods than the best check Sunco.

The genotypes evaluated in 2014 showed highly significant ($p<0.001$) differences in crown rot severity assessed as weighted stem browning (WSB). The crown rot severity was also significantly influenced by treatment (Appendix III, Table 1) and WSB varied from 0.46 to 3.76 with an average of 1.76 ± 0.036, compared to un-inoculated treatments that ranged from 0 to 2.88 with an average of 0.92 ± 0.039 (Appendix III, Table 13). In 2015, significant variation ($p<0.001$) among genotypes for basal stem browning due to the crown rot disease was observed (Appendix III, Table 2). The two scoring methods of crown rot severity; the 0-4 scale in 2014 and the length of the stem showing symptoms in 2015, were compared. The two scoring methods produced inconsistent disease severity (Figure 5.7). The association between the methods was non-significant and the result were not corilated ($R^2 = 0.0217$). However, a group of progenies produced significantly lower disease severity in both scoring methods compared to their parents (1.5-2.25 and 42.7-71.8 mm), so both methods could both identify low severity. These included entries 54 (1.43, and 17.10 mm for the 0-4 scale and length of browning methods, respectively), 68 (1.49, and 14.59 mm), 72 (1.19, and 25.9 mm), 89 (1.13, and 23.94 mm) and 116 (1.25, and 17.58). These entries consistently produced lower disease severity in both scoring methods compared to the best check Sunco (1.69, and 27.1 mm) and the parents. The susceptible check Bellaroi (3.76, and 95.86 mm) rated poorly in both scoring methods.

Relationships between weighted stem browning and mean grain yield (kg ha^{-1}), % screenings, yield loss % and % WH in 2014 and 2015 are presented in Figures 5.8 and 5.9. Grain yield and stem browning had a significant negative association ($r = -0.234$; $p<0.01$) under inoculation in 2015, however this association was not significant in 2014. Linear regression of stem browning on grain yield revealed that grain yield explained only 1.7% and 5.5% of the variation in stem browning in 2014 and 2015, respectively (Figure 5.8a and Figure 5.9a).

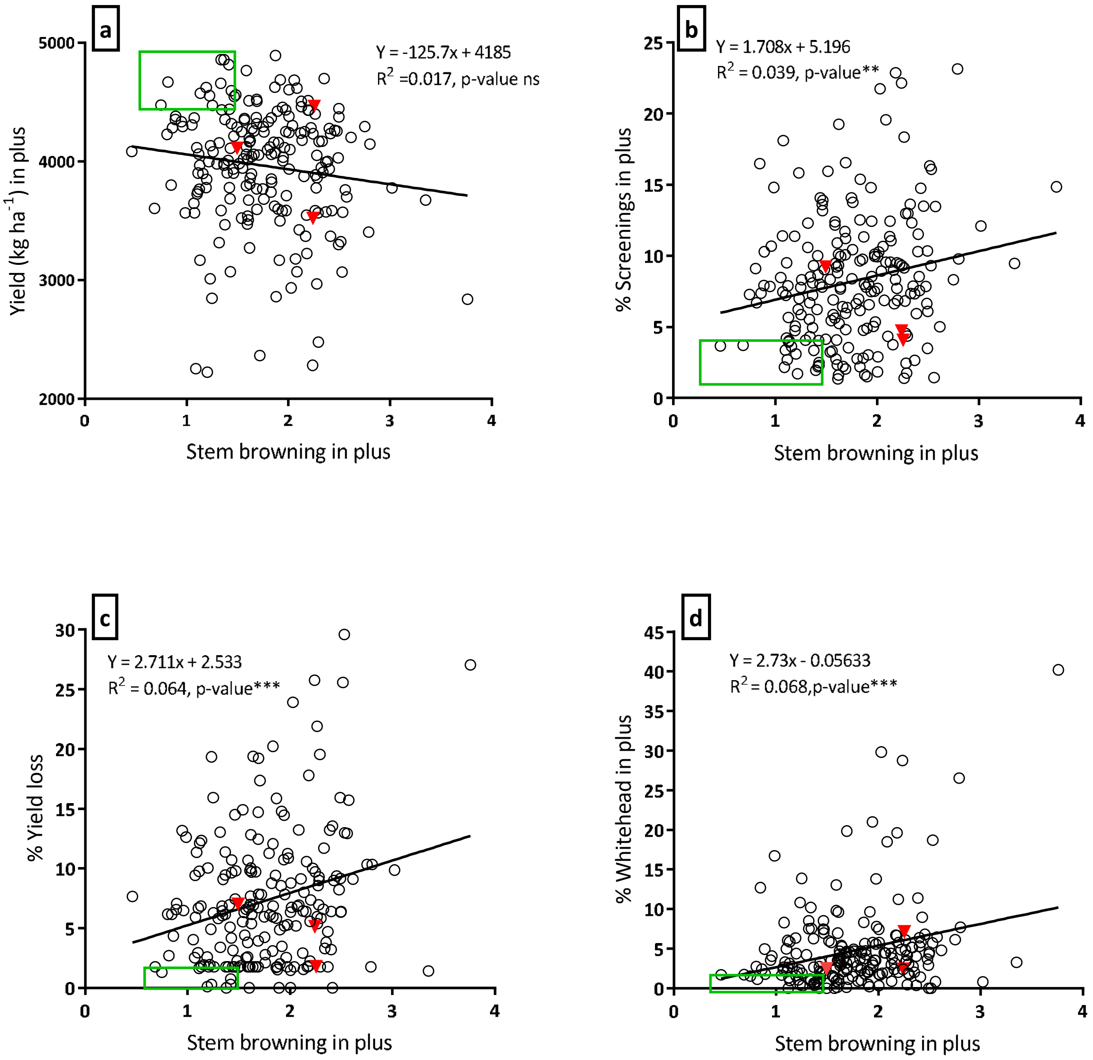


Fig. 5.8: Relationships of disease severity (stem browning obtained from 0-4 scale) with mean a) grain yield (r = -0.129, p = ns), b) percent screenings (r = 0.197, p = <0.01), c) percent yield loss (r = 0.252, p = <0.001) and d) percent white head formation (r = 0.262, p = <0.001) under crown rot inoculum in 2014. The green rectangles indicate genotypes with (a) higher grain yield (b) lower screenings (c) lower yield loss (d) lower disease severity compared to one of the best parents under crown rot severity.

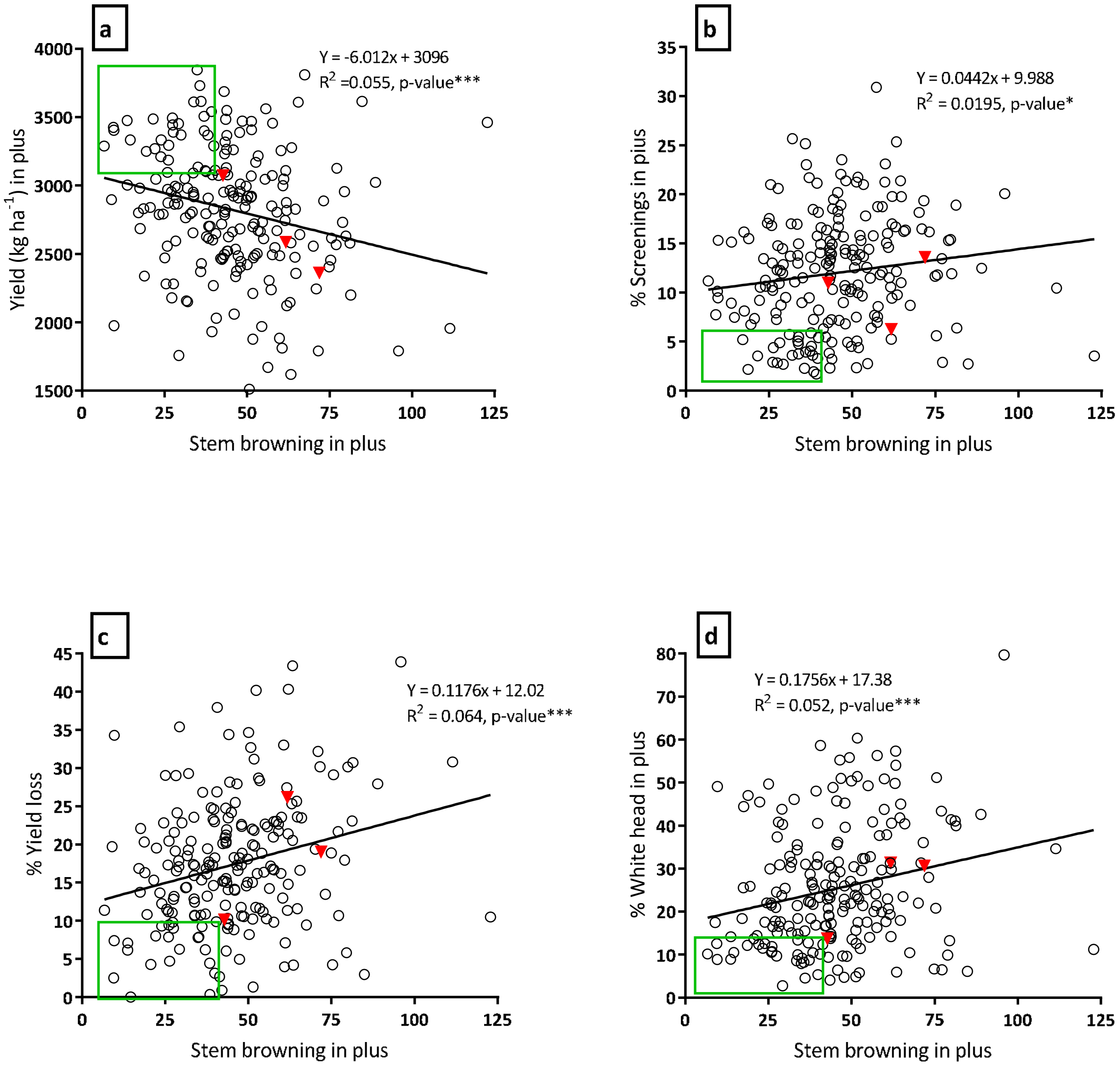


Fig. 5.9: Relationships of disease severity/stem browning (based on infection length) with a) Grain yield (r = -0.234, p = <0.01); b) Percent screenings (r = 0.140, p = <0.05) c) Percent yield loss (r = 0.241, p = <0.001) and d) Percent white head(r = 0.229, p = <0.001) for crown rot in 2015. The green rectangles indicate genotypes with (a) higher grain yield and lower disease severity (b) lower disease severity- % white head and stem browning (c) lower screenings and lower disease severity (d) lower yield loss and stem browning compared to one of the best parents under crown rot severity.

Significant positive relationships were observed between stem browning and % screenings (r = 0.197; p<0.01 and r = 0.140; p<0.05), % yield loss (r = 0.252; p<0.001 and r = 0.253; p<0.001) and % WH (r = 0.262; p<0.001 and r = 0.229; p<0.001) for both 2014 and 2015, respectively (Figures 5.7 and 5.8). Stem browning in the inoculated treatment accounted for 4% of screenings, 6.4% of yield loss and 6.8% of WH in 2014 (Figures 5.8b, c and d). Stem browning also accounted for 1.2% of screenings, 6.4% of yield losses and 5.2% of variation in % WH in 2014 (Figure 5.9b, c and d).

Table 5.6: Comparisons of parents and selected progeny for yield, % yield loss, % screenings, % white heads incidence and stem browning during 2014 and 2015

Genotype	GY (kg ha^{-1})	% yield loss	% screenings	% WH	WSB (0-4 scale/length)
Year 2014					
26	4062	12.11	2.69	0.00	1.11
31	4084	7.64	3.66	1.70	0.46
36	4474	1.31	7.28	1.50	0.74
44	4472	1.91	6.27	5.85	1.25
54	3780	0.75	2.18	0.00	1.42
64	4667	2.70	6.70	1.22	0.81
72	4622	0.10	4.73	1.60	1.19
74	4554	4.91	6.20	2.35	1.22
89	4574	12.33	4.03	1.00	1.13
92	4603	1.48	9.94	1.78	2.00
110	4764	1.77	5.61	0.87	1.58
146	4816	5.08	9.98	1.30	1.41
177	4656	6.48	5.51	1.16	1.33
181	4596	1.92	8.00	1.77	1.43
AUS29529	3519	5.134	4.72	2.41	2.24
Sunco/Pastor	4464	1.778	4.06	7.14	2.26
Syn110	4110	7.014	9.26	2.46	1.41
SED	431.10	6.03	2.99	5.86	0.67
Year 2015					
12	3731	10.74	2.26	8.24	35.66
15	2933	10.63	3.73	18.37	33.84
22	3615	9.23	3.93	4.56	36.06
26	3687	12.03	3.81	9.38	43.05
28	3475	6.18	8.91	8.92	13.65
29	3845	7.79	8.94	7.93	34.85
31	3443	12.82	2.84	9.68	27.47
51	3426	2.53	10.12	12.57	9.48
58	2972	7.89	13.00	10.53	25.98
75	3612	10.75	5.45	13.36	33.84
89	3334	9.31	10.65	17.54	23.94
103	3185	9.45	2.89	10.75	26.11
151	3404	7.40	9.45	8.87	9.60
153	3294	4.71	4.38	16.52	26.28
155	3269	8.01	9.19	12.37	22.10
159	3613	12.44	4.76	9.98	33.83
AUS29529	2586	26.16	6.23	31.30	61.71
Sunco/Pastor	3074	10.11	10.95	13.65	42.73
Syn110	2361	19.00	13.56	30.62	71.88
SED	328.4	8.80	3.53	9.34	5.59

Note: GY = Grain yield (Kg ha^{-1}); % yield loss= Percent yield loss; % screenings = Percent screenings; % WH = Percent white head; WSB= Weighted stem browning; SED= Standard error of difference.

Some of the lines marked with green rectangles in Figures 5.8 and 5.9 showed better performance than any of their parents in both years. Comparisons between parents and their best performing progeny under crown rot inoculum for yield, % yield loss, % screenings, % WH and WSB during 2014 and 2015 are presented in Table 5.6. In 2014, the genotypes 36, 72, and 181 were identified as resistant and tolerant and these lines showed higher grain yield (4474 - 4622 kg ha^{-1}) lower % WH (1.5 - 1.9%), lower WSB (0.75 – 1.19) and reduced % yield loss (0.1 – 1.77%) compared to best performing parents. Entry 89 was also identified as resistant and tolerant and this line had high yield, low % WH, low % yield loss and low WSB as compared to its parents. Genotypes 44, 64, 74, 146 and 177 produced higher grain yield with lower disease severity and genotypes 92 and 110 gave higher grain yield and lower % WH and % yield loss compared to their parents. Genotypes 26 and 31 had lower % WH, % screenings and WSB than their parents. In 2015, entries 12, 22, 28, 29, 31, 51, 68, 75, 89, 103, 151, 153, 155 and 159, were considered to be resistant and tolerant, with higher grain yield (3185 – 3845 Kg ha^{-1}), lower % WH incidence (4.56 – 18.37%), lower WSB (9.48 – 41.33), lower % screenings (2.26 – 10.65%) and reduced % yield loss (0-12.82%) compared to their parents (Table 5.6).

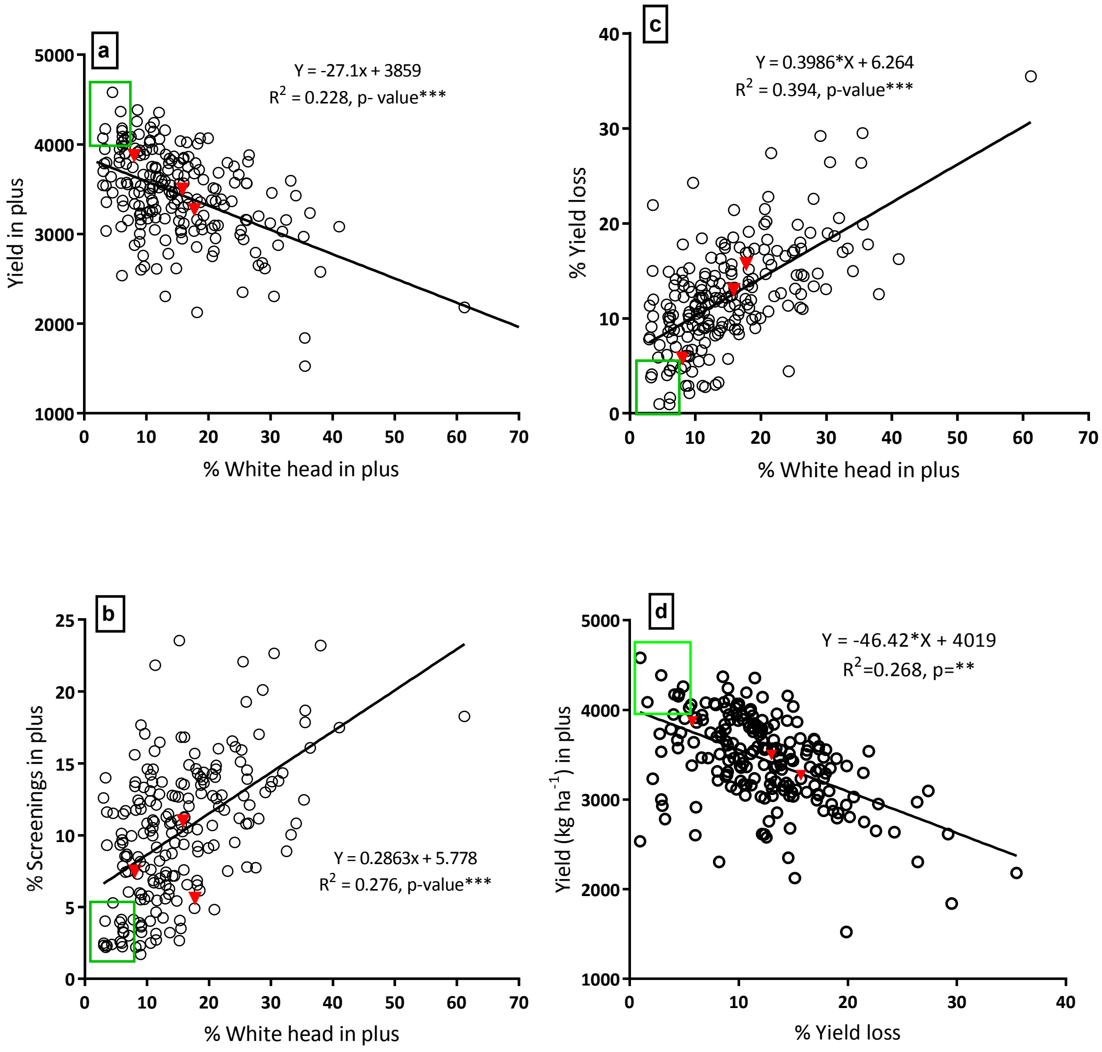


Fig. 5.10: Relationships between disease severity assessed as white heads in the inoculated treatment and a) grain yield (r = 0.478, p = <0.001); b) percent screenings (r = 0.525, p = <0.001); c) percent yield loss (r = 0.630, p = <0.001) and d) relationship between % yield loss and yield (r=0.268, p=<0.001). The green rectangles indicate genotypes that had (a) higher average grain yield and lower disease severity, (b) lower screenings and lower disease severity, (c) lower yield loss and lower disease severity and d) lower % yield loss and higher grain yield compared to at least one of the best parents.

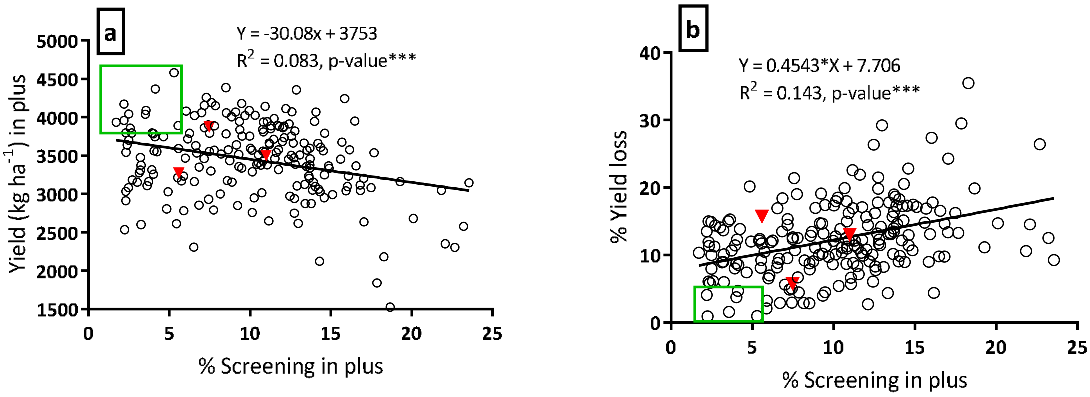


Fig. 5.11: Relationships of percentage screenings under inoculation with a) grain yield (r = -0.288, p = <0.001) in plus; b) percent yield loss (r = 0.391, p = <0.001) averaged over two years, 2014-15. The green rectangles indicate genotypes with (a) higher grain yield and lower screenings (b) lower screenings compared to one of the best parents under crown rot severity.

Genotypes 44, 64, 74, 146 and 177 also had higher grain yield, lower % WH and WSB than their parents. Lower % WH, % screenings and WSB were observed in genotypes 26 and 31 compared to their parents. Correlation coefficients, based on two years of experiments, showed that yield loss was highly positively correlated (r = 0.630, p = <0.001) with % WH (Figure 5.10c). Percentage WH also had a moderate effect on grain yield, seed size and the extent of yield loss (Figures 5.10a, b and c). Percentage yield loss was negatively correlated with grain yield and accounted for 26.8% of total variation in grain yield (Figure 5.10d). Percentage white heads accounted for 22.2%, 27.6% and 39.4% of the total variation in grain yield, % screenings and % yield loss, respectively. Percentage screenings also reduced yield and explained 8.3% of the variation in yield under crown rot pressure (Figure 5.11a). It was also observed that in addition to yield reduction, % screenings increased the total % yield loss. Percentage yield loss also explained 14.1% of the variation in % screenings (Figure 5.11b).

5.4 Discussion

This chapter showed that genetic variation for crown rot tolerance and resistance exists in this wheat population and that these traits improve yield in the presence of crown rot. Genotypic variation for grain yield (kg ha^{-1}) and components of crown rot tolerance/resistance such as TKW, screenings, NDVI, HD, PMD, PH, white head incidence and WSB were observed and are sufficient to exploit in breeding and selection. Shrivelled grain or reduced grain size and weight, % WH and WSB significantly reduced wheat grain in the presence of crown rot disease. Others also reported similar finding in wheat (Burgess *et al.*, 1996; Davies, 2016; Brennan and Murray, 1988). The inoculated environment was observed to suppress grain yield by reducing grain weight and size, decreasing PH and increasing the incidence of % WH. Smiley and Yan (2009) also observed similar reductions in spring wheat yield under crown rot pressure. Clearly, crown rot infection exacerbates WH incidence and stem browning resulting in higher yield loss. This yield loss is also a function of reduced phenotypic values of key yield components such as grain weight and screenings. However, little relationship between crown rot tolerance and resistance was observed. Tolerance is defined as the ability of a genotype to maintain yield under disease conditions (Bingham *et al.*, 2009). Therefore, those genotypes in the current study with lower yield loss calculated from inoculated and un-inoculated paired plots were considered to be crown rot tolerant. The observed mean yield loss ranged from around 1% to 36% (with an average 12.3 ± 0.38% across years), and clearly those genotypes with 5% or lower yield loss were tolerant to the disease. The higher yield loss in 2015 was a function of warmer, drier grain-filling conditions which were more conducive to disease development compared to 2014. Percentage screenings varied from 1.71% to 23.55% (with an average 10.16 ± 0.33) indicating significant variation for the trait with those less than 4% considered tolerant (based on the performance of check cultivars). As expected, the higher screenings observed in 2015 was a function of the more stressed grain-filling environment in that year. Daniel and Simpfendorfer (2008) reported yield losses of 25%, 20% and 58% due to crown rot infection in bread wheat, barley and durum, respectively, and % screenings of 11-15% in wheat and 7-21% in durum. However, while the yield losses might be higher in the Daniel and Simpfendorfer (2008) study, these are to some extent overestimated as they used separate inoculated and un-inoculated blocks rather than more precise paired plots to assess yield loss. Nevertheless, both the current study and the Daniel and Simpfendorfer (2008) study show that economic losses due to crown rot can be significant.

Direct selection for yield loss is effective. However, the estimation of yield loss is expensive and can only be performed when fixed lines with sufficient seed are identified. Indirect selection for QTLs or related traits with higher heritability and favourable correlation with yield under crown rot stress would improve the efficiency of breeding. Moreover, any association between traits can assist the definition of selection criteria in plant breeding. In the current study, the significant positive correlation between yield loss with white head incidence and screenings, and negative correlation with grain yield are an example. White head incidence and screenings were the major contributors to variation in yield loss (39.4% and 14.3%, respectively) and these traits are relatively easy to measure if good crown rot infection is achieved. The percentage of whiteheads also a showed strong positive association with the amount of screenings (with screenings explaining 27.6% of the variation in white heads alone); however this association becomes more robust when TKW is included (Table 5.5). Thus, a combination of white head incidence, screenings and kernel weight can be used to select for yield response under crown rot pressure. These observations support the findings of Klein *et al.* (1991) who found that white head incidence was directly associated with grain yield loss through reduced grain size. Since white head incidence is often affected by post-anthesis drought and other related factors (Brennan and Murray, 1988), estimation of reduction in grain yield and screenings based only on white head incidence would be imprudent (Hollaway *et al.*, 2013). The difference in crown rot expression between 2014 and 2015, as discussed earlier, highlights this risk. Other studies also show that while moist soil during plant establishment enhances plant infection, post-anthesis water stress favours white head incidence in the field (Swan *et al.*, 2000; Hollaway and Exell, 2010). However, genotype-by-environment interaction and the heritability of associated traits will influence the expression of tolerance and resistance. The medium to high heritability (0.46 – 0.79) observed for traits such as TKW, screenings and white head incidence under inoculation indicate that these traits would be effective targets for selection to improve yield under crown rot. The expected selection response of these traits was higher or equivalent in the inoculated treatment to the un-inoculated treatment indicating that their selection would also improve yield potential.

Stem browning was suggested to be a more reliable indicator of crown rot severity than white head incidence in the field (Dodman and Wildermuth, 1987). Stem browning is quantified by assessing the degree of honey-brown discoloration on the lower stem and crown. The more dense the discoloration on the lower stem the greater the crown rot susceptibility (Liu and Ogbonnaya, 2015). However, measurement of stem browning is very laborious and time-consuming and the degree of stem browning varies between years and environments (Smiley and Yan, 2009). This is further complicated by the quantitative nature of the inheritance of crown rot resistance (Li *et al.*, 2010). This study assessed more than 45 thousand tillers of more than 10 thousand plants across years to demonstrate that genetic variation for resistance existed among the tested genotypes. Genotypic variation for stem browning within each population was significant and sufficient to exploit in breeding and selection. However, basal stem browning was very inconsistent and highly influenced by environment and shown to have little influence on grain yield under crown rot pressure. Nevertheless, some genotypes (Entries 54, 68, 72, 89 and 116) showed consistently lower disease severity in both years compared to the best check Sunco and parents (based on disease severity across years). These genotypes could be targeted in breeding and selection.

The minor observed relationship between the degree of basal stem browning and white head incidence, screenings and yield loss suggests that this trait is not an effective target for selection for tolerance, or yield traits more generally, particularly given the time consuming and expensive process of its evaluation. However, the measurement of whiteheads, grain size and screenings may provide a more effective measure of tolerance. White heads had a moderate effect on grain yield screenings and yield loss and are also an important component of crown rot tolerance. In contrast to this study, a positive association between the degree of basal stem browning and yield loss, white head incidence, reduced grain and test weight were reported by Smiley *et al.* (2005). The current study also found a negative association between plant height and stem browning, indicating that taller genotypes had higher resistance or lower crown rot severity. Similarly, two separate studies also reported that taller plants (lacking semi dwarf gene *Rht1*) showed better resistance to crown rot incidence (Collard *et al.*, 2005; Wallwork *et al.*, 2004). However, the genotypes in the current study were all semi-dwarf, thus minor variation in plant height (attributable to modifier genes present in semi-dwarf germplasm) can influence crown rot severity among semi-dwarf materials.

5.5 Conclusion

This chapter demonstrated that genetic variation for resistance and tolerance to crown rot existed in the materials evaluated. Some genotypes were consistent in their response to crown rot infection across years (such as entries 31 ad 89) and these could be used as parents to develop new crown rot resistant and tolerant cultivars. A very weak relationship between yield loss and basal stem browning was observed indicating that selection for this trait is ineffective for the selection of yield under crown rot pressure. Yield loss, white head incidence and screenings however were found to be important traits that can be targeted to improve crown rot tolerance in bread wheat.

CHAPTER 6

Genetic control of crown rot tolerance and resistance in a MARS population (population 3)

6.1 Introduction

Breeding for resistance and tolerance to crown rot is one avenue to improve sustainable wheat production and productivity in areas where this disease causes severe yield losses. The inheritance of crown rot resistance is quantitative and the trait is controlled by many minor genes and QTLs that are highly affected by the environment (Kazan and Gardiner, 2017; Collard *et al.*, 2005; Collard *et al.*, 2006; Ma *et al.*, 2010; Martin *et al.*, 2015). Partial resistance to crown rot has been identified in a range of wheat materials (Kazan and Gardiner, 2017). Clearly, the identification of different genomic regions linked to both crown rot resistance and tolerance would improve the effectiveness of breeding and selection and the performance of cultivars under disease pressure. Quantitative trait loci (QTL) linked to disease resistance have been identified in various crops (Pasam and Sharma, 2014) including crown rot resistance in wheat (Liu and Ogbonnaya, 2015). Until recently, the majority of QTL mapping studies were based on linkage analysis using traditional recombinant inbreed lines and/or doubled haploid populations targeting a small fraction of the natural variation (Rakshit *et al.*, 2012).

Genome wide association studies (GWAS), also referred to as association mapping or linkage disequilibrium mapping (LD), allow a large portion of the natural variation to be evaluated thus expanding the search for QTL linked to complex traits. Large numbers of genotypes are phenotyped and genotyped and marker-trait associations (MTAs) determined (Crossa *et al.*, 2007; Pasam *et al.*, 2012; Huang and Han, 2014; Mwadzingeni *et al.*, 2017). However, many of these MTAs are false positives and validation is required in other materials before they can be effectively targeted in breeding. Recent reductions in the cost of genotyping including sequencing technologies and improvements in data processing have led to increased GWAS application in crop breeding (Pasam and Sharma, 2014). The high density 90K SNP array in wheat has been used to characterize a wide array of hexaploid cultivars including landraces and to implement GWAS (Wang *et al.*, 2014; Cavanagh *et al.*, 2013; Sukumaran *et al.*, 2015; Ain *et al.*, 2015).

Genome-wide association analysis had been successfully used to study complex traits in maize, wheat, rice, barley, sorghum, soybean, sugarcane, potato, grape, forage grasses and fruit trees (Abdurakhmonov and Abdukarimov, 2008; Mohammadi *et al.*, 2015; Huang and Han, 2014; Hwang *et al.*, 2014; Neumann *et al.*, 2011). This strategy has also been used to identify QTL in wheat for globally important diseases such as stripe rust (*Puccinia striiformis* f. sp. *tritici*), leaf rust (*Puccinia triticina*) and stem rust (*Puccinia graminis* f. sp. *tritici*) (Yu *et al.*, 2012; Neumann *et al.*, 2011; Bovill *et al.*, 2010; Crossa *et al.*, 2007). While the genetic control of some cereal diseases such as rust is relatively well understood, the genetic control of crown rot resistance and tolerance is not well known. As with all complex traits, the effectiveness of GWAS is restricted by accurate, effective and relevant phenotyping methods that can be applied to large populations (Chen *et al.*, 2017). GWAS requires accurate phenotypes on a large number of genetically diverse genotypes, generally more than 100, that represent the diversity of the breeding population (Huang and Han, 2014; Pasam and Sharma, 2014).

However, the identification of reliable SNP markers linked to alleles and QTLs associated with resistance and tolerance to crown rot using GWAS has never previously been attempted. A population of 196 progeny derived from a top cross of 3 parental lines; AUS29529, Sunco/Pastor and Syn110 (descried in Chapter 3 Section 3.2), and eight check cultivars were evaluated for yield and key agronomic traits in crown rot inoculated and un-inoculated paired plots. The traits evaluated, apart from stem browning, were chosen because of their moderate to high heritability estimated in Chapter 5. The objectives of this chapter were therefore to: i) identify marker-trait associations and QTLs that explain crown rot resistance and tolerance in a MARS population, ii) establish the genetic relationship if any between resistance and tolerance and iii) identify parents among the base population for recombination in an on-going MARS strategy.

Nevertheless, it should be clarified that while a GWAS analysis was used, the experimental materials were not traditional GWAS populations of unrelated fixed lines. Instead they represented populations derived from three-way crosses that were analysed using a GWAS approach.

6.2 Materials and Methods

6.2.1 Germplasm

A total of 196 progeny from population 3, as described in Chapter 3, Section 3.2, parental material and eight check cultivars were included in the association mapping study. The line name and pedigree information of this experimental material are presented in Appendix III, Table 5 and Chapter 3, Table 3.1. A summary of the numbers of genotypes tested and the traits evaluated is presented in Table 6.1.

Table 6.1: Number of genotypes and traits evaluated each year using GWAS.

Traits	**Year/ Genotype number**	
	2014	**2015**
Normalized difference vegetation index (NDVI)	206	207
Plant height	206	207
Heading days	206	207
Physiological maturity days	206	207
Thousand kernel weight	206	207
Grain yield	206	207
Percent (%) screenings	206	207
Percent (%) white heads	206	207
Weighted stem browning	206	207
Percent (%) yield loss	206	207

6.2.2 DNA extraction, SNP genotyping and KASP marker development

DNA of all 207 lines was extracted in the molecular laboratories at the Plant Breeding Institute, Cobbitty following the modified CTAB method described by Doyle *et al.* (1990). Detailed description of the DNA extraction methodology can be found in Chapter 3, Section 3.3.1.

The DNA of 207 genotypes was genotyped using the Infinium iSelect 90K SNP Assay (Wang *et al.*, 2014), following the protocol recommended by the manufacturer. Approximately 45k SNPs were successfully called in this population. Quality control filtered out SNPs with high missing values and MAF (minor allele frequency) < 0.05. This resulted in a final set of 23367 polymorphic SNPs.

Once progeny carrying significant marker-trait associations were identified for recombination from the GWAS, Kompetitive allele-specific primers (KASP) were developed for key SNP markers to facilitate the selection of progeny. The KASP primers were designed with 101 bp sequence for elucidation the SNPs of interest that ultimately used to develop three primers, two allele specific A1 and A2 primers and a common reverse (C) primer. The molecular configurations of the developed primers and PCR amplification are described in Chapter 3, section 3.8.

6.2.3 Experimental design

Experiments were established as paired row plots, planted with and without crown rot (*F. pseudograminearum*) inoculum in 2014 and 2015 seasons. The experiments were arranged in augmented partially replicated design in 2014 and fully replicated design in 2015. Details are described in Chapter 5.

6.2.4 Phenotyping

The traits phenotyped in the population and used in GWAS are presented in Table 6.2.

Table 6.2: Traits recorded from two years of experiments under inoculated (plus) and un-inoculated conditions and used in GWAS.

Traits		**Year**	
	Unit/ Scale	**2014**	**2015**
Normalized difference vegetation index (NDVI)	NDVI	X[1]	X
Plant height	cm	X	X
Heading days	Days	X	X
Physiological maturity days	Days	X	X
Thousand kernel weight	g	X	X
Grain yield	Kg ha^{-1}	X	X
Screenings	%	X	X
White head	%	X	X
Stem browning	mm	X	X

Yield loss	%	X	X

[1]X indicates that the trait was assessed

6.2.5 Statistical Analysis

6.2.5.1 Phenotypic data analysis

All plot weights were converted into yield in kg ha^{-1} and both un-inoculated and inoculated plots were considered for analysis. The effect of disease on each trait was calculated by estimating the percentage change between un-inoculated (Nil) and inoculated (Plus) plot means. Thus trait response or change (%) = $(M_{\text{un-inoculated}} – M_{\text{treatment}})/ M_{\text{un-inoculated}})*100$; where M= the plot weight. Negative values were set to zero. A total of 207 genotypes that had both phenotypic and genotypic data were analysed. A two-stage analysis was performed. In the first stage, years were analysed independently and best linear unbiased estimators (BLUES) were calculated using genotypes and inoculation treatments as fixed effects and replications within inoculation blocks within rows and plots as random terms in a spatial model. In the second stage, years were combined to estimate overall final BLUES.

6.2.5.2 GWAS analysis

A mixed linear model with kinship matrix and principal components to account for population relatedness was used for the GWA analysis. All the analysis was done using R-package GAPIT Following filtering of the SNP data, phenotype and SNP map files were produced for GWAS analyses. These analyses were performed using the genome-wide complex analysis (GCTA) software (http://cnsgenomics.com/software/gcta/) following the procedure of Yang *et al.* (2011). The model fitted the overall mean (mu) and fixed SNP effects along with the genomic relationship matrix (GRM) to account for population structure in the sample. The model fitted and used to explain population structure is given below:

Y= mu + SNP + random (GRM)

Where y represents population structure in the sample (n1 vector of phenotypes with n being the sample size), mu denotes the overall mean, SNP is the fixed SNP effect and GRM the genomic relationship matrix.

The false discovery rate was p >0.999673 and some traits did not cross this stringent threshold. Therefore, following the linkage disequilibrium analysis only those marker/trait associations with a -$\log_{10}$ P value > 3 ($p<0.001$) were considered significant. The SNP markers used in this study segregated only within the population studied and not all markers are unique to one position. The physical map positions in cM were determined where possible based on anchoring and ordering of next generation sequencing contig assemblies by population sequencing (PopSeq) (Mascher *et al.*, 2013) and the Wang et al (2014) consensus map. Positions in cM were available only for markers that: (i) had a physical position, (ii) were uniquely mapped within a chromosome, and (iii) were segregating in the population. The selected markers therefore had -$\log_{10}$ P>3, either a positive or negative effect on the trait (Appendix IV, Table 1) and where relevant a pleiotropic effect. Chromosomes 1 to 21 as displayed in the Manhattan plots were arranged as 1-7 (1A-7A), 8-14 (1B-7B), and 15-21 (1D-7D). Following the GWAS analysis, Manhattan plots representing $\log_{10}$ (p) values for each SNP association with the trait on the y-axis and the genetic positions on the x-axis were constructed. Unmapped SNPs were assigned to chromosome 22 in each Manhattan plot.

6.3 Results

6.3.1 Marker-trait associations of traits evaluated under crown rot inoculation

A total of 1152 marker trait associations (MTAs) were observed across all traits that were greater than $-\log_{10}$ (p) 3 (Table 6.3). However, when analyzed by year the significant MTAs were 383 in 2014 and 364 in 2015. The MTAs for each trait varied with the highest number detected across all years and inoculation treatments for PMD (428) followed by HD (371), TKW (248), yield (185), % screenings (74), % WH (28) and WSB (5). The A genome had most of the significant MTAs (510) followed by the B genome (456) and D genome (183) (Appendix IV, Table 1) across treatments and years. The highest number of MTAs were identified on chromosomes 5A (427), 2B (272), 5D (114) and 4B (92) and the lowest on chromosomes 6D (1), 7D (2), 4D (5) and 4A (6) (Tables 6.5, 6.6 and 6.7; Appendix IV, Table 1). The significant MTAs from the GWAS are shown in Manhattan plots (Figures 6.1 – 6.5).

Table 6.3: The number of significant marker-trait associations identified for each trait in the inoculated treatment in 2014, 2015 and across both years.

	Year			
Traits[1]	**2014**	**2015**	**Combined**	**Total**
Yield	4	39	142	185
TKW	80	55	113	248
% WH	-	28	-	28
WSB	1	4	-	5
% Screenings	21	35	18	74
PH	20	11	5	36
HD	121	82	168	371
PMD	125	107	196	428
NDVI	11	3	9	23
Total	383	364	651	1398

[1] Yield, TKW, %WH, WSB, PH, HD, PMD and NDVI are Grain yield (Kg ha^{-1}), thousand kernel weight (g), percent white heads, weighted stem browning, plant height (cm), heading days, physiological maturity days and normalized difference vegetation index, respectively.

6.3.2 Marker-trait associations for resistance and tolerance traits

One hundred and forty two markers were significantly associated with grain yield in the inoculated treatment across years (Table 6.3). These significant markers were found on all genomes with the majority located on chromosomes 4B, 3D and 5D (Figure 6.1). These markers individually explained 5.26-11.43 % of the variation in the trait (Appendix IV, Table 1). Fifty-two markers located on chromosomes 2A, 2B, 3B, 3D, 4B, 5D, 6A, 6B and 7B had a significant positive impact on grain yield while others were associated with reduced grain yield under inoculation across years (Appendix IV, Table 1). In total, 229 MTAs were detected for grain yield representing different chromosomal regions in both treatments across the two years (Appendix IV, Table 1) of which fifty-six markers were consistent under both inoculated (plus) and un-inoculated (nil) conditions. Some of these markers were pleiotropic and linked to crown rot tolerance QTLs (based on reduced yield loss in the presence of crown rot) and other traits (Tables 6.6 and 6.7). The majority of these pleiotropic loci were located on chromosome 5D (14).

A total of 248 MTAs were detected for TKW in each year and combined across years in the presence of crown root inoculum (Table 6.3). Two-hundred and twenty eight MTAs were detected for TKW in both treatments across both years of which ninety-four markers were consistent under inoculated (plus) and un-inoculated (nil) conditions (Appendix IV, Table 1). Seventy-two markers had a pleiotropic effect across both treatments and five in the inoculated treatment only (Table 6.5 - 6.7). The greatest numbers of MTAs for TKW were observed on chromosomes 1A (5), 3A (8), 5A (190) and 5D (8) in both treatments. In the presence of crown rot 113 MTAs were observed across years (Table 6.3). These MTAs were detected on all genomes with the majority located on chromosome 5A (Figure 6.1). These markers individually explained 3.15-6.73 % of the variation in the trait (Appendix IV, Table 1).

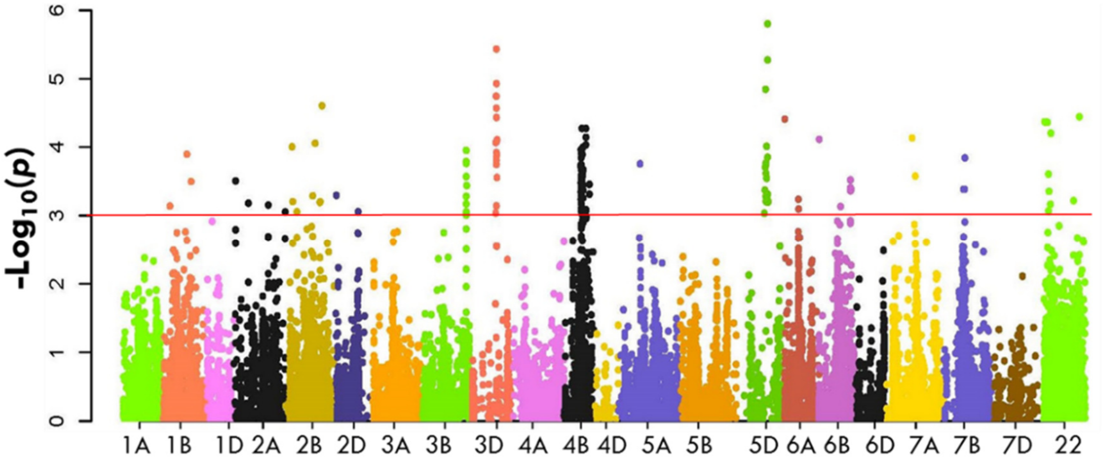


Fig. 6.1: Manhattan plot of grain yield with inoculation. The minimum threshold considered for significance is 3 (P-value=0.001).

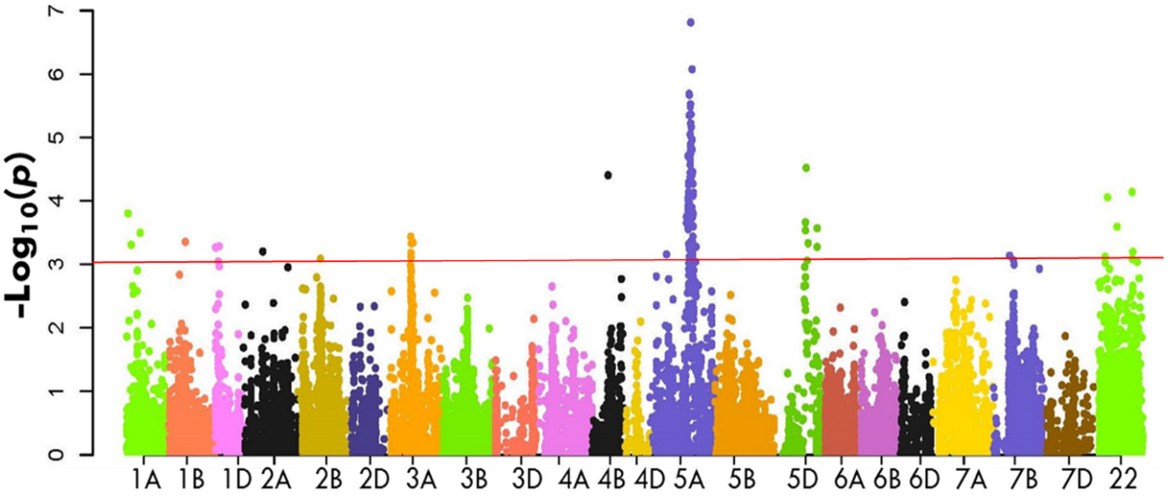


Fig. 6.2: Manhattan plot of TKW with inoculation. The minimum threshold considered for significance is 3 (P-value=0.001).

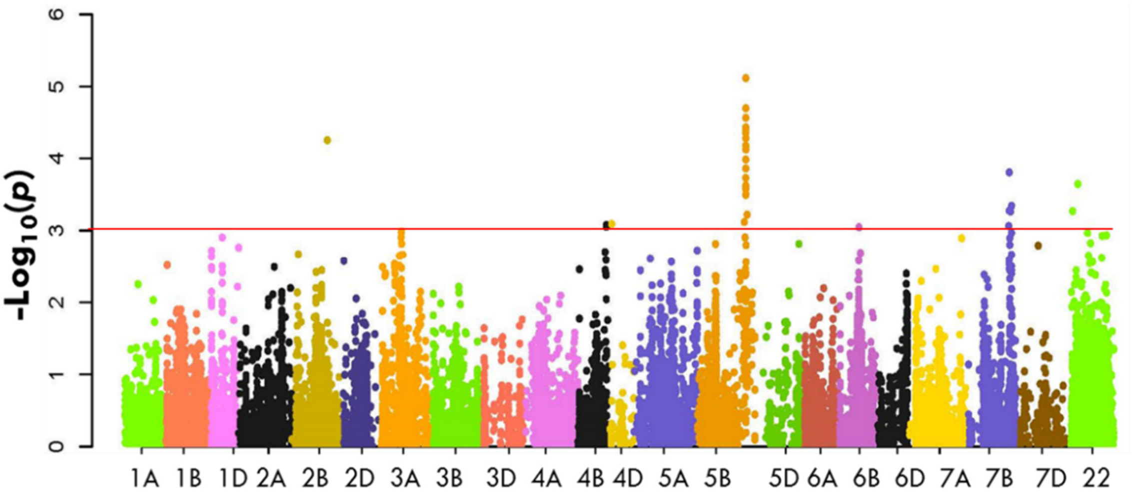


Fig. 6.3: Manhattan plot of % white heads with inoculation. The minimum threshold considered for significance is 3 (P-value=0.001).

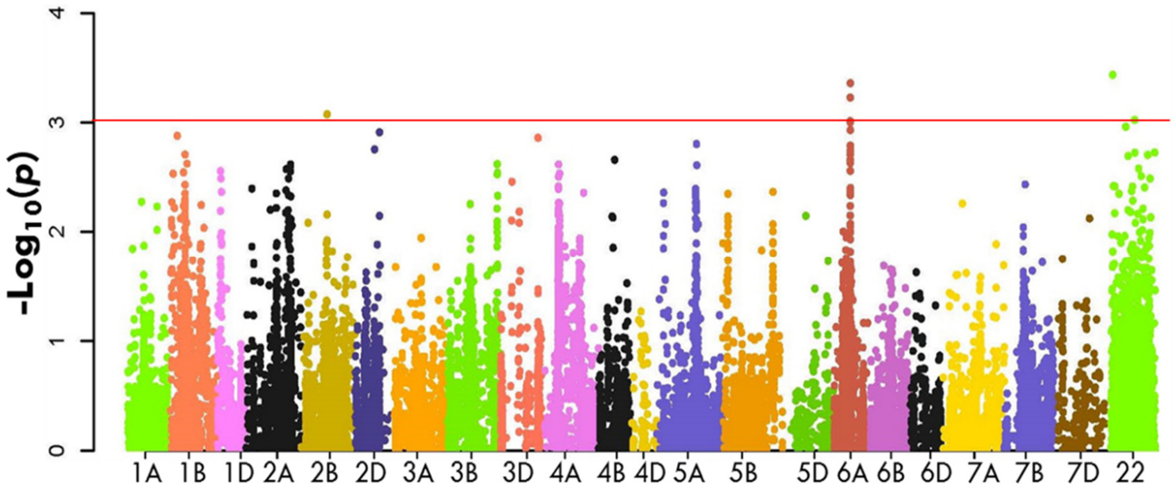


Fig. 6.4: Manhattan plot of stem browning with inoculation. The minimum threshold considered for significance is 3 (P-value=0.001).

Twenty-eight MTAs were found to be significantly associated with % WH under inoculation in 2015, whereas none were observed in 2014 (Table 6.3). Chromosomes 2B, 4B, 4D, 5B, 6B and 7B were associated with % WH with the highest number of MTAs located on chromosome 5B (19) (Table 6.4; Figure 6.3). Each marker explained between 5.06-9.42 % of the variation in the trait (Appendix IV, Table 1). Markers on chromosomes 4B (2), 4D (1) 5B (4), 6B (1) and 7B (4) had a negative effect on white head formation (Appendix IV, Table 1). Seventy-four MTAs were detected for % screenings under inoculation. Twenty-one MTAs were unique to 2014 and 35 to 2015 (Table 6.3). Twenty-one markers were identified on chromosomes 1A, 1B, 2A, 3A, 3B, 5A and 7B with the majority located on chromosomes 3A (7) and 5A (7) in both treatments (Appendix IV, Table 1; Figure 6.5). Markers individually explained between 3.20-4.97 % of the variation in screenings (Appendix IV, Table 1). Three markers (*RAC875_c744_1935, BobWhite_c30009_285* and *Excalibur_rep_c68583_689*) located on chromosomes 1A and 3A were pleiotropic with TKW in the inoculated treatment (Table 6.5). Six MTAs were unique to the inoculated treatment and had a negative effect. These were located on chromosomes 1A (1), 3A (3), 5A (1) and 7B (1) (Appendix IV, Table 1). Five MTAs were detected for WSB (weighted stem browning) under crown rot inoculation; one MTA was unique to 2014 and four to 2015 (Table 6.3). A combined analysis of WSB was not performed as different scoring methods of disease severity were used in each year

(Chapter 5, Figure 5.7). Three MTAs were located on chromosome 6A and two MTA on chromosome 2B (Table 6.4; Figure 6.4) in 2015. Individual markers explained between 5.96-6.81 % of the trait variation (Appendix IV, Table 1). These markers were all associated with reduced stem browning depending on the target allele (Table 6.4).

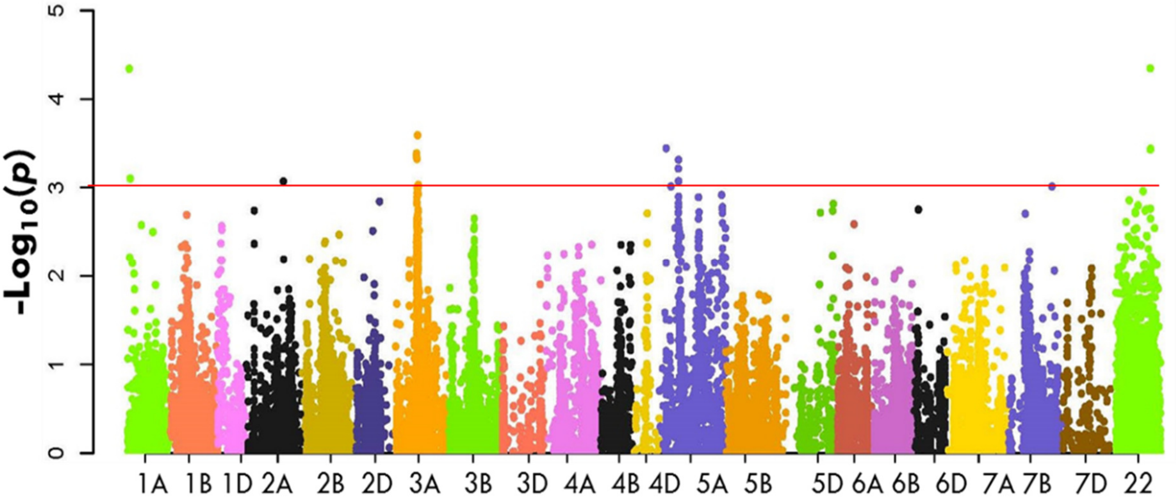


Fig. 6.5: Manhattan plot of % screenings with inoculation. The minimum threshold considered for significance is 3 (P-value=0.001).

6.3.3 Marker-trait associations for other traits

Forty-three MTAs were detected for plant height under crown rot inoculation. Twenty and 11 MTAs were detected for plant height in 2014 and 2015, respectively (Table 6.3). Three MTAs were unique to the inoculated treatment and 10 to the un-inoculated conditions across both years. However, only one MTA (*wsnp_Ex_rep_c107564_91144523*) was consistent in both treatments (Table 6.5-6.7). Individual markers explained between 2.98-5.39 % of the variation in the trait. Seven and 3 markers had a negative effect on plant height in un-inoculated and inoculated treatments, respectively (Appendix IV, Table 1). A total of 371 MTAs were observed for HD in the presence of crown rot (Table 6.3) and 85 MTAs were consistent across both treatments and years. Seventy-five MTAs were pleiotropic in both treatments. Twenty markers located on chromosome 5A had pleiotropic effects on HD, PMD and TKW in both treatments. Pleiotropic relationships were identified for HD, PMD and grain yield on chromosome 5D (15) in both treatments (Table 6.5-6.7). Four markers (*D_GB5Y7FA02IZ73U_152*, *D_contig62661_72*, *Ku_c19010_273* and *Ku_c6176_938*) which were significant in both treatments contributed to reduced height, early maturity and higher grain yield. Fourteen MTAs were pleiotropic for HD and grain yield (Appendix IV, Table 1).

These four SNPs, once validated, could be selected to reduce height, increase earliness and improve grain yield. A total of 428 MTAs were detected for PMD under inoculation in 2014, 2015 and combined across years (Table 6.3). Forty-three MTAs were consistent in both years (Appendix IV, Table 1). Twenty-one MTAs, the majority located on chromosome 5A, had significant effects on PMD and TKW in both treatments (Table 6.5-6.7). Forty-two MTAs were reported for NDVI (Table 6.4). Of these, 3 MTAs had a positive effect on NDVI and were unique to the un-inoculated treatment and four MTAs of positive effect were unique to the inoculated treatment across years (Appendix IV, Table 1).

6.3.4 The genetic relationship between resistance and tolerance

Significant MTAs with unique positions were sorted by chromosome for individual traits. These significantly associated markers linked to resistance and tolerance under inoculation across years, were grouped into forty-eight QTLs located on all genomes (Table 6.4). A total forty-five unique crown rot tolerance QTL were detected on chromosomes 1A (1), 1B (1), 1D (1) 2A (2), 2B (3), 2D (2), 3A (2), 3B (1), 3D (2), 4B (6), 4D (1), 5A (7), 5B (1), 5D (5), 6A (2), 6B (3), 7A (1) and 7B (4) with an R^2 that ranged from 3.19-11.43 % (Table 6.4). A haplotype block of nine markers on chromosome 3A, covering a genetic distance of 269.13 - 280.36 cM, was classified as a major tolerance QTL (QTL_13) with an increased TKW and reduced screenings. The tolerance QTLs_6, 15, 16, 17, 18, 19, 20, 21, 22, 33, 39 and 46 in a haplotype block of 2 SNPs (2B), 6 SNPs (3B), 11 SNPs (3D), 3 SNPs (3D), 22 SNPs (4B), 11 SNPs (4B), 5 SNPs (4B), 4 SNPs (4B), 2 SNPs (4B), 3 SNPs (5D), 5 SNPs (6A) and 2 SNPs (7B), respectively, were associated with increased yield under crown rot inoculation (Table 6.4). One large QTL (27, 28, 29, 30 and 31) located on chromosome 5A covering a genetic distance of 440.73-500.09 cM formed a major haplotype block controlling higher TKW under crown rot pressure. Another major QTL (34, 35 and 36) on chromosome 5D for TKW and grain yield was associated with crown rot tolerance. The marker *Kukri_c41787_141* had a increased (B allele) TKW and grain yield, explaining 3.56% and 5.62% of the variation in TKW and grain yield, respectively. The tolerance QTLs _14 and 25, located on chromosome 3A and 5A respectively, explained 3.2-3.6% of the phenotypic variation for % screenings. These QTLs reduced screenings. Among all the six SNPs, *RAC875_rep_c106044_137* showed the lowest trait value (A=8.64) with R^2 of 3.6%. The QTLs_23, 24, 32, 42, and 48 located on chromosomes

4B, 4D, 5B, 6B and 7B, respectively, reduced % WH and explained between 5.06-9.42% of the variation in the trait. QTL_9 was a haplotype block of three markers covering a genetic distance of 413.94-417.82 cM, and had a positive effect on grain yield and a large negative effect on % WH (Table 6.4). QTL_47 was a haplotype block of four markers covering 470.16-482.15 cM, and reduced both % WH and % screenings. These results helped explain the phenotypic variability for crown rot tolerance discussed in Chapter 5 (Figure 5.10, Table 5.4), where a positive correlation between % WH and % screenings and a negative association between % WH and grain yield was observed. QTL_5 tolerance on chromosome 2A was observed to influence both % screenings and grain yield (Table 6.4). This haplotype block of two SNPs (*RAC875_c64377_350* and *Kukri_rep_c76691_483*) was located at 413.64 cM. However, the marker *RAC875_c64377_350* was associated with increased yield (R^2 = 5.52%) while the SNP marker *Kukri_rep_c76691_483* was associated with reduced screenings (R^2 = 3.28%). A total of three unique QTLs (QTL_7, 8, and 40) associated with crown rot resistance were identified on chromosomes 2B (7 and 8) and 6A (40), respectively. QTLs_7, 8 and QTL_40 reduced stem browning on adult plants and were clearly associated with crown rot resistance. QTL_7 (marker; *Tdurum_contig83066_276*) explained 6.12% of the phenotypic variation in stem browning. QTL_40 (comprising the haplotype of two SNPs; *Ku_c21490_472* and *Ra_c8185_676*) was located at 188.89 cM and explained 5.96-6.49% of the variation for stem browning.

Table 6.4: GWAS results including QTLs identified that were linked to crown rot resistance and tolerance in a MARS population**.**

Traits	SNP	Chro	Target allele		Position	P-Value	-log10(p)	MAF	R^2 (%)	QTL	Ref
TKW	RAC875_c744_1935	1A	**A**=30.68	B=29.40	55.22	0.000157	3.80	0.368	4.17	QTL_1 Tol	(Martin *et al.*, 2015)
%Screenings	RAC875_c744_1935	1A	**A**=10.39	B=10.53	55.22	4.56E-05	4.34	0.368	4.97		(Collard *et al.*, 2005)
%Screenings	Tdurum_contig43475_978	1A	**A**=7.36	B=10.99	66.54	0.000791	3.10	0.440	3.32		
Yield	BS00067024_51	1B	**A**=2758	B=1736	306.49	0.000127	3.90	0.054	7.12	QTL_2 Tol	(Martin *et al.*, 2015)
TKW	BobWhite_c1715_887	1D	**A**=30.21	B=28.59	35.05	0.0009	3.05	0.495	3.19	QTL_3 Tol	
TKW	wsnp_CAP11_c8597_3709328	1D	A=28.79	**B**=30.87	45.36	0.00052	3.28	0.487	3.49		
Yield	Tdurum_contig56157_1595	2A	**A**=2752	B=2290	20.21	0.000313	3.51	0.060	6.27	QTL_4 Tol	(Martin *et al.*, 2015)
Yield	RAC875_c64377_350	2A	**A**=2713	B=2102	413.64	0.000704	3.15	0.065	5.52	QTL_5 Tol	
%Screenings	Kukri_rep_c76691_483	2A	**A**=9.07	B=12.40	413.64	0.00085	3.07	0.383	3.28		
Yield	Kukri_c3507_158	2B	**A**=2914	B=2668	78.23	9.92E-05	4.00	0.145	7.35	QTL_6 Tol	(Martin *et al.*, 2015)
Yield	Excalibur_c4748_360	2B	A=1688	**B**=2704	87.22	0.000628	3.20	0.057	5.62		
WSB	Tdurum_contig83066_276	2B	A=51.24	**B**=42.95	292.15	0.000843	3.07	0.425	6.12	QTL_7 Res	
WSB	Excalibur_c65830_82	2B	**A**=46.82	B=47.40	317.99	0.000671	3.17	0.500	6.2	QTL_8 Res	
Yield	Kukri_c29052	2B	**A**=2734	B=2381	413.94	0.000645	3.19	0.060	5.60	QTL_9 Tol	
Yield	GENE-0862_110	2B	A=2306	**B**=2745	417.82	0.00063	3.20	0.054	5.62		
%WH	Excalibur_c18966_1008	2B	**A**=24	B=31	417.82	5.59E-05	4.25	0.101	7.56		
Yield	BS00063589_51	2B	**A**=2713	B=2095	439.24	2.48E-05	4.60	0.070	8.69	QTL_10 Tol	
Yield	D_contig17313_245	2D	**A**=2766	B=2445	6.13	0.000508	3.29	0.098	5.82	QTL_11 Tol	
Yield	BobWhite_rep_c48966_570	2D	**A**=2686	B=1920	267.98	0.000882	3.05	0.148	5.31	QTL_12 Tol	
TKW	Excalibur_rep_c68583_689	3A	A=29.81	**B**=31.01	269.13	0.000368	3.43	0.207	3.69	QTL_13 Tol	(Martin *et al.*, 2015)
%Screenings	BobWhite_c30009_285	3A	**A**=9.92	B=10.41	269.13	0.000458	3.34	0.158	3.63		
%Screenings	Excalibur_c41477_1272	3A	**A**=9.97	B=10.18	269.13	0.000437	3.36	0.194	3.66		
Screening	Excalibur_rep_c68583_689	3A	A=10.38	**B**=8.90	269.13	0.000412	3.39	0.207	3.69		
TKW	Tdurum_contig93364_355	3A	A=29.76	**B**=30.18	271.98	0.000657	3.18	0.301	3.36		
TKW	BS00098840_51	3A	A=29.58	**B**=30.28	273.07	0.000776	3.11	0.326	3.27		
%Screenings	BobWhite_c35303_192	3A	**A**=9.81	B=11.12	273.07	0.000475	3.32	0.339	3.61		

TKW	wsnp_Ku_c44089_51445136	3A	**A**=30.31	B=29.44	274.44	0.000465	3.33	0.311	3.56		
%Screenings	Ku_c1638_648	3A	**A**=9.79	B=10.79	280.36	0.000257	3.59	0.275	3.96		
%Screenings	IAAV8768	3A	A=10.74	**B**=9.74	288.25	0.000932	3.03	0.334	3.23	QTL_14 Tol	
%Screenings	wsnp_Ex_rep_c69034_67934852	3A	A=10.57	**B**=9.52	288.43	0.000972	3.01	0.332	3.20		
Yield	RAC875_c17373_848	3B	**A**=2719	B=2462	539.26	0.000173	3.76	0.062	6.82	QTL_15 Tol	(Martin *et al.*, 2015)
Yield	RAC875_c23665_68	3B	**A**=2740	B=2688	539.26	0.00027	3.57	0.062	6.40		(Poole *et al.*, 2012)
Yield	RAC875_c35672_136	3B	A=2484	**B**=2731	539.26	0.000112	3.95	0.060	7.24		(Zheng *et al.*, 2014)
Yield	RAC875_c35672_73	3B	**A**=2713	B=2484	539.26	0.000163	3.79	0.057	6.88		(Ma *et al.*, 2010)
Yield	RAC875_c68392_137	3B	**A**=2708	B=2484	539.26	0.000163	3.79	0.057	6.88		
Yield	BS00011605_51	3B	A=2319	**B**=2755	545.17	0.000365	3.44	0.052	6.12		
Yield	RAC875_rep_c74926_682	3D	**A**=2729	B=2419	276.85	8.61E-05	4.07	0.054	7.49	QTL_16 Tol	
Yield	Kukri_c5252_107	3D	A=2456	**B**=2730	280.71	1.81E-05	4.74	0.052	9.00		
Yield	D_GBB4FNX02JKG8H_167	3D	A=2424	**B**=2719	283.69	0.000142	3.85	0.057	7.01		
Yield	CAP12_c470_361	3D	**A**=2732	B=2424	284.57	1.18E-05	4.93	0.060	9.42		
Yield	D_contig09222_937	3D	**A**=2716	B=2319	284.57	0.000179	3.75	0.060	6.79		
Yield	D_contig11810_446	3D	**A**=2732	B=2379	284.57	0.00012	3.92	0.062	7.17		
Yield	Excalibur_c40068_522	3D	A=2315	**B**=2743	284.57	3.70E-06	5.43	0.052	10.57		
Yield	Kukri_c17342_231	3D	**A**=2730	B=2424	284.57	1.81E-05	4.74	0.052	9.00		
Yield	Kukri_c5411_1312	3D	A=2424	**B**=2728	284.57	8.43E-05	4.07	0.057	7.51		
Yield	RAC875_c24641_720	3D	**A**=2721	B=2352	284.57	3.69E-05	4.43	0.052	8.30		
Yield	wsnp_CAP7_rep_c5643_2537213	3D	**A**=2730	B=2424	284.57	2.70E-05	4.57	0.054	8.61		
Yield	Kukri_c19263_346	3D	A=2424	**B**=2729	290.37	0.000279	3.55	0.057	6.38	QTL_17 Tol	
Yield	Kukri_c22857_496	3D	**A**=2743	B=2405	290.37	0.000129	3.89	0.052	7.10		
Yield	Tdurum_contig1015_131	3D	**A**=2725	B=2352	292.51	7.83E-05	4.11	0.052	7.58		
Yield	wsnp_Ex_c296_574790	4B	A=2083	**B**=2761	203.6	0.000332	3.48	0.091	6.21	QTL_18 Tol	(Martin *et al.*, 2015)
Yield	Kukri_c15910_159	4B	A=2325	**B**=2768	203.85	0.000187	3.73	0.101	6.75		(Poole *et al.*, 2012)
Yield	Kukri_c32064_629	4B	A=2193	**B**=2771	203.85	0.00011	3.96	0.104	7.26		(Wallwork *et al.*, 2004)
Yield	RAC875_c104414_76	4B	**A**=2769	B=2288	203.85	0.00018	3.74	0.098	6.79		
Yield	wsnp_Ex_c296_573976	4B	A=2171	**B**=2769	203.85	0.000198	3.70	0.096	6.70		

Yield	Tdurum_contig93160_155	4B	**A**=2766	B=2171	205.73	0.000209	3.68	0.106	6.65	
Yield	Excalibur_c5769_798	4B	A=2765	B=2201	206.89	0.000187	3.73	0.101	6.75	
Yield	Kukri_c26900_996	4B	**A**=2756	B=2201	206.89	0.000257	3.59	0.085	6.45	
Yield	RFL_Contig3363_1294	4B	A=2237	**B**=2757	206.89	0.000386	3.41	0.104	6.07	
Yield	Tdurum_contig47552_957	4B	A=2191	**B**=2745	206.89	0.000349	3.46	0.104	6.17	
Yield	tplb0034b12_591	4B	**A**=2772	B=2196	206.89	0.00018	3.74	0.098	6.79	
Yield	wsnp_Ex_c5769_10136243	4B	**A**=2762	B=2201	206.89	0.000321	3.49	0.104	6.24	
Yield	wsnp_Ex_c5769_10136788	4B	A=2182	**B**=2769	206.89	0.000187	3.73	0.101	6.75	
Yield	wsnp_Ku_rep_c104382_90867406	4B	A=2165	**B**=2752	206.89	0.000515	3.29	0.101	5.80	
Yield	wsnp_Ra_c22945_32440611	4B	**A**=2767	B=2201	206.89	0.000145	3.84	0.080	6.99	
Yield	CAP7_c10839_300	4B	**A**=2770	B=2201	208.51	0.000263	3.58	0.104	6.43	
Yield	Excalibur_rep_c108293_345	4B	**A**=2767	B=2288	208.51	0.000418	3.38	0.109	6.00	
Yield	GENE-2636_193	4B	A=2171	**B**=2761	208.51	0.000292	3.54	0.093	6.33	
Yield	RAC875_c23144_1560	4B	A=2290	**B**=2769	208.51	0.000125	3.90	0.101	7.13	
Yield	wsnp_Ex_c50195_54565006	4B	A=1935	**B**=2761	208.51	0.00019	3.72	0.096	6.74	
Yield	wsnp_Ku_c5502_9765942	4B	**A**=2764	B=2196	208.51	0.000187	3.73	0.101	6.75	
Yield	Ku_c13328_1228	4B	A=1921	**B**=2747	210.85	0.00046	3.34	0.067	5.91	
Yield	wsnp_Ex_c16825_25387841	4B	**A**=2774	B=2196	215.45	0.000122	3.91	0.117	7.15	QTL_19 Tol
Yield	GENE-2422_208	4B	**A**=2748	B=2171	215.51	0.000376	3.43	0.101	6.10	
Yield	RAC875_c89195_138	4B	A=2268	**B**=2763	215.51	0.000309	3.51	0.096	6.28	
Yield	wsnp_Ex_c35910_43971560	4B	A=2288	**B**=2766	215.51	5.33E-05	4.27	0.091	7.95	
Yield	wsnp_Ex_c72198_70679871	4B	**A**=2761	B=2201	215.51	0.000309	3.51	0.096	6.28	
Yield	BobWhite_c11005_236	4B	**A**=2773	B=2177	220.72	0.000418	3.38	0.104	6.00	
Yield	Excalibur_c24563_339	4B	**A**=2754	B=2196	220.72	0.00013	3.88	0.106	7.09	
Yield	Kukri_c12814_763	4B	**A**=2776	B=2171	220.72	0.000127	3.90	0.137	7.12	
Yield	RAC875_c62816_54	4B	**A**=2756	B=2177	220.72	0.000247	3.61	0.101	6.49	
Yield	RAC875_c77652_348	4B	A=2171	**B**=2764	220.72	0.00036	3.44	0.098	6.14	
Yield	Tdurum_contig48088_463	4B	**A**=2769	B=2177	220.72	0.000269	3.57	0.101	6.41	
Yield	Tdurum_contig10466_87	4B	**A**=2748	B=2241	226.2	0.000101	3.99	0.062	7.33	QTL_20 Tol
Yield	BS00022830_51	4B	**A**=2769	B=1760	230.39	0.000426	3.37	0.067	5.98	

Yield	Excalibur_c19547_75	4B	**A**=2724	B=2271	230.39	0.00036	3.44	0.060	6.14		
Yield	IACX6482	4B	**A**=2747	B=2406	230.39	0.000554	3.26	0.057	5.74		
Yield	Excalibur_c19547_1012	4B	**A**=2750	B=2241	232.66	0.000215	3.67	0.070	6.62		
Yield	Ku_c103450_879	4B	**A**=2752	B=2102	262.81	9.32E-05	4.03	0.054	7.41	QTL_21 Tol	
Yield	Kukri_c2148_137	4B	**A**=2751	B=2102	262.81	5.35E-05	4.27	0.054	7.95		
Yield	RAC875_c103017_302	4B	**A**=2768	B=2310	263.93	0.00082	3.09	0.148	5.38		
Yield	GENE-1584_692	4B	**A**=2873	B=2567	264.66	7.20E-05	4.14	0.430	7.66		
Yield	Kukri_c21787_283	4B	A=1454	**B**=2785	305.75	0.000489	3.31	0.130	5.85	QTL_22 Tol	
Yield	wsnp_Ex_c4148_7495656	4B	A=1921	**B**=2766	305.75	0.000351	3.45	0.122	6.16		
%WH	BS00034147_51	4B	A=31.65	**B**=21.57	333.52	0.00084	3.08	0.298	5.12	QTL_23 Tol	
%WH	RAC875_c39339_400	4B	A=32.61	**B**=21.74	333.52	0.00089	3.05	0.308	5.07		
%WH	Ex_c16174_681	4D	**A**=24.91	B=26.40	36.87	0.000813	3.09	0.482	5.15	QTL_24 Tol	(Poole *et al.*, 2012)
%Screenings	Kukri_c12738_882	5A	**A**=8.85	B=12.65	214.57	0.000611	3.21	0.303	3.47	QTL_25 Tol	
%Screenings	wsnp_Ex_c7841_13337935	5A	**A**=8.75	B=12.47	214.57	0.000611	3.21	0.303	3.47		
%Screenings	Excalibur_c17553_84	5A	A=12.64	**B**=8.94	216.63	0.000851	3.07	0.290	3.28		
%Screenings	RAC875_rep_c106044_137	5A	**A**=8.64	B=12.65	216.63	0.000487	3.31	0.303	3.60		
Yield	RFL_Contig727_736	5A	**A**=2737	B=2379	260.89	0.000176	3.76	0.054	6.81	QTL_26 Tol	
TKW	BS00089795_51	5A	A=29.14	**B**=32.59	440.73	0.00013	3.89	0.233	4.28	QTL_27 Tol	
TKW	Ex_c27046_1362	5A	A=29.21	**B**=32.58	440.73	0.000138	3.86	0.231	4.24		
TKW	Ex_c27046_3425	5A	A=29.20	**B**=32.85	440.73	9.81E-05	4.01	0.205	4.44		
TKW	IAAV2473	5A	A=29.15	**B**=32.42	440.73	1.94E-05	4.71	0.251	5.38		
TKW	RAC875_c3046_1764	5A	A=29.23	**B**=32.52	440.73	8.88E-05	4.05	0.241	4.50		
TKW	RFL_Contig3739_2135	5A	A=29.09	**B**=32.46	440.73	0.000143	3.85	0.236	4.22		
TKW	wsnp_Ex_c17523_26244256	5A	A=29.17	**B**=32.25	440.73	2.00E-05	4.70	0.254	5.36		
TKW	wsnp_Ex_c27046_36265198	5A	A=29.11	**B**=33.16	440.73	0.000181	3.74	0.228	4.09		
TKW	wsnp_Ex_c898_1738424	5A	A=29.17	**B**=32.38	440.73	0.000118	3.93	0.231	4.33		
TKW	Excalibur_c37943_221	5A	A=29.11	**B**=32.50	445.69	0.000136	3.87	0.207	4.25		
TKW	Kukri_c29560_455	5A	**A**=32.83	B=29.17	445.69	5.55E-05	4.26	0.228	4.77		
TKW	wsnp_Ex_c11120_18022932	5A	**A**=32.14	B=29.19	445.69	5.13E-05	4.29	0.256	4.81		

TKW	wsnp_Ex_c13258_20911706	5A	**A**=32.21	B=29.22	445.69	0.000144	3.84	0.231	4.22	
TKW	wsnp_Ex_c37943_45584325	5A	A=29.20	**B**=32.43	445.69	0.00015	3.82	0.212	4.20	
TKW	wsnp_Ku_c20011_29589089	5A	**A**=32.80	B=29.10	445.69	7.32E-05	4.14	0.228	4.61	
TKW	wsnp_Ku_c20011_29589289	5A	A=29.09	**B**=33.34	445.69	0.000113	3.95	0.202	4.35	
TKW	wsnp_Ku_c20011_29589514	5A	A=29.16	**B**=32.35	445.69	0.000103	3.99	0.212	4.41	
TKW	wsnp_Ra_c12183_19587379	5A	**A**=32.69	B=29.16	445.69	8.70E-05	4.06	0.231	4.51	
TKW	wsnp_Ku_c3684_6789632	5A	**A**=32.61	B=29.06	446.53	0.00014	3.85	0.199	4.23	
TKW	Kukri_c20011_147	5A	A=28.97	**B**=32.22	447.33	0.000172	3.76	0.285	4.12	
TKW	Excalibur_c7729_144	5A	A=29.14	**B**=32.58	448.42	5.32E-05	4.27	0.202	4.79	
TKW	wsnp_Ex_c31799_40545376	5A	**A**=32.77	B=28.98	448.42	7.60E-05	4.12	0.199	4.58	
TKW	wsnp_Ex_rep_c66689_65011117	5A	**A**=32.26	B=29.04	448.42	0.000132	3.88	0.197	4.27	
TKW	BS00065936_51	5A	A=28.98	**B**=32.58	450.43	2.06E-06	5.69	0.231	6.73	
TKW	RAC875_c13931_205	5A	**A**=31.85	B=29.00	450.43	0.000187	3.73	0.220	4.07	
TKW	Kukri_c33022_198	5A	A=28.97	**B**=31.88	453.34	2.13E-06	5.67	0.155	6.70	QTL_28 Tol
TKW	Tdurum_contig81424_367	5A	A=29.10	**B**=33.04	453.34	4.48E-06	5.35	0.233	6.26	
TKW	Kukri_c6669_145	5A	A=29.04	**B**=34.29	457.14	4.45E-06	5.35	0.158	6.26	
TKW	Excalibur_c24051_502	5A	**A**=34.79	B=29.01	463.65	3.59E-05	4.45	0.176	5.02	
TKW	Kukri_c865_59	5A	**A**=34.36	B=29.03	463.65	2.72E-05	4.57	0.171	5.18	
TKW	wsnp_RFL_Contig2265_1693968	5A	A=29.06	**B**=34.28	463.65	9.13E-06	5.04	0.166	5.83	
TKW	Excalibur_c41710_417	5A	A=28.99	**B**=34.21	464.98	8.80E-06	5.06	0.181	5.85	
TKW	GENE-2794_70	5A	A=29.01	**B**=34.44	464.98	3.27E-06	5.48	0.176	6.44	
TKW	wsnp_Ex_c2185_4094843	5A	A=29.06	**B**=34.73	464.98	2.29E-05	4.64	0.161	5.29	
TKW	BobWhite_c658_377	5A	A=28.95	**B**=33.94	466.78	1.39E-05	4.86	0.189	5.58	QTL_29 Tol
TKW	BS00041063_51	5A	**A**=35.07	B=28.98	466.78	3.01E-06	5.52	0.171	6.49	
TKW	Tdurum_contig50175_875	5A	A=29.02	**B**=34.33	466.78	1.81E-05	4.74	0.184	5.42	
TKW	wsnp_Ex_c55777_58153636	5A	A=29.03	**B**=34.37	466.78	1.64E-05	4.78	0.174	5.48	
TKW	wsnp_Ex_c8424_14192191	5A	**A**=34.29	B=29.25	466.78	1.28E-05	4.89	0.161	5.63	
TKW	wsnp_Ex_c8543_14357385	5A	A=29.36	**B**=34.45	466.81	0.000442	3.35	0.145	3.58	
TKW	Tdurum_contig47120_587	5A	A=29.02	**B**=34.46	469.39	1.54E-07	6.81	0.192	8.33	
TKW	Tdurum_contig69612_781	5A	A=28.84	**B**=34.56	469.39	6.01E-06	5.22	0.199	6.08	

TKW	wsnp_Ex_c5978_10478584	5A	A=28.90	**B**=34.45	473.13	4.33E-06	5.36	0.148	6.28	
TKW	wsnp_Ra_c3966_7286546	5A	A=29.14	**B**=33.99	473.13	1.51E-05	4.82	0.142	5.53	
TKW	IAAV4799	5A	**A**=34.14	B=29.06	475.36	6.85E-06	5.16	0.153	6.00	
TKW	BobWhite_c17445_83	5A	A=28.79	**B**=34.01	484.57	8.47E-07	6.07	0.132	7.27	QTL_30 Tol
TKW	Kukri_c67527_89	5A	**A**=33.75	B=29.20	484.57	3.89E-05	4.41	0.179	4.97	
TKW	Tdurum_contig10086_387	5A	A=29.20	**B**=33.81	484.57	1.55E-05	4.81	0.174	5.51	
TKW	Tdurum_contig54543_888	5A	A=29.00	**B**=33.64	484.57	1.08E-05	4.97	0.192	5.73	
TKW	Tdurum_contig85105_286	5A	A=29.34	**B**=34.45	484.57	0.000129	3.89	0.140	4.28	
TKW	wsnp_BF484028B_Td_2_1	5A	**A**=33.99	B=29.24	484.57	1.10E-05	4.96	0.155	5.72	
TKW	RAC875_c104483_394	5A	A=29.10	**B**=33.93	488	5.25E-05	4.28	0.148	4.80	
TKW	Tdurum_contig54725_586	5A	**A**=34.41	B=29.19	488	0.000181	3.74	0.153	4.09	
TKW	wsnp_Ex_c790_1554988	5A	A=28.57	**B**=31.60	490.41	5.30E-05	4.28	0.407	4.79	
TKW	Jagger_c6618_144	5A	A=28.59	**B**=31.60	492.85	3.48E-05	4.46	0.181	5.04	
TKW	BS00022098_51	5A	**A**=33.10	B=29.10	493.65	8.36E-05	4.08	0.238	4.53	
TKW	RAC875_c7132_134	5A	A=29.31	**B**=33.61	494.25	0.000364	3.44	0.155	3.69	
TKW	wsnp_BG607308A_Ta_2_1	5A	**A**=33.72	B-29.24	498.48	0.000252	3.60	0.194	3.90	QTL_31 Tol
TKW	wsnp_BG607308A_Ta_2_2	5A	A=29.21	**B**=33.91	498.48	0.000159	3.80	0.155	4.16	
TKW	BS00069739_51	5A	A=29.25	**B**=34.00	500.09	7.43E-05	4.13	0.137	4.60	
%WH	BS00067074_51	5B	A=34.91	**B**=23.55	568.44	3.87E-05	4.41	0.207	7.90	QTL_32 Tol
%WH	CAP7_c8713_356	5B	**A**=23.20	B=33.54	568.44	0.000321	3.49	0.212	5.98	
%WH	RAC875_c82589_246	5B	**A**=23.11	B=34.73	568.44	0.000187	3.73	0.194	6.46	
%WH	Tdurum_contig60165_722	5B	**A**=22.80	B=34.73	568.44	4.40E-05	4.36	0.202	7.78	
%WH	RAC875_c14732_461	5B	**A**=23.11	B=34.73	568.44	3.71E-05	4.43	0.197	7.94	
%WH	Kukri_c18410_193	5B	A=34.20	**B**=23.61	568.98	7.53E-05	4.12	0.189	7.29	
%WH	RAC875_rep_c106982_82	5B	A=32.43	**B**=22.57	568.98	2.74E-05	4.56	0.233	8.22	
%WH	Kukri_c18410_409	5B	A=35.52	**B**=22.68	568.98	6.67E-05	4.18	0.212	7.40	
%WH	Tdurum_contig60189_263	5B	**A**=22.87	B=36.22	568.98	0.000265	3.58	0.244	6.15	
%WH	Tdurum_contig60189_192	5B	**A**=22.87	B=36.22	568.98	0.000239	3.62	0.220	6.24	
%WH	Kukri_c18410_349	5B	**A**=22.89	B=35.29	568.98	0.000316	3.50	0.184	5.99	

%WH	RAC875_rep_c109540_64	5B	**A**=22.31	B=37.75	568.98	0.000138	3.86	0.220	6.74		
%WH	Kukri_c4594_825	5B	**A**=22.67	B=34.92	568.98	0.000104	3.98	0.218	6.99		
%WH	BobWhite_c46416_247	5B	**A**=22.93	B=34.73	568.98	2.02E-05	4.70	0.202	8.51		
%WH	RAC875_c1035_65	5B	**A**=23.02	B=34.73	568.98	7.69E-06	5.11	0.205	9.42		
Yield	D_GB5Y7FA02IZ73U_152	5D	A=2385	**B**=2785	338.67	0.000927	3.03	0.161	5.26	QTL_33 Tol	(Zheng *et al.*, 2014)
Yield	D_contig14133_180	5D	**A**=2785	B=2385	344.94	0.000426	3.37	0.158	5.98		(Bovill *et al.*, 2006)
Yield	D_contig62661_72	5D	A=2408	**B**=2781	349.65	0.000197	3.71	0.176	6.70		
Yield	RFL_Contig1091_1538	5D	**A**=2820	B=2320	354.06	1.43E-05	4.84	0.189	9.23	QTL_34 Tol	
Yield	BobWhite_c20106_377	5D	**A**=2773	B=2470	357.85	0.000524	3.28	0.142	5.79		
Yield	BobWhite_c27870_103	5D	**A**=2781	B=2415	357.85	0.000171	3.77	0.140	6.84		
Yield	D_GBB4FNX02GXFL1_268	5D	**A**=2780	B=2407	357.85	0.000624	3.21	0.161	5.63		
Yield	D_GDS7LZN01DW87V_234	5D	**A**=2794	B=2473	357.85	0.000241	3.62	0.184	6.51		
Yield	tplb0055c05_1689	5D	**A**=2764	B=2381	357.85	0.000181	3.74	0.161	6.78		
Yield	wsnp_RFL_Contig2346_1854360	5D	**A**=2785	B=2408	357.85	0.00053	3.28	0.189	5.78		
TKW	D_GDS7LZN01DW87V_234	5D	**A**=30.72	B=27.75	357.85	0.000291	3.54	0.184	3.82		
TKW	wsnp_RFL_Contig2346_1854360	5D	**A**=30.15	B=26.96	357.85	0.000218	3.66	0.189	3.98		
Yield	D_F5XZDLF02IP5IR_228	5D	**A**=2774	B=2377	365.23	0.000287	3.54	0.187	6.35	QTL_35 Tol	
Yield	Ku_c19010_273	5D	A=2415	**B**=2778	365.23	9.75E-05	4.01	0.119	7.37		
TKW	D_F5XZDLF02IP5IR_228	5D	**A**=30.39	B=26.51	365.23	3.02E-05	4.52	0.187	5.12		
Yield	Excalibur_c76347_77	5D	**A**=2776	B=2390	371.54	0.000534	3.27	0.161	5.77		
Yield	Tdurum_contig11553_534	5D	**A**=2774	B=2390	371.54	0.000639	3.19	0.163	5.60		
Yield	BS00000929_51	5D	**A**=2796	B=2320	377.86	1.58E-06	5.80	0.148	11.43		
Yield	IACX3123	5D	**A**=2796	B=2320	377.86	5.34E-06	5.27	0.179	10.20		
Yield	Jagger_c754_272	5D	**A**=2784	B=2356	377.86	0.000141	3.85	0.132	7.02		
Yield	Ku_c6176_938	5D	A=2375	**B**=2777	377.86	0.000487	3.31	0.142	5.86		
TKW	Jagger_c754_272	5D	**A**=30.47	B=25.99	377.86	0.000879	3.06	0.132	3.20		
Yield	Kukri_c41787_141	5D	A=2292	**B**=2752	387.6	0.000632	3.20	0.111	5.62	QTL_36 Tol	
TKW	Kukri_c41787_141	5D	A=26.39	**B**=30.55	387.6	0.000464	3.33	0.111	3.56		
TKW	D_contig79410_237	5D	A=26.39	**B**=30.55	489.95	0.000531	3.27	0.267	3.48	QTL_37 Tol	

TKW	wsnp_Ku_c10877_17896883	5D	**A**=31.84	B=29.38	489.95	0.000269	3.57	0.264	3.86	
Yield	BS00037002_51	6A	A=1926	**B**=2756	9.88	3.92E-05	4.41	0.065	8.25	QTL_38 Tol
Yield	IAAV5346	6A	A=2564	**B**=2740	173.19	0.000581	3.24	0.073	5.69	QTL_39 Tol
Yield	BS00065852_51	6A	A=1921	**B**=2742	175.85	0.000803	3.10	0.057	5.39	
WSB	Ku_c21490_472	6A	A=64.86	**B**=46.41	188.89	0.000593	3.23	0.057	6.49	QTL_40 Res
WSB	Ra_c8185_676	6A	**A**=45.85	B=63.97	188.89	0.000974	3.01	0.054	5.96	
WSB	Tdurum_contig14544_1550	6A	**A**=46.09	B=66.11	190.27	0.000437	3.36	0.101	6.81	
Yield	BS00037003_51	6B	**A**=2698	B=2395	1.28	7.73E-05	4.11	0.075	7.59	QTL_41 Tol
%WH	RAC875_c12879_176	6B	A=25.52	**B**=21.33	220.52	0.000904	3.04	0.135	5.06	QTL_42 Tol
Yield	BobWhite_c3506_1559	6B	A=2584	**B**=2740	377.2	0.000395	3.40	0.057	6.05	QTL_43 Tol
Yield	Kukri_c27662_675	6B	**A**=2744	B=2379	377.2	0.000418	3.38	0.065	6.00	
Yield	RAC875_c31299_1215	6B	**A**=2743	B=2389	377.2	0.000303	3.52	0.062	6.30	
Yield	TA003403-0617	6B	A=1688	**B**=2752	377.2	0.000437	3.36	0.135	5.96	
Yield	RAC875_c45987_132	6B	A=2172	**B**=2749	388.21	0.000418	3.38	0.065	6.00	
Yield	RAC875_rep_c72984_1417	7A	**A**=2708	B=1920	332.69	7.38E-05	4.13	0.057	7.64	QTL_44 Tol
TKW	wsnp_Ex_c12535_19963035	7B	A=29.38	**B**=33.27	224.57	0.000864	3.06	0.142	3.21	QTL_45 Tol
Yield	Tdurum_contig76683_147	7B	**A**=2726	B=2488	236.25	0.000415	3.38	0.054	6.01	
Yield	Excalibur_c13912_587	7B	**A**=2722	B=2379	247.05	0.000415	3.38	0.054	6.01	QTL_46 Tol
Yield	Tdurum_contig19852_242	7B	A=2428	**B**=2730	251.12	0.000144	3.84	0.052	7.00	
%WH	Kukri_c28160_2017	7B	A=28.80	**B**=23.05	470.16	0.000869	3.06	0.282	5.09	QTL_47 Tol
%WH	IACX9217	7B	A=30.6	**B**=22.79	475.92	0.000156	3.81	0.233	6.62	
%WH	JD_c17199_230	7B	A=29.04	**B**=23.13	475.92	0.00053	3.28	0.272	5.53	
%Screenings	BS00022162_51	7B	A=12.21	**B**=9.72	482.15	0.000974	3.01	0.218	3.20	
%WH	Excalibur_c1070_2327	7B	**A**=22.82	B=31.73	490.67	0.000548	3.26	0.262	5.50	QTL_48 Tol
%WH	wsnp_Ex_c4484_8065800	7B	**A**=30.12	B=22.21	502.72	0.000455	3.34	0.254	5.67	

Note: Chro, chromosome; Position, the marker position (cM) determined from a consensus map (Wang et al, 2014); MAF, minor allele frequency, R^2, variance explained by marker on specific trait; QTL, name of the QTL; Ref, the reference QTL previously reported within the same chromosomal regions; Yield, grain yield; TKW, thousand kernel weight; %Screening, Percent screenings; %WH, Percent white heads; WSB, Weighted stem browning; Tol, Tolerance QTL; Res, Resistance QTL. Target allele, a bold letter (**A** or **B**) indicates the target allele that increased resistance and/or tolerance.

Table 6.5: SNPs significantly [-Log10 (p) >3] associated with single or several traits on chromosomes 1A-7A across treatments and years.

1A	2A	3A	4A	5A	6A	7A
BS00021942_51[TKW(NP)]	BS00022382_51[TKW(P)]	BobWhite_c30009_285[TKW(N)Sc(P)]	IAAV8683[PM(NP)]	BobWhite_c14689_172[HD,PM(NP)]	BS00037002_51[Y(NP)]	BobWhite_c156_381[Y(N)]
BS00023419_51[PH(N)]	Excalibur_c12916_123[HD(P)]	BobWhite_c35303_192[Sc(P)]	Ku_c1125_814[PM(NP)]	BobWhite_c15758_79[PM,TKW(NP)]	BS00065852_51[Y(P)]	BS00076379_51[Y(N)]
Excalibur_c12819_216[PM(N)]	Excalibur_c1999_1130[Y(P)]	BS00098840_51[TKW(P)]	RAC875_rep_c102042_172[HD(NP)]	BobWhite_c17445_83[HD,PM,TKW(NP)]	Excalibur_c15109_942[PH(N)]	Excalibur_c109258_1038[Y(N)]
Kukri_rep_c113971_162[HD(P)]	IAAV8700[HD(PN)]	Excalibur_c41477_1272[Sc(P)]		BobWhite_c3675_788[TKW(N)]	Excalibur_c31035_805[PH(N)]	GENE-4897_105[HD(P)]
RAC875_c41145_189[TKW(P)]	Kukri_c136_150[Y(N)]	Excalibur_rep_c68583_689[TKW(NP)Sc(P)]		BobWhite_c658_377[HD(P)PM,TKW(NP)]	Excalibur_c35871_596[PH(NP)]	Ra_c16930_416[HD(P)]
RAC875_c744_1935[TKW(NP)Sc(P)]	Kukri_rep_c76691_483[Sc(P)]	IAAV8768[Sc(P)]		BobWhite_rep_c64315_180[PM(NP)TKW(N)]	IAAV5346[Y(P)]	Ra_c4601_2417[Y(N)]
RAC875_c97040_104[HD(P)]	RAC875_c64377_350[Y(NP)]	Ku_c1638_648[Sc(P)]		BS00022098_51[HD,PM,TKW(NP)]	Ku_c21490_472[WSB(P)]	RAC875_c114809_130[Y(P)]
Tdurum_contig43475_978[Sc(P)]	RAC875_rep_c111906_144[Y(P)]	Tdurum_contig15529_135[TKW(NP)]		BS00022753_51[TKW(N)]	Ra_c8185_676[WSB(P)]	RAC875_c13300_139[Y(N)]
wsnp_CAP11_c710_458019[HD(P)]	RAC875_rep_c72517_1215[Y(N)]	Tdurum_contig93364_355[TKW(P)]		BS00022754_51[HD,PM(NP)TKW(N)]	TA005330-0793[PM(N)]	RAC875_c24411_889[HD(NP)]
	RFL_Contig5625_2578[PM(N)]	wsnp_Ex_rep_c69034_67934852[Sc(P)]		BS00041063_51[HD(P)PM,TKW(NP)]	Tdurum_contig14544_1550[WSB(P)]	RAC875_c28144_448[Y(N)]
	Tdurum_contig15156_730[PM(NP)]	wsnp_Ku_c44089_51445136[TKW(P)]		BS00041911_51[HD,PM,TKW(NP)]	Tdurum_contig17378_299[PH(N)]	RAC875_rep_c72984_1417[Y(P)]
	Tdurum_contig56157_1595[Y(P)]			BS00044408_51[PM(P)TKW(NP)]		TA005578-0927[PM(P)]
	BobWhite_rep_c49768_768[NDVI(P)]			BS00062996_51[SC(P)]		wsnp_CAP7_c949_486485[PM(P)]
				BS00063973_51[HD,PM,TKW(NP)]		wsnp_Ex_c2277_4267788[Y(N)]
				BS00065481_51[PM(NP)]		wsnp_Ex_c2360_4422599[Y(P)]
				BS00065936_51[HD,PM,TKW(NP)]		wsnp_Ex_c8692_14557179[HD,PM(P)]
				BS00067150_51[HD,PM(NP)TKW(N)		wsnp_Ex_c9428_15641609[TKW(N)]
				BS00069739_51[HD,PM,TKW(NP)]		BS00065453_51[NDVI(N)]
				BS00074855_51[PM,TKW(N)]		
				BS00089795_51[TKW(NP)]		
				BS00109908_51[TKW(NP)]		
				Ex_c27046_1362[PM(P)TKW(NP)]		
				Ex_c27046_3425[PM,TKW(NP)]		
				Ex_c898_1319[PM(P)TKW(NP)		

				Excalibur_c11656_1760[PM,TKW(NP)]		
				Excalibur_c17553_84[Sc(P)]		
				Excalibur_c24051_502[HD(P)PM,TKW(NP)]		
				Excalibur_c30482_898[PM,TKW(NP)]		
				Excalibur_c31769_793[HD,PM,TKW(NP)]		
				Excalibur_c34426_723[TKW(NP)]		
				Excalibur_c37943_221[PM,TKW(NP)]		
				Excalibur_c41710_417[HD(P)PM,TKW(NP)]		
				Excalibur_c7729_144[HD(P),PM,TKW(NP)]		
				Excalibur_c92705_94[PM(N)]		
				Excalibur_rep_c103747_193[PM(NP)TKW(N)]		
				GENE-2794_70[HD(P)PM,TKW(NP)]		
				IAAV108[TKW(NP)]		
				IAAV1650[PM(NP)]		
				IAAV2473[PM,TKW(NP)]		
				IAAV4799[TKW(NP)]		
				IACX9023[TKW,PM(PN)]		
				Jagger_c6618_144[HD,PM,TKW(NP)]		
				JD_c15758_288[PM(NP)]		
				Kukri_c12738_882[Sc(P)]		
				Kukri_c20011_147[TKW(P)]		
				Kukri_c29560_455[TKW(NP)]		
				Kukri_c33022_198[HD,PM,TKW(NP)]		
				Kukri_c36397_149[PM(NP)]		
				Kukri_c52733_358[Sc(P)]		
				Kukri_c6669_145[HD(P)PM,TKW(NP)]		
				Kukri_c67527_89[PM(P)TKW(NP)]		
				Kukri_c865_59[HD,PM,TKW(NP)]		

				RAC875_c104483_394[PM,TKW(NP)]		
				RAC875_c13931_205[HD(TKW)]		
				RAC875_c3046_1764[PM(P)TKW(NP)]		
				RAC875_c30566_230[HD,PM(NP),TKW(P)]		
				RAC875_c3964_752[TKW(N)]		
				RAC875_c60453_122[TKW(N)]		
				RAC875_c62807_251[TKW(N)]		
				RAC875_c7132_134[HD,PM,TKW(NP)]		
				RAC875_rep_c106044_137[SC(P)]		
				RAC875_rep_c112818_307[TKW(N)]		
				RAC875_rep_c76193_513[PM,TKW(NP)]		
				RFL_Contig316_572[PM(NP)TKW(P)		
				RFL_Contig3739_2135[TKW(NP)]		
				RFL_Contig727_736[Y(NP)]		
				TA006037-0261[TKW(P)]		
				Tdurum_contig10086_387[HD,PM,TKW(NP)]		
				Tdurum_contig10759_260[PM(P)TKW(NP)]		
				Tdurum_contig10843_745[HD(P)PM,TKW(NP)]		
				Tdurum_contig10843_745[PM,TKW(NP)]		
				Tdurum_contig45823_821[TKW(N)]		
				Tdurum_contig47120_587[HD,PM,TKW(NP)]		
				Tdurum_contig47120_587[HD(P),PM,TKW(NP)]		
				Tdurum_contig50175_875[HD(P),PM,TKW(NP)]		
				Tdurum_contig54543_888[PM(N)TKW(NP)]		
				Tdurum_contig54725_586[HD,PM,TKW(NP)]		
				Tdurum_contig55097_601[TKW(NP)]		
				Tdurum_contig67291_367[PM(P)TKW(NP)]		
				Tdurum_contig69612_781[HD,PM,TKW(NP)]		

				Tdurum_contig81424_367[HD,PM,TKW(NP)]		
				Tdurum_contig85105_286[HD,PM,TKW(NP)]		
				wsnp_BE403211A_Td_2_1[TKW(N)]		
				wsnp_BE426080A_Ta_2_1[Sc(P)]		
				wsnp_BF293620A_Ta_2_3[PM,TKW(P)]		
				wsnp_BF293620A_Ta_2_3[TKW(P)]		
				wsnp_BF484028B_Td_2_1[HD,PM,TKW(NP)]		
				wsnp_BG606780A_Td_2_1[PM(NP)TKW(P)]		
				wsnp_BG607308A_Ta_2_1[HD,PM,TKW(NP)]		
				wsnp_BG607308A_Ta_2_2[HD,PM,TKW(NP)]		
				wsnp_CAP11_c1506_840938[HD,PM,TKW(NP)]		
				wsnp_CAP11_c1506_840951[PM,TKW(N)]		
				wsnp_CD454152A_Ta_2_1[TKW(N)]		
				wsnp_Ex_c11120_18022932[PM,TKW(NP)]		
				wsnp_Ex_c13258_20911706[TKW(NP)]		
				wsnp_Ex_c13942_21820758[PM(NP)]		
				wsnp_Ex_c17523_26244256[OM,TKW(NP)]		
				wsnp_Ex_c18107_26909127[TKW(NP)]		
				wsnp_Ex_c1880_3545329[TKW(P)]		
				wsnp_Ex_c2185_4094843[HD(P)PM,TKW(NP)]		
				wsnp_Ex_c23787_33024604[PM,TKW(P)]		
				wsnp_Ex_c27046_36265198[PM,TKW(NP)]		
				wsnp_Ex_c31799_40545376[HD(P)PM,TKW(NP)]		
				wsnp_Ex_c37943_45584325[PM(NP)]		
				wsnp_Ex_c37943_45584325[TKW(NP)]		
				wsnp_Ex_c44164_50292954[HD(P)PM,TKW(NP)]		
				wsnp_Ex_c55777_58153636[HD(P)PM,TKW(NP)]		
				wsnp_Ex_c5978_10478584[PM,TKW(NP)]		

				wsnp_Ex_c62818_62296773[PM(P)TKW(NP)]		
				wsnp_Ex_c7841_13337935[Sc(P)]		
				wsnp_Ex_c790_1554988[PM,TKW(NP)]		
				wsnp_Ex_c8424_14192191[PM,TKW(NP)]		
				wsnp_Ex_c8543_14357385[HD(P)PM,TKW(NP)]		
				wsnp_Ex_c898_1738424[PM(P)TKW(NP)]		
				wsnp_Ex_rep_c109532_92292121[HD,PM,TKW(NP)]		
				wsnp_Ex_rep_c66689_65011117[PM,TKW(NP)]		
				wsnp_Ku_c20011_29589089[TKW(NP)]		
				wsnp_Ku_c20011_29589289[PM(P)TKW(NP)]		
				wsnp_Ku_c20011_29589514[PM,TKW(NP)]		
				wsnp_Ku_c3684_6789632[PM,TKW(NP)]		
				wsnp_Ku_c40349_48594583[PM,TKW(NP)]		
				wsnp_Ku_c42416_50159250[HD(N)PM,TKW(NP)]		
				wsnp_Ku_c42416_50159402[HD(N)PM,TKW(NP)]		
				wsnp_Ra_c12183_19587379[TKW(NP)]		
				wsnp_Ra_c3966_7286546[TKW(NP)]		
				wsnp_RFL_Contig2265_1693968[HD(P)]		
				wsnp_RFL_Contig2265_1693968[PM,TKW(NP)]		
				wsnp_RFL_Contig4136_4696148[TKW(N)]		

Note: Y, grain yield; TKW, thousand kernel weight; Sc, screenings WH, white heads; WSB, Weighted stem browning HD, heading days; PH, plant height; NDVI, normalized difference vegetation index at 33 Zadock scale; N, nil (un -inoculated) and P, plus (inoculated) treatment across the years. SNPs delineated in the blue colour were associated with a chromosomal region linked to the expression of three different traits under both treatments. Those SNPs delineated in the pink colour were associated with a chromosomal region linked to the expression of two different traits under both treatments along with one trait under either treatment. The name of significant SNPs with traits, gene effects, *P* value of the association and variance explained by markers on specific traits (R^2) are presented in Appendix IV Table 1.

Table 6.6: SNPs significantly [-Log10 (p) >3] associated with single or several traits on chromosomes 1B-7B across treatments and years.

1B	2B	3B	4B	5B	6B	7B
BobWhite_c17044_155[Y(P)]	BobWhite_c2988_2161[TKW(N)]	BS00011605_51[Y(NP)]	BobWhite_c11005_236[Y(P)]	BobWhite_c15406_510[WH(P)]	BobWhite_c3506_1559[Y(NP)]	BS00022162_51[Sc(P)]
BS00066092_51[PM,Y(NP)]	BobWhite_c30112_275[HD(P)PM(NP)]	D_contig64400_391[Y(N)]	BS00022830_51[Y(NP)]	BobWhite_c46416_247[WH(P)]	BS00037003_51[Y(NP)]	BS00049887_51[PM(NP)]

Excalibur_c1453_1310[Y(P)]	BobWhite_c30622_180[HD(P)PM(NP)]	Excalibur_rep_c106461_262[PM(NP)]	BS00034147_51[WH(P)]	BobWhite_s66049_223[WH(P)]	Ex_c2978_640[HD(P)]	BS00068071_51[PM(N)]
RFL_Contig2443_255[Sc(N)]	BobWhite_c40418_289[PM(NP)]	IAAV4641[Y(P)]	BS00087144_51[Y(P)]	BS00067074_51[WH(P)]	Excalibur_c58410_729[PH(N)]	Excalibur_c1070_2327[WH(P)]
tplb0050c03_1003[TKW(NP)]	BS00007901_51[Y(N)]	Kukri_c22748_211[Y(P)]	BS00110365_51[HD,PM(P)TKW(NP)	CAP7_c8713_356[WH(P)	IACX1162[Sc(N)]	Excalibur_c13912_587[Y(NP)]
	BS00029713_51[HD,PM(NP)]	Kukri_c38065_217[Sc(N)]	CAP7_c10839_300[Y(P)]	Excalibur_c23452_352[WH(P)]	Kukri_c27662_675[Y(P)]	IACX9217[WH(P)]
	BS00030497_51[HD,PM(NP)]	RAC875_c17373_848[Y(P)]	CAP8_c1408_167[Y(P)]	Kukri_c18410_193[WH(P)]	RAC875_c12879_176[WH(P)]	JD_c17199_230[WH(P)]
	BS00038217_51[HD,PM(NP)]	RAC875_c23665_68[Y(P)]	Excalibur_c12925_510[Y(P)]	Kukri_c18410_349[WH(P)]	RAC875_c31299_1215[Y(P)]	Kukri_c28160_2017[WH(P)]
	BS00063589_51[Y(P)]	RAC875_c31133_533[Y(P)]	Excalibur_c19547_1012[Y(NP)]	Kukri_c18410_409[WH(P)]	RAC875_c45987_132[Y(P)}	Kukri_c50384_371[WH(N)]
	BS00067337_51[HD,PM(NP)]	RAC875_c35672_136[Y(NP)]	Excalibur_c19547_128[Y(P)]	Kukri_c4594_825[WH(P)]	TA003403-0617[Y(NP)]	Kukri_c64387_218[Y(N)]
	BS00079213_51[HD(P)PM(NP)]	RAC875_c35672_205[Y(P)]	Excalibur_c19547_75[Y(NP)]	RAC875_c1035_65[WH(P)]	wsnp_Ex_c24927_34181611[Y(P)]	RAC875_c11731_112[PM(NP)]
	BS00088575_51[HD(P)]	RAC875_c35672_73[Y(NP)]	Excalibur_c24563_339[Y(P)]	RAC875_c14732_461[WH(P)]	wsnp_Ex_rep_c68169_66940235[PH(P)]	RAC875_c30123_913[TKW(NP)]
	BS00103461_51[HD,PM(P)]	RAC875_c48860_106[HD(NP)]	Excalibur_c38012_393[Y(P)]	RAC875_c82589_246[WH(P)]		TA003961-0636[PM(N)]
	BS00110319_51[HD(P)PM(NP)]	RAC875_c68392_137[Y(NP)]	Excalibur_c5769_798[Y(P)]	RAC875_rep_c106982_82[WH(P)]		Tdurum_contig19852_242[Y(NP)]
	BS00110442_51[HD,PM(NP)]	Excalibur_c34581_339[NDVI(P)]	Excalibur_rep_c108293_345[Y(P)]	RAC875_rep_c109540_64[WH(P)]		Tdurum_contig76683_147[Y(NP)]
	CAP12_rep_c5926_115[HD,PM(P)]	Excalibur_c35491_788[NDVI(P)]	GENE-1584_692[Y(NP)]	Tdurum_contig60165_722[WH(P)]		wsnp_CAP8_c334_304253[HD(NP)]
	CAP12_rep_c5926_51[HD,PM(P)]		GENE-2422_208[Y(P)]	Tdurum_contig60189_192[WH(P)]		wsnp_Ex_c12535_19963035[TKW(P)]
	D_contig36671_269[HD,PM(P)]		GENE-2636_193[Y(P)]	Tdurum_contig60189_263[WH(P)]		wsnp_Ex_c4484_8065800[WH(P)]
	D_F1BEJMU02IKD3X_298[HD,PM(NP)]		IAAV163[Y(NP)]	wsnp_Ex_rep_c68504_67334656[Y(N)]		
	Ex_c12004_1006[PM(P)]		IAAV6327[Y(P)]	wsnp_Ku_rep_c103274_90057407[Y(N)]		
	Excalibur_c1305_662[HD(P)PM(NP)		IACX6482[Y(NP)]	CAP11_c5629_55[NDVI(P)]		
	Excalibur_c18966_1008[WH(P)]		Ku_c103450_879[Y(NP)]	GENE-4579_108[NDVI(P)]		
	Excalibur_c2454_333[Y(P)]		Ku_c13328_1228[Y(P)]			
	Excalibur_c2496_1141[HD(P)]		Kukri_c12814_763[Y(NP)]			
	Excalibur_c25430_183[HD,PM(NP)]		Kukri_c15910_159[Y(P)]			
	Excalibur_c27557_381[HD(P)PM(NP)]		Kukri_c2148_137[Y(NP)]			
	Excalibur_c43482_196[HD,PM(NP)]		Kukri_c21787_283[Y(P)]			
	Excalibur_c4748_360[Y(P)]		Kukri_c26900_996[Y(P)]			
	Excalibur_c53027_302[HD(P)PM(NP)]		Kukri_c32064_629[Y(NP)]			
	Excalibur_c6097_2208[HD(NP)]		Kukri_c5502_2513[Y(P)]			
	Excalibur_c6111_411[HD,PM(NP)]		Kukri_rep_c103450_1504[Y(P)]			
	Excalibur_c64276_565[HD,PM(NP)]		RAC875_c103017_302[Y(P)]			
	Excalibur_rep_c101660_546[HD,PM(P)]		RAC875_c104414_76[Y(NP)]			
	Excalibur_rep_c68899_1400[HD(P)]		RAC875_c15807_669[Y(P)]			
	Excalibur_rep_c68899_191[HD,PM(NP)]		RAC875_c23144_1560[Y(NP)]			
	GENE-0862_110[Y(P)]		RAC875_c39339_400[WH(P)]			
	IAAV1101[HD,PM(NP)]		RAC875_c62816_54[Y(P)]			
	IACX6223[HD(P),PM(PN)]		RAC875_c77652_348[Y(P)]			
	Jagger_c36_213[HD,PM(P)]		RAC875_c89195_138[Y(P)]			
	Jagger_c8098_88[HD,PM(P)]		RAC875_rep_c109069_89[Y(P)]			
	JD_c11869_1297[HD,PM(NP)]		RFL_Contig3363_1294[Y(P)]			
	JD_c11869_1300[HD,PM(NP)]		Tdurum_contig10466_87[Y(NP)]			
	JD_c39990_130[HD(P)}		Tdurum_contig42107_1978[Y(P)]			
	Kukri_c106282_114[HD(P)PM(NP)]		Tdurum_contig42107_2206[Y(P)]			
	Kukri_c12616_844[HD,PM(P)]		Tdurum_contig42229_113[PH(P)]			

	Kukri_c15043_326[HD(P)PM(NP)]		Tdurum_contig47552_957[Y(P)]			
	Kukri_c17483_568[PM(P)]		Tdurum_contig48088_463[Y(P)]			
	Kukri_c27574_725[HD,PM(P)]		Tdurum_contig86933_317[Y(P)]			
	Kukri_c29052_75[Y(P)]		Tdurum_contig93160_155[NP(P)]			
	Kukri_c29272_363[HD,PM(P)]		tplb0034b12_591[Y(NP)]			
	Kukri_c3507_158[Y(NP)]		wsnp_Ex_c16825_25387841[Y(NP)]			
	Kukri_c40637_223[HD(NP)]		wsnp_Ex_c296_573976[Y(NP)]			
	Kukri_c43403_346[HD(P)]		wsnp_Ex_c35910_43971560[Y(NP)]			
	Kukri_c43403_412[HD,PM(P)]		wsnp_Ex_c37437_45183236[Y(NP)]			
	Kukri_c43403_594[HD(P)PM(NP)]		wsnp_Ex_c40815_47789152[Y(P)]			
	Kukri_c5904_80[HD,PM(NP)]		wsnp_Ex_c4148_7495656[Y(P)]			
	Kukri_c67627_393[HD(P)]		wsnp_Ex_c50195_54565006[Y(NP)]			
	Kukri_rep_c69288_529[PM(P)]		wsnp_Ex_c5769_10136243[Y(P)]			
	Kukri_rep_c76670_262[HD(P)PM(NP)]		wsnp_Ex_c5769_10136788[Y(P)]			
	RAC875_c26415_350[HD,PM(NP)]		wsnp_Ex_c72198_70679871[Y(P)]			
	RAC875_c3302_1411[HD,PM(NP)]		wsnp_Ku_c5502_9765942[Y(P)]			
	RAC875_c37837_889[HD(P),PM(NP)]		wsnp_Ku_c7453_12833586[Y(P)]			
	RAC875_c55059_202[HD(P)]		wsnp_Ku_rep_c104382_90867406[Y(NP)]			
	RAC875_c76533_442[HD,PM(P)]		wsnp_Ra_c22945_32440611[Y(NP)]			
	RAC875_c86069_65[HD,PM(NP)]		wsnp_Ra_rep_c69724_67278233[Y(P)]			
	RAC875_rep_c113555_122[HD(P)]		wsnp_Ex_c4125_7456528[NDVI(P)]			
	RFL_Contig996_350[HD,PM(NP)]					
	RFL_Contig996_818[HD,PM(NP)]					
	TA001567-0999[HD(P)]					
	TA005827-0874[PM,HD(P)]					
	Tdurum_contig12293_1003[PM(NP)]					
	Tdurum_contig18901_188[HD,PM(NP)]					
	Tdurum_contig19415_271[HD(P),PM(NP)]					
	Tdurum_contig28227_304[HD(P)]					
	Tdurum_contig29620_125[HD,PM(P)]					
	Tdurum_contig29620_285[TKW(P)]					
	Tdurum_contig30989_79[HD,PM(NP)]					
	Tdurum_contig36804_220[HD,PM(NP)]					
	Tdurum_contig47202_1699[HD,PM(NP)]					
	Tdurum_contig60978_352[HD(P)PM(NP)]					
	Tdurum_contig61293_131[HD(P)]					
	Tdurum_contig62458_179[HD(P)]					
	Tdurum_contig62458_179[PM(NP)]					
	Tdurum_contig62852_302[HD(P)PM(NP)]					
	Tdurum_contig62852_538[HD,PM(NP)]					
	Tdurum_contig62852_592[HD,PM(NP)]					
	Tdurum_contig68806_537[HD,PM(NP)]					
	Tdurum_contig74936_264[HD,PM(P)]					
	Tdurum_contig74936_387[HD(P)PM(NP)]					

	Tdurum_contig7526_301[HD,PM(P)]					
	Tdurum_contig81323_291[HD,PM(NP)]					
	Tdurum_contig83066_276[WSB(P)]					
	tplb0045o20_1168[HD,PM(NP)]					
	tplb0045o20_699[HD,PM(NP)]					
	wsnp_Ex_c47157_52450090[Y(P)]					
	wsnp_Ex_c5239_9272511[HD(P)PM(NP)]					
	wsnp_Ex_c57_116914[HD(P)]					
	wsnp_Ex_c66052_64232430[HD,PM(P)]					
	wsnp_Ex_c741_1456698[HD,PM(NP)]					
	wsnp_Ex_rep_c101349_86725007[Y(P)]					
	wsnp_Ex_rep_c67391_65971023[HD,PM(NP)]					
	wsnp_JD_c29939_23694256[PM(NP)]					
	wsnp_Ku_c23305_33210628[HD,PM(P)]					
	wsnp_Ku_c23305_33210841[PM(P)}					
	wsnp_Ku_c31_62657[HD,PM(P)]					
	wsnp_Ku_c34759_44069854[HD,PM(NP)]					
	wsnp_Ra_c11493_18637928[HD(P)]					
	Kukri_c36026_68[NDVI(N)]					
	RAC875_c52566_447[NDVI(P)]					
	Tdurum_contig74936_456[NDVI(P					

Note: Y, grain yield; TKW, thousand kernel weight; Sc, screenings WH, white heads; WSB, Weighted stem browning HD, heading days; PH, plant height; NDVI, normalized difference vegetation index at 33 Zadock scale; N, nil (un -inoculated) and P, plus (inoculated) treatment across the years. SNPs delineated in the violet colour were associated with a chromosomal region linked to the expression of one or two different traits under both treatments. The name of significant SNPs with traits, gene effects, *P* value of the association and variance explained by markers on specific traits (R^2) are presented in Appendix IV Table 1.

Table 6.7: SNPs significantly [-Log10 (p) >3] associated with single or several traits on chromosomes 1D-7D across treatments and years.

1D	**2D**	**3D**	**4D**	**5D**	**6D**	**7D**
BobWhite_c1715_887[TKW(P)]	BobWhite_rep_c48966_570[Y(NP)]	BS00023217_51[Y(NP)]	Ex_c16174_681[WH(P)]	BobWhite_c20106_377[HD,PM,Y(NP)]	Tdurum_contig8741_194[PH(N)]	IAAV4510[HD(N)]
BobWhite_c359_1026[HD,PM,Y(NP)]	D_contig17313_245[Y(P)]	CAP12_c470_361[Y(NP)]	Kukri_c64744_1087[PM(P]	BobWhite_c27870_103[HD,PM,Y(NP)]		Kukri_c15912_2019[NDVI(P)]
GENE-0014_822[HD(P),PM(NP)]	Excalibur_c94336_103[PM(N)]	D_contig09222_937[Y(NP)]	RAC875_rep_c105922_169[PH(P)]	BS00000929_51[HD(P)Y(NP)]		
IAAV7856[Y(N)]	Excalibur_c94336_68[PM(N)]	D_contig11810_446[Y(NP)]	wsnp_Ex_rep_c107564_91144523[PH(NP)]	D_contig14133_180[HD,PM,Y(NP)]		
Jagger_c3179_499[PM(N)]	Kukri_c23961_636[PM(N)]	D_contig79290_372[Y(P)}		D_contig62661_72[HD,PM,Y(NP)]		
Kukri_c17177_1575[TKW(N)]	D_GCE8AKX02I8TJ5_334[NDVI(P)]	D_F5XZDLF02HWOJZ_227[Y(P)]		D_contig79410_237[TKW(P)]		
Kukri_c26168_713[HD,PM(NP)]		D_GBB4FNX02JKG8H_167[Y(NP)]		D_F5XZDLF02IP5IR_228[HD(NP)TKW,Y(P)]		

wsnp_CAP11_c8597_3709328[TKW(NP)]		Excalibur_c40068_522[Y(NP)]		D_GB5Y7FA02IZ73U_152[HD,PM,Y(NP)]		
wsnp_JD_c5316_6447231[TKW(P)]		Kukri_c17342_231[Y(NP)]		D_GBB4FNX02GXFL1_268[HD,PM,Y(NP)]		
wsnp_JD_rep_c48890_33141899[PM(NP)]		Kukri_c19263_346[Y(NP)]		D_GDS7LZN01DW87V_234[HD,PM,Y(NP)TKW(P)]		
		Kukri_c22857_496[Y(NP)]		Excalibur_c76347_77[HD,PM, Y(NP)]		
		Kukri_c32139_2473[HD(NP)]		IACX3123[HD,PM,Y(PN)]		
		Kukri_c5252_107[Y(NP)]		Jagger_c754_272[HD,PM,Y(NP)TKW(P)]		
		Kukri_c5411_1312[Y(NP)]		Ku_c19010_273[HD,PM,Y(NP)]		
		RAC875_c24641_720[Y(NP)]		Ku_c6176_938[HD,PM,Y(NP)]		
		RAC875_rep_c74926_682[Y(NP)]		Kukri_c41787_141[HD,Y,TKW(NP)]		
		Tdurum_contig1015_131[Y(NP)]		Kukri_rep_c110911_477[HD(NP)]		
		wsnp_CAP7_rep_c5643_2537213[Y(NP)]		RFL_Contig1091_1538[HD,PM,Y(NP)]		
				Tdurum_contig11553_534[HD,PM,Y(NP)]		
				tplb0055c05_1689[HD,PM,Y(NP)]		
				wsnp_Ku_c10877_17896883[TKW(P)]		
				wsnp_RFL_Contig2346_1854360[HD,Y(NP)PM,TKW(P)]		

Note: Y, grain yield; TKW, thousand kernel weight; Sc, screenings WH, white head; WSB, Weighted stem browning HD, heading days; PH, plant height; NDVI, normalized difference vegetation index at 33 Zadox scale; N, nil (un -inoculated) and P, plus (inoculated) treatment across the years. SNPs delineated in the blue colour were associated with a chromosomal region linked to the expression of three different traits under both treatments. The name of significant SNPs with traits, gene effects, *P* value of the association and variance explained by markers on specific traits (R^2) are presented in Appendix IV Table 1.

6.3.5 The identification of parents for the first recombination in a MARS scheme

The GWA analysis identified 1152 significant marker-trait associations across traits, treatments and years (Appendix IV, Table 1). However, these MTAs represented the total number of significant markers and many SNPs were located in the same region. To identify new parents for recombination in the MAS scheme, only those markers and traits of greatest effect under crown rot inoculation and that occupied a unique position on the chromosome were selected and genotypes carrying complementary combinations of markers and traits identified. SNPs which appeared only under inoculation and that had the greatest effect on the grain yield, % WH and WSB were identified (Table 6.8). These included 6, 3 and 6 markers for the three traits, respectively. These SNPs had unique positions on each chromosome and each marker explained 6-11% of the variation in grain yield, 5-9% in % white heads and 6-7% in WSB. Six SNPs had a positive effect on grain yield in both treatments. These were located on chromosomes 1B, 3B, 5A, 5D, 6A and 7B and explained between 7-10% of the variation in grain yield. Seven SNPs had a positive effect on yield only in the un-inoculated treatment. These were located on 2A, 2B, 2D, 3D, 4B, 5B and 7A and explained between 22 - 25% of the trait variation. These 7 markers were considered yield-potential QTLs only. The entries 31, 53, 69, 89, 74 and 176 were selected based on their complementary sets of favourable SNP markers and their phenotypic responses. Entries 31, 53, 69 contained the highest multiple marker trait associations (23) followed by entries 89 (22), 74 (21) and 176 (21) (Table 6.8). In total, 29 linked SNP markers associated with the target traits (Table 6.8) located in different chromosomal regions were selected and converted into a KASP panel (see Chapter 3). The KASP assay was then used to genotype the progeny derived from recombination of the above parents. The derived progeny are still under multiplication as of the submission date of this thesis.

Table 6.8: Parents selected among the base population for recombination in a MARS strategy.

Traits	SNPs	Chro.	cM	R^2 (%)	31[1]	53	69	89	74	176
Yield plus	Tdurum_contig56157_1595	2A	20.21	6	1	1	1	1	1	1
	BS00063589_51	2B	439.24	9	1	1	1	1	1	1
	D_contig17313_245	2D	6.13	6	1	1	1	1	1	1
	Excalibur_c40068_522	3D	284.57	11	1	1	1	1	1	1
	wsnp_Ex_c35910_43971560	4B	215.51	8	1	1	1	0	0	1
	RAC875_rep_c72984_1417	7A	332.69	8	1	1	1	1	1	1
Yield Nil and Plus	BS00067024_51	1B	306.49	7	1	1	1	1	1	1
	RAC875_c35672_136	3B	539.26	7	1	1	1	1	1	1
	RFL_Contig727_736	5A	260.89	7	1	1	1	1	1	1
	BS00000929_51	5D	377.86	10	1	1	1	1	1	1
	BS00037002_51	6A	9.88	8	1	1	1	1	1	1
	Tdurum_contig19852_242	7B	251.12	7	1	1	1	1	1	1
Yield (nil)	RAC875_rep_c72517_1215	2A	614.77	22	1	1	1	1	1	1
	IAAV7856	2B	78.23	23	0	0	0	0	1	0
	Kukri_c3507_158	2B	78.23	23				0	0	
	BobWhite_rep_c48966_570	2D	267.98	23	1	1			1	1
	Kukri_c5252_107	3D	280.71	25	1	1	1	1	1	1
	Tdurum_contig10466_87	4B	226.2	24	1	1	1	1	1	1
	wsnp_Ku_rep_c103274_90057407	5B	36.44	22	1	1	1		1	1
	wsnp_Ex_c2277_4267788	7A	382.54	23	1	1	0	1	0	1
White head(plus)	Excalibur_c18966_1008	2B	417.82	8	0	0	0	1	1	0
	BS00034147_51	4B	333.52	5	1	1	1	1	1	1
	RAC875_c1035_65	5B	568.98	9	1	1	1	1		1
	RAC875_c12879_176	6B	220.52	5	0	0	1	1	1	0
	IACX9217	7B	475.92	7	0	1	1	1	0	1
	wsnp_Ex_c4484_8065800	7B	502.72	6	1	1	0	0	0	0
WSB (Plus)	Excalibur_c65830_82	2B	317.99	6			1	1	0	
	Tdurum_contig83066_276	2B	292.15	6	1	1	1	0	0	0
	Tdurum_contig14544_1550	6A	190.27	7	1	0	1	1	1	0
Total significant markers					23	23	23	22	21	21

[1] Note: 1 and 0 represent presence and absence of the marker, respectively. Chro, chromosome; Pos (cM), the marker position; R^2, variance explained by marker on specific trait

6.4 Discussion

A large number of significant MTAs linked to crown rot resistance and tolerance traits were detected on the A genome followed by the B and D genomes. While it could be concluded that the contribution of the A and B genomes is more important compared to D, the result was influenced by the generally poorer marker coverage of the D genome. This is an issue with all marker systems in wheat (Semagn *et al.*, 2006; Cavanagh *et al.*, 2013; Wang *et al.*, 2014). Nevertheless, earlier studies have made similar conclusions that the A and B genomes contribute more to key traits in wheat (Sun *et al.*, 2017). Grain yield under crown rot pressure is the principal trait wanted by breeders and farmers. In the current study, QTLs with a specific effect on crown rot resistance and tolerance were discovered. This study revealed that no QTL was observed that was linked to both resistance measured by stem browning and tolerance, thus it can be concluded that the genetic control of these traits is different. This is a new finding and the first time that the genetic control of both resistance and tolerance has been compared. Nevertheless, the QTLs on chromosome 3B and 4B identified in the current study for partial resistance (there is no complete resistance) to crown rot in wheat were also reported by Martin *et al.* (2015) and Poole *et al.* (2012).

TKW was an important trait linked to crown rot tolerance in the current study. Those genotypes with better yield and lower screenings under crown rot inoculation generally had higher TKW (Chapter 5, Appendix III, and Table 5 - 7) although it was difficult to separate this from yield potential as the same QTLs were also present in un-inoculated treatments (Table 6.7). Earlier reports revealed that shrivelled grain or reduced grain size and weight significantly reduced grain yield in the presence of crown rot disease (Burgess *et al.*, 1996; Brennan and Murray, 1988). In addition, MTAs and QTLs on chromosome 5A governing TKW were reported by Wang *et al.* (2017) and Sukumaran *et al.* (2015) while MTAs and QTLs on chromosomes 3A and 4B for TKW were reported by Chen *et al.* (2017) under un-inoculated growing conditions. In addition, another QTL on chromosome 3A for TKW under drought stress has been reported by Bennett *et al.* (2012). The current study found that MTAs on chromosomes 3A, 5A, 4B, 1D and 5D have a positive influence on TKW under both treatments whereas MTAs on chromosomes 2A, 1B, 2B and 7B were important for increasing grain weight under inoculation (Appendix IV, Table 1). Co-localized MTAs for TKW and yield, and separate MTAs for the same traits were previously observed to increase grain yield (Sukumaran *et al.*, 2018). The current study also found co-localized MTAs for TKW and yield on chromosomes 2A, 2B, 4B, 5D and 7A, and separate MTAs for both traits that influenced grain yield.

Previous genetic mapping studies reported crown rot resistance QTLs on chromosomes 1A, 1B and 3A for seedling and adult plant response in bi-parental doubled haploid populations (Martin *et al.*, 2015). A seedling resistance QTL (designated Qcrs.cpi-5D) on chromosome 5D was found to explain 31.1% of the phenotypic variability in the glasshouse (Zheng *et al.*, 2014). This study did not find any resistance MTA linked with crown rot resistance on chromosome 5D, however many genomic regions associated with yield potential and tolerance to crown rot were identified (Table 6.7).

Yield loss from crown rot is a function of reduced phenotypic values of principle yield components such as grain weight and screenings and higher screenings will also decrease the seed germination rate (Shahi *et al.*, 2015). A number of QTLs for % screenings were detected in the current study and some of these (QTLs_1 and 13) were co-located with TKW. Others have observed similar co-localization of QTL between kernel weight and kernel diameter under rain-fed conditions (Edae *et al.*, 2014). MTAs associated with lower % screenings in the inoculated treatment were found on chromosomes 1A, 2A, 3A, 5A and 7B. Ma'arup (2016) also detected MTAs on chromosome 3A and 7B for lower % screenings in rain-fed conditions.

The suppression of grain yield through reduced grain weight and grain size under inoculation observed in the current study was also associated with an increased incidence of white heads. The incidence of white heads on mature plants in the presence of stem browning was reported to measure resistance to crown rot in Australia (Liu and Ogbonnaya, 2015). However, the formation of white heads is highly influenced by moisture stress during grain filling, with post-anthesis drought increasing the incidence (Smiley *et al.*, 2005; Klein *et al.*, 1991). While many MTAs for % WH were identified in the current study, two QTLs located on chromosomes 2B and 7B also appeared to influence tolerance, as described as yield loss. These QTL are obvious targets for breeding and selection once they are validated in other materials. The observed co-location of MTAs for % WH with physiological maturity, reduced grain weight and grain yield in the current study clearly indicates that later maturity increases disease stress and % WH thus lowering yield (Appendix 5, Table 1). This observation has not been reported previously, although would be highly seasonally dependant. However, there were no co-located QTL for % WH and WSB indicating that stem browning did not influence the formation of white heads. These results are in agreement with Smiley *et al.* (2005) who reported that white head formation was highly influenced by environmental conditions. Of the three WSB QTL found in the current study located on chromosomes 2B and 6A, only the

2B QTL has been reported previously by Martin *et al.* (2015). Clearly, stem browning, while effective in determining resistance, is not genetically associated with tolerance to crown rot and this supports the observation in Chapter 5 that resistance measured by stem browning and tolerance were largely uncorrelated. This is the first confirmed report of the lack of relationship between crown rot resistance and tolerance.

6.5 Conclusion

The current study identified the putative genetic control of important traits such as yield, TKW, screenings, % WH and WSB under crown rot pressure. This study was also the first report of the genetic control of tolerance to crown rot disease in wheat. A total of 48 QTL were associated with either resistance or tolerance and 9 previously reported QTL for resistance were confirmed. Resistance associated with basal stem browning was always independent of tolerance, although there was a relationship between whitehead formation and tolerance (assessed as reduced yield loss). The entries 31, 53, 69, 89, 74 and 176 were selected for recombination based on complementary sets of favorable SNP markers and phenotypic responses to the disease. The selected lines were subsequently recombined in recombination cycle to combine different alleles into a single genotype using KASP.

CHAPTER 7

Genetic control of crown rot resistance in two MARS populations (populations 1 and 2) and the effectiveness of recombination

7.1 Introduction

Pyramiding of QTLs for complex traits that individually offer a small portion of the trait variance using traditional MAS or MABC has been largely ineffective because of unfavourable linkages and the impacts of environment and genetic background on trait expression (Young and Tanksley, 1989). The improvement of complex traits via phenotypic recurrent selection is generally possible (Wiersma *et al.*, 2001; Posadas *et al.*, 2014), however, the long selection cycles and difficulty in identifying unique genes or alleles restricts the practicability of this breeding method. This is particularly the case for crown rot, as strong interactions between disease expression and the environment make phenotyping challenging. As described earlier, MARS is an alternative strategy that allows targeted recombination of gene effects through recurrent selection (Monds *et al.*, 2005; Bernardo and Charcosset, 2006). However, since every MARS population is operated independently, the QTL information generated may not be translatable to other populations. To the author's knowledge, there is no earlier report of the use of MARS to improve resistance to crown rot in wheat. This chapter aimed to: i) identify QTLs that explain crown rot resistance in two MARS populations ii) combine markers linked to these QTL into single backgrounds using marker-assisted recurrent selection and iii) confirm the resistance of lines carrying multiple sources of resistance.

7.2 Materials and Methods

7.2.1 Experimental conditions

Crown rot resistance was assessed in field experiments conducted during 2012-2017 at the IA Watson Grains Research Centre at Narrabri, NSW (30° 20′S latitude and 149° 45′E longitude; elevation of 212 m above sea level) and in a pot test conducted at Plant Breeding Institute, Cobbitty, NSW 2570 during the summer and winter of 2012 (for details see chapter 4.2). Both populations 1 and 2 were phenotyped in all experiments (see chapter 3.4 for details). A summary of the experiments conducted in each year is given in Table 7.1. The recombination of lines selected from the MARS strategy and the production of doubled haploid progeny was conducted at The Plant Breeding Institute (PBI), The University of Sydney, Cobbitty. All experiments conducted in 2016 and 2017 were sown under natural conditions and no irrigation was applied during crop growth. The experimental field was prepared using discs before sowing. Recommended fertilizer practice for this region of NSW was adopted following a pre-sowing soil nutrient analysis. The amount of fertilizer applied to the experimental fields is presented in Chapter 5, Table 5.1.

Table 7.1: Summary of experiments conducted to assess crown rot resistance during 2012-2017

Year	Location	Number of lines tested		Generation[1]
		Population 1	Population 2	
2012 (Summer)	Pot	250	225	Base population
2012 (Winter)	Pot	250	225	Base population
2012 (Winter)	Field	250	225	Base population
		3	3	Parents
		2	2	Checks
2016	Field	755	436	Doubled haploid SR
2017	Field	99	99	Doubled haploid SR
		25	74	Doubled haploid DR
		8	6	Base population
		3	3	Parents
		6	10	Checks
2017	Field	99	99	Doubled haploid SR
		8	6	Base population
		3	3	Parents
		10	10	Checks

[1] SR, Single recombinant; DR, Double recombinant

Weather data was collected from a weather station at the IA Watson Grains Research Centre at Narrabri in 2017 (Figure 7.1). Rainfall and daily mean minimum and maximum temperatures were recorded from the time of sowing to harvest. Total rainfall was described as the rainfall received during the active plant growing period or the time between sowing and physiological maturity. The weather station data is available at the following link: http://ozforecast.com.au/cgi-bin/aws_export.cgi?aws=11250

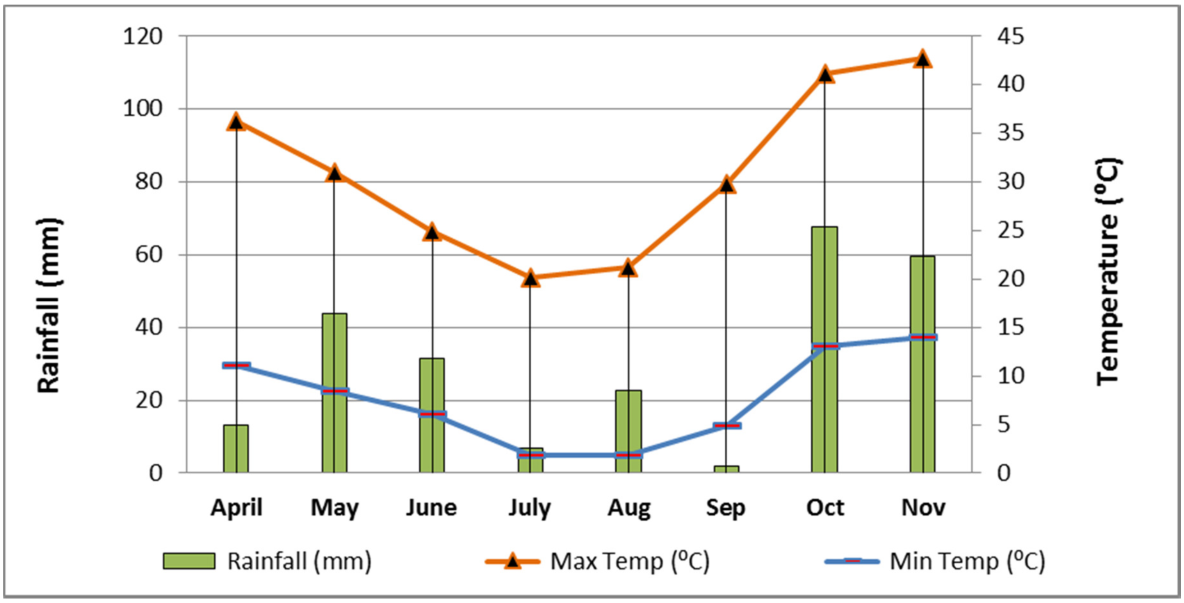


Fig. 7.1: Monthly total rainfall and mean minimum and maximum temperature in 2017.

7.2.2 Genetic materials

The development of populations 1 and 2 is outlined in chapter 3, Figures 3.1 and 3.2. Two populations consisting of 250 lines (MARS population 1) and 225 lines (MARS population 2) were derived from top crosses- between three polymorphic crown rot resistant parents. The details of these crosses and the parents are described in Chapter 3, Section 3.2. These populations were advanced to the F_2 generation, and individual plants were selected on the basis of stripe rust resistance and agronomic adaptability. These selected plants were grown as $F_{2:3}$ single rows in the following generation and genotyped using a 9K Infinium SNP assay. Details of the genotyping of both populations are described in Chapter 3, Section 3.4. A crown rot resistance phenotype was established by growing $F_{2:4}$ plants in the glasshouse and $F_{2:5}$ plants in the field under high disease pressure. Resistance to crown rot was determined by the degree of symptom development, including the extent of stem browning. Details of the phenotyping in pot and field are described in Chapter 3, Section 3.5.

GWAS was completed to identifying SNPs that were significantly associated with stem browning in both populations. The numbers of these significant markers were subsequently reduced by eliminating redundant markers (those found in the same genomic region) and maintaining those with higher individual effects on stem browning. Based on these marker effects and their complementarity, 8 and 6 lines were retained from the base population to cross as parents in the first recombination cycle of populations 1 and 2, respectively. The process of SNP detection was described earlier in Chapter 3, section 3.5 and marker effect estimation in Chapter 6, section 6.3.5.

In the first recombination cycle, simple and complex crosses were made among selected progeny carrying complementary markers alleles. These intercross derived progeny were advanced to the F_2 generation and genotyped for previously identified significant SNP makers from both populations using a KASP panel. The KASP panel development was described in Chapter 3, section 3.5. A list of the selected markers and their primer sequences are presented in Chapter 3, Table 3.3.

At the end of the 1st recombination cycle, plants were selected based on the number of recombined favourable marker-alleles. Seventy-three plants carrying 10-12 target and 41 plants carrying 9-12 markers for crown rot resistance were identified from populations 1 and 2, respectively. Approximately 10 doubled haploids were then produced per plant using the wheat-maize wide cross system, to fix all loci. Detail of the recombination cycles and production of doubled haploids was described in Chapter 3, sections 3.6 and 3.7. From the 1st recombination cycle, 6 and 5 plants carrying 10-12 markers were selected from populations 1 and 2, respectively, based on the complementary of their favourable marker-alleles. These selected genotypes were hybridized within each population in three-way crosses to produce the 2nd recombination cycle. A total of 85 plants (29 plants from population 1 and 56 from population 2) were genotyped with the KASP panel. Six plants carrying 18-19 markers and 14 plants carrying 18-22 markers were selected from populations 1 and 2, respectively. Approximately 10 doubled haploids were then made on these 20 selected plants from the 2nd recombination cycle.

Finally, the parents, base population and homozygous recombined doubled haploid lines from the 1st and 2nd recombination cycles were evaluated phenotypically in field trials to assess crown rot resistance and tolerance. The steps followed in the development of MARS populations 1 and 2 including details of the 1st and 2nd recombination cycles was described in Chapter 3, Figures 3.1 and 3.2. The number of lines evaluated at each stage of the MARS process for crown rot resistance is summarized in Table 7.2.

Table 7.2: Stages of MARS process

Year	Activity[1]	Population 1 Number of lines/plants tested	Population 2 Number of lines/plants tested
2012	Crown rot resistance phenotype produced from the base population (Pot test-summer)	250	225
2012	Crown rot resistance phenotype produced from the base population (Pot test-winter)	250	225
2012	Crown rot resistance phenotype produced from the base population (Field test-winter)	250	225
2013	Base population used for SR	8	6
2014	SR plant selection for KASP assay	352	415
2014	SR plant selection (10-12 markers combined) for DH	73	41
2014-15	DH production and seed increase (SR)	755	436
2016	Field evaluation of DH (SR)	755	436
2015	Selection of plants from SR for DR F_1 top	6	5
2016	DR F_1 plant selected for DH (18-19 and 18-22 markers combined for population 1 and 2) using KASP genotyping	9	16
2016-17	DH production and seed increase (DR)	25	74
2017	Doubled haploid lines (SR and DR) phenotyping at field level for CR resistance and tolerance	124	173

[1] SR, Single recombinant; DR, Double recombinant; DH, Doubled haploid

Two separate resistance trials for each of populations 1 and 2 were conducted under crown rot disease pressure in 2016 and 2017 at the IA Watson Grains Research Centre at Narrabri. Experiments were sown at a row spacing of 50 cm and row length of 130 cm. The production of crown rot inoculum and its application in field plots was described in Chapter 3, Section 3.5.1. The seeding rate was of 50 kg ha^{-1} to establish a plant population of approximately 200 seed m^{-2}. The doubled haploid lines from the first round recombination of both populations 1 and 2 were evaluated on the basis of stripe rust and tan spot diseases in 2016. In 2017, the experiment was conducted using the same materials evaluated in the 2016 experiment, with the addition of the double recombinant DH material (Table 7.1). The checks used were Suntop, Sunguard, Mace, Spitfire and EGA Gregory for population 1 and Suntop, Sunguard, Mace, Sunco, Spitfire, EGA Gregory, Lancer, EGA Wylie, 2_49 and EGA Bellaroi for population 2. Extra checks were included in population 2 as extra space was available. The list of recombinant parents used for these experiments can be found in Chapter 3, Table 3.4.

In addition, two crown rot yield-loss experiments were conducted in 2017. The experimental material for MARS population 1 consisted of recombinant 98 lines selected in 2016 resistance experiments, 8 recombinant parents (from the base population), 3 parental lines of the base population (AUS29529, 2.49/Cunningham//Kennedy and Sunco) and 9 checks (Suntop, Sunguard, Mace, Spitfire, EGA Gregory, lancer, EGA Wylie, 2-29 and EGA Bellaroi). The experimental material of MARS population 2 consisted of recombinant 99 DH lines selected in 2016, 6 recombinant parents (from the base population), 3 parental lines of the base population (CSCR16, 2.49/Cunningham//Kennedy, Sunco/2*Pastor) and the checks (Suntop, Sunguard, Mace, Sunco, Spitfire, EGA Gregory, Lancer, EGA Wylie, 2_49 and EGA Bellaroi). The genotypes were sown in replicated paired plots with (plus) and without (minus) inoculum of *F. pseudograminearum.* Inoculum was delivered to each furrow at the rate of 2.5 gm^{-1} just above the seed during seeding using the fertilizer applicator on a mechanical seeder. Complete details of seeding rate and plot size are provided in Chapter 5, section 5.2.6.

7.2.3 Experimental design and the establishment of field experiments

All four experiments were laid out in paired-plot randomized complete block designs with two replications and standard management practices for wheat at the IA Watson Grains Research Centre at Narrabri were followed.

7.2.4 Phenotyping

All materials were assessed for CR resistance in 2017. Ten plants per each plot were randomly collected when mature and subsequently stored at room temperature until assessment. Leaf sheaths were removed from individual plants and 6 individual tillers were assessed for stem discoloration as described in Chapter 3, sections 3.4.3. Resistance was calculated by the extent of stem browning along the stem, measured in mm from the base of each stem.

7.2.5 Assessment of agronomic traits

Agronomic traits such as grain yield, TKW, percentage of white heads (% WH), percentage screenings and yield loss were measured and calculated on the field experiments in 2017. Details are described in Chapter 5, section 5.2.10.

7.2.6 Statistical analysis

The GenStat 18th Edition (www.vsin.co.uk) statistical software package was used to analyse the stem browning data. The Residual Maximum Likelihood (REML) function of GenStat was used to conduct a Linear Mixed Model (LMM) analysis of each trait. Genotypes were considered fixed terms and tillers within plants within entries and replications as random terms in the model.

The REML function of GenStat was used to estimate yield loss and to test differences among genotypes and between groups of genotypes (parents, base population and recombinants) and treatments. Genotypes and treatments (inoculum) were considered fixed terms and plots within treatments and treatments within replications as random terms in the model. Means were separated using Fisher's protected least significant difference test at $P < 0.05$. Broad sense heritability (H^2), genetic advance and response to selection or genetic gain% are described in Chapter 5, section 5.2.11.

7.3 Results

7.3.1 Genome-wide association analysis

GWAS was conducted using the methodology described in Chapter 6. In total, 444 and 404 SNP markers were significantly associated at $P<0.001$ (or $–\text{Log10}(p)> 2$) based on the false discovery rate with the target resistance trait; stem browning, in both populations 1 and 2, respectively. Those markers that were not polymorphic were subsequently discarded. Chromosome location was then determined using population sequencing information as described in Chapter 6. The B genome had the most significant MTAs (268) followed by the A genome (101) and D genome (60) in population 1, similarly the highest number of significant MTAs were detected on the B genome (175) followed by the A genome (171) and D genome (47) in population 2 (Figure 7.2). Not all SNPs had unique map positions and redundant markers were removed. Finally, a total of 23 SNP markers located in unique chromosomal regions across the genome that explained a significant portion of the variation in crown rot resistance were selected from both populations 1 and 2 (Table 7.3). The selected SNPs were subsequently converted into a Kompetitive allele-specific primers (KASP) panel and the progeny derived from crosses among the parents were genotyped and selected using the KASP panel. This was performed for both the first and second recombination cycles using the KASP panel.

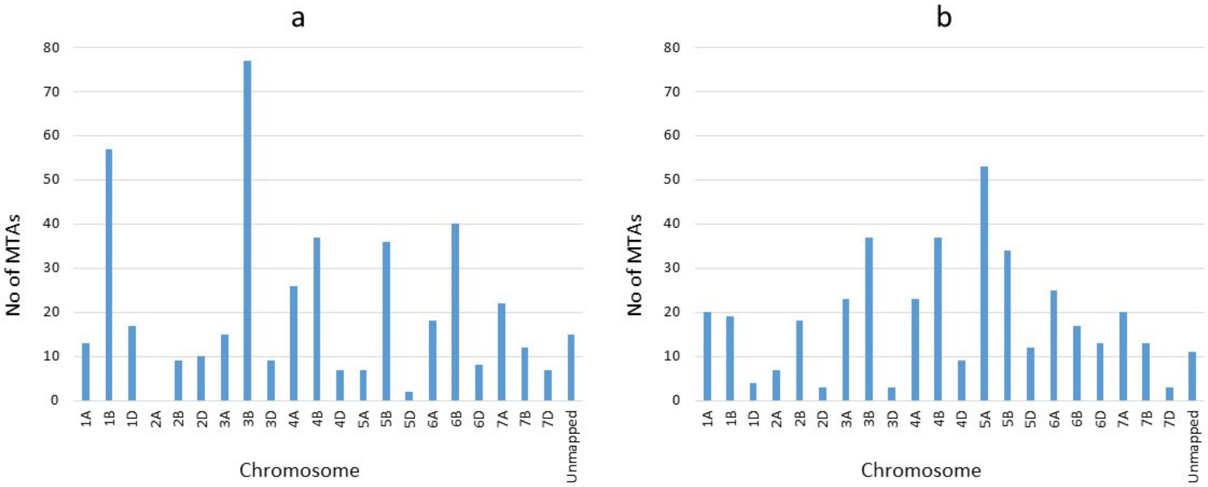


Fig 7.2: Distribution of MTAs across the genome in population 1(a) and 2(b)

Table 7.3 Selected markers from the GWAS that best explained crown rot resistance in MARS populations 1 and 2

Markers	Chromosome	Position[1]	Previous reports of QTL on the same chromosome arm
wsnp_Ku_c183_358844(IWA6649)	1A	27.071	(Martin *et al.*, 2015; Collard *et al.*, 2005)
IAAV2694(IWB34600)	1A	93.61	
CAP7_c821_239(IWB14279)	1A	130.09	
BobWhite_c1027_1127(IWB38)	1A	149.82	
Excalibur_c21898_1423(IWB23711)	1B	8.3607	Martin *et al.* (2015)
Ra_c16069_1820(IWB51198)	1B	64.099	
BS00070139_51(IWB10444)	1B	68.037	
Tdurum_contig13117_1316(IWB67865)	1B	86.073	
wsnp_Ex_c3372_6195001(IWA3446)	1D	75.036	(Collard *et al.*, 2005; Collard *et al.*, 2006; Bovill *et al.*, 2010; Martin *et al.*, 2015)
BS00062567_51(IWB8864)	2Dx	82.821	(Martin *et al.*, 2015)
IACX11310(IWB35687)	3B	72.018	(Bovill *et al.*, 2010; Ma *et al.*, 2010; Li *et al.*, 2010; Poole *et al.*, 2012; Zheng *et al.*, 2014; Martin *et al.*, 2015)
BS00072994_51(IWB10632)	3B	85.517	
BS00079029_51(IWB11049)	3B	140.51	
BS00035307_51(IWB8008)	4A	11.598	
Ku_c3385_521(IWB39213)	4B	71.914	(Martin *et al.*, 2015; Poole *et al.*, 2012; Wallwork *et al.*, 2004)
BS00032003_51(IWB7864)	5B	0.4281	
BobWhite_c6094_447(IWB4087)	5B	69.191	
RAC875_c60007_199	6B		
BobWhite_c33300_159(IWB2616)	7A	45.245	Poole *et al.* (2012)
BS00097659_51(IWB12011)	7A	113.3	
Kukri_rep_c70199_506(IWB49992.1)	7A	213.2	
wsnp_JD_c1219_1766041(IWA5797)	7A	241.4	
wsnp_be352570B_Ta_2_1(IWA4)	7B	67.473	

[1] Genetic map position reported in Wang *et al.* (2014)

7.3.2 Effect of recurrent selection on the expression of crown rot resistance

There were significant (*p*<0.001) differences observed among genotypes for stem browning in both populations 1 and 2. Significant (*p*<0.001) differences in resistance were also noted between the parents, base population, single recombinants, double recombinants and check cultivars in both populations (Table 7.4 and Appendix V, Table 1 and 2). The MARS approach produced significant changes in stem browning as markers were accumulated through recurrent selection. Table 7.4 summarizes the stem browning of five groups of genotypes evaluated under crown rot pressure in both populations.

Table 7.4: Wald statistics from variance component analyses of stem browning in populations 1 and 2.

Stem browning (mm)				
Population 1				
Fixed term	Wald statistic	d.f.	F statistic	F pr
Entry	1638.33	139	11.79	<0.001
Groups (Parent, BP, SR, DR, Check)[1]	299.6	4	74.9	<0.001
Population 2				
Entry	2242.45	191	11.74	<0.001
Groups (Parent, BP, SR, DR, Check) [1]	374.99	4	93.75	<0.001

[1] BP, Base population; SR, Single recombinant; DR, Double recombinant

Considerable reduction in stem browning or disease severity was observed after two rounds of recombination in both MARS populations (Tables 7.5 and 7.6). Mean stem browning reduced steadily with each generation and the accumulation of markers linked to crown rot resistance in population 1. The parental value of 38.33 ± 9.75 was considerably higher than the double recombinant stem browning of 19.11 ± 1.86 (Figure 7.3). The parents and all derived materials were significantly more resistant than the check cultivars. However, the trend was different in population 2 (Figure 7.4). In this population, the parents were very resistant (21.32 ± 5.508) and not significantly different to the double recombinants (22.73 ± 1.04), because some marker-gene combinations did not express under the prevailing environmental conditions. Nevertheless, there was a steady improvement in resistance between the base population and the double recombinants as increasing numbers of markers were accumulated. However, when the mean value of the top 10% from both single (15.38) and double recombinants (8.09) was considered, stem browning had reduced significantly (Figure 7.5).

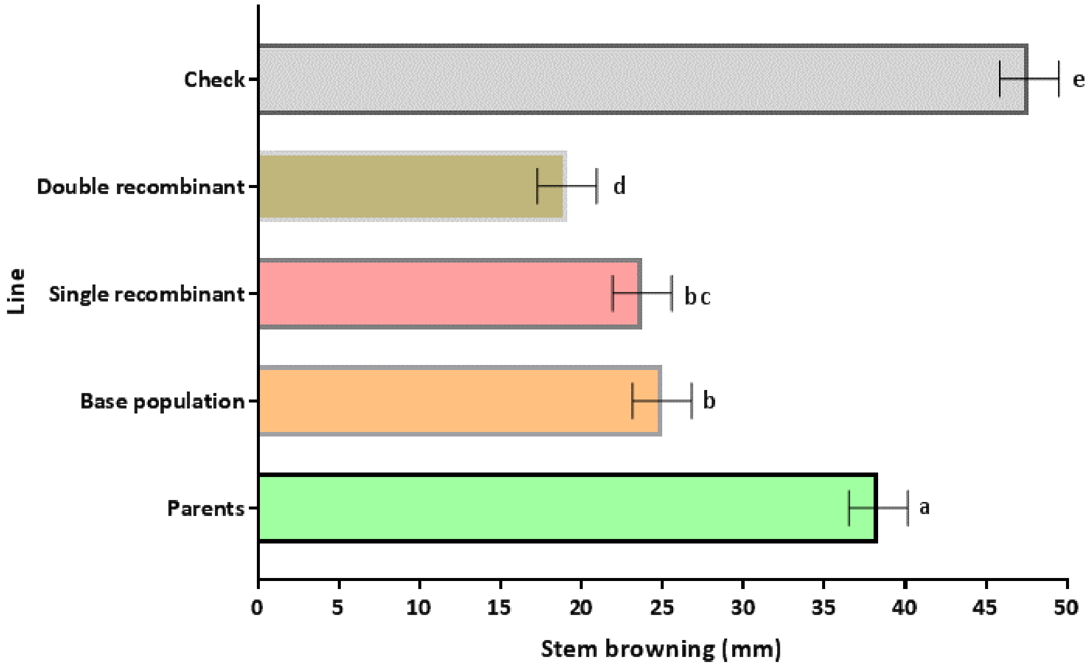


Fig. 7.3: Comparison of parents, base population, single recombinants, double recombinants and check cultivars for stem browning in MARS population 1. Different letters indicate significance at P<0.05 based on Fisher's protected least significant difference test.

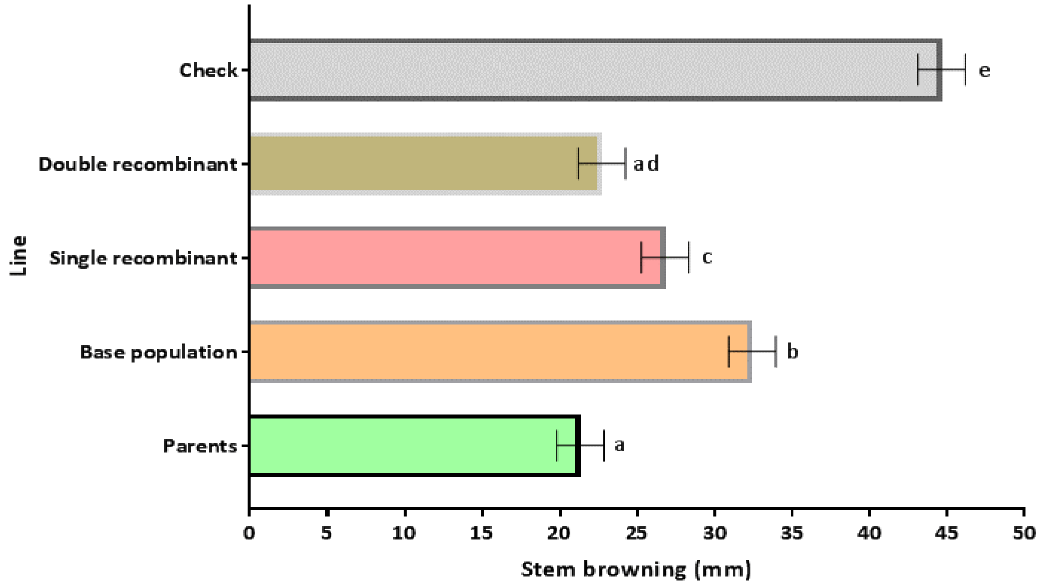


Fig. 7.4: Comparison of parents, base population, single recombinants, double recombinants and check cultivars for stem browning in MARS population 2. Different letters indicate significance at P<0.05.

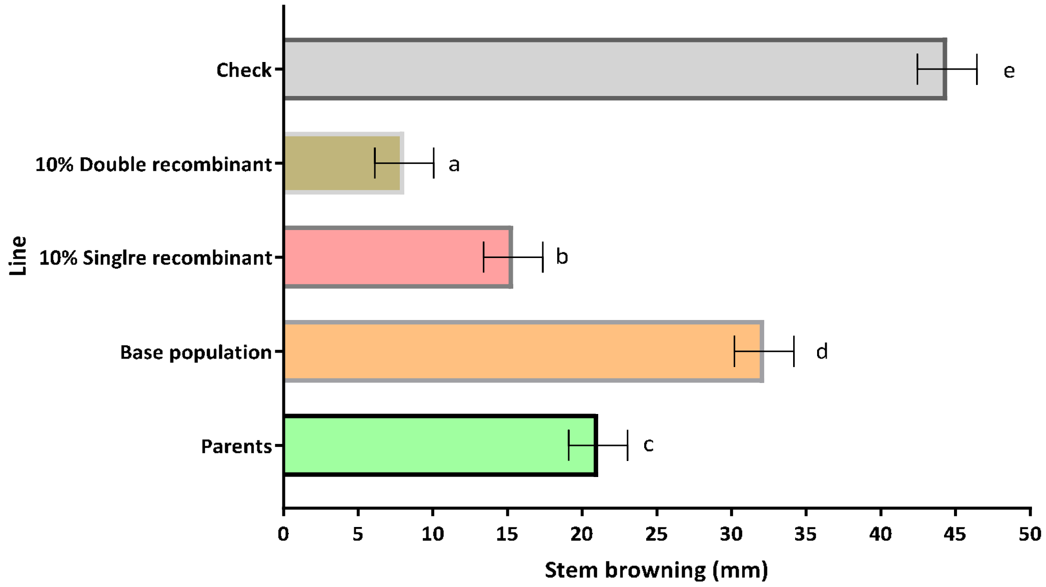


Fig. 7.5: Comparison of the top 10% recombinants compared to the parents, base population and check cultivars for stem browning in MARS population 2. Different letters indicate significance at P<0.05.

The broad sense heritability for stem browning in the base population, single and double recombinants of population 1 was 0.12, 0.11 and 0.21, respectively (Table 7.5). The reduction in disease severity of the double recombinants over the parents, base population and checks was 50.1%, 16.2% and 59.9%, respectively (Table 7.5). However, the reduction in disease severity of the single recombinants over the parents, base population and checks was 38%, 4.9% and 50.2%, respectively (Table 7.5).

Table 7.5: Mean stem browning (mm), broad sense heritability, GA (genetic advance), percentage genetic gain over the mean, percentage gain over the base population, percentage gain over the parents and percentage gain over the checks in MARS population 1.

Line	Mean	Heritability	GA	Genetic gain %	Gain over Base population%	Gain over Parent%	Gain over check%
Check	47.66						
Parent	38.33						
Base population	24.97	0.12	3.60	14.40			
Recombination	22.8	0.12	3.76	16.49			
Single recombination	23.74	0.11	3.22	14.14	-4.93	-38.06	-50.19
Double recombination	19.11	0.21	6.65	29.15	-16.18	-50.14	-59.90

The broad sense heritability for stem browning in the base population, single and double recombinants of population 2 was 0.12, 0.16 and 0.30, respectively (Table 7.6). The mean percentage genetic gain after two cycles of recombination was 38.9. After the second cycle of MARS, there was a marked decrease in disease severity on the double recombinant material. The reduction in disease severity of the single recombinants over the base population and checks was 17.3%, and 40%, respectively while the reduction in disease severity of the double recombinant over the base population and checks was 29.9%, and 49%, respectively (Table 7.6). However, compared to parents the increase in disease severity was recorded in both cycles, but a marked reduction in disease severity of the top 10% single and double recombinants over the parents was evident. While stem browning was used to evaluate resistance in both the field, several other traits related to tolerance and resistance were also evaluated in yield loss trials. These include grain yield, % yield loss, TKW, % screenings and % WH. These traits were assessed to understand the impact of crown rot on yield and its components.

Table 7.6: Mean stem browning (mm), broad sense heritability, GA (genetic advance), percentage genetic gain over the mean, percentage gain over the base population, percentage gain over the parents and percentage gain over the checks in MARS population 2.

Line	Mean	Heritability	GA	Genetic gain%	Gain over Base population%	Gain over Parent%	Gain over check%
Check	44.64						
Parent	21.32						
Base population	32.41	0.12	3.88	11.98			
Recombination	24.99	0.22	6.34	25.41			
Single Recombination	26.80	0.16	4.41	16.44	-17.31	25.70	-39.96
Double Recombination	22.73	0.30	8.84	38.89	-29.87	6.61	-49.08

7.3.3 Effect of recurrent selection for resistance on yield loss

7.3.3.1 MARS Population 1

Grain yield under crown rot pressure is the dominant trait wanted by breeders and farmers. Analysis showed that both genotype and inoculum had a significant ($p<0.001$) impact on grain yield, TKW, % screenings, % WH and stem browning (Table 7.7). However, the genotype x inoculum interaction, while significant for % screenings and % WH, was not significant for grain yield and TKW. Mean grain yield and TKW were higher in un-inoculated treatments as expected. Higher % screenings and % WH were recorded under inoculation. Group effects (e.g. parents, base population, single recombinants and checks) were highly significant ($p<0.001$) for % screenings and stem browning (Appendix V, Table 3). The yield was not assessed on the double recombinants due to insufficient seed at the time of evaluation. Inoculum effects were significant for all traits except TKW. There was no significant group x inoculum interaction for all traits (Appendix V, Table 3).

The means of each genotype grouping (parents, base population, single recombinants and check cultivars) for a range of traits including yield in both treatments are summarized in Table 7.8. The single recombinants did not significantly differ for grain yield, TKW and % yield loss compared to other genotype groups. However, they produced significantly higher % screenings, % WH and stem browning under inoculation compared to the parental group. The mean % screenings and % WH incidence of the single recombinants was not significantly different from the mean of the base population and check cultivars. As expected, the mean stem browning of the single recombinants was significantly lower than that of the base population.

Table 7.7: Wald statistics from tests of fixed effects for traits evaluated in inoculated (plus) and un-inoculated (nil) environments in MARS population 1

	Wald statistics				
Source of variation	Yield	TKW	% Screenings	% WH	Stem browning (mm)
Genotype	187.37**	1470.08**	592.94**	343.45**	2197.55**
Inoculum	306.2**	19.87**	302.72**	284.37**	-
Genotype X Inoculum	117.15^{ns}	143.28^{ns}	228.27**	356.72**	-
	Treatment means				
Nil	3193	34.51	2.087	0.536	-
Plus	2372	33.62	4.048	10.154	-
SED	47.97	0.203	0.116	0.58	-
LSD	94.02	0.88	0.66	1.48	-

** indicates significance at P<0.01, ns indicates no significance. % Screenings, Percent screenings; % WH, percent white heads.

Table 7.8: Means of four groups of entries (founder parents, base population, single recombinants and check cultivars) from population 1 for yield, TKW, % screenings, % WH, stem browning and % yield loss in both inoculated (plus) and un-inoculated (minus) conditions.

Group	Yield		TKW		% screenings		% WH		Stem browning	%Yield loss
	Minus	Plus	Minus	Plus	Minus	Plus	Minus	Plus	Plus	
Parent	3274aA	2542aA	36.12aA	35.59aA	1.142aA	2.26aA	0.00aA	1.63bA	10.17A	21.38A
Base population	3010aA	2456aA	34.35aA	33.8aA	2.941aBD	4.62aB	1.234aA	7.59aAB	17.31C	22.1A
Single recombinants	3211aA	2355bA	34.29aA	33.38aA	2.125aAB	4.08bBC	0.17aA	10.42bB	14.31B	26.24A
Check	3292aA	2513bA	34.39aA	34.03aA	1.723aAC	3.46aAC	0.155aA	8.51bB	13.41B	25.02A

Note: Different upper case letters in columns represent significant differences at the P<0.05 probability level (LSD$_{0.05}$) and different lower case letters in rows show significant differences at the P<0.05 probability level (LSD$_{0.05}$).

Comparisons among the check cultivars, parents, base population and the top 10% of single recombinants selected on the basis of high grain yield under crown rot pressure are presented in Table 7.9. The top 10% of single recombinants had higher mean grain yield (3001 kg ha^{-1}) under inoculation than the parents, base population and check cultivars. The gain in grain yield of the selected single recombinant entries under inoculation over the parents, base population and checks was 19%, 23% and 19%, respectively. However, a respective reduction in TKW of 11.4%, 9.6% and 7.9% was observed. Compared to the parents, base population and check cultivars, the reduced yield loss of the single recombinants was 5.3%, 28.4% and 38.6%, respectively. Percentage WH incidence in the single recombinants was 57.6% and 62.1% lower than the base population and check cultivars, respectively. The observed decline in disease severity of the single recombinants over the parents, base population and checks was 54.7%, 47.4% and 66.7%, respectively.

Table 7.9: Comparison of the top 10% of single recombinants with the parents, base population and check cultivars for yield, TKW, % screenings, % WH, yield loss and WSB under crown rot disease in population 1

Traits	Single recombinant	Base population	Parent	Checks	Increase over parents%	Increase over base population%	Increase over checks%
Yield (Nil)	3579	2992	3254	3301	9.99	19.62	8.42
Yield (Plus)	3001	2438	2522	2522	18.99	23.09	18.99
TKW (Nil)	31.79	35.21	35.86	34.35	-11.35	-9.70	-7.45
TKW (Plus)	31.32	34.64	35.34	33.99	-11.38	-9.57	-7.86
%Screenings (Nil)	1.95	2.95	1.14	1.73	70.54	-33.91	12.26
%Screenings (Plus)	3.51	4.64	2.25	3.47A	55.60	-24.25	1.15
%WH (Plus)	3.06	7.22A	2.33	8.06	31.12	-57.61	-62.05
%Yield Loss	15.49	21.64	16.35	25.23	-5.26	-28.42	-38.60
WSB (Plus)	8.53	16.23	18.84	25.65	-54.72	-47.44	-66.74

Note: TKW = Thousand kernel weight (g); Yield = Grain yield (Kg ha^{-1}); % screenings = Percentage screenings, % WH = Percentage white heads; WSB= Weighted stem browning (mm). Different upper case letters in rows represent significance differences at the P<0.05 probability level ($LSD_{0.05}$)

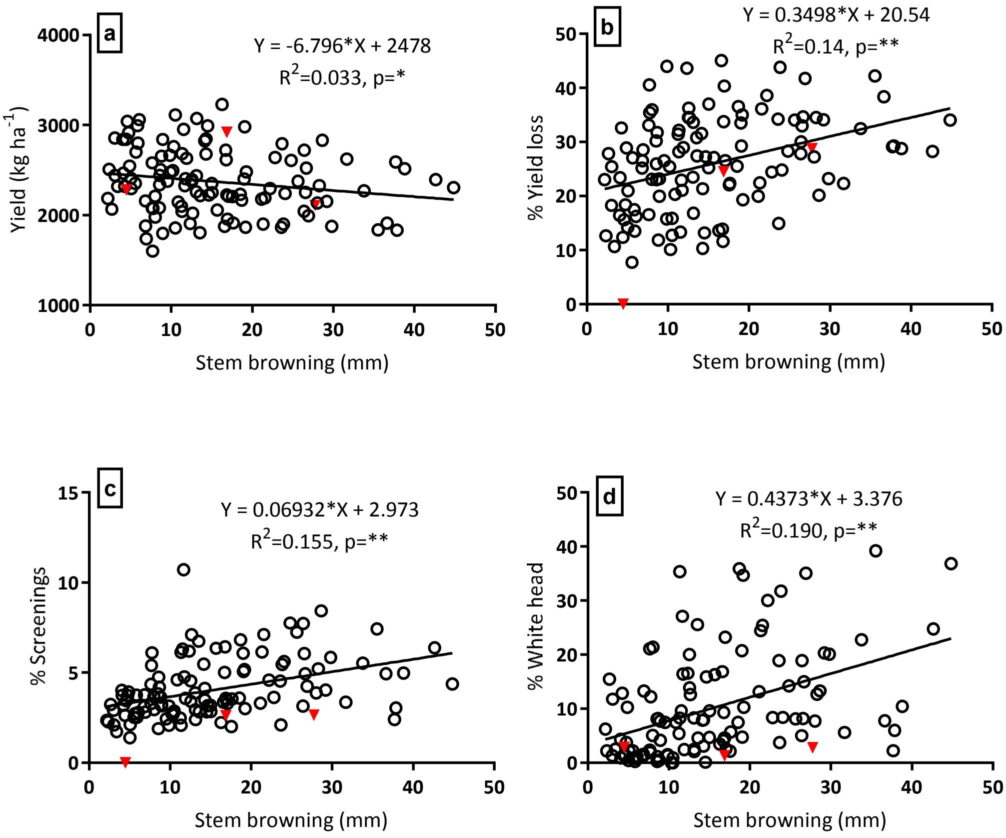


Fig. 7.6: Relationship of disease severity /stem browning and mean a) Grain yield (r = -0.18, p = <0.04); b) Percent yield loss (r = 0.37, p = <0.01) c) Percent screenings (r = 0.39, p = <0.001) and d) Percent white head (r = 0.43, p = <0.001) for crown rot in population 1.

In the inoculated treatment, stem browning explained 3%, 14%, 15%, 19% and 19% of the variation in grain yield, % yield loss, % screenings and % WH, respectively (Figures 7.6). Significant positive correlations were observed between % yield loss and % screenings and % screenings accounted for 11.8% yield variation (Figure 7.7). Significant positive correlations between % WH, % yield loss and % screenings were observed while a significant negative correlation between % WH and grain yield was observed (Figure 7.8b, c and a). Percentage WH accounted for 31.8% of % yield loss, 34.1% of % screenings and 17% of the variation in grain yield. A significant negative relationship was observed between % yield loss and grain yield and % yield loss accounted for 29.4% of the variation in grain yield (Figure 7.8d).

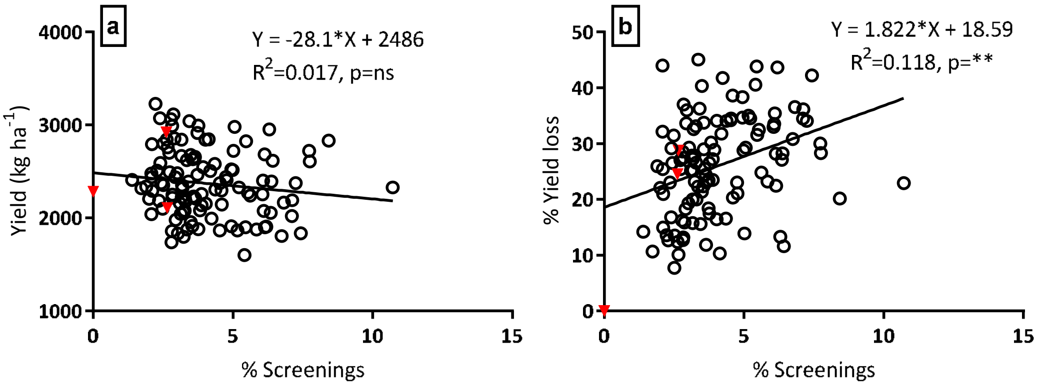


Fig. 7.7: Relationship of percent screenings and mean a) Grain yield (r = -0.13, p = ns); b) Percent yield loss (r = 0.30, p = <0.001) for crown rot in population 1.

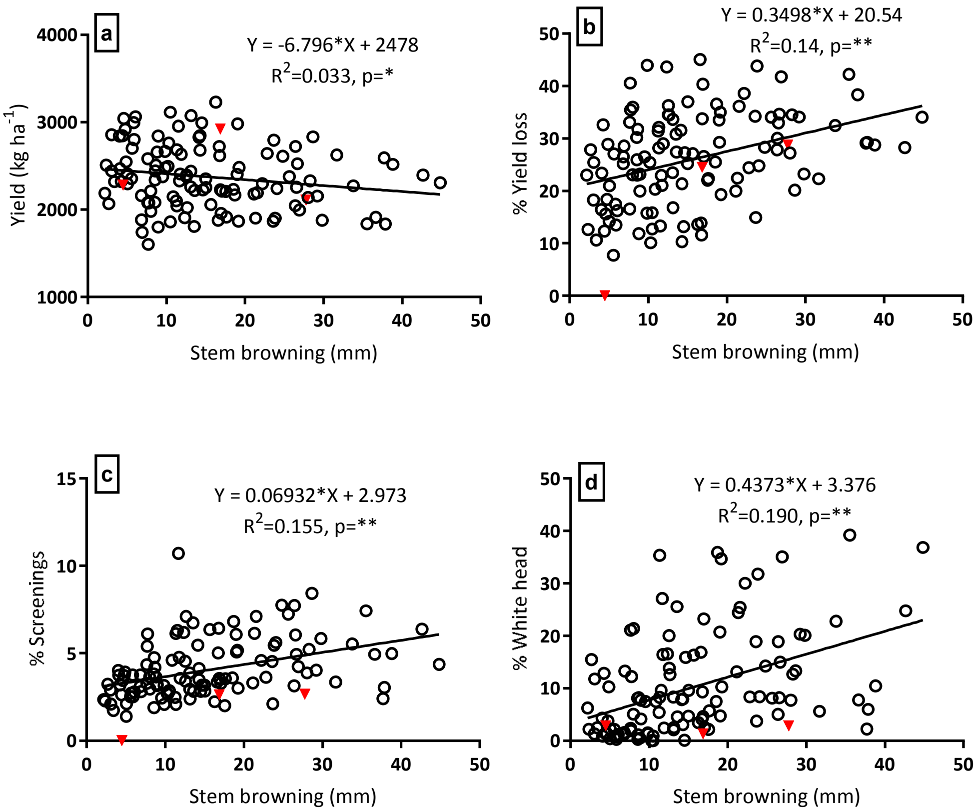


Fig. 7.8: Relationship of percent white head and mean a) Grain yield (r = -0.41, p = <0.001); b) Percent yield loss (r = 0.56, p = <0.001) c) Percent screenings (r = 0.58, p = <0.001) and d) grain yield and % yield loss (r = -0.54, p = <0.001) for crown rot in population 1.

7.3.3.2 MARS Population 2

Highly significant (p<0.001) differences were observed in genotypic effects for all traits as presented in Table 7.10. Inoculum effects were also significant (P<0.001) for all traits, however, there were no significant genotype x inoculum interactions were observed for any trait. Average grain yield (3487 ± 42.55) and TKW (38.40 ± 0.248), were higher in the un-inoculated treatment (Appendix V, Table 8). However, as expected, mean % screenings was higher in the inoculated treatment than the un-inoculated treatment. Highly significant (p<0.001) group effects (e.g. parent, base population, single recombinant and check) were noticed for % screenings and stem browning (Appendix V, Table 4). Significant inoculum effects were observed for grain yield, TKW and % screenings as presented in Appendix V, Table 4. There was no significant group x inoculum interaction for all traits evaluated.

Table 7.10: Wald statistics from tests of fixed effects for traits evaluated in inoculated (plus) and un-inoculated (nil) environments in MARS population 2

	Wald statistics			
Source of variation	Yield	TKW	% screenings	Stem browning
Genotype	327.6**	476.42**	572.05**	1670.04**
Inoculum	74.56**	86.75**	309.06**	
Genotype X Inoculum	128.79^{ns}	131.03^{ns}	149.39^{ns}	
	Treatment mean			
Nil	3290	38.39	1.493	
Plus	2567	36.75	3.05	
SED	87.14	0.21	0.91	
LSD	170.79	0.4	0.176	

** indicates significance at P<0.01, ns indicates no significance

The means of each genotype grouping (parents, base population, single recombinants and check cultivars) for a range of traits including yield in both treatments are presented in Table 7.11. The single recombinants did not significantly differ for grain yield, % screenings and % yield loss compared to parents, base population and checks genotypes, however, mean TKW of the single recombinants was significantly (p<0.05) higher than the mean of the parents under inoculation. The mean TKW of single recombinants was not significantly different to the mean of the base population in both treatments. The mean stem browning of the single recombinant group was not significantly lower than the parental group and base population, but was significantly lower than the check cultivars.

Table 7.11: Means of four groups of entries (founder parents, base population, single recombinants and check cultivars) from population 2 for yield, TKW, % screenings, stem browning and yield loss in both inoculated (plus) and un-inoculated (minus) conditions.

Line	Yield		TKW		% screenings		Stem browning	%Yield loss
	Minus	Plus	Minus	Plus	Minus	Plus	Plus	
Parent	2845aA	2344aA	36.11aA	34.62aA	1.12aA	2.59aA	23.17B	20.04A
Base population	3227aA	2462bA	39.30aB	37.79aC	1.84aA	3.57bAB	19.58B	21.36A
Single Recombination	3394aA	2588bA	38.59aB	36.88bBC	1.71aA	3.22bA	21.67B	19.74A
Check	3334aA	2312bA	36.52aAC	35.50aAB	1.44aA	2.77bAC	16.33A	22.42A

Note: Different upper case letters in columns represent significant differences at the P<0.05 probability level ($LSD_{0.05}$) and different lower case letters in rows show significant differences at the P<0.05 probability level ($LSD_{0.05}$).

The mean comparisons of the parents, base population, check cultivars and the top 10% of single recombinants selected on the basis of higher grain yield under crown rot pressure are shown in Table 7.12. After the first round of MARS, some lines showed higher grain yield under crown rot. The top 10% of single recombinants had higher mean grain yield (3037 kg ha^{-1}) than the parents (2312 kg ha^{-1}), base population (2453 kg ha^{-1}) and check cultivars (2333 kg ha^{-1}) under crown rot. The group of selected single recombinant entries also had higher mean grain yield than the parental group, base population and check cultivars without inoculation. Mean TKW was higher than the parents and check cultivars in both treatments and higher than the base population without inoculation. Mean % yield loss of the single recombinants was lower than the parents, base population and check cultivars while % screenings under inoculation was lower than the base population. Stem browning of the top 10% of single recombinants was lower than the parents, base population and checks. The maximum gain in grain yield of the selected single recombinant entries under inoculation over the parents was 31.4%, 30.18% compared to the checks and 23.8% over the base population. In contrast, the maximum decrease in yield loss was 27%, 26.9% and 16.7% over the base population, check cultivars and parents, respectively. The observed decrease in stem browning of single recombinants compared to the parents, base population and checks was 32.6% and 20%, 5%, respectively, while the percentage decrease in screenings under inoculation compared to the base population was 21.3%. In population 2, stem browning did not have any significant impact on grain yield, % yield loss and % screenings (Figure 7.9a, b and c). Percentage screenings did not influence grain yield nor % yield loss (Figure 7.9d and e). A significant negative relationship was observed between % yield loss and grain yield (Figures 7.9f).

Table 7.12: Percentage change of the top 10% of single recombinants compared to the parents, base population and check cultivars for yield, TKW, % screenings, % yield loss and WSB under crown rot disease in population 2

Traits	Single recombinant	Base population	Parents	Checks	Gain over parents%	Gain over base population%	Gain over checks%
Yield (Nil)	3683	3219	2831	3333	30.10	14.41	10.50
Yield (Plus)	3037	2453	2312	2333	31.36	23.81	30.18
TKW (Nil)	40.42	39.24	36	36.54	12.28	3.01	10.62
TKW (Plus)	37.25	37.81	34.77	35.5	7.13	-1.48	4.93
%Screenings (Nil)	1.916	1.839	1.228	1.416	56.03	4.19	35.31
%Screenings (Plus)	2.819	3.583	1.094	2.778	157.68	-21.32	1.48
%Yield Loss	16.34	22.38	19.62	22.35	-16.72	-26.99	-26.89
Stem browning	15.63	19.53	23.2	16.45	-32.63	-19.97	-4.98

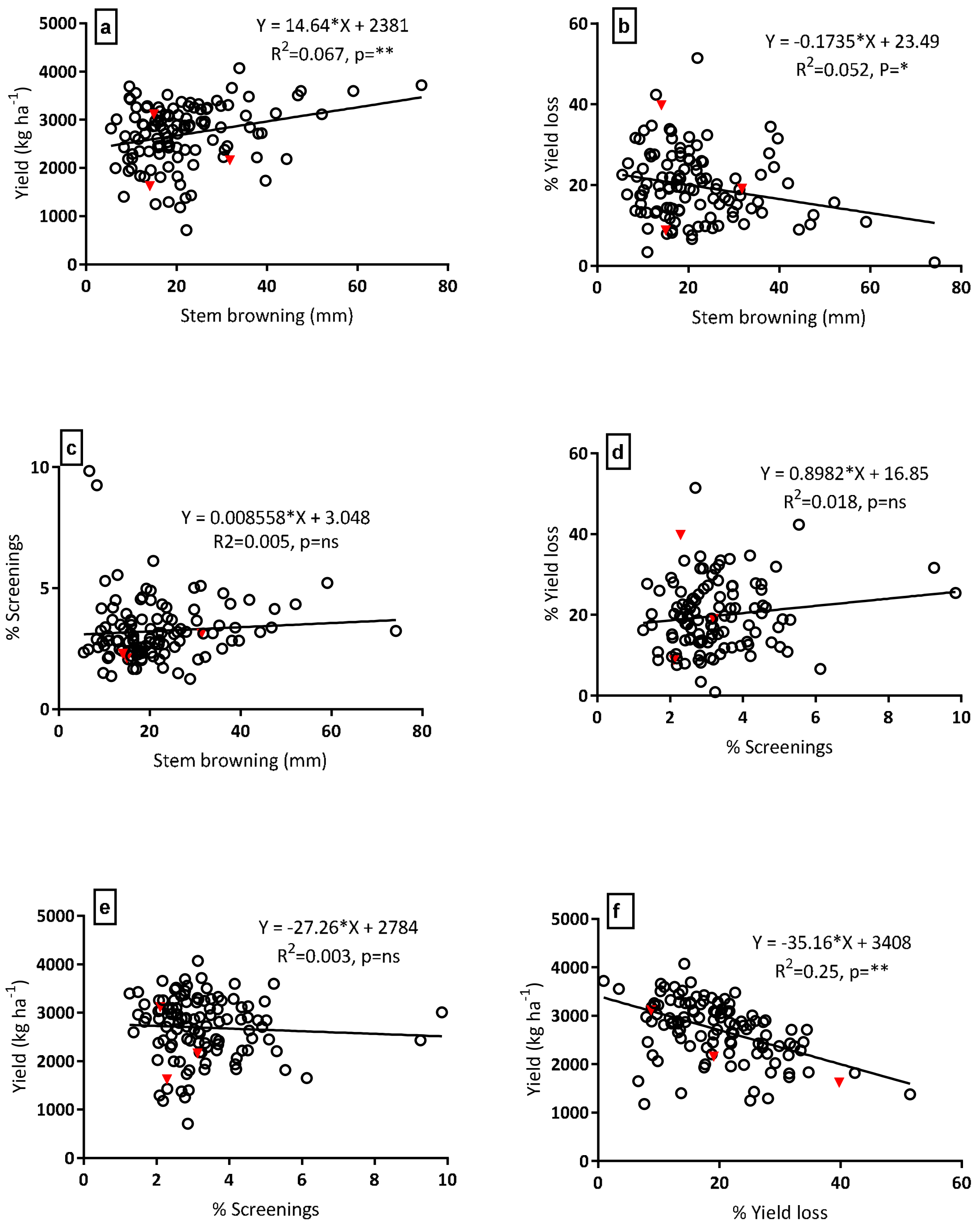


Fig. 7.9: Relationship of disease severity /stem browning and mean a) Grain yield (r = 0.26, p = <0.04); b) Percent yield loss (r = -0.22, p = <0.01) c) Percent screenings (r = 0.07, p = ns), Percent screening and mean d) Percent yield loss (r = 0.13, p = ns); e) Grain yield (r = -0.05, p = ns), and percent yield loss and mean f) grain yield (r = -0.49, p = <0.001) for crown rot in population 2

7.4 Discussion

GWAS detected a large number of significant MTAs linked to crown rot resistance on all genomes in both populations. However, these were reduced by selecting only those regions that were consistent across disease screenings experiments and that explained the greatest portion of the genetic variance for stem browning. Thus 23 SNP markers representing 23 putative QTLs were identified across both populations. These represented 9, 12 and 2 QTLs distributed on the A, B and D genomes, respectively. As in previous GWAS studies, the A and B genomes contributed more MTAs than the D genome (Ullah, 2018; Zegeye *et al.*, 2014; Allen *et al.*, 2013). Previous studies reported significant QTLs for crown rot resistance on chromosome 3B in the Australian crown rot resistant cultivar Sunco under field conditions (Poole *et al.*, 2012). Another study identified regions on chromosomes 1A and 2D linked to adult plant resistance (Martin *et al.*, 2015). Furthermore, QTLs for stem browning in unique positions on chromosomes 1A, 1B, 1D, 3B, 4B and 7A were also reported in previous studies of wheat (Martin *et al.*, 2015; Bovill *et al.*, 2010; Collard *et al.*, 2005). We have identified QTLs in all the above chromosomal regions. However, the significant MTAs on chromosomes 4A, 5B, 6B and 7B in the current study are unique and could either be new regions as no QTLs have been reported previously on these chromosomes, or false positives. These will need to be confirmed. Nevertheless, even though there was some pedigree similarity between population 3 and populations 1 and 2, the locations of many of the QTL are different to those identified in Chapter 6. This can be explained by what did differ among the crosses; with the key parents AUS29529, CSCR16 a SYN110 contributing unique variation to each population.

The level of resistance of a genotype is determined by the extent of stem browning on the lower stem and crown (Liu and Ogbonnaya, 2015). Plants with reduced length of stem browning are considered resistant to crown rot. Highly significant differences were observed among the genotypes in each population and among the groups of germplasm in each population including parents, base population, single recombinants, double recombinants and check cultivars (Table.7.4). The observed increased resistance to crown rot with increasing accumulation of SNP markers linked to resistance, in populations 1 (Figure 7.3) validates the use of MARS for the genetic improvement of complex traits. While a similar trend was observed in population 2 between the base population and the double recombinants, the parents exhibited an equivalent degree of resistance to the double recombinants (Figure 7.4). However, when the mean value of the top 10% of both single and double recombinants was compared, a marked increase in resistance to crown rot was observed (Figure 7.5). This result typifies the complexity of this disease. However, the steady improvement in resistance through the accumulation of significant marker effects identified in the base population once again validated the effectiveness of MARS. This approach is a strategy for improving intractable diseases and as such other favourable traits are concurrently selected and improved. This was the case in population 2.

While stem browning under high disease pressure was the primary selection target in this MARS strategy, yield loss was assessed to evaluate the impact of improved resistance on other traits including grain yield, particularly given that the outputs of this strategy are to enter commercial breeding programs. While the means of the different groups (parents, base population and single recombinants) were not significantly different for yield in both populations, there was a trend to higher yield in the recombinants. This became much stronger when the top 10% of single recombinants were selected and compared for yield. These selected materials were 19% and 31% higher yielding than the parents in populations 1 and 2, respectively. These single recombinant lines with high yield and improved resistance to crown rot, including entries 80, 81, 82, 87 and 89 in population 1 and 51, 59, 75, 77 and 86 in population 2, (Appendix V, Table 5 and Table 8) can be used in applied wheat breeding as parents to improve adaptation. The single recombinants (the double recombinants were not included in yield loss trial) were clearly higher yielding than the parents and carried higher resistance to crown rot (Table 7.9 and 7.12). This is clearly a successful breeding outcome from the MARS approach. MARS has been used in maize to improve grain yield under drought stress (Beyene *et al.*, 2015; Beyene *et al.*, 2016). These authors reported a consistent improvement in genetic gain in eight maize populations compared to the parents. There is one report of the successful use of MARS in wheat (Jain *et al.*, 2014). In this study, 4-8 favourable QTLs identified in the base population for yield, drought and heat adaptive traits, were recombined and progenies with superior grain yield compared to check cultivars and parents identified. Recurrent selection (without the assistance of molecular markers) was also successfully used to improve disease resistance in barley (leaf rust), oats (crown rust) and rice (leaf blast) (Reinhold *et al.*, 1993; Diaz-Lago *et al.*, 2002; Vales *et al.*, 2009). However, none of these diseases was as genetically complex as crown rot in wheat.

An important component of grain yield is TKW, and the recombinant DH lines did not significantly differ in TKW from other groups of materials. The mean TKW of the top 10% of selected recombinant lines, in fact, was higher than parents and check cultivars in population 2 and lower than the parents, base population and checks in population 1. These differences are probably artefacts of the two populations. Yield is a balance between grain number and grain size, and optimization of yield may lead to a decrease in grain weight in some circumstances (Foulkes *et al.*, 2010). The Jain *et al.* (2014) study also found both positive and negative changes in TKW in a MARS breeding strategy. The relatively poor association observed between stem-browning and yield under crown rot pressure highlights the strong influence of environment on disease expression (see Chapter 5). The same results were observed in populations 1 and 2 where basal stem browning was very inconsistent and highly influenced by environment and revealed to have little influence on grain yield and a moderate influence on % screenings and % WH in population 1 only, while stem browning did not influence on grain yield, % screenings under crown rot pressure in population 2. Stem browning showed to some extent a positive association in population 1 since stem browning accounted for 14% variation in % yield loss. In contrast, stem browning was not associated with grain yield and % yield loss in population 2. Similar observations were made by Smiley *et al.* (2005) that the degree of stem browning on adult plants is greatly affected by the environmental conditions, resulting in enormous variation year to year, paddock to paddock and even within paddocks in the same year and the yield reduction does not associate with the degree of stem browning. In the current study, however, % WH had a significant positive correlation with % yield loss and % screenings, and a negative correlation with grain yield. Percentage WH accounted for 32% and 17% of total variation in screenings and grain yield, respectively. Percentage WH was also the major contributor to variation in yield loss (31.8%). Similar results were also observed in Chapter 5 in population 3 (Table 5.5, Figure 5.9 and 5.10).

Yield loss is a measure of the disease tolerance of a genotype (Smiley and Yan, 2009). In the current study, mean yield loss of the top 10% of recombinants was generally lower than the precursor materials following MARS for crown rot resistance. However, the stem browning of the top 10% of single recombinant lines was much lower (decreasing by up to 67% and 33% in populations 1 and population 2, respectively). This is the first report of the improvement in crown rot incidence of wheat using MARS. Mean yield loss between the single recombinants and other groups was not significant, but the decrease in yield loss of the top 10% of recombinants was up to 39% and 27% in populations 1 and 2, respectively. However, it is likely that this will be enhanced once the double recombinants are evaluated. Massman *et al.* (2013) observed that yield improved between the first and second round of recombination in a MARS strategy in maize. Nevertheless, the selected single recombinants in the current study did provide a substantial yield improvement, although these responses would need to be validated in new head-to-head comparisons.

7.5 Conclusion

This study validated the effectiveness of MARS for improving crown rot resistance in wheat. The recombined materials with accumulated MTAs produced significantly improved resistance compared to their constituent materials. While no strong relationship between resistance and tolerance (determined as yield under crown rot pressure) was observed, the selected single recombinant lines did have much higher yield and resistance compared to their constituents. While these materials will need to be validated in other environments, they do provide a valuable source of improved adaptation to crown rot for plant breeders.

It should also be noted that this chapter was an examination of a breeding methodology and not a pure QTL study. While none of the markers were validated, the validation of the approach was in the performance of the derived progeny that were developed by recombining these significant markers. The use of markers in this way vastly reduced the numbers of lines that had to be phenotyped in the development of new lines and helped target the crossing at the different stages of recombination.

CHAPTER 8

General discussion

Crown rot is considered to be the second most important disease (economically) in Australia (Chakraborty *et al.*, 2006), with estimates of economic losses of $79 million annually in wheat and $97 million when combined with barley (Murray and Brennan, 2009b; Murray and Brennan, 2010). Crown rot can cause up to 100% crop losses (Stephens *et al.*, 2008; GRDC, 2009) and an 89% reduction in average yield in Australia (Klein *et al.*, 1991). A number of control measures have been demonstrated to be at least partially effective (Golkari *et al.*, 2008; Simpfendorfer, 2012d; Simpfendorfer *et al.*, 2006), while no fungicides are effective at controlling this disease (GRDC, 2009) . Therefore, a combination of cultivars with improved resistance and/or tolerance to crown rot and optimised crop management is the only sustainable strategy to control this disease. To breed for crown rot resistance/tolerance it is first necessary to identify sources of variation within the accessible germplasm. Partial resistance and tolerance to crown rot have been identified in a range of wheat materials both in Australia and other parts of the world (Smiley and Yan, 2009; Liu and Ogbonnaya, 2015). Incorporation of these sources into elite germplasm, however, has proven challenging due to association of resistance with poor agronomic traits including low yield potential, poor grain quality, tall plant height and undesirable maturity. In addition, the genetic control of the resistance and tolerance is generally complex, with many minor genes and QTL controlling the plant response (Bovill *et al.*, 2006; Ma *et al.*, 2010; Poole *et al.*, 2012; Martin *et al.*, 2015). Molecular markers, once identified, could be used in MAS, MABC, genomic selection and MARS to accelerate the development of desired germplasm (Beyene *et al.*, 2016; Agostinelli *et al.*, 2012). However, not all molecular approaches are appropriate or equally effective. In this study, a MARS strategy was evaluated to pyramid the many minor genes controlling the crown rot response in a short period of time. The premise was that the QTL thus identified would be effective in the recombinants of the same population. To demonstrate the practicalities of using MARS for improving crown rot resistance and tolerance in wheat, three populations were developed and the phenotyping approach optimized. The impact of recombination on disease expression, yield loss and other traits was then assessed and positive responses were observed.

8.1 Optimizing phenotyping for adult plant resistance

A pot test was suggested to be a reliable, repeatable and effective method for phenotyping crown rot disease resistance at the mature plant stage. This was because the inoculum and growing conditions could be managed. To validate this premise, the pot test was compared to field screening and it was concluded that field screening was in fact more relevant and provided better range in the data. The pot test was clearly too severe to identify the critical partial resistance phenotype. This may have been a result of lack of control over spore concentration in the development of the inoculum and finer control may have reduced the intensity of the disease expression.

To establish disease at the seedling stage requires good surface soil moisture (Swan *et al.*, 2000) and low rainfall and higher temperature at the adult plant stage (drought or a stressed environment) (Backhouse and Burgess, 2002; Hollaway *et al.*, 2013). The weather at Narrabri in 2012 (Figure 4.1) was conducive to the establishment and expression of crown rot. The field experiments followed standard wheat practices in a conducive environment and were thus more relevant than the pot experiments which were conducted in glasshouses. The range of variation in stem browning in field experiments was much greater than that observed for the pot experiments (Tables 4.1 and 4.2). The higher rainfall observed in June-July (disease establishment period) and very low rainfall in September- October (Figure 4.1) will have aided the field screening. The inability of the pot experiments to identify partial resistance was a function of excessive inoculum which was not representative of actual practice. The seedlings grew through the inoculum on the pot surface and this created an epidemic that was too severe. Differences in soil compactness could also have produced different water-holding capacities in each pot which may have produced different water stress thus affecting the development of stem browning (Li *et al.*, 2008). The growing conditions (e.g. water application and temperature) in the glasshouse may also have contributed to the excessive expression of crown rot in pots. Crown rot resistance is highly complex and greatly influenced by environment (Collard *et al.*, 2005; Bovill *et al.*, 2006; Wallwork *et al.*, 2004); the pot-test conditions may be better optimized using different soil, temperature and lower inoculum levels. However, the field tests are simply more relevant to farmer conditions and these can also be managed using defined inoculum and irrigation. For this reason field phenotyping was used extensively in the thesis to evaluate adult plant resistance.

8.2 The genetic variation for crown rot tolerance and resistance

Tolerance is very important for ensuring high yield in the presence of the pathogen. However, resistance is vital for reducing inoculum loads in the field and maintaining the health of the farming system. Others have observed a positive relationship between crown rot resistance in spring wheat and tolerance (Nicol *et al.*, 2007). Tolerance was defined by Bingham *et al.* (2009) as little or reduced yield loss in the presence of pathogen inoculum. It is generally measured by comparing yield loss in inoculated and un-inoculated plots (Smiley and Yan, 2009). Resistance in contrast, is the ability of a plant to restrict the infection and growth of the disease by the pathogen throughout the plant (Agrios, 2005). In Australia, stem browning on adult plants are commonly used to measure resistance (Liu and Ogbonnaya, 2015). White head incidence greatly influences kernel weight and increases the proportion of shrivelled grains, thus reducing grain yield (Hollaway and Exell, 2010). Shrivelled grain increases % screenings, reduces the quality of wheat and has an adverse effect on the value of the crop (Nuttall *et al.*, 2017).

Although stem browning is a reliable method of measuring crown rot resistance, it is highly laborious and very expensive and the expression of white heads, which is easier to assess, depends entirely on the environment (Smiley *et al.*, 2005; Smiley and Yan, 2009). For example, the evaluation of all components of MARS populations 1 and 2 in 2017 required the evaluation of over 45,000 tillers. Clearly, the availability of molecular markers linked to improved resistance would be very cost effective. This study also attempted to combine tolerance and resistance. While several studies have assessed both resistance and tolerance to crown rot in the field, none have used inoculated and un-inoculated paired plots. Instead, the treatments have been separate blocks, often un-replicated (Daniel and Simpfendorfer, 2008; Martin *et al.*, 2015; Wallwork *et al.*, 2004; Smiley and Yan, 2009). Variation in the soil highly influences disease infection and expression thus affecting grain yield and other traits. Paired plots overcome these limitations, although are difficult and expensive to establish and manage, and cannot be used in wide scale breeding programs. The current study revealed that under inoculation, grain yields were significantly reduced by increasing % screenings, %

WH and WSB compared to un-inoculated plots (Chapter 5, Table 5.2; Appendix III, Table 1, 2, 5, 6 and 7). The observed genotypic differences in grain yield, TKW, % screenings, % WH and WSB were sufficient to exploit in breeding and selection. However, the expression of these traits was highly influenced by differences in rainfall and temperature between years (Chapter 5, Figure 5.1 and 5.2). In 2014, the average rainfall was lower during June-July and the post-anthesis period was wetter and cooler than 2015. Therefore, disease establishment and expression was better in 2015. These differences typify the challenges of phenotyping crown rot.

Percentage yield loss, the measure of tolerance, was also higher in 2015 (17.4%) compared to 2014 (7.3%) due the environmental differences. Drier warmer conditions, as experienced in 2015, accelerated the production of more white heads with shrivelled and sub-standard grain (Burgess *et al.*, 2001; Obanor and Chakraborty, 2014). The positive correlation between white head incidence and screenings helped explain their influence on greater yield loss. More shrivelled grain reduces grain weight and eventually yield. If kernel weight can be maintained in the presence of the disease (with fewer screenings) then yield can be improved. Klein *et al.* (1991) also reported a direct association between yield losses and white head incidence which was linked to reduced grain size. Although others suggested that it would be erroneous to estimate yield reduction and screenings based on whitehead incidence (Hollaway *et al.*, 2013), given the seasonal influences. Stem browning is generally used to measure crown rot resistance but the degree of stem browning varies from year to year due to variation in environments (Smiley and Yan, 2009). This was also observed in the current study. Although stem browning was significantly correlated with white head incidence, yield loss and grain yield in 2015, its overall contribution to these traits was very low (Chapter 5, Figure 5.8, 5.9; Chapter 7, Figure 7.6 and 7.9). On the contrary, white head incidence explained 39% of the variation in yield loss and 22.8% of the reduction in grain yield. Tolerant genotypes were characterized by lower yield loss, fewer screenings, reduced white head incidence and higher grain yield and kernel weight (Chapter 5, Table 5.5, Figure 5.4, 5.5 and 5.6; Appendix III, Table 5, 6, 7, 12 and 14), while resistant and tolerant genotypes had consistently lower stem browning, white head incidence, yield loss and screenings and higher TKW (Chapter 5, Table 5.6 and Appendix III; Chapter 7, Appendix V).

Clearly, genetic variation for crown rot tolerance and resistance was identified in the current study using inoculated and un-inoculated paired plots and this variation was sufficient to exploit in breeding and selection. However, whiteheads are a function of the plant's ability to cope with infection and continue to yield. It does not measure the amount of fungus in the plant, and the experimental data revealed that white head formation was weakly correlated with the degree of stem browning but moderately to strongly associated with yield, screenings and yield loss. Therefore, white head incidence can be used to assess tolerance, while stem browning is only a measure of resistance. Stem browning was effective in determining resistance only and was not associated with tolerance determined as yield under crown rot pressure or yield loss.

8.3 Genetics of resistance and tolerance to crown rot

GWAS identified 142 markers linked to grain yield under inoculation (Chapter 6). Of all the SNPs identified, *BS00000929_51* located on chromosome 5D explained the highest phenotypic variation (R^2 = 11.4%) (Table 6.4). Some markers had pleiotropic effects with TKW (Table 6.5) and 227 markers linked to TKW were common to both treatments. Markers on chromosome 5A explained the largest variation in TKW (6-8.33%). In 2015, 28 MATs were identified for white head incidence although none were found in 2014 due to the less favourable environment for white head expression. Chromosomes 5B, 6B and 7B tended to be associated with reduced white head incidence. These are new findings as no previous reports on the genetic control of white head incidence have been published. However, markers for resistance, assessed as stem browning, on chromosomes 2B, 4B, and 4D were identified earlier on the same chromosome arms (Wallwork *et al.*, 2004; Poole *et al.*, 2012). Six unique markers on chromosomes 1A, 3A, 5A, and 7B were linked to reduced screenings under inoculation and three markers, located on 1A and 3A, had a pleiotropic effect with TKW (Chapter 6, Table 6.5). Others also found stem browing QTLs on 1A and 3A (Martin *et al.*, 2015). However, no one has reported QTL for any trait linked to resistance or tolerance on chromosome 7B. In the current study, two markers located on chromosomes 2B and 6A were linked to reduced stem browning on adult plants. Martin *et al.* (2015) and Poole *et al.* (2012) also found stem browning resistant markers on 2B.

Of the 23 SNP markers located in unique chromosomal regions across the genome and used for MARS recombination (Table 7.3), none were located chromosomes 2B or 6A. Previous GWAS have reported more MTAs on the A and B genomes than the D genome (Ullah, 2018; Zegeye *et al.*, 2014; Allen *et al.*, 2013) and the current study was no exception. However, Liu and Ogbonnaya (2015) and Powell *et al.* (2017) found more resistance QTLs were located on the B and D genomes than the A genome.

In population 3 (Chapter 6), four MTAs located on chromosome 5D were common in both treatments and these markers had a pleiotropic effect on shorter days to flowering, early maturity and higher grain yield. Once validated, these markers could be used for selecting genotypes with reduced height, increased earliness and improved grain yield. The current study also revealed QTLs with a specific but independent effect on crown rot resistance and tolerance. A total of 45 QTL were identified for crown rot tolerance (Chapter 6, Table 6.4) and some of these were co-localised with other traits including screenings, TKW and yield. Three unique QTLs (7, 8 and 40) were identified for resistance and reduced stem browning. A further five unique QTLs (23, 24, 32, 42 and 40) reduced white head incidence. QTL_9 on chromosome 2B reduced white heads and increased grain yield while QTL_47 on chromosome 7B reduced both white heads and screenings.

However, no genomic region or MTA for stem browning was co-located with other traits (% white heads, grain yield, % screenings, TKW), indicating that the genetic control of resistance was not related to the genetic control of tolerance. These results are supported by the phenotypic results of chapter 5 (Figure 5.7, 5.8), where resistance associated with stem browning was only weekly related to tolerance assessed as yield loss.

The newly identified genomic regions related to resistance and tolerance still require validation before they are used extensively in MAS. Population 3 (Chapter 6) was developed to validate these findings. Twenty-nine markers that were related to resistance and tolerance traits were selected and six genotypes carrying complementary sets of alleles were identified for crossing. Few of these SNP markers occupy similar chromosome regions to those identified in populations 1 and 2, indicating that the inheritance of resistance and tolerance is different in this population. However, at the writing of this thesis, the 1st cycle recombinants from population 3 have yet to be genotyped and assessed for crown rot resistance and tolerance.

In future, a genomic selection approach might allow all the additive effects and markers associated with crown rot resistance and tolerance to be combined. However, a better phenotyped and more extensive training population will need to be developed upon which to base genomic estimated breeding values for each material.

8.4 MARS as a practical way to pyramid genes in wheat breeding

There are several limitations to using recurrent selection in a self-pollinated crop such as wheat. These include recombination, which is difficult to achieve among many progeny, and the identification of progeny for recombination that are polymorphic or carry complementary alleles. MARS overcomes both limitations as progeny are selected for recombination based on their marker profile, thus fewer and better targeted crosses are made during the recombination phases. The approach also overcomes the important issue of QTL expression in unrelated backgrounds; a constant problem in crown rot genetics (Bovill *et al.*, 2010).

Significant and gradual reduction in disease severity was obtained in MARS populations 1 and 2 with cycles of recombination. This reduction was even greater when the best single and double recombinants were selected and compared to the parents, base population and checks. Even though the double recombinants in population 2 were equivalent to the parents for stem browning, these materials were higher-yielding. Thus a high level of resistance was transferred to genotypes with superior yield. This underpins the MARS approach which follows a pragmatic breeding philosophy. Selection for agronomic type and other characters is practiced throughout the MARS processes. The MARS strategy also allowed many markers to be combined in a very short time period (just 4-years). Up to 22 SNP markers were combined in single plant progeny. To achieve a similar outcome using backcrossing would take considerably longer. The improvement in crown rot resistance observed in this study was consistent with improved trait values reported in other crops (Beyene *et al.*, 2015; Beyene *et al.*, 2016).

Yield gains up to 31% were observed in selected single recombinants under crown rot pressure compared to the parental materials and similar improvements in stem browning, kernel weight and screenings were observed, although the parents tended to have lower screenings. This probably reflects the increased selection pressure applied to the parents for seed size by the breeders who developed the parental materials.

The effectiveness of using MARS is detailed in Chapter 7. The study showed that resistance to crown rot increased through the accumulation of SNP markers linked to resistance in both, and validates the use of MARS for genetic improvement of crown rot disease in wheat. It can be comfortably concluded that the MARS approach produced significant and positive changes in stem browning as markers were accumulated through recurrent selection.

8.5 Conclusion

The key findings of this research experiments are given below:

- Pot-based screening for disease severity at the adult plant stage was inconsistent and considered to be unreliable. Field screening was consistent and more reliable and adopted to assess crown rot response (Chapter 4).
- Response to crown rot was consistent across years in some genotypes (entries 31 and 89) and these can be used as parents for developing resistant and tolerant cultivars (Chapter 5)
- Tolerance and resistance were poorly related when basal stem browning was measured as resistance (Chapter 5, Chapter 7)
- White head incidence, screenings and yield loss can be targeted to improve crown rot tolerance in bread wheat (Chapter 5, Chapter 7)
- Selection for tolerance to crown rot was more effective than resistance for improving yield (Chapter 5)
- Putative genetic control of yield, TKW, screenings, white head and stem browning under crown rot pressure were identified (Chapter 6)
- First report, although not yet validated, of the genetic control of tolerance to crown rot disease in wheat (Chapter 6)

- New QTL independently associated with resistance and tolerance identified and 9 previously identified QTL for resistance confirmed (Chapter 6)
- White head incidence was associated with resistance and tolerance but, basal stem browning was independent of tolerance (Chapter 6, Chapter 5 and Chapter 7)
- Recombined materials that accumulated 18-22 markers produced significantly improved resistance compared to their constituent materials (Chapter 7)
- MARS was an effective and rapid way to improve crown rot resistance and/or tolerance using marker information in wheat (Chapter 7)
- MARS was an effective strategy to combine many markers for genes of minor effect in a short time-frame

Overall, the results obtained in these studies is of high significance to improving crown rot resistance and tolerance and could be used in a variety development program.

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Appendix

Appendix I

Table 1: List of SNPs (62) significantly associated with stem browning across pot test summer, pot test winter and field test winter for population 1.

ID	Markers	Chromosome	$-Log_{10}(p)$	Target allele		Entry
34600	IAAV2694	1AL	2.32	AA		13
80192	wsnp_Ku_c183_358844	1AS	2.13		BB	47
10049	BS00067434_51	1BL	2.44		BB	102
10823	BS00075663_51	1BL	2.6		BB	30
67865	Tdurum_contig13117_1316	1BL	2.22		BB	88
51921	Ra_c35710_395	1BL	2.82	AA		82
12484	BS00110148_51	1BL	2.15	AA		102
51198	Ra_c16069_1820	1BL	2.46	AA		93
10997	BS00078228_51	1BL	2.33	AA		31
7076	BS00022429_51	1BS	4		BB	206
23711	Excalibur_c21898_1423	1BS	3.16	AA		100
77798	wsnp_Ex_c3372_6195001	1DL	2.6	AA		103
8257	BS00041010_51	2BL	3.4		BB	33
49084	Kukri_rep_c105330_552	2DL	3.7	AA		49
11934	BS00095512_51	2DS	3.16	AA		24
8864	BS00062567_51	2DS	3.4		BB	27
30974	Excalibur_rep_c68583_1067	3AS	2.02	AA		136
35687	IACX11310	3B_	2.31	AA		221
48415	Kukri_c9571_73	3B_	2.8		BB	12
7902	BS00032694_51	3B_	3.52		BB	220
11049	BS00079029_51	3B_	2.7	AA		85
45539	Kukri_c45513_83	3B_	2.36	AA		108
48859	Kukri_rep_c103205_101	3B_	3		BB	95
8382	BS00044942_51	3B_	2.6	AA		89
9387	BS00064876_51	3B_	3		BB	94
68425	Tdurum_contig15586_563	4AL	2.57		BB	98
9906	BS00066891_51	4AL	3.7	AA		44
24962	Excalibur_c30378_673	4AL	4	AA		25
8008	BS00035307_51	4AS	3	AA		60
79848	wsnp_JD_c64_103934	4AS	3.4		BB	60
62565	RAC875_rep_c69370_218	4BL	2.14	AA		188
78061	wsnp_Ex_c4148_7494801	4BL	2.41	AA		177
7783	BS00030571_51	4BL	3.1	AA		178
39213	Ku_c3385_521	4BL	2.05		BB	178
35773	IACX1632	4BL	2.42		BB	171
78083	wsnp_Ex_c42133_48794975	4DL	2.15		BB	61
5418	BobWhite_rep_c63943_76	5AL	2.05		BB	21

7044	BS00022366_51	5BL	2.02	BB	181
7716	BS00029345_51	5BL	4	BB	29
10444	BS00070139_51	5BL	2.64	AA	29
34448	IAAV178	5BL	3.7	AA	28
6814	BS00021946_51	5BL	2.25	AA	93
7633	BS00026678_51	5BL	2.18	AA	30
4087	BobWhite_c6094_447	5BL	2.37	BB	106
71751	Tdurum_contig47071_1322	5BL	2.38	BB	34
68150	Tdurum_contig14130_315	5BS	2.44	AA	119
7864	BS00032003_51	5BS	2.44	AA	114
11318	BS00083715_51	5BS	2.52	AA	118
68149	Tdurum_contig14130_245	5BS	2.57	AA	121
40294	Kukri_c10243_475	5DL	2.31	BB	147
6503	BS00011962_51	6AL	2.26	AA	149
44476	Kukri_c3570_1817	6AL	2.36	AA	138
33818	GENE-4184_410	6DL	2.02	BB	52
48854	Kukri_rep_c103186_134	6DL	2.16	AA	99
79633	wsnp_JD_c1219_1766041	7AL	2.03	BB	89
49992	Kukri_rep_c70199_506	7AL	2.31	BB	47
14786	CAP8_c4980_112	7AL	2.38	BB	161
2616	BobWhite_c33300_159	7AS	2.77	BB	189
12457	BS00110010_51	7AS	2	BB	83
78046	wsnp_Ex_c41150_48040078	7AS	2.05	AA	214
12011	BS00097659_51	7AS	2.16	BB	86
8604	BS00051607_51	7DL	2.22	BB	27

Table 2: List of SNPs (132) significantly associated with stem browning across pot test summer, pot test winter and field test winter for population 2.

ID	Markers	Chromosome	-Log$_{10}$(p)	Target allele	Entry
34600	IAAV2694	1AL	2.77	AA	2
59764	RAC875_c63359_1671	1AL	2.051	AA	124
42798	Kukri_c2338_533	1AL	2	BB	138
57894	RAC875_c43002_382	1AL	2.004	BB	144
62751	RAC875_rep_c71093_1070	1AL	2.032	AA	131
38	BobWhite_c1027_1127	1AL	2.268	BB	40
78789	wsnp_Ex_c7684_13109335	1AL	2.319	BB	144
14279	CAP7_c821_239	1AL	2.796	AA	133
59941	RAC875_c6537_584	1BL	2.013	BB	126
3159	BobWhite_c4126_442	1BL	2.215	BB	33
77798	wsnp_Ex_c3372_6195001	1DL	3.097	AA	3
1174	BobWhite_c18406_110	2AL	2.215	AA	2
77643	wsnp_Ex_c298_580660	2BL	2.276	BB	130
69372	Tdurum_contig27907_216	2BL	2.022	BB	87
9207	BS00064155_51	2BS	3.097	AA	3
6117	BS00009807_51	2BS	3.097	BB	3

34673	IAAV3165	2BS	3.097	AA		3
76198	wsnp_Ex_c10596_17293192	2BS	3.097		BB	3
76199	wsnp_Ex_c10596_17293363	2BS	3.097	AA		3
11823	BS00093755_51	2BS	3.097		BB	3
77910	wsnp_Ex_c3685_6723631	2BS	3.097	AA		3
26054	Excalibur_c39493_251	2BS	4		BB	2
77019	wsnp_Ex_c19371_28311667	2BS	2.201	AA		64
81154	wsnp_Ra_c4321_7860456	2BS	2.276		BB	61
78796	wsnp_Ex_c7776_13247365	2BS	2.284	AA		73
40771	Kukri_c12212_182	3AL	2.194		BB	2
11609	BS00089400_51	3AL	2.77		BB	2
75430	wsnp_BE443995B_Ta_2_2	3AL	2.004	AA		57
75843	wsnp_CAP11_c2438_1258747	3AL	2.131	AA		62
78539	wsnp_Ex_c5997_10512308	3AL	2.222	AA		63
12652	CAP11_c1022_66	3AL	2.187	AA		40
34803	IAAV3924	3B_	2.444		BB	3
10632	BS00072994_51	3B_	2.585	AA		130
77063	wsnp_Ex_c19778_28779907	3B_	2.721	AA		131
73871	Tdurum_contig93431_485	3B_	2.854	AA		130
72895	Tdurum_contig62502_90	3DL	2.194		BB	2
34384	IAAV1461	4AL	2.149		BB	35
75338	wsnp_BE398523A_Ta_2_1	4AL	2.222	AA		31
35330	IAAV7376	4AL	2.244	AA		36
9697	BS00066024_51	4BL	2.143		BB	2
80790	wsnp_Ku_rep_c68318_67259259	4BL	2.174		BB	2
10761	BS00074787_51	4BL	2.18		BB	2
12310	BS00107247_51	4BL	2.18	AA		2
11605	BS00089282_51	4BL	2.18	AA		2
80379	wsnp_Ku_c31283_41033384	4BL	2.215	AA		2
11688	BS00091035_51	4BL	2.229	AA		2
36336	IACX9010	4BL	2.244		BB	2
34713	IAAV3421	4BL	2.432		BB	4
10924	BS00077411_51	4BL	2.444	AA		3
78061	wsnp_Ex_c4148_7494801	4BL	2.444	AA		3
3246	BobWhite_c4256_213	4BL	2.469		BB	3
48196	Kukri_c89906_197	4BL	2.469		BB	3
72441	Tdurum_contig55374_309	4BL	2.469	AA		3
75726	wsnp_BG604404B_Ta_2_1	4BL	2.523		BB	3
1043	BobWhite_c17457_89	4BL	2.77		BB	2
38919	Ku_c24961_1176	4BL	2.77		BB	2
12222	BS00104279_51	4BL	3.097	AA		3
42555	Kukri_c21787_283	4BL	3.097	AA		3
58701	RAC875_c5087_310	4BL	3.097	AA		3
34794	IAAV3896	4BL	3.155		BB	3
7783	BS00030571_51	4BL	2.097	AA		14
36446	Jagger_c1432_289	4BL	2.009		BB	51

20947	Ex_c57212_719	4BS	2.18	AA		2
10599	BS00072206_51	4BS	2.201		BB	2
8746	BS00058659_51	4BS	2.229		BB	2
71830	Tdurum_contig47622_234	4BS	2.745		BB	2
73063	Tdurum_contig67399_676	4BS	2.745		BB	4
77270	wsnp_Ex_c22740_31947788	4BS	2.77	AA		2
11207	BS00081724_51	4DL	2.444		BB	3
12209	BS00103682_51	4DL	2.444		BB	3
19353	D_GDS7LZN02F0W89_230	4DL	2.444	AA		3
78083	wsnp_Ex_c42133_48794975	4DL	2.469		BB	3
45192	Kukri_c4210_240	4DL	2.481		BB	3
7083	BS00022436_51	4DL	3.097	AA		3
48622	Kukri_rep_c101259_81	4DL	3.097	AA		3
75531	wsnp_BE497160D_Ta_2_1	4DL	2.066		BB	25
77262	wsnp_Ex_c2266_4247520	4DS	2.387	AA		36
53644	RAC875_c13_2330	5AL	2.174		BB	2
79442	wsnp_Ex_rep_c68515_67349904	5AL	2.18		BB	2
9056	BS00063425_51	5AL	2.194	AA		2
9138	BS00063822_51	5AL	2.194		BB	2
9139	BS00063823_51	5AL	2.194	AA		2
38790	Ku_c21587_754	5AL	2.194	AA		2
72022	Tdurum_contig49844_958	5AL	2.194	AA		2
74436	tplb0031i04_452	5AL	2.194	AA		2
7967	BS00034304_51	5AL	2.194		BB	2
7966	BS00034303_51	5AL	2.77	AA		2
9723	BS00066127_51	5AL	2.77		BB	2
53640	RAC875_c13_1965	5AL	2.77	AA		2
7718	BS00029347_51	5AS	2.194	AA		2
61548	RAC875_rep_c106118_339	5AS	2.509	AA		2
61034	RAC875_c9150_2945	5BL	2.06		BB	42
78852	wsnp_Ex_c831_1625061	5BS	2.432		BB	3
11167	BS00081120_51	5BS	2.509	AA		2
787	BobWhite_c15454_63	5DL	2.194	AA		2
40294	Kukri_c10243_475	5DL	2.481		BB	3
78020	wsnp_Ex_c4063_7344449	5DL	2.481		BB	3
39426	Ku_c43151_811	5DL	3.097	AA		3
24946	Excalibur_c30234_130	6AL	2.022		BB	30
73927	Tdurum_contig9503_575	6AL	2.06	AA		28
64047	RFL_Contig2765_669	6AL	2.585		BB	26
73091	Tdurum_contig68217_361	6BL	2.432	AA		3
39239	Ku_c3481_732	6BL	2.456		BB	3
14044	CAP7_c3697_87	6BL	2.481	AA		3
51320	Ra_c18658_1048	6BL	2.481	AA		3
47632	Kukri_c75359_152	6BL	2.481	AA		3
76566	wsnp_Ex_c1383_2651887	6BL	2.481	AA		3
12742	CAP11_c204_238	6BL	2.509		BB	3

7387	BS00023032_51	6BL	3.097	AA		3
58149	RAC875_c45515_65	6BL	3.097	AA		3
70643	Tdurum_contig41142_267	6BL	3.097	AA		3
79881	wsnp_JD_c7795_8868122	6BL	2.222		BB	26
59482	RAC875_c60007_199	6BL	2.036		BB	27
12395	BS00109036_51	6BL	2.215		BB	27
58733	RAC875_c5129_280	6BL	2.658		BB	27
10702	BS00074024_51	6DL	2.481		BB	3
24903	Excalibur_c2991_320	6DL	2.076		BB	19
28231	Excalibur_c63713_892	6DL	2.292	AA		25
58435	RAC875_c484_601	6DL	2.638	AA		10
29541	Excalibur_c96134_152	6DS	2.337	AA		25
2616	BobWhite_c33300_159	7AS	2.301		BB	2
10719	BS00074230_51	7AS	2.481	AA		3
78046	wsnp_Ex_c41150_48040078	7AS	2.481	AA		3
76513	wsnp_Ex_c13248_20898211	7AS	2.569		BB	2
5207	BobWhite_rep_c58252_112	7AS	2.77		BB	2
75977	wsnp_CAP12_c3056_1439567	7AS	2.77	AA		2
50066	Kukri_rep_c70864_638	7AS	2.796		BB	2
10367	BS00068863_51	7AS	2.886		BB	2
52818	Ra_c9427_300	7AS	3.097	AA		3
60377	RAC875_c75528_355	7AS	2.092	AA		69
36370	IACX9283	7AS	2.409		BB	16
75336	wsnp_be352570B_Ta_2_1	7BS	2.409		BB	12

Table 3: Unique SNPs and their primer sequences identified and a KASP panel of 78 markers produced from both population 1 and 2

Marker	ID	Chro[1]	Pos[2]	Primer Sequence
BobWhite_c1027_1127	IWB38	1A	462.61	AGTCTGGGAAGCGCGCACCAGCTGGAGCTGGGCGATGGTCGACTCCGACC[A/G]CTCCCAGGTAGACTAGAAGGCAAAGATACGCTCAGGCGACTGTGCTGCCA
CAP7_c821_239	IWB14279	1A	401.68	CTGTCCATGTAGATGACACACTAGCAGAAGAAAGGAATTTGCGGTGGAAT[T/C]AGCTGGTGTGTTCCCATCCTGTAAAGCATCTCATCATGTCAACCATACAC
IAAV2694	IWB34600	1A	289.05	AGCCGTAACCAAACATATATACAAATCGAGCATCTAGGAAAGGCTGGGTAGTCAAACACCGAAACGTGGCAGCCGAGCTGAAATCAC[A/C]GATATGAGCTACGGTCGTGACTACTACTCAGAAGCTATAAGCAGATGTAACCAAATCTACAGATGATCGGGCCGTAGTTGTACGTTAAATCATGAATACT
Kukri_c2338_533	IWB42798	1A	406.22	TTTGCAGTAAGTAGCAGGACTGGATTCTCCAGATGCATTACTTGATTGCT[A/G]ttcgtggattctccagatccacgaacaggattaagctaggtggcaagttc
RAC875_c43002_382	IWB57894	1A	439.42	CTTGTTTTGGTTGGAGCCGCTTTAAAATCTGGAAAGATGCAGCTTCTTAT[T/C]GTCTGTGCTTTGTTCTACGTACTCTTTCTGAGGGCACCATCTTTTATGCG
RAC875_rep_c71093_1070	IWB62751	1A	404.32	CTGTGGACTGTGCCAGCCTTGGATCCATGCCTGACATTGAGTTCACCATT[A/G]gtggcaagaagtttgcgctgaaaccagaagagtatatcctgaaggttggc
BS00021946_51	IWB6814	1B	215.54	GCAGCTGCGGCTCACCTACAGCAAGCCAAGAGACAAGCGAAAGAACAGGG[A/G]TACTGTCACCATGTCGCAGCTGCCTCGCCTACCGCTGGATTCTTCCATGC
BS00022429_51	IWB7076	1B	100.21	TCGATGCCGTGAGAAAAGGAGTGGCCGAGCACCACAACACCATCAACCTC[A/G]TCATCAACGGTATCGAGGACGAAGAGGAGTATGTCCAGGAGGCTGGAGAT
BS00029345_51	IWB7716	1B	208.49	TGGGAAGGCCTTAAACTTTGATGTCGTCACAGTTAGGATGAGGCTGCGAC[A/G]GCGGCCCTGCAGACCCTGTAAGTTGTTGAAGTGGCGTGAAGGAAAAACCG
BS00041010_51	IWB8257	1B	208.49	AACATCGTCAGTGGATGGAAATGGTGGCAATTCATCCTGCATGGCTGATG[T/C]TTGCAATGAAATTAGTTCCTGCAATGCTTCACCCATGGAATATAGTGGCA
BS00067434_51	IWB10049	1B	215.54	CGTTGTATGGTCAAAGTCTTTATTTCTGGAATTTGGTATCAATCAAACTA[T/C]TGATGTGCTGCAACTTAAAGTGGTCTGGTGAAAGCGCCTTGAGGAAATAC
BS00070139_51	IWB10444	1B	218.35	AAGCAACTGACTGCTCGCTCTTGTTTGGATGTAGTCCGTTCAGCGTGTCC[A/C]AGGTACTGAATAATGTAGGTCGTCAGGTACTCGGATCTTGACGTGAGCAC
BS00075663_51	IWB10823	1B	218.35	CCTGATTTGTGATAAAAATGGTGTATGCTAGCTCTGCGCCTCTGCCACAC[A/G]CATTAGTCTTTGTTTTTAGTCATGCTCAATGCAGCATTTTGAGTGTGATT
BS00078228_51	IWB10997	1B	220.59	TAGCCTGCTTAGTGCATCCAGATACACATTTTTTACCAGTTAATCAAGTT[A/C]TCTGTTCTCAAGTTATCTAATGAGTTCAAAAAAGTTTCTCTAATTTGATA
BS00110148_51	IWB12484	1B	216.28	CAGATTTGTCGGCGAAGAATCACAAATGTCATATCAGTGCGGCACCACAC[A/C]GTAAGAGGACCAATCAGGACAATCTTCCTGCAGAGCATCAGAGTTTACAA
Excalibur_c21898_1423	IWB23711	1B	31.34	CATTTTTAGGTTGACGTTGGCAGTAGTAGCCCTGTCGTCCGCCTTGCCCG[T/C]GCTTCCTTCAGAAGGATGATCTTGTTCGTGCGATGAAGCGGTGGCCATAT
Ra_c15153_324	IWB51154	1B	204.86	ATCCAAACTAGAATTTCTCTTGACGGATGACTTGACGGGAGTCCTTACCG[T/C]GCCCATCTGCAGACTCCTCTCTTCCTCCCTCACCCAATTAATCTTTTGGG
Ra_c16069_1820	IWB51198	1B	206.01	GAGTACAGCACATCAAAGCCGAAAAGGCTCAAGCTACTCCCCGTGTCCAA[T/C]CGCCATACACTCATTTGTCTGCCTTGCCGCTCGCAAAAGTGTGGGGGATT
Ra_c35710_395	IWB51921	1B	273.29	GGTCGAAGCTGTTAGAAATTTAGAAAGAGTGATTTGGGCCGGTCCCATTG[T/G]TGATGTTTATCCTGGGACAAACGAGGATGATGTGTTGGTGCCGCCATTGT
Ra_c3837_797	IWB51977	1B	227.17	GAGCTTGCGAGAAATTCTTAGCAGTTCTCTTAGTTCTCAAATGCAGCAGC[T/G]AGAAAATAAGTAAAAATACAATTATAAAAAAGTACATTATGTAGTTGCCA
Tdurum_contig13117_1316	IWB67865	1B	274.87	TGCCTGGTTACGGTTGCGTTTACTTATTTGTATGTTAAATCTTCCTAGTC[T/C]TGTATATATGGCTGCATCTTTCAGCTTGTCTATGAGCGAATTGTCTTTGG
wsnp_Ex_c3372_6195001	IWA3446	1D	120.64	CATCCGAAGCAGGCGAAGTATTTGGACAATCCTCTAGAGGAAATCCGCAAAGGCCGGAATTGTTCCGGTAAATCGAAGGGTCGGTCAACGTCTGCATCTG[T/G]CTCCCAGTAGGTATCTTGCCTGACAAATGATTGTTCGAGATGTTGAATGTGCTGAGCCCGGACAAGATCGAGATGCTCTGTGGAATGTTTCCATAAAGCT
BobWhite_c22273_227	IWB1572	2Dx	222.41	AGCTGGCTCCAGAAGAACGGCTTCCACTCCCTGGCCCGACCCACCTAGCT[T/C]GCCAGAGAGACCATCAAGACCAGCTCCACCGCGCGCCGCCTTCATCCACC
BS00062567_51	IWB8864	2Dx	222.41	GGTGGCGGGGCAGTCGACGGGCCCTGGGCATGCCGGCGCACGCGTTCTCG[T/C]CGACCAATGGGCTATTCTCCGGGACGCATTGGGGGTGCTCAGCGGCTTCG
CAP11_c1022_66	IWB12652	3A	476.16	TGTAGTTGTCAATTTCATTTCTGGTAACATGAACATACTGATCAGTAGCC[A/C]TAGCATTCAGTCCTGGCTTCTTGGCCACTTGAATAGAGGAGACAGATGTA
IAAV4781	IWB34922	3A	270.96	GAGTAAACCAACCTGTGAGTATTTATTTGCACACATGTTCTTTTGTTGCACAAATTATTTGCGGAGATGTTGATAAGTGCTGCTCTGGGGTAAATATGTG[T/C]GGTAGTTTAGGGACAAACCTGTGTATTAACTTCATTTGTAAGAAGTGGATCGGATCGCGAAGGATACTTAGGCACATGTTCTAGTAGGAACNGTAATAGA
BS00032694_51	IWB7902	3B	282.75	aatcagttaaagaaagagcttgccatgatcaagaggcttgaacaagatag[T/C]TCTAAGCTCTTTGAGCTTGAAGGTTCTGATACTCTTGGATCACAGTTCCG
BS00044942_51	IWB8382	3B	558.39	ACAAATAGATGGCAACCAACACTTCAGCAACAGATTATTCATCAGCAGGC[A/G]CACAGCCACAGATTGACAGACGACTCCTGGAGGCAGCCACATCGGGTGAT
BS00064876_51	IWB9387	3B	558.39	AAAGATAATTTACGATTTACAAGATACAATTAGGAGATGGCCAAATGTTC[T/C]AATGAAGATGGACGGAGGCACACCAAAAGCAGACTAAGAAACATACAAAA
BS00072994_51	IWB10632	3B	342.02	TATAAATAAGCTGCAGTGCAGCTAGTTCTGGTGTACAATAGTTGCGAGAA[A/G]TCAATGTCCACTACCAAGTACCACTGACACAAAATGCTGAAATGTGGTAT
BS00079029_51	IWB11049	3B	561.95	ACTTCTTCCATTTCTCTGCCTCCCTCTTCCATAACTTGCTTATCCAGAAT[T/C]GCTGACAAATTGCCTTGTGTGAATAAGGTACAAAAATGTGTAACAAGGCC
Excalibur_rep_c68583_1067	IWB30974	3B	250.24	ACTCATGCGGATCCTGCTTTGGGCGTGAATGGTGTCCGTGTCGATCTTGC[A/G]TGGTTCCAAGCTACAGCATTAGGGTATTGCCAACTGGGTCTTGTTGTTTA
IACX11310	IWB35687	3B	288.03	CCTAGAGAAGTAGTGCCTTTTTGATTCCCCTCGAGAGCTAACAAAGGCTCATCCTCGGGTACAGTACTAGTGTGAGTGCCTGTTGGATATTTACCTAGTT[T/C]AGGCATCGCGTTTTCTTCAGATGCCAGAACCGGAAGCTTCTCCTCTTCACCATCAAAGGTCTCTCCTGGTGGTGGAGAAAGCATCTTGAACACATATGTG
Kukri_c45513_83	IWB45539	3B	558.39	TGTCTTGGAAACCGACGAAGTGAGTAGCAACAAGATATGTTCAATGTTTG[T/C]AGGCTGTATAAAATGCTTATATCTTCAGGAAGTGATTCGATATAACTTCT
Kukri_c9571_73	IWB48415	3B	280.43	AGAGATCTGGTGCAGAAGGTCCCGGATGGTTGCATATTTACCATCGTCTC[A/C]GACTCATGCCACAGTGGTGGCCTACTGGACAAGGCAAAGGAACAGATAGG
Kukri_rep_c103205_101	IWB48859	3B	558.39	AAGGGGAGACACCGCTTGTAACCGCCGTTACACATGGTCATGCCTTCGTG[T/G]CTTCTTTTTAGTTGGACGCTGCCATCGACTAGGATTGAGACAGGTAATC

BS00035307_51	IWB8008	4A	45.36	CGGCGGCGACGGTGATGCATCAGGATCCAACAAATTTTAAATTTCTGCTA[T/C]GTAGTTCATTTAGCGTGCGCGCTGAGTGCGTACGTCGTTGGTTCAGGTCT
BS00066891_51	IWB9906	4A	430.71	gggggaacactactagtagtatcttataagctactaccgctccggcgcga[T/C]GAGCCATCAACCATCCGTCCATCATCGCGGCGAATCAAAGCGAATTATTG
Excalibur_c30378_673	IWB24962	4A	296.48	CTCCGGCAAGCATAGCAGAACAACATCCTCGCCCAGCCACTCTGCGGCCG[T/C]GGTGTGCGCCGTCGCCAGCAGGAGGAGAAGCAAGGTCTTGTGGAGCATCT
Tdurum_contig15586_563	IWB68425	4A	402.97	AAATGTGAATGGAGTACAAGGATATACATGGACCTCGAGCCTGCCTAGAT[T/C]attgagtttgagaacatgaaccctacattgttctcaagtttgagccttgt
wsnp_JD_c64_103934	IWA6137	4A	45.36	TGGGTCTGGGTGCAGCCGAGACGACAAAGTACTTGATGTCAATCTGATCATGGTTGCTGGATCAGCTCAGGATGGGGAATATGCGRGTCACGTGCTCGAA[T/C]GGAACAGTGTCGGCTGTGTTCTTCTTGAGTTCGGGGTGATTGAACTCGTTGCGCGGAAGGACAATCAGTTGGGAGCGTGCACCCTTCTCAATGACCCATC
BS00022366_51	IWB7044	4B	305.75	TCGACATCTACCTCGAAAATGCTATGAAGGCATTGCAAGCAATCCAGAAT[A/G]TCGTCCACAGCCACACCAACAACACCTAGCTCTGTTCTTGGGAGCTCGGT
BS00030571_51	IWB7783	4B	217.73	CTACCGGCGGCAGTTCGTTTTGGTTGAGAGGGCGTGCTTTCCAAGTGAAT[A/G]ATCTGAACGGTAGTGCCTCTTACTAATTTTTCTCTTAGCTATTTGGGTTA
Jagger_c1432_289	IWB36446	4B	194.25	GATGATAAGCTCCAATTCTTTTATGATGGGCAAGGGTTCATGTCCCTCCA[A/G]CTAAACCAGGACCAAGCTGACTTCATCTTTTATGATGTTTCTGGGAAAGT
Ku_c3385_521	IWB39213	4B	209.83	AATCTGAGCCGACCTTTAGTCAACACGGGAGCACTTCCATTAAAAATGAA[T/C]GAAAGGTCATGGGATATGCAGAAGAATTGTGGTGGTGAGAGCCTGTTGCT
RAC875_rep_c69370_218	IWB62565	4B	209.83	cagccggactccaccgcgtgggattgttaacctgtcttaatttgtatgct[T/C]CGAAACTGGTTCAAGACTTCATCCATTCTGCTGCGTTTATCAGGAAATCT
wsnp_Ex_c4148_7494801	IWA3780	4B	305.75	CGATATGCTCAGTCGTAGTTTCCATTTCATTAAGAGAACTGATTACATCCAATATATCAGGTCTCTTTTTCACGTCGTATGACATGCAGAGTGCAGCAAT[T/C]TCAATGCATTTGGTTACTTGCTCTGATCCCAGTGGTGGATACTTGCCTGATTTATTCCACCTGTACCTCCATCTTCTAAGTATATTTTTTATGTTAGGCT
wsnp_BE497160D_Ta_2_1	IWA286	4D	160.46	TTCGCCAAGCTTGGTGAACAGGTCCGTTCAGATACTAACATCCATCGCACCACATAGCTC[T/C]GAGATGATCACTCTACTGAACATGAATTATGAATGTCTGGAAGAATRATCTAGGGTACTA
wsnp_Ex_c42133_48794975	IWA3815	4D	160.99	ATTTAGTAATTTGTCRCYTGATTTCTTCCCTAAAGTGGATGCTTCAACAAYTGATATTGCCTGGCTTACTTTTCCTGTATGCAGTAATTCGTTCACAATG[T/C]AGCTGAAAGCTGGGACATCAGAACATTCTGTTTTCAGCATAGACTGTACCAAGTCCTTGCATCGTTCTGCATCAAACCATGATAGTGAAGAGAATGCAAA
BobWhite_rep_c63943_76	IWB5418	5A	367.76	TTTCTTTACTCTTAGGAACAGGGTAAACATATCACCGTACAGGTAACATA[T/G]ATGTTACAGTTATGTCGTACAAATTGATCTTCAGAATTCAGAAACATCAC
BobWhite_c6094_447	IWB4087	5B	214.95	CACGGTGCTCGAATGGGCCTCCAAACAGGCATACATGATGCAAGACCCGA[T/C]GATCGAGAACTTGTTGCCAGAGGCCAAGATCAGGTTGGAGCTGTACCAAT
BS00026678_51	IWB7633	5B	377.23	ATGCACCTTCTCACCAAGCCTGGCCTTTGCGGCAAACAAGGTAGCAGCTA[T/C]ATTCTCCAAACCCTTCAATCCAATTTCTCTTAACTGGGAAAGAGGCCTCA
BS00032003_51	IWB7864	5B	1.33	GGCGGTCCCTCTGGTGTGGCCGAGCCATGCCGGCTCCGACCCGTCTGGCC[T/C]GGCTCGCAGAGAAGAGAGAGGGCTGTCTAACCTGAAACCTAGGTACCAGA
BS00083715_51	IWB11318	5B	34.9	ACCACGGGCTCCACACCGCGTATTGCCAGTTCCCTGACCCCGAAGAAGAT[A/G]TACAACTGGAGGAGATTCGGACCGTCGGGAACGATGAGGACGGCGGAGGT
RAC875_c9150_2945	IWB61034	5B	179.66	GAAGTTGTCCGTGCAGGATGTAAATCAGCTGGAGCTTGCTAAAAGGTTGG[T/C]AACAGGGGATCCCCATGATGGCTCTCGTGTCCGAAGACAAAGGGAATTGA
Tdurum_contig14130_245	IWB68149	5B	34.9	GTCGGACAACTAACCGAACCGCTAACCCAACCCGTTCATCATGTGGCCGC[T/C]catgcaactgtacagagcgatatatacaggccgtacaagtttttttttcc
Tdurum_contig14130_315	IWB68150	5B	34.9	atatatacaggccgtacaagtttttttttcctttttctttttgaaaaaa[A/G]AGAGCGGGTTATAGATCATACATATACAAAGTACACAAGACACATTAGAG
Tdurum_contig47071_1322	IWB71751	5B	375.54	cactgagatttttaatgggactaccactgagagttgtgagcttcattcac[T/C]GAGAGTCGCTATAAGTTGAAAATAAGCTTGTATCTGTGGCGGCCGCTTCC
BS00011962_51	IWB6503	6A	339.47	CACAACGGCCTGCTACCTGTCGCCGCATAGGGTGTCGATCGCTCCTTTTT[T/C]TCTTTTTCATTCGCCGCACCAACTTTTAGGACTTTTTATTTCCATGTGAA
CAP11_c7092_120	IWB13032	6A	329.71	ATTGGACACAGAGATGAGGCAAGCTTGGGCATAGCAGGTCGTGTCGCTGG[A/C]GATGGGTCCATCCCATCAAGCCGCCTGGAAGGCCTGGGCAAACTGCAGCC
Kukri_c3570_1817	IWB44476	6A	339.47	CCAGTGGAAGCAGGCAGCTACCTGTTGTTGTATTCTAGTGTATGCGTGTG[T/C]GCTCAGTCCCTGCTTGTGTTGTTGTAACATTATTATTAACTGGTGATGAA
Kukri_rep_c103186_134	IWB48854	6A	338.95	TGGCTTCGGAATTCCCGCCAACCRCAGGAAAATCCATCGCTGCGCTCAGC[A/G]GGCCTAGTCAGATTCGTGTCACGGCGGGCATTGTCCAGCTCGGCGACCAC
wsnp_CAP12_rep_c4048_1842112	IWA1000	6A	332.79	CCCGATGCCATCATCTCCGGGGAGTGGCCCGAGAACTTCTCCCTCCTCAGCTACGACGACCTCCGCGCATACCTCCAGTCACAGCAGCAGCAGCARCAAC[A/G]ACAACCATCCCATGCCGGCGATCAGCAGCGGGGGCCTCTCCTGCGTGAGGCCATGTCGACGCCCGTGCTGATGGTCACAGCGGAGCAGGCGCTGGTGGAG
BS00109036_51	IWB12395	6B	269.77	AAGTTGTTGAGAAGCTCGAACAGCAGGACGAAAACCTGAAGGAGGTGTAC[T/C]GAATCCTTGCCCATGAGCTTCCGGCAGAGTTCATGAGCCAACCCATTGGT
RAC875_c5129_280	IWB58733	6B	269.77	AGGGGTGGCCTGTACACAGATCAGATGTTGAATCCTTATGTTTATATATC[A/G]CATGCATGATGATTTACATTACAAAATGTATTACTTCCCCGCCGCAGAAG
RAC875_c60007_199	IWB59482	6B	269.77	ACCTGAAGGAGGTGTACTGAATCCTTGCCCATGAGCTTCCGGCAGAGTTC[A/G]TGAGCCAACCCATTGGTGACCTTCTCCCTCATACCATCTTGCTGGGCCTC
BobWhite_c33300_159	IWB2616	7A	132.86	TCGATATCTGGAATGTACACAGCATGCTCGCAGTTGAGCCAAACTTGATT[A/G]CAAATTTACACACCTGCAGCTCCTCATTGTTAGCCCGAACTACGTACAGA
BS00097659_51	IWB12011	7A	332.69	AAGCCCAAGAAAGGGTATCTGAATTCTGATGGAGCTGGATTGTTCAACAC[A/G]CCAAAGGTGTACTAGTTCAGACTTCATGTATACATGTATACATCAAGCCC
BS00110010_51	IWB12457	7A	332.69	TGGGACCCACTGCAATTAATATCTAGGAATTGCTATATAACATCCTGAGA[T/C]TAGAAAAGTATTTCCTTAGGAAATTCAACAAGAACCAGATCTTTGTACAT
CAP8_c4980_112	IWB14786	7A	637.2	ctctagaggaagctacctaccccccctccccccctgctgttccggggcatgg[T/C]GGCGCTCTGATCCCGTCTAGCTGTATATTAATAAGCAGACTGTATGTTGT
IACX9283	IWB36370	7A	345.35	TTTTTTGGTGTACAGCAGTGAGATTACATTGCAGACAGCGAGTGTAC[C/G]AAGATAACAGTTTCACAGCAAATTTAGAAGCAGGTCATAAGACCCCGGTACGTAACACTATAACATTGCTGCTTCTTCCTACGGTCCTGAAATCTCTAGT
Kukri_c10243_475	IWB40294	7A	635.34	TGGTACAATCCTATATAAGGGAGCCGAGCTTGGGAGGCAACTTAGAGATA[A/C]TGTTCCTGATCAAGGACAGCGTTGGAAGGTGCTGGCTGACTTTTGGGCAG
Kukri_rep_c105330_552	IWB49084	7A	372.34	CGAGAGAAATGGTTCAAATGCTGATATGAGGTCAATGTGTTTGATAATCT[A/G]GGGTATTTCTCGTGCATATGCGGCCTGTTCGAGCACATGGGTATGGTCTG
Kukri_rep_c70199_506	IWB49992	7A	626.06	ACTACTACTGAATGGGAGCTTCTGAATGATATGAAGGCCGTGTGGCTTCG[T/C]AGCCCCAAGGAGGTTACTGAAGAAGAGTATGCAAAGTTTTACCACTCACT

wsnp_Ex_c41150_48040078	IWA3760	7A	314.23	TGGAGGAATGTCCAGTCCATACAAACCGTAGTGATGCTAGTGGAATCATACATACCAAAATAAACTGTAGCGATGACAGCGGAATCAAAATACTATGAAA[T/G]ACTTGCATTGTTTGTCTTGATAACTGCTACGATTTCAAAATCGAGCCAATAAACCATGGTGATGCCAGTGGAATACAAAATATGAAAGATTTGCATTTGT
wsnp_JD_c1219_1766041	IWA5797	7A	708.87	TTAGGAACAACAAACTCATTGGTTCTATCCCTGCTACCTTTGGGAGTTTGGTTAATCTCACTAGCTTGGTCCTATGGGACAACCAACTCTTTGGACGTAT[T/C]CCTCCAGAATTAGGTTATCTCATGAACTTAGAAGAGTTAGGACTTAGCAACAACAAACTCGTGGGTTCCCTCCCTGATATGTTTGGAAATTTGACCAAGC
wsnp_be352570B_Ta_2_1	IWA4	7B	216.02	GCTCGCTACATTGGCAAATAACTAAATTAGCAACTGAATGCACTGAAAATTGGAATCATT[T/C]GGATCTTGGATAGTTTATAAAAACAGTTACACATTTTATAACTATGCAGCAAAGCAACTT
BS00051607_51	IWB8604	7D	323.05	CATCGCGGTGAAAGCCATCGAGACGGCGGTGGTATTCGTCGCCAGATCGG[A/G]GAGGACGGCGAGCGAGATCAAGATCAAGTGCCAGAACCTCTCCGACCGTG

Note: Chro[1], chromosome; Pos[2], the marker position (cM)

Table 4: Media composition for Gamborg's B5 and MS-Murashige and Skoog mediums for comparison

Component (mg/L)	G5893 Gamborg's B-5 medium	M5524 MS medium
Ammonium nitrate		1650
Ammonium sulfate	134	
Boric acid	3	6.2
Calcium chloride anhydrous	113.24	332.2
Cobalt chloride • 6H2O	0.025	0.025
Cupric sulfate • 5H2O	0.025	0.025
Na2-EDTA	37.25	37.26
Ferrous sulfate • 7H2O	27.85	27.8
Magnesium sulfate	122.09	180.7
Manganese sulfate • H2O	10	16.9
Molybdic acid (sodium salt) • 2H2O	0.25	0.25
Potassium iodide	0.75	0.83
Potassium nitrate	2500	1900
Potassium phosphate monobasic		170
Sodium phosphate monobasic	130.5	
Zinc sulfate • 7H2O	2	8.6
Organics (mg/L)		
myo-Inositol	100	100
Nictotinic acid (free acid)	1	0.5
Pyridoxine • HCl	1	0.5
Thiamine • HCl	10	0.1
Glycine		2
Grams of powder to prepare 1 L	3.2	4.3
pH 1 0.5 at room temperature	4	3.9

See more at: http://www.sigmaaldrich.com/life-science/molecular-biology/plant-biotechnology/tissue-culture-protocols/classic-plant-media.html#sthash.HaovdRH4.dpuf and Gamborg *et al.* (1968)

Appendix II

Table 1: Stem browning score (0-4 scale) of MARS population 1 and population 2 in pot and field screenings and entry number of the material used.

Population 1				**Population 2**			
Entry	Winter (Field)	Summer (Pot)	Winter (Pot)	Entry	Field (winter)	Summer (Pot)	Winter (Pot)
1	2.7277	3.8	2	1	1.088	4	2.5
2	2.061	4	2	2	0.8	3.95	2.75
3	0.568	3.1	1.85	3		4	3
4	0.2149	4	0.553	4		3.95	3.6
5		3.9	2.5	5	2.023	4	2.6
6	0.2015	3.65	2.2	6			

7		3.9	1.8
8	0.5479	3.95	2
9	1.305	4	1.25
10	1.3454	3.75	3.7
11	1.0621	4	1.7
12		3.3	2.05
13		3.9	2
14	0.973	4	1.05
15		3.95	2.45
16		4	2.7
17	1.4621	3.8	2.9
18	0.061	3.8	1.85
19	0.8369	4	2.75
20	0.5745	3.95	1.65
21	0.5599	4	2.1
22	0.2167	3.95	3.3
23	0.061	3.95	1.75
24		4	2.3
25	0.061	3.65	0.55
26		4	1.6
27		3.9	0.853
28		3.8	2.329
29	0.5559	4	2.2
30	1.6974	3.95	2.15
31		3.35	1.879
32	0.1199	4	2
33	0.961	4	1.65
34	0.3994	4	3
35		4	2.15
36		3.95	1
37	0.9726	4	2
38		4	2.2
39	0.8959	3.9	1.8
40		3.8	2.6
41		4	0.65
42	1.3092	3.95	3.3
43	0.7604	3.95	2.15
44	0.8707	4	2
45	2.1325	4	1.65
46	1.1456	3.6	2.5
47	1.2793	3.6	2.5
48	0.6261	3.9	2.5
49	0.9205	4	2.25
50	0.8285	3.9	2.8
51	0.4485	3.8	1.65
52	0.7885	4	2.1
53	1.3	4	2.7
54	2.3699	4	2.4
55	0.4534	4	1.75
56	0.0455	4	2.2

7	1.628	4	3.25
8		4	2.85
9	0.861	3.85	2.65
10	2.609	3.8	2.9
11	0.657	3.9	2.6
12		3.8	2.2
13	0.202	4	2.4
14	1.574	4	2.55
15	0.936	4	3.65
16	0.226	3.95	2.9
17		4	2.6
18		4	2.7
19	0.167	4	1.55
20	0.855	3.75	2
21		4	4
22	1.238	4	3.1
23	0.485	4	2.55
24		3.9	3.5
25	0.401	4	3.65
26		4	2
27	0.239	3.85	3.3
28	0.403	4	2.35
29	0.031	4	3.75
30	1.318	3.9	4
31		3.9	3.5
32	0.756	4	3.115
33	1.292	4	3.1
34	0.886	4	3.25
35		4	2.6
36	0.905	4	2.8
37	0.031	4	2.1
38	0.884	4	0.5
39	1.036	4	1.15
40		4	2.9
41	0.719	4	2.05
42		4	3.15
43	1.308	4	2.35
44	1.109	4	3
45	0.946	4	3.2
46	0.461	3.8	4
47	1.759	4	3.5
48	1.04	4	3
49	1.361	4	2.75
50	1.034	4	3
51	1.252	4	1.8
52		4	2.05
53		4	2.3
54	0.106	4	2.15
55	0.969	4	2.4
56	1.578	4	1.9

57	1.2357	4	2.1
58	1.0702	3.9	2.25
59	1.1564	3.65	2.25
60		3.95	2
61	1.1071	3.9	2.9
62	0.054	3.75	2.2
63	1.3553	3.75	2.4
64	1.2034	3.9	2
65	0.211	4	3
66	1.561	4	1
67	1.6024	4	2.5
68	0.5696	4	1.85
69	1.0261	4	2
70		4	2.25
71	1.9359	3.65	2.65
72		3.9	2.3
73	0.7285	4	2.2
74		4	3.5
75	0.7044	4	3.1
76	1.4326	3.9	2.35
77	0.6999	4	2.35
78		3.9	2.4
79	0.4772	4	2
80	1.589	3.7	2.5
81	0.7029	4	2
82	1.3233	4	2.1
83		3.8	0.647
84	1.5957	4	2.3
85		4	2.75
86	0.7319	4	1.8
87	0.8759	4	3
88	0.4866	4	2.7
89	1.8965	3.7	2.229
90	1.5637	4	1.95
91		4	2.15
92	1.4739	4	2.8
93	1.8277	3.6	3.25
94	0.6095	3.9	2.55
95		4	2.529
96	0.3147	3.65	3
97	1.1114	4	2.4
98	0.8865	4	2.95
99		3.75	1.5
100	0.9068	4	0.9
101	1.0606	3.95	1.85
102		4	0.747
103	1.211	3.9	2.7
104	0.8607	4	0.447
105	0.9073	4	2.8
106	0.3297	3.8	2.5

57		3.95	0.8
58		4	4
59	0.294	4	4
60	0.664	3.7	3
61	1.093	4	4
62	1.206	4	3.1
63	1.122	4	3.6
64		4	3.6
65	0.569	3.9	4
66		4	3
67		4	4
68	0.978	4	4
69	1.607	4	1.5
70	1.122	4	2.8
71	0.007	4	3.1
72	1.396	4	2.5
73	1.178	4	2.9
74	1.06	4	2.85
75	0.984	4	3.5
76		4	4
77	0.059	4	3.25
78	0.561	4	3.9
79	1.163	4	2.65
80	1.443	4	2.4
81	2.048	4	4
82	0.886	4	4
83		4	3.15
84		4	4
85		4	3.6
86	1.281	4	3.4
87	1.433	4	3.6
88	0.594	4	4
89	1.251	4	3.5
90		3.85	3.7
91	1.317	4	3.15
92	0.894	3.95	3.4
93		4	1.6
94		4	2.95
95	1.212	4	4
96		4	4
97	1.202	4	4
98	1.433	3.95	3.65
99		3.95	3.25
100	1.253	4	2.4
101	1.437	4	3.3
102	1.166	3.9	2.85
103	1.06	4	3.4
104	0.717	4	3.1
105	1.622	3.8	3.35
106	1.61	4	3.4

107		4	2.25
108	1.2457	4	1.55
109	0.9741	4	2.7
110	0.9571	4	1.25
111		4	2.7
112	0.2315	4	2.5
113	0.7883	4	2.65
114	1.2971	3.9	2.75
115	1.1979	4	1.95
116	0.994	4	2.65
117	1.2934	3.8	2.65
118	0.428	4	2.15
119	0.5749	3.85	1.45
120	0.8045	4	2
121		3.75	2.2
122	0.211	3.75	0.5
123	0.654	3.9	2
124	0.3612	4	3.25
125	0.0001	4	2.7
126	0.7608	4	2.85
127	0.9961	4	2
128	1.2409	4	1.8
129	0.989	4	2.25
130		3.45	3.7
131	0.6413	3.95	0.65
132		4	1.85
133		4	2
134	0.2653	3.75	2.6
135	0.244	4	2.1
136		4	2.5
137	0.5239	4	3.25
138	0.8622	4	2.35
139	1.9196	3.95	1.5
140	0.811	4	2.25
141	0.9821	3.7	2.4
142		3.9	2.7
143		4	2.75
144	0.811	4	1.45
145	1.24	4	2.5
146	0.9493	3.65	3.2
147	1.2159	4	4
148	0.2173	3.9	2.2
149	0.3126	4	2.1
150	1.3341	4	2.8
151	1.5739	4	2.8
152	0.5557	4	2.1
153	0.2065	4	2.8
154		3.9	2.75
155	0.8295	3.85	1.25
156		4	2.25

107	1.045	4	3.5
108	1.504	4	3.4
109	1.266	4	2.75
110	0.755	3.95	2.5
111	1.37	4	0.885
112	1.109	4	3.2
113		4	1.4
114	1.28	4	2
115		4	3.8
116	1.191	4	3.4
117	1.364	4	3.9
118	0.904	4	3.6
119	1.082	4	3.7
120	0.031	4	4
121	1.033	3.9	2.85
122	0.796	4	4
123		4	3.85
124	1.323	4	3.05
125	1.144	3.9	2.25
126	0.746	4	3
127		4	2.7
128	1.414	4	4
129	1.065	4	3.85
130	1.065	4	3.65
131	0.513	4	3.4
132	1.631	4	4
133		4	3.65
134		4	2.6
135		4	3.75
136		4	4
137		4	3.251
138	2.732	4	3.5
139	1.481	4	3.8
140	0.632	4	4
141	1.645	4	4
142	0.349	4	4
143		4	4
144	0.993	4	3.15
145	1.575	4	3.5
146	0.753	3.9	4
147	0.803	3.9	4
148		4	4
149	1.09	4	3.2
150	1.68	4	4
151	0.662	4	3.6
152	0.925	4	4
153		3.85	1.85
154	1.561	4	2.2
155		3.9	4
156		4	3.8

157	1.3304	3.9	1.9
158	0.7641	4	1.4
159	0.9012	4	1.65
160	1.389	4	1.55
161	0.1856	4	2.25
162	1.1358	3.85	2.5
163	1.1189	4	1.85
164		4	2.5
165	2.2399	4	2.55
166	0.4519	4	2.7
167		3.6	1.8
168	1.0424	3	1.65
169	0.061	4	1
170	0.8532	3.9	1.85
171		4	2.65
172	0.7524	4	1.65
173		4	1.9
174	1.0652	3.9	2.15
175	1.284	4	2.7
176	0.8967	4	3.65
177	0.53	3.8	3.5
178	0.8243	3.9	2.25
179	1.1258	4	3.25
180		3.95	2
181		4	2.6
182	0.061	3.9	3.8
183	1.2712	3.7	3.65
184	1.0703	3.85	3.6
185	1.5428	3.95	2.85
186	0.4344	3.9	2.95
187	0.8809	4	2.95
188	1.4389	4	4
189	0.8603	3.75	2.45
190	1.2844	4	2.6
191	0.4691	4	1.25
192	0.8467	3.75	3.7
193	0.6403	4	3
194		3.55	2.75
195	1.661	4	3.5
196	0.0226	4	2.9
197	0.061	3.65	4
198		4	1.65
199	0.5038	4	4
200	0.5659	3.85	3.8
201		3.7	3.75
202	1.2651	4	3.7
203		4	3.35
204	0.0001	3.747	1.85
205		4	2.6
206	0.6617	3.9	1.5

157		4	3.5
158	0.53	4	3.65
159		4	2.25
160		4	4
161		4	2.8
162	1.349	4	4
163		4	3.2
164	1.386	3.9	1.7
165		4	4
166	0.68	3.9	3.1
167	0.587	3.7	3.4
168		3.75	2.9
169	1.057	4	4
170	0.665	4	2
171		4	3.2
172		4	2.8
173		4	4
174		4	3.05
175		4	3.4
176		4	3.7
177	0.879	4	3.9
178	0.552	4	3.25
179	0.767	4	3.8
180	1.708	4	3.8
181		4	3.6
182	1.201	4	2.25
183	0.51	4	3
184	1.228	4	4
185	0.484	4	3.3
186		4	3.5
187		4	4
188	0.219	4	3.7
189	0.106	4	4
190		3.95	4
191		4	2.35
192		4	3.5
193		4	4
194		4	3.5
195	0.657	4	2.7
196	0.894	4	3.35
197	1.061	4	3.65
198	0.513	4	3.1
199		4	3.2
200	0.66	4	3.6
201	0.98	4	3.5
202	0.94	3.9	4
203		4	3.2
204		4	4
205	0.106	4	4
206		4	3.3

207	1.6735	4	2.95
208		3.5	3.553
209	1.0947	4	3.5
210		3.75	1.75
211	1.284	3.7	1.6
212		3.65	3.65
213	1.3148	4	3.2
214		4	4
215	0.9702	4	3.95
216		3.7	3
217	0.8872	3.75	2.2
218	1.0928	4	3.65
219	0.455	4	3.6
220	1.6649	4	3
221		3.55	1.2
222		3.5	2.553
223	0.138	3.65	3.1
224	0.4181	3.75	3.3
225	0.368	3.8	1.95
226	1.5177	4	2.95
227	0.8205	3.75	4
228		3.75	3.3
229	0.1309	3.65	3.05
230	0.561	4	1.8
231		3.65	3.15
232		4	2.45
233	1.0051	3.9	2.5
234	0.2899	4	3.4
235		4	2.9
236	1.061	4	3.35
237	1.5485	4	3.1
238	0.4763	4	2.95
239	1.2409	4	2.4
240	1.0972	3.9	3.65
241	0.6256	3.55	2.65
242	0.3768	3.6	2.5
243	1.2914	3.9	2.95
244	1.2601	3.75	2.9
245	0.411	3.95	3.1
246	1.5973	3.65	3.35
247		3.9	2.9
248	0.364	3.75	3
249	1.634	4	2.4
250	1.9285	4	2.65
2-49/Cunningham//Kennedy	1.9679	4	3.625
AUS 29529	2.2782	3.6	2.55
Batavia Check (PBI)	1.254	4	3.55
Sunco - Parent	1.2451	4	4
Sunco check (PBI)	1.0325	4	3.25

207	1.015	3.8	4
208	0.375	3.9	3.3
209		4	3.45
210		4	3.5
211		4	2.95
212		4	3.3
213	0.962	4	3.2
214		4	3.6
215	1.187	4	3.6
216	0.762	3.85	2.9
217		4	3.6
218	1.354	3.8	3
219	1.726	4	4
220	0.823	4	3.5
221		3.9	2.15
222		4	3.8
223	1.941	4	3.2
224	0.031	3.8	3.65
225	1.029	4	2.75
2-49/Cunningham//Kennedy	1.964	2.85	3.35
Batavia Check (PBI)	1.245	4	3.3
CSCR 16	1.567	2.75	1.9
3 check (PBI)	1.086	3.149	2.4
SUNCO/2*PASTOR	2.43	3.975	3.8

Appendix III

Table 1: Wald statistics from REML analysis for test of fixed effect, summary statistics and treatment [inoculated (Plus) and un-inoculated (Nil) plot] means of evaluated traits in environments in 2014

					Wald statistics					
Source of variation		d.f	GY	TGW	%Screenings	NDVI	HD	PMD	PH	% WH	WSB
Genotype (G)		205	693.6***	1488.9**	1012.46***	564.1***	7611.3***	2788.3***	1814.8***	228.0ns	306.2***
Treatment (T)		1	79.4***	1.3^{ns}	71.05***	62.1***	1.2^{ns}	1.7^{ns}	14.6***	77.9***	366.0***
G x T		205	368.4***	255.3^{ns}	113.5***	216.9^{ns}	92.9^{ns}	2316.8***	151.1^{ns}	407.5***	218.0^{ns}
					Genotype						
SED			405.30	2.93	2.76	0.019	1.41	1.71	4.35	5.51	0.49
LSD			800.03	5.77	5.45	0.036	2.78	3.37	8.58	10.87	0.97
% CV			12.13	9.20	34.36	3.77	1.07	1.11	3.87	174.27	51.95
h^2	Nil		0.62	0.67	0.81	0.00	0.97	0.89	0.88	0.00	0.31
	Plus		0.58	0.85	0.74	0.31	0.97	0.89	0.86	0.26	0.29
GA	Nil		895.32	7.35	7.10	0.00	11.69	8.05	16.33	0.00	0.39
	Plus		857.54	9.25	7.02	0.02	11.76	8.00	16.07	3.11	0.36
					Treatment means						
Nil			4229.00a	33.18a	7.13a	0.81a	113.7a	152.4a	97.91a	1.58a	0.93a
Plus			3962.00b	32.91a	8.22b	0.75b	113.7a	152.5a	97.52b	4.87b	1.77b
SED			30.52	0.22	0.15	0.008	0.054	0.04	0.019	0.342	0.05
LSD			59.88	0.43	0.29	0.02	0.11	0.08	0.21	0.67	0.10

Note: *** indicates significance level at p= ≤0.001, ** indicates significance level p= ≤0.01, * indicates significance level at p= ≤0.05 and ns = non-significant. Min = Minimum; Max = Maximum; h^2 = Heritability; LSD = Least significant difference; SED = Standard error of differences GA = Genetic advance (5%); GG = Genetic gain (Genetic advance % of mean); GY = Grain yield (Kg ha^{-1}); TGW = 1000- grain weight (g); % Screenings = Percent screenings ; NDVI = Normalized difference vegetation index; HD = Heading days; PMD = Physiological maturity days; PH = Plant height (cm); % WH = Percent white heads; WSB= Weighted stem browning. Treatment mean followed by different letters indicates significance at ≤ 0.05.

Table 2: Wald statistics from REML analysis for test of fixed effect, summary statistics and treatment [inoculated (Plus) and un-inoculated (Nil) plot] means of evaluated traits in environments in 2015

Wald statistics											
Source of variation		d.f	GY	TGW	%Screenings	NDVI	HD	PMD	PH	% WH	WSB
Genotype (G)		206	1250.3***	3778.1***	1443.5***	701.0***	8694.3***	800.1***	2115.8***	605.1***	4481.0***
Treatment (T)		1	519.1***	358.1***	258.4***	177.9***	5.6*	0.9^{ns}	8.4**	1183.3***	-
G x T		206	308.1**	314.3**	272.9*	287.3*	123.6^{ns}	211.2^{ns}	98.2^{ns}	493.4***	-
Genotype											
SED			283.2	1.28	2.89	0.01	1.05	1.76	4.63	7.54	5.59
LSD			555.17	2.50	5.67	0.08	2.06	3.44	9.08	14.78	10.95
% CV			12.30	6.20	49.10	1.60	1.30	0.89	6.00	70.20	77.00
h^2	Nil		0.54	0.83	0.59	0.32	0.91	0.77	0.68	0.24	-
	Plus		0.50	0.76	0.61	0.39	0.88	0.72	0.80	0.42	0.68
GA	Nil		499.26	5.86	5.61	0.01	7.02	3.46	13.27	2.12	-
	Plus		504.77	4.98	7.05	0.01	6.62	3.17	14.77	12.44	77.57
Treatment means											
Nil			3409.00a	29.53a	7.71a	0.82a	110.80a	144.80a	98.43a	2.40a	
Plus			2823.00b	27.24b	12.00b	0.80b	110.90a	144.60a	97.45b	25.40b	
SED			25.69	0.12	0.27	0.002	0.06	0.15	0.31	0.67	
LSD			50.40	0.24	0.52	0.003	0.12	0.29	0.61	1.31	

Note: *** indicates significance level at p= ≤0.001, ** indicates significance level p= ≤0.01, * indicates significance level at p= ≤0.05 and ns = non-significant. Min = Minimum; Max = Maximum; h^2 = Heritability; LSD = Least significant difference; SED = Standard error of differences GA = Genetic advance (5%); GG = Genetic gain (Genetic advance % of mean); GY = Grain yield (Kg ha^{-1}); TGW = 1000- grain weight (g); % Screenings = Percent screenings; NDVI = Normalized difference vegetation index; HD = Heading days; PMD = Physiological maturity days; PH = Plant height (cm); % WH = Percent white heads. Treatment mean followed by different letters indicates significance at ≤ 0.05.

Table 3: Correlation coefficients based on means of 7 agronomic and yield contributing traits evaluated under inoculated (Plus) and un-inoculated (Nil) environment in 2014

Traits	*NDVI Nil*	*NDVI Plus*	*PH Nil*	*PH Plus*	*HD Nil*	*HD Plus*	*PMD Nil*	*PMD Plus*	*TGW Nil*	*TGW Plus*	*GY Nil*	*GY Plus*	*%Sc Nil*	*%Sc Plus*	*%WH Nil*	*%WH Plus*	*WSB nil*	*WSB Plus*
NDVI Nil	1																	
NDVI Plus	0.73***	1																
PH Nil	-0.22**	-0.30***	1															
PH Plus	-0.23***	-0.30***	0.99***	1														
HD Nil	0.43***	0.54***	-0.24***	-0.24***	1													
HD Plus	0.42***	0.54***	-0.23***	-0.23***	0.99***	1												
PM Nil	0.40***	0.50***	-0.28***	-0.29***	0.88***	0.88***	1											
PM Plus	0.41***	0.51***	-0.27***	-0.28***	0.91***	0.91***	0.96***	1										
TGW Nil	-0.32***	-0.37***	0.31***	0.32***	-0.65***	-0.64***	-0.66***	-0.68***	1									
TGW Plus	-0.25***	-0.35***	0.32***	0.33***	-0.68***	-0.68***	-0.68***	-0.69***	0.85***	1								
GY Nil	0.06	0.09	-0.22**	-0.21**	0.07	0.07	0.27***	0.25***	-0.21**	-0.22**	1							
GY Plus	0.14*	0.15*	-0.18**	-0.17*	0.00	0.00	0.20**	0.19**	-0.18**	-0.15*	0.87***	1						
%Sc Nil	0.21**	0.27***	-0.34***	-0.35***	0.53***	0.53***	0.52***	0.54***	-0.71***	-0.66***	0.04	-0.04	1					
%Sc Plus	0.26***	0.37***	-0.34***	-0.35***	0.61***	0.61***	0.59***	0.61***	-0.74***	-0.75***	0.07	-0.05	0.88***	1				
%WH Nil	0.06	0,08	-0.08	-0.09	0.19**	0.19**	0.19**	0.20**	-0.21**	-0.18**	-0.16*	-0.25***	0.33***	0.38	1			
%WH Plus	0.08	0.11	-0.07	-0.08	0.33***	0.33***	0.30***	0.30***	-0.34***	-0.36***	-0.20**	-0.38***	0.49***	0.59	0.77***	1		
WSB Nil	-0.03	-0.03	-0.04	-002	-0.11	-0.10	-0.13	-0.13	0.03	0.02	-0.14*	-0.13	0.05	0.06	0.12	0.02	1	
WSB Plus	0.04	0.00	-0.15*	-0.15*	-0.08	-0.08	-0.02	-0.04	-0.08	-0.09	0.00	-0.13	0.19**	0.20**	0.28***	0.26***	0.24***	1
%Yield loss	-0.14	-0.08	-0.11	-0.11	0.18	0.19	0.18**	0.17*	-0.11	-0.18**	0.16*	-0.31***	0.25***	0.32***	0.27***	0.46***	-0.04	0.25***

Note: *** indicates significance level at p= ≤0.001, ** indicates significance level p= ≤0.01 and * indicates significance level at p= ≤0.05. Correlation coefficients not highlighted are non-significant. NDVI = Normalized difference vegetation index; PH = Plant height (cm); HD = Heading days; PMD = Physiological maturity days; TGW = 1000- grain weight (g); GY = Grain yield (Kg ha^{-1}); % Sc = Percent screenings, % WH = Percent white heads; WSB= Weighted stem browning and %YL = Percent yield loss.

Table 4: Correlation coefficients based on means of 7 agronomic and yield contributing traits evaluated under inoculated (Plus) and un-inoculated (Nil) environment in 2015

Traits	*NDVI Nil*	*NDVI Plus*	*PH Nil*	*PH Plus*	*HD Nil*	*HD Plus*	*PMD Nil*	*PMD Plus*	*TGW Nil*	*TGW Plus*	*GY Nil*	*GY Plus*	*%Sc Nil*	*%Sc Plus*	%WH Nil	%WH Plus	WSB Plus	%Yield loss
NDVI Nil	1																	
NDVI Plus	0.55***	1																
PH Nil	-0.09	-0.11	1															
PH Plus	-0.10	-0.11	0.97***	1														
HD Nil	0.36***	0.33***	-0.33***	-0.36***	1													
HD Plus	0.35***	0.31***	-0.34***	-0.37***	0.99***	1												
PM Nil	0.33***	0.34***	-0.34***	-0.37***	0.83***	0.82***	1											
PM Plus	0.25***	0.25***	-0.27***	-0.29***	0.57***	0.56***	0.72***	1										
TGW Nil	-0.23***	-0.40***	0.36***	0.39***	-0.48***	-0.48***	-0.56***	-0.42***	1									
TGW Plus	-0.25***	-0.37***	0.37***	0.40***	-0.50***	-0.49***	-0.56***	-0.41***	0.92***	1								
GY Nil	-0.15*	-0.15*	0.02	0.03	-0.53***	-0.53***	-0.33***	-0.13	0.33***	0.30***	1							
GY Plus	-0.18**	-0.12	0.09	0.11	-0.56***	-0.56***	-0.37***	-0.19**	0.29***	0.39***	0.81***	1						
%Sc Nil	0.26**	0.36***	-0.27***	-0.31***	0.43***	0.43***	0.48***	0.37***	-0.76***	-0.73***	-0.30***	-0.34***	1					
%Sc Plus	0.31**	0.31***	-0.29***	-0.33***	0.51***	0.51***	0.52***	0.41***	-0.76***	-0.83***	-0.34***	-0.50***	0.83***	1				
%WH Nil	-0.01	-0,08	-0.09	-0.11	0.16*	0.16*	0.14*	0.07	-0.22**	-0.23***	-0.33***	-0.42***	0.26***	0.34***	1			
%WH Plus	0.10	0.006	-0.05	-0.07	0.30**	0.30***	0.12	0.12	-0.31***	-0.43***	-0.36***	-0.63***	0.35***	0.48***	0.65***	1		
WSB Plus	-0.02	-0.02	-0.19**	-0.20**	0.21**	0.23***	0.22**	0.16*	-0.06	-0.12	-0.13	-0.23***	0.12	0.14*	0.18**	0.23***	1	
%Yield loss	0.11	-0.01	-0.16*	-0.17*	0.26***	0.26***	0.21**	0.19**	-0.08	-0.27***	-0.06	-0.63***	0.19**	0.41***	0.30***	0.60***	0.24***	1

Note: *** indicates significance level at p= ≤0.001, ** indicates significance level p= ≤0.01 and * indicates significance level at p= ≤0.05. Correlation coefficients not highlighted are non-significant. NDVI = Normalized difference vegetation index; PH = Plant height (cm); HD = Heading days; PMD = Physiological maturity days; TGW = 1000- grain weight (g); GY = Grain yield (Kg ha^{-1}); % Sc = Percent screenings, % WH = Percent white heads; WSB= Weighted stem browning and %YL = Percent (%) yield loss.

Table 5: Mean for genotype x inoculum of grain yield (kg ha^{-1}) in 2014, 2015 and across years.

		Grain yield (kg ha^{-1})					
		2014		**2015**		**Combined**	
Entry	**Genotype**	**Nil**	**Plus**	**Nil**	**Plus**	**Nil**	**Plus**
1	PBICR-08-008-#2	4208	4158	3663	3319	4098	3947
2	PBICR-08-008-#7	4019	3907	3161	2521	3819	3355
3	PBICR-08-008-#8	4549	4179	3645	3216	4371	3948
4	PBICR-08-008-#9	3415	3539	3149	3074	3129	3231
5	PBICR-08-008-#10	3745	4082	2552	2455	3300	3534
6	PBICR-08-008-#11	3518	3623	3578	3051	3568	3315
7	PBICR-08-008-#16	5332	4624	3677	3250	4435	3837
8	PBICR-08-008-#22	4083	3861	2811	1619	3090	2303
9	PBICR-08-008-#23	5088	4318	3415	2121	4142	3097
10	PBICR-08-008-#27	4654	4203	3655	2698	4448	3865
11	PBICR-08-008-#29	4892	4334	3117	2280	3569	3063
12	PBICR-08-008-#37	3422	3904	4064	3731	3850	3859
13	PBICR-08-008-#38	4506	4196	4530	3560	4798	4038
14	PBICR-08-008-#39	4422	4100	3854	2624	4207	3562
15	PBICR-08-008-#44	2861	2861	3484	2933	3143	2913
16	PBICR-08-008-#45	3793	3225	2596	2281	2647	2350
17	PBICR-08-008-#46	4366	4423	3627	3074	4322	4258
18	PBICR-08-008-#47	3646	3682	2830	2158	3395	3206
19	PBICR-08-008-#48	4147	4060	3295	2663	3721	3364
20	PBICR-08-008-#49	4724	4170	3628	2669	4074	3376
21	PBICR-08-008-#50	4505	4460	3224	2718	3984	3713
22	PBICR-08-008-#51	3444	3471	3974	3615	3836	3700
23	PBICR-08-008-#52	4428	4302	3150	2721	4104	3944
24	PBICR-08-008-#53	4419	4248	3198	2245	3974	3332
25	PBICR-08-008-#55	5152	4856	3639	2984	4417	3887
26	PBICR-08-008-#56	4599	4062	4143	3687	4308	3798
27	PBICR-08-008-#57	4225	4009	3961	3367	3403	3214
28	PBICR-08-008-#62	4528	3982	3719	3475	4157	3783
29	PBICR-08-008-#63	4059	4116	3974	3845	4053	3901
30	PBICR-08-008-#64	4142	4243	3390	2602	3940	3562
31	PBICR-08-008-#65	4440	4084	3805	3443	3782	3373
32	PBICR-08-008-#68	3869	3585	3028	2146	3551	2993
33	PBICR-08-008-#69	3593	3298	3953	2980	3675	3152
34	PBICR-08-008-#70	3217	3508	3249	2732	3306	3275
35	PBICR-08-008-#71	4889	4040	3413	2842	3782	3156
36	PBICR-08-008-#72	4583	4474	3584	2422	4231	3558
37	PBICR-08-008-#73	4224	3863	3258	2626	3654	3184
38	PBICR-08-008-#74	3323	3179	2461	2178	2506	2305
39	PBICR-08-008-#75	4256	3967	3100	2828	3822	3519
40	PBICR-08-008-#76	4639	4374	3660	2863	4232	3795

41	PBICR-08-008-#77	3937	3796	2670	1811	3553	3096
42	PBICR-08-008-#80	4043	3886	4183	3487	4351	3934
43	PBICR-08-008-#81	4401	4174	4439	3370	4848	4157
44	PBICR-08-008-#82	4758	4472	3528	2952	4466	4007
45	PBICR-08-008-#83	4237	3584	3569	2649	3556	2637
46	PBICR-08-008-#85	4088	3726	3277	2786	3943	3509
47	PBICR-08-008-#86	4548	4276	3570	3130	3706	3507
48	PBICR-08-008-#89	4573	4513	3606	3078	3943	3752
49	PBICR-08-008-#90	4133	3949	3505	2805	3530	3106
50	PBICR-08-008-#91	3647	2934	2618	1758	2572	1840
51	PBICR-08-008-#94	4733	4687	3495	3426	4446	4386
52	PBICR-08-008-#97	4550	4347	3228	2789	3876	3568
53	PBICR-08-008-#98	4542	3999	3723	3462	4046	3592
54	PBICR-08-008-#99	3742	3780	3325	2800	3621	3257
55	PBICR-08-008-#100	4396	3967	3628	3070	4252	3791
56	PBICR-08-008-#101	4252	3980	3583	2829	4081	3719
57	PBICR-08-008-#103	4404	4061	2569	1932	3489	3155
58	PBICR-08-008-#104	4787	4164	3322	2972	4366	3896
59	PBICR-08-008-#107	4081	4132	3426	3011	4219	4023
60	PBICR-08-008-#108	3757	3547	3641	2912	3621	3172
61	PBICR-08-008-#109	4356	3595	3371	2567	3770	3029
62	PBICR-08-008-#111	2811	2282	1920	1670	1929	1525
63	PBICR-08-008-#112	4529	4283	2185	1512	3463	2947
64	PBICR-08-008-#113	4832	4667	3457	2866	4465	4068
65	PBICR-08-008-#114	4711	4505	4096	3456	4252	3851
66	PBICR-08-008-#115	4414	4439	3115	2402	3969	3754
67	PBICR-08-008-#116	3590	3271	3892	3493	3760	3462
68	PBICR-08-008-#118	4490	4288	3442	3334	4583	4581
69	PBICR-08-008-#119	4690	3851	3751	2957	4082	3297
70	PBICR-08-008-#123	4579	4379	4409	3810	4337	4057
71	PBICR-08-008-#124	4638	4379	3551	2908	4111	3659
72	PBICR-08-008-#125	4559	4622	3691	3097	4161	4060
73	PBICR-08-008-#126	4868	4510	3199	2429	4307	3675
74	PBICR-08-008-#127	4894	4554	3434	2496	4077	3640
75	PBICR-08-008-#129	4711	4334	4111	3612	4750	4369
76	PBICR-08-008-#130	4185	3775	3677	2910	3822	3336
77	PBICR-08-008-#133	3990	3586	3607	2521	3816	2951
78	PBICR-08-008-#134	4815	4617	3868	3389	4213	3879
79	PBICR-08-008-#136	3790	3745	3510	3103	4036	3746
80	PBICR-08-008-#137	3468	3072	3263	2200	3602	2806
81	PBICR-08-008-#138	4907	4029	3073	2557	4154	3471
82	PBICR-08-008-#140	3563	3072	2398	1884	3029	2679
83	PBICR-08-008-#141	3338	2968	3426	2994	3447	3031
84	PBICR-08-008-#145	4089	3673	2694	2338	3541	3122
85	PBICR-08-008-#146	3333	3371	2685	2060	3260	2856

86	PBICR-08-008-#147	3794	3675	3665	2952	4467	3937
87	PBICR-08-008-#148	4664	4292	3549	2669	4185	3596
88	PBICR-08-008-#150	2511	2253	2455	2467	2726	2602
89	PBICR-08-008-#151	5398	4574	3595	3334	4657	4192
90	PBICR-08-008-#153	3862	3317	2717	1791	3369	2751
91	PBICR-08-008-#154	4502	4051	3404	2806	3780	3376
92	PBICR-08-008-#156	4638	4603	3548	2949	4394	4068
93	PBICR-08-008-#157	3727	3648	2785	2334	3338	3115
94	PBICR-08-008-#160	4670	4295	3597	2611	4284	3881
95	PBICR-08-008-#162	4145	3778	3114	3078	3819	3434
96	PBICR-08-008-#163	4019	3895	2964	2702	2876	2931
97	PBICR-08-008-#164	4485	4251	3198	3003	4101	3914
98	PBICR-08-008-#165	3962	3997	3652	3452	4275	4171
99	PBICR-08-008-#166	4539	4308	3230	2446	4052	3791
100	PBICR-08-008-#167	4498	4228	3694	3170	4462	3984
101	PBICR-08-008-#168	4717	4255	3489	2887	4231	3862
102	PBICR-08-008-#169	3023	3369	3109	2150	3318	3044
103	PBICR-08-008-#170	3395	3169	3452	3185	3605	3310
104	PBICR-08-008-#171	4799	4698	3873	3388	4379	4071
105	PBICR-08-008-#173	3975	3899	3436	3408	4097	4088
106	PBICR-08-008-#174	4442	4318	3992	3484	4306	3947
107	PBICR-08-008-#175	4766	4369	3454	3136	3689	3462
108	PBICR-08-008-#176	4318	4168	3197	2459	3661	3248
109	PBICR-08-008-#177	2608	2478	4633	2994	3853	3109
110	PBICR-08-008-#178	4711	4764	3664	2792	4470	4142
111	PBICR-08-008-#180	4229	3068	3613	2471	3642	2616
112	PBICR-08-008-#181	4786	4367	3133	2268	4066	3502
113	PBICR-08-008-#182	4119	3572	3277	2924	3703	3201
114	PBICR-08-008-#183	4310	3901	3791	3097	3701	3050
115	PBICR-08-008-#184	4362	3761	4157	3549	4507	3957
116	PBICR-08-008-#185	3421	2846	2850	2684	3058	2792
117	PBICR-08-008-#186	4862	4055	3255	2896	4121	3350
118	PBICR-08-008-#187	3794	3599	4001	3368	4300	3795
119	PBICR-08-008-#188	4237	3826	3653	2921	3919	3536
120	PBICR-08-008-#189	4448	3324	3315	3045	3535	2875
121	PBICR-08-008-#190	4637	4431	3412	2807	3967	3575
122	PBICR-08-008-#191	4249	3768	3893	3469	4094	3544
123	PBICR-08-008-#193	4756	4249	3519	2825	4145	3547
124	PBICR-08-008-#196	3501	3574	3485	2578	3636	3387
125	PBICR-08-008-#198	4526	4263	3596	2915	3835	3233
126	PBICR-08-008-#199	4728	4893	3508	2792	4041	3808
127	PBICR-08-008-#200	4210	3874	3905	3232	3978	3475
128	PBICR-08-008-#202	4424	4251	3750	2876	4192	3576
129	PBICR-08-008-#203	4984	4684	3749	3256	4477	4113
130	PBICR-08-008-#204	4606	4524	3709	2489	4407	3539

131	PBICR-08-008-#205	3722	3770	3210	2999	3637	3733
132	PBICR-08-008-#206	4000	3566	3321	2494	3924	3235
133	PBICR-08-008-#207	3800	3566	2831	2370	3260	3046
134	PBICR-08-008-#209	4231	4022	3365	3290	3853	3785
135	PBICR-08-008-#210	3359	3404	3187	2486	2918	2578
136	PBICR-08-008-#212	4353	3901	3431	2501	3526	2850
137	PBICR-08-008-#213	4388	4294	3120	2594	3666	3406
138	PBICR-08-008-#214	4116	4116	4243	3541	4454	4043
139	PBICR-08-008-#215	3871	3686	3592	3264	3717	3467
140	PBICR-08-008-#218	4892	4366	3802	3400	4605	4242
141	PBICR-08-008-#219	4968	4455	3876	3471	4048	3554
142	PBICR-08-008-#221	4881	4546	3455	2631	3580	2940
143	PBICR-08-008-#223	5204	4856	3759	3289	4352	4086
144	PBICR-08-008-#225	4027	3801	2651	1876	3487	2874
145	PBICR-08-008-#227	3895	3742	2815	1956	3740	3160
146	PBICR-08-008-#228	5031	4816	3339	3277	4256	4180
147	PBICR-08-008-#229	3327	3465	3468	2850	3584	3171
148	PBICR-08-008-#230	3660	3780	2987	2357	3394	3041
149	PBICR-08-008-#231	4826	4235	3445	2765	3895	3386
150	PBICR-08-008-#232	4086	3583	2868	2212	3693	3083
151	PBICR-08-008-#233	4223	4059	3979	3404	4190	4150
152	PBICR-08-008-#234	4067	3713	2845	1976	3313	2649
153	PBICR-08-008-#235	4126	3994	3520	3294	3957	3745
154	PBICR-08-008-#236	3997	3768	2852	2374	3388	3160
155	PBICR-08-008-#237	4610	4110	3440	3269	4261	3890
156	PBICR-08-008-#240	4744	4096	3471	2920	4416	4022
157	PBICR-08-008-#241	4173	4155	3501	2818	3928	3607
158	PBICR-08-008-#242	2747	2365	2825	2306	2844	2612
159	PBICR-08-008-#243	4411	4433	4081	3613	4226	4080
160	PBICR-08-008-#244	2085	2225	2745	2612	2257	2535
161	PBICR-08-008-#247	3300	3604	3143	2472	3368	3161
162	PBICR-08-008-#248	4775	4284	3398	2535	4150	3459
163	PBICR-08-008-#250	4502	4035	3548	2641	4309	3683
164	PBICR-08-008-#252	4940	4434	3160	2557	4147	3664
165	PBICR-08-008-#253	3439	3010	2202	1969	2500	2124
166	PBICR-08-008-#254	4725	4146	3241	3047	4230	3840
167	PBICR-08-008-#255	4558	4124	3483	2654	4027	3318
168	PBICR-08-008-#256	3738	3981	2707	2239	3293	3146
169	PBICR-08-008-#257	4503	4277	3512	2893	3355	3016
170	PBICR-08-008-#258	3914	4013	3064	2660	3691	3574
171	PBICR-08-008-#259	4236	4071	3675	3047	3962	3568
172	PBICR-08-008-#260	4400	4239	3116	2955	3825	3662
173	PBICR-08-008-#261	4153	4354	3589	3112	3411	3381
174	PBICR-08-008-#262	4679	4234	3512	2980	4355	3821
175	PBICR-08-008-#263	4227	3935	3674	3614	3802	3639

176	PBICR-08-008-#267	4519	4399	4077	3023	4447	3663
177	PBICR-08-008-#268	5005	4656	3253	2683	4203	3752
178	PBICR-08-008-#269	3845	3587	3918	3109	4247	3795
179	PBICR-08-008-#270	4652	4562	3813	2964	3973	3568
180	PBICR-08-008-#271	4565	4256	3392	2830	3638	3083
181	PBICR-08-008-#273	4245	4596	2962	2794	3630	3648
182	PBICR-08-008-#274	4498	4121	3528	2745	3927	3290
183	PBICR-08-008-#275	4812	4352	3549	3108	4249	4022
184	PBICR-08-008-#276	4560	4161	3207	2581	3975	3429
185	PBICR-08-008-#278	4539	3702	3704	3262	4013	3452
186	PBICR-08-008-#280	4221	3944	3258	2546	3998	3515
187	PBICR-08-008-#283	4519	4214	3363	2476	3959	3364
188	PBICR-08-008-#284	3689	3425	2847	2471	2980	2616
189	PBICR-08-008-#285	4144	3567	3626	3126	3485	3033
190	PBICR-08-008-#289	3652	3935	2951	2840	2727	3002
191	PBICR-08-008-#291	3982	3808	3444	2873	3179	2758
192	PBICR-08-008-#292	3174	3167	2564	2487	2783	2781
193	PBICR-08-008-#293	4212	4005	3196	2731	3554	3237
194	PBICR-08-008-#294	4169	3522	3484	3092	4202	3552
195	PBICR-08-008-#298	3643	3766	3054	2405	3434	3356
196	PBICR-08-008-#299	4170	3936	3521	2919	3769	3453
197	AUS29529	3628	3519	3506	2586	3890	3271
198	Sunco/Pastor	4348	4464	3393	3074	3939	3872
199	Syn110	4483	4110	2896	2361	3964	3498
200	Suntop	4790	4446	4262	3608	4828	4356
201	Sunguard	4524	4361	3855	3506	4163	3886
202	Sunco	4813	4507	3284	2954	4002	3631
203	Spitfire			3724	3210		
204	Gregory	4549	4431	3524	2615	4161	3595
205	Bellaroi	3832	2838	2743	1791	3269	2181
206	Batavia	4177	3498	3238	2029	3939	2972
207	Wylie	4276	3850	3501	2702	3934	3335
Mean		**4229**	**3962**	**3409**	**2823**	**3851**	**3448**
Minimum		**2085**	**2225**	**1920**	**1512**	**1929**	**1525**
Maximum		**5398**	**4893**	**4633**	**3845**	**4848**	**4581**
Standard Error of Mean		**38.110**	**35.230**	**30.810**	**32.810**	**34.480**	**34.590**
Standard Error of difference (SED)		**431.10**		**328.40**		**294.00**	
LSD (5%) (Genotype x environment)		**851.35**		**644.32**		**576.83**	
LSD (5%) (Genotype)		**800.03**		**555.17**		**424.89**	

Table 6: Mean for genotype x inoculum of TKW (g) in 2014, 2015 and across years.

		TKW (g)					
		2014		2015		Combined	
Entry	Genotype	Nil	Plus	Nil	Plus	Nil	Plus
1	PBICR-08-008-#2	30.83	31.19	28.38	25.65	29.55	28.32
2	PBICR-08-008-#7	21.51	25.15	25.78	23.36	24.65	24.96
3	PBICR-08-008-#8	29.96	28.74	24.82	24.09	27.76	26.58
4	PBICR-08-008-#9	33.26	33.13	29.1	26.98	30.25	28.96
5	PBICR-08-008-#10	29.14	22.01	32.05	30.06	29.76	26.63
6	PBICR-08-008-#11	36.8	38.64	33.31	30.3	34.69	33.91
7	PBICR-08-008-#16	27.45	30.99	28.35	27.52	29.32	29.37
8	PBICR-08-008-#22	29.05	27.64	26.58	23.91	26.71	24.53
9	PBICR-08-008-#23	36.53	36.44	30.75	26.3	33.15	30.57
10	PBICR-08-008-#27	35.53	34.99	31.82	29.58	34.41	32.78
11	PBICR-08-008-#29	27.61	28.84	25.32	21.9	26.34	25.64
12	PBICR-08-008-#37	39.51	38.98	35	33.84	37.73	36.24
13	PBICR-08-008-#38	41.48	40.73	32.46	27.26	37.36	34.68
14	PBICR-08-008-#39	33.7	32.57	29.69	24.3	31.23	28.69
15	PBICR-08-008-#44	42.15	42.25	37.34	33.78	39.65	37.67
16	PBICR-08-008-#45	27.63	26.55	23.78	24.24	24.23	23.58
17	PBICR-08-008-#46	38.11	34.46	31.75	29.86	34.61	32.45
18	PBICR-08-008-#47	28.7	30.24	25.92	24.58	28.16	27.85
19	PBICR-08-008-#48	30.3	29.85	27.84	24.36	28.69	26.6
20	PBICR-08-008-#49	34.17	35.15	29.91	26.11	31.34	29.71
21	PBICR-08-008-#50	27.9	29.49	25.31	22.93	26.73	25.92
22	PBICR-08-008-#51	41.55	40.74	37	33.19	39.35	37.75
23	PBICR-08-008-#52	32.35	29.77	24.95	24.38	28.7	27.77
24	PBICR-08-008-#53	28.01	27.85	27.11	24.17	27.76	26.13
25	PBICR-08-008-#55	36.36	35.38	27.52	24.44	31.53	29.54
26	PBICR-08-008-#56	43.98	41.12	36.94	35.83	40.64	38.66
27	PBICR-08-008-#57	36.85	35.4	33.57	32.12	34	33.47
28	PBICR-08-008-#62	32.26	29.59	26.81	26.02	29.33	27.2
29	PBICR-08-008-#63	31.5	32.86	28.19	26.99	29.65	29.23
30	PBICR-08-008-#64	45.34	39.44	34.83	32.53	39.82	35.1
31	PBICR-08-008-#65	41.87	40.35	35.71	33.69	37.85	36.13
32	PBICR-08-008-#68	29.29	27.79	28.65	24.23	28.92	25.91
33	PBICR-08-008-#69	36.34	41.08	35.03	32.08	36.04	37.18
34	PBICR-08-008-#70	44.37	43.31	38.04	34.08	40.74	38.14
35	PBICR-08-008-#71	30.6	30.33	28.84	26.04	28.91	28.1
36	PBICR-08-008-#72	32.4	38.61	29.14	25.82	30.43	32.12
37	PBICR-08-008-#73	41.95	41.01	37.67	33.4	40.03	37.47
38	PBICR-08-008-#74	34.59	34.39	33.25	30.9	33.49	32.29
39	PBICR-08-008-#75	32.5	31.75	27.19	26.42	29.58	29.23
40	PBICR-08-008-#76	33.43	29.77	30.62	27.28	32.71	29.99
41	PBICR-08-008-#77	24.01	24.3	22.35	24.89	23.53	24.87
42	PBICR-08-008-#80	42.68	41.92	40.43	34.78	42.19	39.25

43	PBICR-08-008-#81	39	40.74	32.99	28.9	35.09	32.93
44	PBICR-08-008-#82	31.09	32.87	27.35	26	29.26	29.17
45	PBICR-08-008-#83	29.05	27.95	30.22	26.53	29.23	26.09
46	PBICR-08-008-#85	31.96	30.88	26.37	23.73	29.15	27.65
47	PBICR-08-008-#86	29.62	29.85	29.09	26.2	28.97	27.74
48	PBICR-08-008-#89	31.56	33.55	27.5	24.55	30.04	29.62
49	PBICR-08-008-#90	28.85	27.27	27.92	26.63	28.22	26.82
50	PBICR-08-008-#91	30.38	23.64	27.54	25.82	27.37	23.17
51	PBICR-08-008-#94	30.05	29.23	26.27	28.35	28.24	29.05
52	PBICR-08-008-#97	31.51	30.88	26.56	25.69	29.25	28.48
53	PBICR-08-008-#98	34.48	34.52	28.77	28.03	30.74	30.69
54	PBICR-08-008-#99	38.06	40.07	34.96	33.81	36.7	37.25
55	PBICR-08-008-#100	37.55	35.87	29.49	28.9	34.51	33.95
56	PBICR-08-008-#101	39.95	41.57	31.44	29.38	35.98	34.76
57	PBICR-08-008-#103	29.68	27.92	25.47	23.68	27.2	25.09
58	PBICR-08-008-#104	33.55	31.06	26.56	26.29	30.79	29.12
59	PBICR-08-008-#107	30.91	35.61	25.99	25.61	29.16	30.91
60	PBICR-08-008-#108	35.24	33.69	32.1	29.26	33.6	31.64
61	PBICR-08-008-#109	28.11	26.36	27.24	27.01	27.51	26.88
62	PBICR-08-008-#111	22.23	24.68	25.59	25.34	23.63	24.11
63	PBICR-08-008-#112	32.34	34.04	28.8	25.16	30.09	29.18
64	PBICR-08-008-#113	39.31	40.86	29.15	26.72	35.14	34.1
65	PBICR-08-008-#114	25.99	20.35	33.11	30.13	30.26	28.01
66	PBICR-08-008-#115	36.38	33.51	24.38	26.25	30.22	30.08
67	PBICR-08-008-#116	38.67	39.38	28.86	27.55	33.91	33.5
68	PBICR-08-008-#118	39.33	35.71	29.06	28.99	34.5	32.57
69	PBICR-08-008-#119	39.86	33.34	32.01	30.39	36.22	31.72
70	PBICR-08-008-#123	31.34	35.39	27.93	27.43	29.15	30.89
71	PBICR-08-008-#124	29.38	30.16	26.47	24.34	28.14	27.84
72	PBICR-08-008-#125	33.6	32.43	28.19	25.14	31	29.37
73	PBICR-08-008-#126	32.82	29.39	26.29	22.07	28.73	25.88
74	PBICR-08-008-#127	37.03	34.69	31.52	26.92	34.17	30.38
75	PBICR-08-008-#129	35.03	32.22	29.83	27.64	32.55	29.8
76	PBICR-08-008-#130	33.95	30.9	27.11	25.01	30.45	28.24
77	PBICR-08-008-#133	31.83	30.06	29.01	23.96	29.91	26.55
78	PBICR-08-008-#134	30.83	32.83	30.38	27.65	30.95	30.12
79	PBICR-08-008-#136	36.29	35.11	31.37	29.93	34.56	33.17
80	PBICR-08-008-#137	41.42	40.74	37.05	30.73	39.17	35.89
81	PBICR-08-008-#138	34.02	32.19	27.08	24.73	30.81	28.55
82	PBICR-08-008-#140	23.51	24.65	24.42	21.99	23.82	22.85
83	PBICR-08-008-#141	38.74	38.15	30.85	30.72	34.77	34.29
84	PBICR-08-008-#145	28.56	28.2	25.91	24.73	27.46	26.67
85	PBICR-08-008-#146	35.3	37.73	34.44	30.82	35.08	34.24
86	PBICR-08-008-#147	33.61	35.33	28.97	26.93	32.2	30.54
87	PBICR-08-008-#148	32.09	33.86	27.57	23.61	29.96	27.97
88	PBICR-08-008-#150	36.44	39.65	31.13	29.61	34.18	33.96

89	PBICR-08-008-#151	36.94	33.88	27.87	28.57	33.07	31.64
90	PBICR-08-008-#153	26.55	26.64	27.81	25.54	27.45	26.69
91	PBICR-08-008-#154	33.55	31.35	26.21	23.96	30.26	27.53
92	PBICR-08-008-#156	27.01	29.12	24.87	22.69	26.6	26.07
93	PBICR-08-008-#157	29.89	29.52	24.08	24.21	27.19	26.58
94	PBICR-08-008-#160	32.94	34.86	29.02	24.73	30.88	30.45
95	PBICR-08-008-#162	30.03	29.24	26.65	26.77	28.63	27.99
96	PBICR-08-008-#163	36.35	32.44	30.72	28.42	32.85	29.98
97	PBICR-08-008-#164	29.94	28.05	27.03	25.94	28.45	27.55
98	PBICR-08-008-#165	40.2	41.17	37.03	33.42	39.41	37.61
99	PBICR-08-008-#166	28.9	30.98	24.97	23.57	26.53	27.52
100	PBICR-08-008-#167	28.75	29.41	28.59	26.06	29.21	28.34
101	PBICR-08-008-#168	31.86	32.47	26.93	25.61	29.51	29.36
102	PBICR-08-008-#169	37.72	37.4	28.6	24.84	34.26	31.43
103	PBICR-08-008-#170	35.76	37.08	30.7	30.2	33.71	33.28
104	PBICR-08-008-#171	31.61	36.56	27.26	26.1	29.99	30.81
105	PBICR-08-008-#173	36.78	37.47	34.99	29.75	35.56	33.35
106	PBICR-08-008-#174	28.1	26.91	26.85	24.76	27.26	25.46
107	PBICR-08-008-#175	33.82	32.15	29.62	27.25	30.76	28.48
108	PBICR-08-008-#176	32.25	31.19	27.52	26.19	29.47	28.01
109	PBICR-08-008-#177	43.63	42.95	37.35	33.47	40.84	38.78
110	PBICR-08-008-#178	37.32	33.88	29.71	26.84	33.73	31.06
111	PBICR-08-008-#180	30.24	28.35	28.26	24.52	28.72	25.93
112	PBICR-08-008-#181	34	33.4	25.33	24.78	29.36	29.91
113	PBICR-08-008-#182	26.68	26.85	27.07	26.28	26.86	26.57
114	PBICR-08-008-#183	28.8	28.53	29.89	27.41	29.6	27.05
115	PBICR-08-008-#184	40.97	41.48	35.44	33.67	38.49	38.26
116	PBICR-08-008-#185	34	30.35	29.38	26.09	31.49	28.6
117	PBICR-08-008-#186	33.48	33.46	31.35	29.33	32.64	31.41
118	PBICR-08-008-#187	44.32	43.4	33.75	31.78	39.83	38.07
119	PBICR-08-008-#188	28.32	26.83	28.64	24.23	28.62	26.01
120	PBICR-08-008-#189	28.04	21.24	28.76	26.77	29.08	24.87
121	PBICR-08-008-#190	33.44	31.59	28.45	25.62	31.33	28.88
122	PBICR-08-008-#191	41.11	42.86	39.76	36.78	40.33	39.75
123	PBICR-08-008-#193	32.49	31.29	28.65	26.59	30.58	29.26
124	PBICR-08-008-#196	36.43	33.83	31.88	25.47	32.29	30.36
125	PBICR-08-008-#198	27.86	27.04	26.61	24.75	26.81	25.5
126	PBICR-08-008-#199	34.69	35.72	28.15	24.9	31.43	29.97
127	PBICR-08-008-#200	44.41	38.48	37.96	32.68	41.03	35.66
128	PBICR-08-008-#202	32.37	34.02	32.09	27.84	31.59	30.46
129	PBICR-08-008-#203	28.91	30.73	25.72	23.99	27.42	27.35
130	PBICR-08-008-#204	31.33	29.66	28.93	26.71	29.87	28.51
131	PBICR-08-008-#205	33.97	31.67	29.04	28.57	31.93	31.45
132	PBICR-08-008-#206	28.87	28.88	26.89	24.51	28.42	27.65
133	PBICR-08-008-#207	26.47	23.27	24.8	21.91	25.1	22.3
134	PBICR-08-008-#209	34.24	32.86	29.09	28.89	31.96	31.18

135	PBICR-08-008-#210	22.31	22.39	24.27	22.04	22.88	21.4
136	PBICR-08-008-#212	35.35	33.05	31.57	29.55	32.7	31.47
137	PBICR-08-008-#213	35.76	35.09	29.67	25.26	31.85	29.79
138	PBICR-08-008-#214	32.68	32.79	31.86	29.12	33.65	31.13
139	PBICR-08-008-#215	36.47	35.29	31.42	28.43	33.52	31.38
140	PBICR-08-008-#218	28.83	38.46	24.81	23.98	27.58	31.56
141	PBICR-08-008-#219	37.18	34.75	33.56	31.09	34.1	31.66
142	PBICR-08-008-#221	27.01	26.48	26.23	22.76	25.92	23.33
143	PBICR-08-008-#223	33.5	32.36	27.2	25.02	30.58	29.09
144	PBICR-08-008-#225	25.96	23.66	31.34	27.65	29.45	25.58
145	PBICR-08-008-#227	36.96	36.04	32.19	28.86	34.72	32.45
146	PBICR-08-008-#228	32.97	28.68	29.08	27.98	30.9	28.74
147	PBICR-08-008-#229	37.2	35.22	32.13	27.87	34.73	31.21
148	PBICR-08-008-#230	26.83	26.49	25.59	23.7	26.25	24.47
149	PBICR-08-008-#231	31.86	32.43	28.74	26.99	30.96	30.26
150	PBICR-08-008-#232	28.04	26.62	25.48	22.98	27.16	25.26
151	PBICR-08-008-#233	35.04	47.29	31.23	28.78	33.58	38.49
152	PBICR-08-008-#234	34.85	35.74	31.13	27.35	33.05	30.74
153	PBICR-08-008-#235	43.18	39.35	35	32.74	37.89	36.52
154	PBICR-08-008-#236	28.45	38.41	24.76	22.74	25.85	30.59
155	PBICR-08-008-#237	35.9	38.96	32.29	31.15	33.8	35.6
156	PBICR-08-008-#240	33	32.1	28.51	27.31	31.55	30.45
157	PBICR-08-008-#241	29.68	31.25	26.57	24.48	27.86	26.42
158	PBICR-08-008-#242	36.27	38.76	32.54	29.23	35.15	34.54
159	PBICR-08-008-#243	32.08	31.32	30.11	28.45	30.42	29.51
160	PBICR-08-008-#244	40.12	41.59	38	37.65	39.04	39.87
161	PBICR-08-008-#247	41.57	42.61	37.99	34.64	39.69	38.48
162	PBICR-08-008-#248	29.64	28.96	27.29	23.55	28.52	26.6
163	PBICR-08-008-#250	37.95	36	29.89	26.16	34.53	31.68
164	PBICR-08-008-#252	29.12	27.95	27.11	23.99	27.96	25.92
165	PBICR-08-008-#253	29.41	29.76	27.46	25.13	27.22	25.34
166	PBICR-08-008-#254	32.08	31.22	30.03	26.58	31.31	29.44
167	PBICR-08-008-#255	30.36	29.11	26.93	24.85	28.08	26.38
168	PBICR-08-008-#256	23.65	23.36	21.38	20.56	22.47	21.94
169	PBICR-08-008-#257	32.07	32.24	32.33	28.24	30.87	28.75
170	PBICR-08-008-#258	27.16	31.87	22.66	22.07	24.72	26.9
171	PBICR-08-008-#259	38.49	37.73	31.07	29.37	33.55	32.54
172	PBICR-08-008-#260	30.57	27.55	24.55	24.19	27.43	25.6
173	PBICR-08-008-#261	25.96	29.79	27.24	25.55	25.74	27.56
174	PBICR-08-008-#262	25.3	27.61	25.28	24.18	26.26	25.74
175	PBICR-08-008-#263	36.18	37.56	34.24	32.55	35.49	35.4
176	PBICR-08-008-#267	33.77	33.71	31.68	26.52	32.53	29.82
177	PBICR-08-008-#268	32.14	32.67	25.16	23.97	28.45	27.58
178	PBICR-08-008-#269	43.56	41.27	40.63	38.29	41.76	40.49
179	PBICR-08-008-#270	31.78	31.31	28.75	25.15	29.85	27.92
180	PBICR-08-008-#271	36.43	34.65	34.52	32.3	34.77	34.15

181	PBICR-08-008-#273	29.07	28.77	27.35	25.7	27.71	27.61
182	PBICR-08-008-#274	29.93	30.7	27.06	25.14	28.73	28.31
183	PBICR-08-008-#275	34.18	34.7	32.82	31.22	33.05	33.41
184	PBICR-08-008-#276	29.48	28.86	29.91	27.29	30	28.7
185	PBICR-08-008-#278	30.88	27.33	28.92	27.21	30.32	27.75
186	PBICR-08-008-#280	32.52	35.8	29.8	26.6	31.28	31.49
187	PBICR-08-008-#283	28.27	29.38	26.14	23.96	26.34	26.64
188	PBICR-08-008-#284	37.59	34.67	33.58	30.35	34.91	31.91
189	PBICR-08-008-#285	45.09	45.26	40.57	38.57	42.37	41.19
190	PBICR-08-008-#289	32.05	32.55	31.01	29.71	30.7	30.73
191	PBICR-08-008-#291	33.44	34.6	32.75	29.65	31.87	30.71
192	PBICR-08-008-#292	39.54	36.4	33.21	30.39	36.64	33.72
193	PBICR-08-008-#293	25.41	23.05	24.67	24.23	24.21	23.16
194	PBICR-08-008-#294	36.16	36.73	30.43	29.68	33.27	32.8
195	PBICR-08-008-#298	32.81	30.65	28.84	25.91	29.89	28.55
196	PBICR-08-008-#299	29.15	29.3	27.86	24.64	28.74	27.53
197	AUS29529	39.28	37.19	33.05	29.44	36.31	32.88
198	Sunco/Pastor	29.29	29.42	25.45	24.51	27.36	26.59
199	Syn110	30.09	29.09	26.53	24.28	28.16	26.45
200	Suntop	18.63	33.51	28.21	26.99	24.1	30.36
201	Sunguard	31.44	30.35	26.12	23.71	28.17	27.05
202	Sunco	29.5	29.95	26.37	24.02	27.4	26.35
203	Spitfire	-	-	27.87	27.52	-	-
204	Gregory	31.95	33.06	27.32	24.36	29.73	29.41
205	Bellaroi	36.65	36.7	29.92	26.48	33	31.08
206	Batavia	32.62	30.58	27.48	23.84	29.95	27.28
207	Wylie	35.52	33.36	28.4	26.74	31.58	30
Mean		**33.18**	**32.9**	**29.53**	**27.24**	**31.29**	**30.03**
Minimum		**18.63**	**20.35**	**21.38**	**20.56**	**22.47**	**21.4**
Maximum		**45.34**	**47.29**	**40.63**	**38.57**	**42.37**	**41.19**
Standard Error of Mean		**0.350**	**0.355**	**0.261**	**0.237**	**0.292**	**0.280**
Standard Error of difference (SED)		**3.51**		**3.53**		**1.73**	
LSD (5%) (Genotype x environment)		**6.91**		**3.01**		**3.39**	
LSD (5%) (Genotype)		5.77		**2.50**		**2.50**	

Table 7: Mean for genotype x inoculum of % screenings in 2014, 2015 and across years.

		% screenings					
		2014		2015		Combined	
Entry	**Genotype**	**Nil**	**Plus**	**Nil**	**Plus**	**Nil**	**Plus**
1	PBICR-08-008-#2	5.80	4.90	7.56	14.53	6.99	9.34
2	PBICR-08-008-#7	13.71	12.32	8.30	14.88	10.72	13.50
3	PBICR-08-008-#8	9.25	11.08	17.76	21.00	13.71	16.48
4	PBICR-08-008-#9	2.59	4.08	2.33	6.31	2.95	5.89
5	PBICR-08-008-#10	8.11	8.31	4.79	5.59	6.62	6.70
6	PBICR-08-008-#11	3.45	2.82	2.31	5.72	2.88	3.92
7	PBICR-08-008-#16	10.03	11.32	10.88	6.72	11.19	9.37
8	PBICR-08-008-#22	16.79	19.26	16.59	25.35	17.09	22.67
9	PBICR-08-008-#23	9.63	11.21	12.71	19.78	10.85	16.03
10	PBICR-08-008-#27	2.48	5.02	3.95	9.96	3.54	7.17
11	PBICR-08-008-#29	7.22	7.85	12.66	20.59	9.96	14.24
12	PBICR-08-008-#37	1.69	1.95	1.23	2.26	1.75	2.59
13	PBICR-08-008-#38	1.21	1.33	2.40	6.37	1.52	3.52
14	PBICR-08-008-#39	7.32	10.27	10.32	19.45	8.44	14.54
15	PBICR-08-008-#44	1.98	1.63	1.55	3.73	1.61	2.31
16	PBICR-08-008-#45	18.36	22.87	16.88	20.98	17.89	22.08
17	PBICR-08-008-#46	6.18	7.79	3.30	7.50	4.65	7.30
18	PBICR-08-008-#47	10.61	10.44	11.63	16.99	11.41	13.66
19	PBICR-08-008-#48	12.60	12.17	10.09	17.80	11.27	14.86
20	PBICR-08-008-#49	5.38	7.34	8.46	13.66	7.01	10.68
21	PBICR-08-008-#50	7.82	9.55	8.46	12.95	8.18	11.47
22	PBICR-08-008-#51	1.48	2.74	1.08	3.93	1.11	2.49
23	PBICR-08-008-#52	7.69	8.92	9.53	13.85	8.01	11.06
24	PBICR-08-008-#53	13.93	13.77	11.00	16.46	12.31	14.90
25	PBICR-08-008-#55	3.92	6.69	10.08	14.46	7.55	11.29
26	PBICR-08-008-#56	1.73	2.70	2.55	3.81	1.45	2.31
27	PBICR-08-008-#57	4.04	6.22	2.09	4.93	3.30	5.52
28	PBICR-08-008-#62	5.16	8.10	6.37	8.91	6.06	8.52
29	PBICR-08-008-#63	6.25	5.03	4.20	8.95	5.26	7.43
30	PBICR-08-008-#64	1.33	1.83	1.23	3.27	2.14	4.06
31	PBICR-08-008-#65	2.47	3.66	1.38	2.84	1.93	3.26
32	PBICR-08-008-#68	13.81	14.75	9.72	16.67	11.59	15.10
33	PBICR-08-008-#69	2.65	3.49	1.85	3.59	1.94	3.02
34	PBICR-08-008-#70	1.73	2.33	0.88	2.75	1.82	3.15
35	PBICR-08-008-#71	7.02	7.79	4.93	10.09	6.08	8.88
36	PBICR-08-008-#72	7.56	7.29	9.25	13.80	8.59	10.79
37	PBICR-08-008-#73	1.50	2.45	-1.02	4.49	1.35	2.72
38	PBICR-08-008-#74	6.15	6.87	3.42	7.24	4.29	6.52
39	PBICR-08-008-#75	4.50	5.65	7.94	11.00	6.21	8.22
40	PBICR-08-008-#76	4.91	6.08	5.21	10.91	4.17	7.50
41	PBICR-08-008-#77	12.73	12.39	11.79	16.02	12.32	14.04
42	PBICR-08-008-#80	1.14	1.40	1.13	3.52	0.95	1.71

43	PBICR-08-008-#81	4.01	5.24	3.87	9.47	4.17	7.17
44	PBICR-08-008-#82	3.79	5.85	7.44	13.00	5.32	8.86
45	PBICR-08-008-#83	14.90	18.34	9.30	14.91	11.58	17.06
46	PBICR-08-008-#85	7.61	7.23	9.93	14.06	8.80	10.52
47	PBICR-08-008-#86	11.20	11.52	10.17	13.93	11.18	13.08
48	PBICR-08-008-#89	7.04	9.52	12.45	15.75	9.30	12.57
49	PBICR-08-008-#90	9.72	13.63	5.88	12.07	8.05	12.91
50	PBICR-08-008-#91	17.20	21.75	7.67	12.83	12.42	17.86
51	PBICR-08-008-#94	7.80	6.56	9.34	10.12	8.79	8.50
52	PBICR-08-008-#97	6.32	6.90	6.41	13.45	6.10	10.12
53	PBICR-08-008-#98	4.03	5.93	2.03	3.52	3.40	5.58
54	PBICR-08-008-#99	1.59	2.19	2.42	5.19	2.06	4.02
55	PBICR-08-008-#100	2.39	4.95	5.34	7.49	3.91	6.25
56	PBICR-08-008-#101	3.69	4.06	4.06	8.19	4.01	6.15
57	PBICR-08-008-#103	4.98	6.16	10.56	21.14	8.39	13.91
58	PBICR-08-008-#104	8.80	10.10	11.06	13.00	10.03	11.70
59	PBICR-08-008-#107	7.94	7.01	11.57	13.98	9.78	10.31
60	PBICR-08-008-#108	7.85	8.32	5.36	8.72	6.12	8.60
61	PBICR-08-008-#109	11.22	16.56	10.00	13.44	10.47	14.32
62	PBICR-08-008-#111	21.03	22.16	11.26	15.78	15.74	18.68
63	PBICR-08-008-#112	5.16	7.37	6.66	12.51	6.28	10.26
64	PBICR-08-008-#113	3.13	6.70	6.82	11.97	4.65	9.11
65	PBICR-08-008-#114	11.83	12.44	4.95	8.57	8.76	11.28
66	PBICR-08-008-#115	5.65	8.64	15.58	10.29	11.48	9.50
67	PBICR-08-008-#116	1.58	1.61	8.08	12.30	5.05	7.16
68	PBICR-08-008-#118	1.34	4.13	6.82	7.46	3.96	5.30
69	PBICR-08-008-#119	5.78	9.66	5.44	6.81	4.59	7.57
70	PBICR-08-008-#123	7.48	7.71	5.91	8.68	7.05	8.54
71	PBICR-08-008-#124	8.51	10.28	11.09	18.45	10.17	14.20
72	PBICR-08-008-#125	4.22	4.73	6.14	10.57	5.21	7.01
73	PBICR-08-008-#126	6.36	8.81	12.44	23.02	10.00	15.69
74	PBICR-08-008-#127	5.23	6.21	5.78	11.28	5.89	9.15
75	PBICR-08-008-#129	1.10	2.77	3.38	5.45	2.17	4.14
76	PBICR-08-008-#130	11.01	12.10	9.40	15.67	10.61	13.70
77	PBICR-08-008-#133	9.19	9.96	7.22	18.54	8.26	14.59
78	PBICR-08-008-#134	10.15	9.54	10.17	14.76	9.25	11.82
79	PBICR-08-008-#136	4.09	4.21	2.77	5.88	3.21	4.64
80	PBICR-08-008-#137	2.19	2.49	0.33	6.36	2.10	4.84
81	PBICR-08-008-#138	3.16	6.64	12.05	18.15	7.57	12.72
82	PBICR-08-008-#140	17.61	19.57	16.68	21.25	15.98	20.11
83	PBICR-08-008-#141	3.66	4.53	5.74	4.50	4.82	4.93
84	PBICR-08-008-#145	9.52	10.90	11.19	15.49	10.30	13.38
85	PBICR-08-008-#146	4.64	6.62	3.13	7.15	3.95	6.84
86	PBICR-08-008-#147	9.60	9.47	7.58	12.72	7.99	10.83
87	PBICR-08-008-#148	7.53	8.32	9.60	18.74	8.99	13.71
88	PBICR-08-008-#150	1.95	2.16	2.92	5.45	2.02	3.26

89	PBICR-08-008-#151	3.34	4.04	8.99	10.65	6.16	7.61
90	PBICR-08-008-#153	8.91	10.59	9.94	19.35	8.56	12.75
91	PBICR-08-008-#154	10.90	12.97	10.49	13.25	10.87	13.70
92	PBICR-08-008-#156	9.36	9.94	12.54	18.26	10.51	14.08
93	PBICR-08-008-#157	9.69	11.40	18.68	22.04	14.16	16.82
94	PBICR-08-008-#160	9.66	10.67	8.86	14.42	9.09	12.10
95	PBICR-08-008-#162	6.51	6.82	9.13	10.30	7.45	8.74
96	PBICR-08-008-#163	4.63	7.67	3.90	7.25	4.44	7.43
97	PBICR-08-008-#164	8.83	10.11	12.58	15.12	11.57	12.43
98	PBICR-08-008-#165	1.69	1.71	1.60	2.69	1.59	2.20
99	PBICR-08-008-#166	8.23	8.48	14.90	21.37	11.74	14.62
100	PBICR-08-008-#167	8.95	9.09	10.13	15.29	8.60	11.49
101	PBICR-08-008-#168	7.03	7.84	11.52	16.18	9.24	12.03
102	PBICR-08-008-#169	6.47	8.54	14.66	25.66	10.26	16.82
103	PBICR-08-008-#170	2.21	3.02	1.96	2.89	1.99	3.22
104	PBICR-08-008-#171	6.62	7.85	9.45	10.71	9.57	12.60
105	PBICR-08-008-#173	1.83	3.62	2.29	5.05	1.58	3.56
106	PBICR-08-008-#174	13.49	14.08	8.89	13.40	10.91	13.99
107	PBICR-08-008-#175	10.14	11.70	9.47	11.51	9.06	11.53
108	PBICR-08-008-#176	9.95	12.99	8.65	16.37	9.95	14.60
109	PBICR-08-008-#177	1.92	4.36	1.41	4.88	1.32	3.63
110	PBICR-08-008-#178	4.51	5.61	9.57	17.05	7.00	10.94
111	PBICR-08-008-#180	9.20	9.30	7.98	17.52	8.32	12.98
112	PBICR-08-008-#181	4.64	7.47	12.83	18.16	8.96	12.55
113	PBICR-08-008-#182	15.60	16.09	15.53	17.50	15.74	17.03
114	PBICR-08-008-#183	9.81	13.59	7.61	15.24	8.78	13.87
115	PBICR-08-008-#184	1.46	1.42	1.44	3.21	1.34	2.20
116	PBICR-08-008-#185	3.61	7.79	2.10	8.11	2.79	7.74
117	PBICR-08-008-#186	5.20	6.36	4.45	7.73	4.68	6.85
118	PBICR-08-008-#187	1.02	1.50	2.08	3.61	1.46	2.67
119	PBICR-08-008-#188	14.90	15.38	12.90	21.25	13.63	17.68
120	PBICR-08-008-#189	14.25	16.33	8.07	11.46	10.67	13.41
121	PBICR-08-008-#190	5.75	6.87	10.35	16.95	8.02	11.76
122	PBICR-08-008-#191	2.80	2.04	1.36	2.33	2.01	2.33
123	PBICR-08-008-#193	6.57	8.99	8.98	11.70	7.98	10.92
124	PBICR-08-008-#196	6.89	7.33	8.00	18.90	7.40	12.79
125	PBICR-08-008-#198	8.76	13.49	7.00	13.32	7.52	13.63
126	PBICR-08-008-#199	7.15	8.01	5.56	11.09	6.82	10.83
127	PBICR-08-008-#200	1.50	3.74	0.14	2.30	0.80	3.22
128	PBICR-08-008-#202	7.50	8.35	4.92	9.41	6.36	8.66
129	PBICR-08-008-#203	9.16	10.66	10.64	15.03	9.28	12.22
130	PBICR-08-008-#204	5.39	5.95	7.99	15.81	6.98	11.61
131	PBICR-08-008-#205	7.94	10.07	11.28	14.60	10.01	12.12
132	PBICR-08-008-#206	12.03	14.81	10.27	18.74	10.33	16.09
133	PBICR-08-008-#207	11.98	18.10	13.04	25.17	12.85	21.84
134	PBICR-08-008-#209	2.49	3.29	4.41	5.40	2.97	4.02

135	PBICR-08-008-#210	24.33	23.13	13.55	23.10	19.07	23.21
136	PBICR-08-008-#212	10.29	9.49	5.03	9.65	7.55	9.24
137	PBICR-08-008-#213	7.07	8.38	8.71	12.21	8.26	10.52
138	PBICR-08-008-#214	3.28	3.36	2.16	1.68	2.57	2.50
139	PBICR-08-008-#215	3.37	4.04	3.72	7.23	3.61	5.99
140	PBICR-08-008-#218	6.90	12.54	19.07	21.69	12.88	15.85
141	PBICR-08-008-#219	4.43	7.49	3.04	4.92	4.30	7.48
142	PBICR-08-008-#221	12.89	13.91	11.62	11.90	12.67	12.75
143	PBICR-08-008-#223	7.43	7.24	8.94	11.16	8.10	9.95
144	PBICR-08-008-#225	14.83	16.48	4.25	10.77	9.69	13.78
145	PBICR-08-008-#227	2.06	2.19	3.73	10.46	2.91	6.55
146	PBICR-08-008-#228	6.50	10.00	6.49	9.76	6.32	9.48
147	PBICR-08-008-#229	2.65	3.35	3.50	6.96	3.16	5.75
148	PBICR-08-008-#230	12.41	11.36	12.84	19.75	12.10	15.94
149	PBICR-08-008-#231	6.93	7.54	8.06	13.70	7.04	10.40
150	PBICR-08-008-#232	12.71	14.79	12.59	21.73	12.14	17.49
151	PBICR-08-008-#233	8.34	6.43	6.23	9.45	7.15	7.85
152	PBICR-08-008-#234	4.07	5.34	4.56	15.32	4.59	11.16
153	PBICR-08-008-#235	3.00	2.65	2.15	4.38	3.42	4.12
154	PBICR-08-008-#236	13.55	14.09	16.78	23.52	15.62	19.28
155	PBICR-08-008-#237	7.26	2.28	6.11	9.19	6.33	5.55
156	PBICR-08-008-#240	5.97	6.63	10.70	14.35	7.82	9.69
157	PBICR-08-008-#241	10.22	12.30	10.59	16.98	10.21	14.37
158	PBICR-08-008-#242	3.12	3.53	3.62	7.68	3.04	5.46
159	PBICR-08-008-#243	6.05	7.50	6.82	4.76	6.28	6.05
160	PBICR-08-008-#244	2.04	3.10	2.86	1.92	1.43	2.25
161	PBICR-08-008-#247	2.21	3.69	1.30	4.37	1.57	3.73
162	PBICR-08-008-#248	9.27	9.43	10.39	18.88	9.45	13.72
163	PBICR-08-008-#250	6.67	8.54	9.91	16.34	7.91	12.00
164	PBICR-08-008-#252	6.43	8.53	9.49	16.80	7.85	12.68
165	PBICR-08-008-#253	10.71	15.83	9.59	12.56	9.95	14.29
166	PBICR-08-008-#254	7.95	9.78	8.82	11.51	8.30	10.79
167	PBICR-08-008-#255	6.94	9.46	7.72	13.78	7.29	11.76
168	PBICR-08-008-#256	14.98	15.96	24.13	30.90	19.34	23.55
169	PBICR-08-008-#257	7.99	9.95	4.24	10.34	6.66	10.72
170	PBICR-08-008-#258	9.23	9.21	18.90	20.18	15.62	16.15
171	PBICR-08-008-#259	4.12	4.76	5.11	10.53	4.88	7.79
172	PBICR-08-008-#260	10.86	11.36	12.90	15.40	11.70	13.34
173	PBICR-08-008-#261	13.06	9.30	9.76	14.05	11.57	11.07
174	PBICR-08-008-#262	7.54	9.31	12.83	16.15	10.08	12.77
175	PBICR-08-008-#263	2.62	2.88	1.32	2.74	1.76	2.40
176	PBICR-08-008-#267	8.15	9.15	6.55	12.48	7.53	11.18
177	PBICR-08-008-#268	4.94	5.52	9.66	14.38	7.49	9.97
178	PBICR-08-008-#269	2.13	4.32	1.90	4.03	2.28	3.94
179	PBICR-08-008-#270	8.67	9.03	10.29	15.91	9.69	13.52
180	PBICR-08-008-#271	1.83	2.22	1.89	2.16	1.93	2.48

181	PBICR-08-008-#273	8.26	8.01	9.58	13.60	9.11	11.22
182	PBICR-08-008-#274	7.29	6.96	7.27	10.56	7.64	10.15
183	PBICR-08-008-#275	7.74	7.90	3.49	5.22	5.67	6.56
184	PBICR-08-008-#276	8.84	9.76	5.67	12.14	7.08	10.82
185	PBICR-08-008-#278	11.14	13.46	10.24	16.68	10.93	15.61
186	PBICR-08-008-#280	4.69	5.45	32.21	11.79	18.66	9.31
187	PBICR-08-008-#283	10.27	13.17	10.86	21.37	10.53	16.56
188	PBICR-08-008-#284	2.02	4.33	2.01	6.94	2.14	5.43
189	PBICR-08-008-#285	21.80	1.75	1.42	2.87	11.70	2.31
190	PBICR-08-008-#289	7.62	7.80	4.55	7.33	6.87	8.16
191	PBICR-08-008-#291	11.28	9.31	5.95	10.20	8.61	10.14
192	PBICR-08-008-#292	2.75	3.94	4.06	8.98	2.71	5.90
193	PBICR-08-008-#293	10.98	12.43	9.66	15.29	10.38	14.60
194	PBICR-08-008-#294	2.89	3.24	3.58	5.05	2.95	4.24
195	PBICR-08-008-#298	9.64	7.88	7.73	11.66	8.62	9.31
196	PBICR-08-008-#299	9.52	10.30	3.81	14.94	6.55	12.39
197	AUS29529	2.73	4.73	1.78	6.23	2.56	5.60
198	Sunco/Pastor	4.00	4.06	6.50	10.95	4.88	7.49
199	Syn110	7.83	9.22	13.50	13.56	10.17	11.00
200	Suntop	8.39	10.35	12.56	16.22	9.67	12.87
201	Sunguard	3.59	5.85	6.87	9.47	5.67	7.80
202	Sunco	3.53	4.82	4.20	7.90	3.90	6.65
203	Spitfire			7.90	11.25		
204	Gregory	6.05	7.71	7.73	11.80	6.92	10.02
205	Bellaroi	7.84	14.85	10.61	20.07	9.37	18.28
206	Batavia	6.28	8.01	8.30	16.60	7.54	12.47
207	Wylie	4.23	5.04	7.33	12.48	6.26	9.47
Mean		**7.13**	**8.21**	**7.71**	**12.00**	**7.42**	**10.12**
Minimum		**1.02**	**1.33**	**0.00**	**1.68**	**0.80**	**1.71**
Maximum		**24.33**	**23.13**	**32.21**	**30.9**	**19.34**	**23.55**
Standard Error of Mean		**0.29**	**0.31**	**0.32**	**0.40**	**0.27**	**0.33**
Standard Error of difference (SED)		**3.00**		**3.53**		**2.67**	
LSD (5%) (Genotype x environment)		**5.91**		**6.92**		**5.24**	
LSD (5%) (Genotype)		**5.45**		**5.67**		**3.77**	

Table 8: Mean for genotype x inoculum of normalize difference vegetative index (NDVI) in 2014, 2015 and across years.

		NDVI					
		2014		**2015**		**Combined**	
Entry	**Genotype**	**Nil**	**Plus**	**Nil**	**Plus**	**Nil**	**Plus**
1	PBICR-08-008-#2	0.7988	0.7156	0.8181	0.7956	0.8102	0.7584
2	PBICR-08-008-#7	0.8427	0.7694	0.821	0.8167	0.8348	0.7987
3	PBICR-08-008-#8	0.819	0.7489	0.8253	0.815	0.8221	0.7801
4	PBICR-08-008-#9	0.8082	0.7223	0.8192	0.8075	0.8119	0.7741
5	PBICR-08-008-#10	0.8335	0.8245	0.8241	0.8156	0.8286	0.8193
6	PBICR-08-008-#11	0.8302	0.7442	0.8167	0.77	0.8225	0.7585
7	PBICR-08-008-#16	0.8282	0.7704	0.8283	0.8006	0.8257	0.7831
8	PBICR-08-008-#22	0.8081	0.7649	0.8233	0.8015	0.814	0.7947
9	PBICR-08-008-#23	0.8291	0.7538	0.8327	0.8068	0.8324	0.7792
10	PBICR-08-008-#27	0.8439	0.7738	0.8155	0.7549	0.8292	0.7676
11	PBICR-08-008-#29	0.8136	0.7464	0.8304	0.8161	0.8247	0.7794
12	PBICR-08-008-#37	0.8155	0.7483	0.8248	0.7895	0.8205	0.7727
13	PBICR-08-008-#38	0.8061	0.7329	0.8175	0.7996	0.8108	0.7619
14	PBICR-08-008-#39	0.8171	0.7592	0.829	0.786	0.8271	0.7725
15	PBICR-08-008-#44	0.8275	0.7311	0.8187	0.7846	0.8243	0.7594
16	PBICR-08-008-#45	0.8203	0.752	0.833	0.8214	0.8282	0.7849
17	PBICR-08-008-#46	0.83	0.7649	0.8219	0.7982	0.8264	0.7868
18	PBICR-08-008-#47	0.8449	0.7601	0.8233	0.8152	0.8309	0.784
19	PBICR-08-008-#48	0.8125	0.7562	0.8258	0.812	0.8193	0.7836
20	PBICR-08-008-#49	0.7846	0.752	0.8186	0.7946	0.805	0.7696
21	PBICR-08-008-#50	0.817	0.7477	0.8194	0.809	0.817	0.7775
22	PBICR-08-008-#51	0.8012	0.7181	0.8145	0.7751	0.8063	0.7436
23	PBICR-08-008-#52	0.8293	0.7732	0.8277	0.7925	0.8299	0.7865
24	PBICR-08-008-#53	0.8429	0.7982	0.8188	0.8051	0.8287	0.7996
25	PBICR-08-008-#55	0.7974	0.717	0.812	0.7884	0.8054	0.7516
26	PBICR-08-008-#56	0.8136	0.7216	0.8251	0.7893	0.8174	0.7616
27	PBICR-08-008-#57	0.796	0.7473	0.8327	0.8093	0.8089	0.768
28	PBICR-08-008-#62	0.824	0.7868	0.829	0.7982	0.8265	0.7926
29	PBICR-08-008-#63	0.8153	0.7675	0.8254	0.7786	0.8179	0.7713
30	PBICR-08-008-#64	0.8317	0.7529	0.8225	0.7939	0.8273	0.7763
31	PBICR-08-008-#65	0.7599	0.6755	0.806	0.7891	0.7844	0.7316
32	PBICR-08-008-#68	0.8281	0.7855	0.8232	0.7867	0.8255	0.7849
33	PBICR-08-008-#69	0.8052	0.7157	0.822	0.8108	0.8148	0.7684
34	PBICR-08-008-#70	0.8321	0.7744	0.8217	0.8074	0.8274	0.7901
35	PBICR-08-008-#71	0.8102	0.7423	0.8232	0.7915	0.8166	0.7698
36	PBICR-08-008-#72	0.7705	0.7465	0.8199	0.7681	0.7915	0.757
37	PBICR-08-008-#73	0.8128	0.7413	0.825	0.7653	0.8185	0.7539
38	PBICR-08-008-#74	0.7869	0.6965	0.8323	0.7994	0.8079	0.7479
39	PBICR-08-008-#75	0.8226	0.7289	0.8252	0.8084	0.8258	0.7679
40	PBICR-08-008-#76	0.8144	0.7739	0.8218	0.7992	0.8155	0.7792
41	PBICR-08-008-#77	0.8486	0.7456	0.8356	0.8011	0.8406	0.7762

42	PBICR-08-008-#80	0.8302	0.7798	0.8225	0.7857	0.829	0.7832
43	PBICR-08-008-#81	0.8361	0.7786	0.8229	0.8074	0.8293	0.7911
44	PBICR-08-008-#82	0.8212	0.769	0.8209	0.8039	0.8201	0.7882
45	PBICR-08-008-#83	0.7801	0.7547	0.8142	0.7967	0.7928	0.7708
46	PBICR-08-008-#85	0.8032	0.7266	0.8222	0.7866	0.8141	0.7565
47	PBICR-08-008-#86	0.8173	0.7471	0.8232	0.8077	0.8216	0.7745
48	PBICR-08-008-#89	0.7937	0.7501	0.8206	0.8042	0.8038	0.7669
49	PBICR-08-008-#90	0.8271	0.777	0.8286	0.8049	0.8261	0.7879
50	PBICR-08-008-#91	0.8215	0.7607	0.8318	0.8041	0.8289	0.7793
51	PBICR-08-008-#94	0.8484	0.7858	0.8213	0.8104	0.8329	0.7959
52	PBICR-08-008-#97	0.8206	0.7473	0.8213	0.8048	0.8256	0.7798
53	PBICR-08-008-#98	0.8002	0.7225	0.7964	0.7721	0.7978	0.7476
54	PBICR-08-008-#99	0.8135	0.743	0.8199	0.8018	0.8168	0.77
55	PBICR-08-008-#100	0.8012	0.7409	0.8233	0.814	0.8103	0.7693
56	PBICR-08-008-#101	0.8104	0.7762	0.8208	0.7955	0.8169	0.7848
57	PBICR-08-008-#103	0.8162	0.7543	0.8153	0.7716	0.8132	0.7638
58	PBICR-08-008-#104	0.8147	0.7613	0.8259	0.8083	0.8249	0.7906
59	PBICR-08-008-#107	0.817	0.7459	0.8274	0.8015	0.8219	0.775
60	PBICR-08-008-#108	0.8226	0.7548	0.8195	0.7524	0.82	0.7497
61	PBICR-08-008-#109	0.8157	0.7737	0.8147	0.8036	0.8124	0.7873
62	PBICR-08-008-#111	0.826	0.76	0.8262	0.7971	0.8284	0.7831
63	PBICR-08-008-#112	0.8249	0.7514	0.8292	0.8176	0.8268	0.7853
64	PBICR-08-008-#113	0.833	0.7783	0.8261	0.8183	0.8262	0.7973
65	PBICR-08-008-#114	0.8206	0.7752	0.8265	0.7818	0.8263	0.7806
66	PBICR-08-008-#115	0.8231	0.7635	0.8133	0.7993	0.8147	0.7806
67	PBICR-08-008-#116	0.7989	0.7475	0.8156	0.8063	0.8064	0.7825
68	PBICR-08-008-#118	0.8233	0.7698	0.8184	0.806	0.8129	0.7866
69	PBICR-08-008-#119	0.8209	0.7527	0.8258	0.8064	0.8237	0.7793
70	PBICR-08-008-#123	0.825	0.7685	0.8196	0.7844	0.8269	0.7809
71	PBICR-08-008-#124	0.7812	0.7159	0.8117	0.7894	0.7937	0.747
72	PBICR-08-008-#125	0.8269	0.7563	0.8214	0.8088	0.8205	0.7768
73	PBICR-08-008-#126	0.8268	0.7658	0.8227	0.7781	0.8243	0.7724
74	PBICR-08-008-#127	0.7858	0.7572	0.8208	0.7944	0.8066	0.777
75	PBICR-08-008-#129	0.8105	0.7494	0.7905	0.7474	0.7993	0.7505
76	PBICR-08-008-#130	0.8014	0.7638	0.8278	0.7911	0.8121	0.7842
77	PBICR-08-008-#133	0.8183	0.7557	0.8199	0.7899	0.8195	0.7722
78	PBICR-08-008-#134	0.7805	0.7146	0.8181	0.7889	0.7971	0.7594
79	PBICR-08-008-#136	0.7996	0.7352	0.8224	0.792	0.8062	0.7626
80	PBICR-08-008-#137	0.8212	0.7532	0.8194	0.7722	0.8227	0.7647
81	PBICR-08-008-#138	0.8294	0.7452	0.8311	0.7981	0.8307	0.7712
82	PBICR-08-008-#140	0.8489	0.7997	0.8279	0.8274	0.8379	0.8164
83	PBICR-08-008-#141	0.8014	0.7295	0.8244	0.8038	0.8136	0.7664
84	PBICR-08-008-#145	0.8207	0.7102	0.8264	0.7976	0.8236	0.7566
85	PBICR-08-008-#146	0.8204	0.7795	0.8186	0.7813	0.819	0.7857
86	PBICR-08-008-#147	0.7908	0.728	0.7853	0.7626	0.7874	0.7462
87	PBICR-08-008-#148	0.8253	0.7557	0.8271	0.7959	0.8247	0.774

88	PBICR-08-008-#150	0.8251	0.7813	0.7995	0.7807	0.8118	0.7886
89	PBICR-08-008-#151	0.7836	0.7126	0.8107	0.7692	0.7997	0.7423
90	PBICR-08-008-#153	0.8229	0.786	0.8286	0.8198	0.8297	0.8003
91	PBICR-08-008-#154	0.8118	0.7599	0.814	0.7852	0.812	0.7699
92	PBICR-08-008-#156	0.8625	0.7913	0.8298	0.8117	0.8451	0.7999
93	PBICR-08-008-#157	0.8357	0.7599	0.8303	0.8054	0.8317	0.7841
94	PBICR-08-008-#160	0.8105	0.7619	0.8269	0.8222	0.8193	0.793
95	PBICR-08-008-#162	0.8453	0.7684	0.8208	0.7943	0.8344	0.7804
96	PBICR-08-008-#163	0.8017	0.6986	0.8171	0.7991	0.8074	0.7434
97	PBICR-08-008-#164	0.8333	0.7609	0.8343	0.8145	0.8317	0.7913
98	PBICR-08-008-#165	0.825	0.7626	0.8166	0.7554	0.8201	0.7566
99	PBICR-08-008-#166	0.8151	0.7415	0.8239	0.79	0.8195	0.7675
100	PBICR-08-008-#167	0.8166	0.7658	0.8233	0.8103	0.8236	0.793
101	PBICR-08-008-#168	0.8106	0.7451	0.8268	0.8175	0.8186	0.7772
102	PBICR-08-008-#169	0.8	0.7296	0.8184	0.8068	0.8138	0.7701
103	PBICR-08-008-#170	0.7715	0.7081	0.802	0.7863	0.7895	0.7491
104	PBICR-08-008-#171	0.8334	0.7567	0.8262	0.7938	0.8271	0.773
105	PBICR-08-008-#173	0.8263	0.7715	0.8261	0.8065	0.8269	0.7923
106	PBICR-08-008-#174	0.8241	0.7646	0.8239	0.7952	0.8245	0.7805
107	PBICR-08-008-#175	0.8185	0.763	0.8333	0.8141	0.8246	0.7845
108	PBICR-08-008-#176	0.8119	0.7431	0.8189	0.7906	0.8172	0.7693
109	PBICR-08-008-#177	0.8008	0.742	0.8172	0.7987	0.8067	0.7665
110	PBICR-08-008-#178	0.8076	0.771	0.8288	0.7926	0.8217	0.7814
111	PBICR-08-008-#180	0.7988	0.7324	0.8177	0.8006	0.8102	0.7707
112	PBICR-08-008-#181	0.7987	0.7489	0.8169	0.8094	0.8093	0.7793
113	PBICR-08-008-#182	0.8178	0.7533	0.8254	0.8167	0.818	0.7888
114	PBICR-08-008-#183	0.8256	0.7771	0.8378	0.8065	0.8301	0.7898
115	PBICR-08-008-#184	0.7819	0.6949	0.809	0.7745	0.7964	0.7365
116	PBICR-08-008-#185	0.7944	0.7231	0.8124	0.7891	0.8031	0.7541
117	PBICR-08-008-#186	0.8012	0.7361	0.8305	0.7821	0.8136	0.7592
118	PBICR-08-008-#187	0.7824	0.7074	0.8223	0.7877	0.8078	0.7495
119	PBICR-08-008-#188	0.8059	0.7272	0.8207	0.7897	0.8169	0.7619
120	PBICR-08-008-#189	0.8002	0.7281	0.8253	0.8021	0.8177	0.7679
121	PBICR-08-008-#190	0.8226	0.7428	0.8302	0.786	0.8229	0.7606
122	PBICR-08-008-#191	0.815	0.7471	0.8127	0.7928	0.8133	0.7695
123	PBICR-08-008-#193	0.8146	0.7423	0.8134	0.7935	0.8134	0.7679
124	PBICR-08-008-#196	0.8139	0.7722	0.8193	0.7956	0.8149	0.7763
125	PBICR-08-008-#198	0.8473	0.7746	0.836	0.8089	0.8404	0.7882
126	PBICR-08-008-#199	0.8208	0.7262	0.8224	0.7831	0.8249	0.7583
127	PBICR-08-008-#200	0.7718	0.7246	0.8268	0.7712	0.7992	0.7505
128	PBICR-08-008-#202	0.8265	0.7613	0.8273	0.7984	0.8283	0.7803
129	PBICR-08-008-#203	0.8294	0.7884	0.8092	0.8015	0.8162	0.7953
130	PBICR-08-008-#204	0.8111	0.7611	0.822	0.7773	0.8167	0.7716
131	PBICR-08-008-#205	0.7947	0.7474	0.82	0.7821	0.808	0.7638
132	PBICR-08-008-#206	0.8245	0.7648	0.8261	0.8071	0.8257	0.7835
133	PBICR-08-008-#207	0.8275	0.785	0.8371	0.8137	0.8312	0.8026

134	PBICR-08-008-#209	0.8151	0.7464	0.8329	0.8262	0.8201	0.7808
135	PBICR-08-008-#210	0.8184	0.7418	0.8253	0.812	0.8188	0.7832
136	PBICR-08-008-#212	0.7721	0.7234	0.8172	0.8169	0.7991	0.7729
137	PBICR-08-008-#213	0.8208	0.7622	0.8361	0.7937	0.8287	0.7777
138	PBICR-08-008-#214	0.7968	0.7125	0.7997	0.7592	0.7955	0.7342
139	PBICR-08-008-#215	0.8243	0.7373	0.8161	0.7878	0.8195	0.7625
140	PBICR-08-008-#218	0.8633	0.8102	0.821	0.8241	0.8397	0.816
141	PBICR-08-008-#219	0.7914	0.7222	0.8228	0.8003	0.8054	0.7593
142	PBICR-08-008-#221	0.8104	0.7526	0.8199	0.8	0.819	0.7807
143	PBICR-08-008-#223	0.825	0.7529	0.8236	0.7913	0.8249	0.7725
144	PBICR-08-008-#225	0.824	0.7624	0.8236	0.8022	0.8222	0.7845
145	PBICR-08-008-#227	0.8224	0.7594	0.8215	0.7779	0.8195	0.7676
146	PBICR-08-008-#228	0.817	0.7399	0.8242	0.791	0.8225	0.7698
147	PBICR-08-008-#229	0.8018	0.7416	0.8215	0.8055	0.8139	0.7773
148	PBICR-08-008-#230	0.8085	0.7595	0.824	0.7928	0.8164	0.776
149	PBICR-08-008-#231	0.7838	0.7329	0.8133	0.789	0.7942	0.7506
150	PBICR-08-008-#232	0.8151	0.7736	0.8315	0.8043	0.8224	0.7916
151	PBICR-08-008-#233	0.8221	0.7626	0.825	0.8065	0.8266	0.7841
152	PBICR-08-008-#234	0.8212	0.7739	0.814	0.7814	0.818	0.7769
153	PBICR-08-008-#235	0.7831	0.7149	0.816	0.7713	0.7981	0.7377
154	PBICR-08-008-#236	0.8208	0.7684	0.8199	0.8105	0.8175	0.7808
155	PBICR-08-008-#237	0.7877	0.7083	0.8131	0.8029	0.7996	0.7579
156	PBICR-08-008-#240	0.8075	0.7465	0.8404	0.8125	0.826	0.7824
157	PBICR-08-008-#241	0.8387	0.7639	0.8272	0.792	0.8305	0.777
158	PBICR-08-008-#242	0.7956	0.7219	0.8046	0.7708	0.8043	0.7494
159	PBICR-08-008-#243	0.8331	0.7403	0.8262	0.819	0.8292	0.7765
160	PBICR-08-008-#244	0.811	0.7084	0.8213	0.7773	0.8143	0.7396
161	PBICR-08-008-#247	0.8194	0.7783	0.8155	0.7817	0.8166	0.7877
162	PBICR-08-008-#248	0.8289	0.76	0.8334	0.7957	0.832	0.7774
163	PBICR-08-008-#250	0.826	0.7772	0.8314	0.8138	0.8281	0.794
164	PBICR-08-008-#252	0.8319	0.7734	0.8266	0.8092	0.8307	0.7925
165	PBICR-08-008-#253	0.8463	0.7945	0.8209	0.7964	0.8294	0.7918
166	PBICR-08-008-#254	0.8213	0.7584	0.8286	0.8018	0.8279	0.7803
167	PBICR-08-008-#255	0.8206	0.7789	0.8306	0.8138	0.8312	0.7985
168	PBICR-08-008-#256	0.8175	0.7843	0.8383	0.8088	0.8306	0.7947
169	PBICR-08-008-#257	0.8137	0.7706	0.8259	0.7899	0.8157	0.7685
170	PBICR-08-008-#258	0.8171	0.7505	0.8205	0.8022	0.8175	0.7748
171	PBICR-08-008-#259	0.8403	0.758	0.8234	0.7839	0.8316	0.7741
172	PBICR-08-008-#260	0.8313	0.7838	0.8216	0.8138	0.8237	0.7971
173	PBICR-08-008-#261	0.8186	0.7549	0.8207	0.8087	0.8186	0.782
174	PBICR-08-008-#262	0.8158	0.7472	0.8269	0.8085	0.819	0.7753
175	PBICR-08-008-#263	0.7737	0.6864	0.8175	0.7948	0.7968	0.7384
176	PBICR-08-008-#267	0.8291	0.7844	0.8274	0.8023	0.8289	0.7942
177	PBICR-08-008-#268	0.8283	0.7776	0.826	0.8008	0.8256	0.7884
178	PBICR-08-008-#269	0.8157	0.7327	0.8124	0.7764	0.8141	0.7545
179	PBICR-08-008-#270	0.7922	0.7175	0.8246	0.7946	0.8092	0.7539

180	PBICR-08-008-#271	0.7386	0.653	0.8135	0.7934	0.7804	0.7269
181	PBICR-08-008-#273	0.8399	0.7807	0.8395	0.7826	0.8389	0.781
182	PBICR-08-008-#274	0.8231	0.7583	0.8281	0.8207	0.8291	0.7871
183	PBICR-08-008-#275	0.8358	0.7561	0.8354	0.8113	0.8346	0.7819
184	PBICR-08-008-#276	0.8206	0.781	0.829	0.7834	0.8251	0.7826
185	PBICR-08-008-#278	0.7886	0.7618	0.8346	0.8186	0.8153	0.7918
186	PBICR-08-008-#280	0.8212	0.7418	0.8147	0.7969	0.8151	0.7706
187	PBICR-08-008-#283	0.8048	0.7585	0.8263	0.801	0.8165	0.7794
188	PBICR-08-008-#284	0.8082	0.7552	0.8214	0.7828	0.8148	0.7671
189	PBICR-08-008-#285	0.7938	0.7045	0.8167	0.7527	0.8012	0.738
190	PBICR-08-008-#289	0.7891	0.7234	0.8103	0.8062	0.8016	0.7627
191	PBICR-08-008-#291	0.809	0.721	0.821	0.7927	0.8127	0.7631
192	PBICR-08-008-#292	0.7299	0.7238	0.8055	0.7899	0.7634	0.7481
193	PBICR-08-008-#293	0.8264	0.7945	0.8197	0.8117	0.8225	0.8039
194	PBICR-08-008-#294	0.7925	0.7183	0.8062	0.7829	0.8007	0.7523
195	PBICR-08-008-#298	0.8355	0.7858	0.8353	0.8105	0.8357	0.8006
196	PBICR-08-008-#299	0.8234	0.76	0.8288	0.817	0.8297	0.7919
197	AUS29529	0.823	0.7613	0.8238	0.7929	0.8258	0.7745
198	Sunco/Pastor	0.8242	0.7613	0.8085	0.7914	0.8177	0.7805
199	Syn110	0.8338	0.78	0.8228	0.8158	0.8281	0.7974
200	Suntop	0.8012	0.7591	0.8051	0.7794	0.8013	0.766
201	Sunguard	0.8209	0.7602	0.8139	0.7879	0.8157	0.774
202	Sunco	0.8111	0.7577	0.8198	0.7907	0.8202	0.7792
203	Spitfire			0.822	0.7912		
204	Gregory	0.8236	0.7369	0.8138	0.8026	0.8186	0.7693
205	Bellaroi	0.8023	0.735	0.7972	0.7227	0.7996	0.7284
206	Batavia	0.812	0.7689	0.8247	0.8083	0.8189	0.7887
207	Wylie	0.7813	0.7232	0.8143	0.768	0.798	0.7442
Mean		**0.8142**	**0.7516**	**0.8218**	**0.7961**	**0.8179**	**0.7739**
Minimum		**0.73**	**0.653**	**0.785**	**0.723**	**0.763**	**0.727**
Maximum		**0.863**	**0.825**	**0.84**	**0.827**	**0.845**	**0.819**
Standard Error of Mean		**0.001**	**0.002**	**0.001**	**0.001**	**0.001**	**0.001**
Standard Error of difference (SED)		**0.02**		**0.01**		**0.01**	
LSD (5%) (Genotype x environment)		**0.044**		**0.023**		**0.016**	
LSD (5%) (Genotype)		**0.036**		**0.08**		**0.022**	

Table 9: Mean for genotype x inoculum of number of days to heading in 2014, 2015 and across years.

		Days to heading (Days)					
		2014		2015		Combined	
Entry	Genotype	Nil	Plus	Nil	Plus	Nil	Plus
1	PBICR-08-008-#2	110.8	110.7	109.7	107.9	110.5	109.5
2	PBICR-08-008-#7	126.9	126.6	116.4	113.9	122.8	120.1
3	PBICR-08-008-#8	114.1	114.1	111.5	111.7	113	113
4	PBICR-08-008-#9	107.4	108.8	108.3	108.5	107.5	108
5	PBICR-08-008-#10	131.4	131.8	125.3	125.2	128.3	128.3
6	PBICR-08-008-#11	109.1	109.1	107.3	107.6	108.2	108.2
7	PBICR-08-008-#16	118.9	119.3	112.4	112.5	115.8	115.8
8	PBICR-08-008-#22	119.4	119.5	115.2	115.5	117.6	117.6
9	PBICR-08-008-#23	115.1	115	112.8	112.9	113.7	113.7
10	PBICR-08-008-#27	114.6	114.7	111.1	111.1	113.1	113.1
11	PBICR-08-008-#29	114	114	112.4	112.3	113.3	113.3
12	PBICR-08-008-#37	105.7	105.8	106	105.9	106.1	106.1
13	PBICR-08-008-#38	101.8	100.8	105.5	105.5	103.7	103.2
14	PBICR-08-008-#39	109.2	109.2	106.6	107.1	107.9	108.1
15	PBICR-08-008-#44	107.7	108	105.9	106.4	107.2	107.5
16	PBICR-08-008-#45	119.8	119.7	112.5	112.2	116.1	116.1
17	PBICR-08-008-#46	111.1	110.5	108.6	108.5	109.9	109.7
18	PBICR-08-008-#47	119.9	119.6	112.9	112.8	116.5	116.5
19	PBICR-08-008-#48	112.1	111.9	110	110.5	111.2	111.2
20	PBICR-08-008-#49	116.2	116.2	115	114.8	115.4	115.4
21	PBICR-08-008-#50	109.5	109.5	106.6	107.1	108.1	108.4
22	PBICR-08-008-#51	101.8	101.4	106.2	106.4	104	104
23	PBICR-08-008-#52	114.4	114.1	109.4	109.4	111.6	111.6
24	PBICR-08-008-#53	113.7	112.4	111.6	114.1	111.4	113.4
25	PBICR-08-008-#55	107.7	107.6	106.8	107	107.6	107.6
26	PBICR-08-008-#56	108.6	108.8	107.7	107.4	108.3	108.3
27	PBICR-08-008-#57	110.4	110.6	110.1	110.1	110.2	110.2
28	PBICR-08-008-#62	113.9	115.1	110.5	110.8	112.4	112.9
29	PBICR-08-008-#63	110.8	111.2	108.6	109.4	109.9	110.2
30	PBICR-08-008-#64	110.4	110.5	108	108.2	109.2	109.2
31	PBICR-08-008-#65	108	108.1	107.6	107.4	108.2	108.2
32	PBICR-08-008-#68	119	119	117.7	117.4	118.2	118.2
33	PBICR-08-008-#69	104.9	103.8	105.4	106.2	104.6	104.3
34	PBICR-08-008-#70	109.7	109.6	106.8	106.2	107.7	107.7
35	PBICR-08-008-#71	114.4	114.4	111.6	112	112.9	112.9
36	PBICR-08-008-#72	114.7	114.7	111.3	111.3	112.9	112.9
37	PBICR-08-008-#73	109.6	109.6	107.9	107.8	108.6	108.6
38	PBICR-08-008-#74	113.9	113.7	112	112	112.6	112.6
39	PBICR-08-008-#75	115.8	115.8	107.9	108.6	111.8	112.1
40	PBICR-08-008-#76	115.4	115.2	111.7	111.3	113.3	113.3
41	PBICR-08-008-#77	126.5	126.7	122	122.1	124.4	124.4

42	PBICR-08-008-#80	111.5	110.3	106.4	106.8	109.2	108.7
43	PBICR-08-008-#81	111.7	111.8	110.2	109.3	110.9	110.9
44	PBICR-08-008-#82	114.6	115.1	112.9	113	113.6	113.8
45	PBICR-08-008-#83	108.7	108.5	108.3	107.9	108.1	108.1
46	PBICR-08-008-#85	116.3	116.3	110.2	110	113.4	113.4
47	PBICR-08-008-#86	108.8	108.7	107	107.3	108.3	108.3
48	PBICR-08-008-#89	112.3	112.6	110.4	110.7	111.7	111.7
49	PBICR-08-008-#90	116.3	116.7	114.1	113.5	115.5	115.3
50	PBICR-08-008-#91	126.1	126	121.6	121.1	123.9	123.9
51	PBICR-08-008-#94	118.9	118.6	114.1	114.3	116.5	116.5
52	PBICR-08-008-#97	117.3	117.2	112.1	112.3	115	115
53	PBICR-08-008-#98	110.6	109.8	107.3	108.1	109.2	109
54	PBICR-08-008-#99	104.8	104.8	102.5	103.8	103.7	104.4
55	PBICR-08-008-#100	113.3	113.5	111.4	111.9	112.4	112.4
56	PBICR-08-008-#101	103.8	103.7	102.8	104.5	103.1	104.1
57	PBICR-08-008-#103	117.6	117.5	118.1	118.7	118.2	118.4
58	PBICR-08-008-#104	117.3	117.2	113.3	113.2	115.1	115.1
59	PBICR-08-008-#107	114.9	114.9	112.5	112.5	113.5	113.5
60	PBICR-08-008-#108	110.6	109.5	110.9	111.2	110.4	110.1
61	PBICR-08-008-#109	118.8	118.4	115.5	116.2	116.8	117.1
62	PBICR-08-008-#111	129.9	129.9	123.3	122.9	126.8	126.8
63	PBICR-08-008-#112	116.6	116.5	122	121.8	119.6	119.6
64	PBICR-08-008-#113	110.4	110.4	111.6	112.5	111	111.2
65	PBICR-08-008-#114	114.5	114.5	109.7	110.1	111.5	111.5
66	PBICR-08-008-#115	109.6	109.9	109.9	109.7	109.6	109.6
67	PBICR-08-008-#116	108.1	108.5	107.9	108	108.2	108.5
68	PBICR-08-008-#118	112.1	112.1	109.6	109.9	110.6	110.9
69	PBICR-08-008-#119	117.3	117.1	110.7	111.1	114.5	114.2
70	PBICR-08-008-#123	113.4	113.4	108.8	108.6	111.5	111.5
71	PBICR-08-008-#124	116.4	116.3	112.3	112.5	114.4	114.4
72	PBICR-08-008-#125	112.9	112.9	109.4	109.2	111.2	111.2
73	PBICR-08-008-#126	117.7	117.7	111.4	114.6	114.9	116.2
74	PBICR-08-008-#127	117.8	117.8	116.1	116.4	117	117
75	PBICR-08-008-#129	111.2	111.4	108.2	108.3	109.8	109.8
76	PBICR-08-008-#130	107.7	107.7	107	108.2	107.8	108
77	PBICR-08-008-#133	114.5	114.5	110.7	111.3	112.9	112.9
78	PBICR-08-008-#134	106.4	106.5	107.4	107.6	106.9	106.9
79	PBICR-08-008-#136	105.2	105	104.3	104.5	105.3	105.6
80	PBICR-08-008-#137	108.9	108.9	107.6	107.5	108.1	108.1
81	PBICR-08-008-#138	117.3	117.4	112.3	112.1	115	115
82	PBICR-08-008-#140	126.8	126.8	121.5	121.4	124.4	124.4
83	PBICR-08-008-#141	104.4	104.3	105	104.9	104.4	104.4
84	PBICR-08-008-#145	120.1	120.1	117.9	116.6	119.4	119.2
85	PBICR-08-008-#146	110.5	110.8	106.2	105.3	108.7	108.7
86	PBICR-08-008-#147	104.4	104.1	106.6	107.6	105.2	105.7
87	PBICR-08-008-#148	119.9	119.9	115.9	116.4	118	118.3

88	PBICR-08-008-#150	113.3	113.5	111.9	112.1	112.6	112.6
89	PBICR-08-008-#151	109.7	109.7	106.4	106.9	108	108.3
90	PBICR-08-008-#153	127.2	127.2	122.9	122.8	124.9	124.9
91	PBICR-08-008-#154	110.6	109.6	109.4	109.8	109.6	109.4
92	PBICR-08-008-#156	117.4	115.5	111.4	110.3	114.2	113.2
93	PBICR-08-008-#157	120.7	120.8	113.2	113.5	116.8	116.8
94	PBICR-08-008-#160	117.2	117	115.3	114.6	115.8	115.5
95	PBICR-08-008-#162	111.3	111.3	107.4	107.4	109.9	109.9
96	PBICR-08-008-#163	106.5	106.6	104.8	105.5	105.9	106.2
97	PBICR-08-008-#164	116.6	116.8	112	111.8	114.7	114.7
98	PBICR-08-008-#165	110	109.7	107.3	108.1	108.7	108.7
99	PBICR-08-008-#166	119	119	112.8	112.5	115.8	115.8
100	PBICR-08-008-#167	115.9	116	113.5	113.2	114.4	114.4
101	PBICR-08-008-#168	116.5	116.5	111.2	111.4	113.8	113.8
102	PBICR-08-008-#169	109.9	109.8	108.6	108.5	109.1	109.1
103	PBICR-08-008-#170	102.2	101.5	104.7	105	103.6	103.6
104	PBICR-08-008-#171	116.6	116.7	112.3	112.1	114.4	114.4
105	PBICR-08-008-#173	111.8	112.2	108.1	108.1	110	110.3
106	PBICR-08-008-#174	116.4	116.2	111.6	111.7	114.1	114.1
107	PBICR-08-008-#175	116.5	116.5	112.9	113.9	115.5	115.7
108	PBICR-08-008-#176	110.2	110.2	107	107.5	108.9	109.1
109	PBICR-08-008-#177	108.6	108.6	107.5	107.3	108.2	108.2
110	PBICR-08-008-#178	117.2	117.1	111.5	111.9	114.4	114.6
111	PBICR-08-008-#180	113.9	113.8	108.3	108	110.9	110.9
112	PBICR-08-008-#181	116.4	116.5	113.2	112.9	114.5	114.5
113	PBICR-08-008-#182	114.8	115.1	110.5	110.4	112.7	112.7
114	PBICR-08-008-#183	119.7	120.2	115.2	115.5	117.4	117.7
115	PBICR-08-008-#184	108.6	107.2	106.9	106.8	107.8	107.1
116	PBICR-08-008-#185	114.4	114.6	111	111	112.8	112.8
117	PBICR-08-008-#186	111.9	110.8	110.8	110.9	111.6	111.1
118	PBICR-08-008-#187	102	101.8	105.9	107.1	103.4	103.4
119	PBICR-08-008-#188	117.8	117.8	112.3	112.8	115.1	115.4
120	PBICR-08-008-#189	119.6	119.6	115.7	118	117.5	118.7
121	PBICR-08-008-#190	115.6	115.7	113	113	114.2	114.2
122	PBICR-08-008-#191	106.6	106.5	107.4	107.2	106.6	106.8
123	PBICR-08-008-#193	116.9	116.1	115.5	115	116.4	115.6
124	PBICR-08-008-#196	114.6	114.9	111.6	111.5	112.6	112.6
125	PBICR-08-008-#198	115.7	115.5	110.7	110.3	113	113
126	PBICR-08-008-#199	110.7	110.5	110.7	110.7	110	110
127	PBICR-08-008-#200	107.1	107.1	107	108.5	106.6	107.1
128	PBICR-08-008-#202	116.5	116.6	112.1	111.9	114.5	114.5
129	PBICR-08-008-#203	116.1	115.8	110.9	111	113.6	113.6
130	PBICR-08-008-#204	112.4	112.5	107.3	107.8	110.7	110.7
131	PBICR-08-008-#205	110.5	110.7	107.5	107.8	109.1	109.3
132	PBICR-08-008-#206	118.9	118.9	111.2	111.5	114.8	114.8
133	PBICR-08-008-#207	129	129	122.2	122	125.6	125.6

134	PBICR-08-008-#209	110.1	110.3	107.9	107.7	109.1	109.1
135	PBICR-08-008-#210	116.7	116.7	111.3	111.3	114.2	114.2
136	PBICR-08-008-#212	115.9	115.8	112.6	112.3	113.7	113.7
137	PBICR-08-008-#213	117.5	117.5	112	112.1	115	115
138	PBICR-08-008-#214	108.9	107.4	108.2	106.7	107.9	107.4
139	PBICR-08-008-#215	110.4	110.3	108.2	108.4	109.3	109.3
140	PBICR-08-008-#218	117.5	117.9	112.3	112.8	115.2	115.2
141	PBICR-08-008-#219	107.9	108.2	103.9	103.8	106.5	106.5
142	PBICR-08-008-#221	117.9	117.9	111.4	111.7	114.8	114.8
143	PBICR-08-008-#223	111.1	112.1	109.7	109.5	110.2	110.7
144	PBICR-08-008-#225	117	116.5	118	117.9	117.7	117.5
145	PBICR-08-008-#227	121.1	121.1	117.9	118.5	119.7	119.7
146	PBICR-08-008-#228	117.8	117.8	112.6	112.8	115	115
147	PBICR-08-008-#229	105.7	105.9	106.7	106.8	106.4	106.4
148	PBICR-08-008-#230	120	120.4	117.1	117.4	118.8	118.8
149	PBICR-08-008-#231	108.6	109.8	107.6	107.1	108.2	108.7
150	PBICR-08-008-#232	117.2	117.1	110.2	110.4	113.6	113.6
151	PBICR-08-008-#233	107.8	107.7	106.4	106.1	107	107
152	PBICR-08-008-#234	121.2	121.4	118.8	118.7	119.6	119.6
153	PBICR-08-008-#235	108.5	108.6	106.9	106.5	106.9	106.9
154	PBICR-08-008-#236	119.2	119.3	111.7	112.4	115.6	115.9
155	PBICR-08-008-#237	108.9	108.8	107.4	107.7	108	108.2
156	PBICR-08-008-#240	117.5	117.6	115.5	115.1	116.6	116.6
157	PBICR-08-008-#241	114.1	113.7	110.3	110.2	111.9	111.9
158	PBICR-08-008-#242	114.8	114.7	109.7	110.5	112.7	112.9
159	PBICR-08-008-#243	108.7	108.7	107.6	108.1	108	108.3
160	PBICR-08-008-#244	107.6	107.5	108.1	108.6	108	108.3
161	PBICR-08-008-#247	108.5	108.5	107.6	108.4	107.7	107.9
162	PBICR-08-008-#248	116.9	116.9	110.8	110.8	114.1	114.1
163	PBICR-08-008-#250	110.7	110.6	108.4	108.5	109.2	109.2
164	PBICR-08-008-#252	115.6	115.6	118.7	118.4	117.4	117.1
165	PBICR-08-008-#253	129.8	129.4	120	120.1	125.1	125.1
166	PBICR-08-008-#254	115.6	115.6	112	112	113.9	113.9
167	PBICR-08-008-#255	114.4	114.3	111.5	111.2	112.1	112.1
168	PBICR-08-008-#256	128.9	128.9	122.2	121.3	125	124.8
169	PBICR-08-008-#257	109.4	109.5	110.2	110	109.4	109.4
170	PBICR-08-008-#258	118.5	117	112.4	112.1	115.5	114.7
171	PBICR-08-008-#259	107.3	107.4	109	109.1	107.8	108
172	PBICR-08-008-#260	115.9	115.7	110.5	110.5	113.3	113.3
173	PBICR-08-008-#261	113	112.8	110.9	110.8	111.5	111.5
174	PBICR-08-008-#262	116.5	116.5	111.6	111.8	114.1	114.1
175	PBICR-08-008-#263	102.2	102.2	104.6	105.5	103.4	103.9
176	PBICR-08-008-#267	111.4	111.4	108.4	107.9	110.1	110.1
177	PBICR-08-008-#268	118.1	118	110.9	111.2	115.3	115.3
178	PBICR-08-008-#269	104.7	104.5	104.7	105.6	105	105.2
179	PBICR-08-008-#270	115.7	115.7	111.9	112.3	113.9	113.9

180	PBICR-08-008-#271	104.3	104.7	106.5	106.3	105.3	105.3
181	PBICR-08-008-#273	117.6	117.7	112.1	112.3	114.7	114.7
182	PBICR-08-008-#274	116.1	116	112.1	112.1	113.8	113.8
183	PBICR-08-008-#275	111.8	111.7	109.3	109.2	110.4	110.4
184	PBICR-08-008-#276	116.4	116.3	110.4	110.4	113.4	113.4
185	PBICR-08-008-#278	116.6	117.9	112.7	113	114.8	115.3
186	PBICR-08-008-#280	113.4	113.4	110.2	109.9	112	112
187	PBICR-08-008-#283	116.3	116.6	111.7	113	113.6	113.9
188	PBICR-08-008-#284	108	108.3	105.8	106.9	106.9	107.7
189	PBICR-08-008-#285	102.4	102.5	105.7	107.4	103.7	104.7
190	PBICR-08-008-#289	107.9	107.8	105.9	106.4	106.7	107
191	PBICR-08-008-#291	107.8	107.9	106.2	106.6	107.1	107.4
192	PBICR-08-008-#292	113.3	113.5	110.8	110.3	112.2	111.9
193	PBICR-08-008-#293	129.9	129.8	122.4	122	126.1	126.1
194	PBICR-08-008-#294	107.8	107.2	107	106.8	107.6	107.4
195	PBICR-08-008-#298	127.2	127.2	119.2	119.2	122.9	122.9
196	PBICR-08-008-#299	115.6	115.9	108.6	108.8	112.5	112.5
197	AUS29529	110.7	110.8	108.5	108.6	109.6	109.6
198	Sunco/Pastor	110.8	110.8	108.9	109.7	109.9	110.4
199	Syn110	115.4	115.5	109.9	109.8	112.7	112.5
200	Suntop	109.8	109.9	109.8	111.1	109.7	109.9
201	Sunguard	113.5	112.6	109.2	109	111.3	110.8
202	Sunco	111.3	111.2	108.1	108.5	109.6	109.6
203	Spitfire			105.8	105.9		
204	Gregory	116.1	116.9	115.5	116.4	115.4	116.1
205	Bellaroi	112.6	113.3	107.4	107.8	110.2	110.7
206	Batavia	117	116.9	111.3	111.2	113.7	113.7
207	Wylie	114.8	114.7	110.8	110.6	112	112.3
Mean		**113.7**	**113.7**	**110.8**	**110.9**	**112.3**	**112.3**
Minimum		**101.8**	**100.8**	**102.5**	**103.8**	**103.1**	**103.2**
Maximum		**131.4**	**131.8**	**125.3**	**125.2**	**128.3**	**128.3**
Standard Error of Mean		**0.402**	**0.405**	**0.295**	**0.288**	**0.342**	**0.338**
Standard Error of difference (SED)		**1.45**		**1.19**		**0.92**	
LSD (5%) (Genotype x environment)		**2.85**		**2.33**		**1.80**	
LSD (5%) (Genotype)		**2.78**		**2.06**		**1.31**	

Table 10: Mean for genotype x inoculum of number of days to maturity in 2014, 2015 and across years.

		Days to Physiological Maturity (Days)					
		2014		**2015**		**Combined**	
Entry	**Genotype**	**Nil**	**Plus**	**Nil**	**Plus**	**Nil**	**Plus**
1	PBICR-08-008-#2	152.5	152.7	145.1	145	149.2	149.2
2	PBICR-08-008-#7	160.9	161	149.1	146.1	156	154
3	PBICR-08-008-#8	153.1	153.2	146	146.3	149.8	149.8
4	PBICR-08-008-#9	146.1	146.2	139.7	140.1	142.8	143
5	PBICR-08-008-#10	163.2	163.4	150.4	150.3	157	156.9
6	PBICR-08-008-#11	147.5	147.5	141.1	141.4	144.8	144.7
7	PBICR-08-008-#16	156.7	156.7	146.6	146.9	152	152
8	PBICR-08-008-#22	156.3	156.4	147.3	146.5	151.2	150.7
9	PBICR-08-008-#23	154.9	155	146.6	146.5	150.6	150.6
10	PBICR-08-008-#27	152.4	152.5	145.2	145.2	149.3	149.3
11	PBICR-08-008-#29	155.3	155.4	146.6	146.2	150.3	150.4
12	PBICR-08-008-#37	145.4	145.4	140.9	140.9	143.2	143.1
13	PBICR-08-008-#38	142.9	142.9	141.7	141.1	142.5	142.3
14	PBICR-08-008-#39	152.4	152.4	142.2	141	147	146.5
15	PBICR-08-008-#44	148.8	149	142.6	142.8	145.7	145.6
16	PBICR-08-008-#45	154.4	154.5	146	145.7	149.2	149.1
17	PBICR-08-008-#46	152.3	152.3	143.9	143.9	148.5	148.5
18	PBICR-08-008-#47	157.9	157.7	145.7	145.8	152.1	152.2
19	PBICR-08-008-#48	150.7	150.7	144.9	144.2	147.7	147.5
20	PBICR-08-008-#49	152.5	152.5	146.9	146.6	149.6	149.3
21	PBICR-08-008-#50	150.2	150	142.9	142.9	146.8	146.8
22	PBICR-08-008-#51	143.9	144.7	136.8	139.4	142	142.1
23	PBICR-08-008-#52	153.9	153.8	146.7	146.7	150.8	150.8
24	PBICR-08-008-#53	153.7	153.9	144.6	146.8	149.2	150.6
25	PBICR-08-008-#55	149.9	150.1	142.5	143.1	146.7	147
26	PBICR-08-008-#56	148.7	147.8	142.6	142.5	145.5	145
27	PBICR-08-008-#57	150.7	150.7	144.1	144.8	146.3	146.5
28	PBICR-08-008-#62	152.3	152.4	144.6	144.7	148.9	148.9
29	PBICR-08-008-#63	149.5	149.5	145.5	145.4	148.3	148.4
30	PBICR-08-008-#64	148.1	148.1	140.4	140.5	144.6	144.5
31	PBICR-08-008-#65	149.3	149.3	143.8	143.6	145.8	145.8
32	PBICR-08-008-#68	154.3	154.4	146.1	145.9	150.3	150.4
33	PBICR-08-008-#69	144.2	144.3	138.6	139.2	141.4	141.7
34	PBICR-08-008-#70	149.7	149.9	140.8	140.7	145.5	145.5
35	PBICR-08-008-#71	152.8	152.9	144.9	144.9	148.5	148.5
36	PBICR-08-008-#72	153.4	153.5	145.1	145.2	149.4	149.4
37	PBICR-08-008-#73	146.4	146.3	141.2	141.3	143.7	143.7
38	PBICR-08-008-#74	150.1	150.1	144.2	144.1	146	146.4
39	PBICR-08-008-#75	151	151.6	142	142.1	147.1	147.4
40	PBICR-08-008-#76	154.9	154.9	144.6	144.8	149.7	149.6
41	PBICR-08-008-#77	159	159.1	148.7	148.8	154.5	154.5

42	PBICR-08-008-#80	149.5	149.1	142.9	142.9	146.9	146.6
43	PBICR-08-008-#81	151.8	151.9	145.6	146.2	150.3	150.2
44	PBICR-08-008-#82	152.8	152.8	146.4	146.2	150.2	150.2
45	PBICR-08-008-#83	153.4	153.2	144.2	144.3	147.7	147.8
46	PBICR-08-008-#85	155	154.9	144.3	144	150.1	150.1
47	PBICR-08-008-#86	151	151.1	144.3	144.7	147.2	147.5
48	PBICR-08-008-#89	152.8	152.8	144.4	144.5	148.1	148.5
49	PBICR-08-008-#90	155.2	155.5	147.6	147.1	150.9	150.6
50	PBICR-08-008-#91	161.2	161.2	149	149	153.8	153.9
51	PBICR-08-008-#94	155.2	155	146	146.1	151.1	151.1
52	PBICR-08-008-#97	156.2	156.3	145.6	145.6	151.1	151.1
53	PBICR-08-008-#98	148.2	147.2	143	143.3	145.7	145.2
54	PBICR-08-008-#99	144.4	144.4	139	139	141.9	141.9
55	PBICR-08-008-#100	154.3	154.3	145.1	145.1	149.9	149.9
56	PBICR-08-008-#101	145.2	145.4	138.5	139.7	142.4	143.1
57	PBICR-08-008-#103	155.2	155.3	145.9	145.9	150.7	151.1
58	PBICR-08-008-#104	155.8	155.8	149.5	149.1	152.7	152.7
59	PBICR-08-008-#107	154.3	154.2	144.9	144.7	150.1	150.1
60	PBICR-08-008-#108	150.7	150.5	145.4	146	148.1	147.5
61	PBICR-08-008-#109	156.8	156.8	147.4	147.5	152.2	152.2
62	PBICR-08-008-#111	161	161.2	149.7	149.6	154.5	154.5
63	PBICR-08-008-#112	153.8	152.7	150.3	150.4	152.1	151.6
64	PBICR-08-008-#113	151.8	151.9	144.7	145	149.3	149.3
65	PBICR-08-008-#114	155.4	155.5	143.3	142.9	149.4	149.1
66	PBICR-08-008-#115	150.4	150.6	145	144.8	148.3	148.3
67	PBICR-08-008-#116	145.8	146.1	144.9	144.5	145.8	145.6
68	PBICR-08-008-#118	150.1	150.2	144.5	144.5	148.9	148.9
69	PBICR-08-008-#119	155.9	155.1	147.2	147.3	151.3	150.8
70	PBICR-08-008-#123	152.7	152.7	145.3	145.8	149.4	149.6
71	PBICR-08-008-#124	153.8	153.9	146.2	146.2	150.1	150.1
72	PBICR-08-008-#125	152.5	152.5	143.6	143.4	148.5	148.5
73	PBICR-08-008-#126	155.2	155.2	146	145.6	151.7	151.4
74	PBICR-08-008-#127	156.4	156.5	147.2	146.2	151.4	151.7
75	PBICR-08-008-#129	149.2	149.3	143.7	143.5	147	147
76	PBICR-08-008-#130	145.3	145.3	142.4	142.4	143.8	143.8
77	PBICR-08-008-#133	151.3	151.4	143.5	143.6	147.3	147.3
78	PBICR-08-008-#134	146.7	146.9	142.6	142.8	144.7	144.8
79	PBICR-08-008-#136	147.7	147.7	142.1	142.1	145.7	145.7
80	PBICR-08-008-#137	149.5	149.6	142.3	142.1	146.4	146.3
81	PBICR-08-008-#138	157.7	158.1	145.6	146	152.2	152.4
82	PBICR-08-008-#140	159.4	159.4	148.4	148.4	154.1	154.1
83	PBICR-08-008-#141	147	147	140.1	140.9	144.2	144.4
84	PBICR-08-008-#145	159.6	159.6	145.3	145	152.6	152.7
85	PBICR-08-008-#146	149.5	149.6	142.1	142	146.8	146.4
86	PBICR-08-008-#147	147.3	147.4	145.3	145.4	147.4	147.4
87	PBICR-08-008-#148	156.6	156.6	146.2	146.5	152.1	152.1

88	PBICR-08-008-#150	147.2	147.3	144.9	144.9	147	147
89	PBICR-08-008-#151	150.6	150.7	142.1	142.2	147.3	147.3
90	PBICR-08-008-#153	159.7	159.8	150.6	150.5	155.4	155.4
91	PBICR-08-008-#154	151.7	151.5	142.9	143	147.4	147.4
92	PBICR-08-008-#156	154.4	153.5	144.2	144	150	149.5
93	PBICR-08-008-#157	141.5	157.5	145.3	144.6	143.3	151.4
94	PBICR-08-008-#160	155.2	155.2	147.1	147.1	152.1	152.1
95	PBICR-08-008-#162	150.6	149.9	143.3	143.4	147.3	147.1
96	PBICR-08-008-#163	150	149.7	141.2	141.3	144.7	144.7
97	PBICR-08-008-#164	156	156	147.1	147.1	152.3	152.3
98	PBICR-08-008-#165	148.1	147.5	142.5	143	146.1	146.1
99	PBICR-08-008-#166	156.1	155.6	145.3	145.2	151.2	151
100	PBICR-08-008-#167	154.6	154.7	146.4	147.3	151.2	150.8
101	PBICR-08-008-#168	153.7	153.7	144.9	144.5	150	149.7
102	PBICR-08-008-#169	148.2	148.1	142.7	142.7	145.8	145.7
103	PBICR-08-008-#170	144.8	144.8	141	140.9	142.5	142.9
104	PBICR-08-008-#171	155.2	155.3	145.7	146.1	151	151.2
105	PBICR-08-008-#173	154.8	155	144.2	144.8	150.6	150.8
106	PBICR-08-008-#174	154.7	154.7	145.8	145.8	150.2	150.2
107	PBICR-08-008-#175	155.3	155	148.5	148.4	150.6	150.9
108	PBICR-08-008-#176	151.4	151.5	144.9	144.8	148.4	148.4
109	PBICR-08-008-#177	146.6	146.6	142.2	142.4	145.3	145.5
110	PBICR-08-008-#178	156.1	156.1	147.2	147.2	151.9	152.3
111	PBICR-08-008-#180	150.7	150.8	143.3	143.2	146.8	146.8
112	PBICR-08-008-#181	154.8	154.9	146.5	146.2	150.9	150.9
113	PBICR-08-008-#182	152.2	152.2	145.2	144.8	148.9	148.6
114	PBICR-08-008-#183	157.5	157.5	148.9	148.2	152.8	152.3
115	PBICR-08-008-#184	147.4	147.7	143.1	143	145.9	145.9
116	PBICR-08-008-#185	150.7	149.8	143.6	143.8	147.1	146.6
117	PBICR-08-008-#186	151.7	151.7	145.5	145.6	149.2	149.2
118	PBICR-08-008-#187	145.5	145.5	140.5	140.9	143.7	143.3
119	PBICR-08-008-#188	154.5	154.6	147	146.5	151.2	150.9
120	PBICR-08-008-#189	155.1	155.2	148.2	147.5	151	150.7
121	PBICR-08-008-#190	154.9	154.7	145.9	145.3	149.7	149.9
122	PBICR-08-008-#191	145.3	145.4	142.8	143.4	144.3	144.5
123	PBICR-08-008-#193	154.6	154.3	147.6	147	151.7	151.2
124	PBICR-08-008-#196	152.5	152.5	145.5	145	149.4	149.2
125	PBICR-08-008-#198	154.3	154.2	145.9	145.5	149.9	149.3
126	PBICR-08-008-#199	151.6	151.7	143	144.1	147.2	147.7
127	PBICR-08-008-#200	146.9	146.8	142.5	142.5	144.4	144.4
128	PBICR-08-008-#202	154.1	154.2	145.9	145.6	150	150
129	PBICR-08-008-#203	154.3	154.4	144.5	145	149.7	150
130	PBICR-08-008-#204	157.7	157.8	146.6	146.8	152.2	152.2
131	PBICR-08-008-#205	150	148.3	142	142.4	146.8	146
132	PBICR-08-008-#206	156	156.2	145.9	145.5	151.5	151.2
133	PBICR-08-008-#207	161.3	161.1	149	149.1	155.4	155.4

134	PBICR-08-008-#209	151.5	151.5	143	143	147.2	147.2
135	PBICR-08-008-#210	153.2	153.2	144.7	144.6	148	148
136	PBICR-08-008-#212	152.9	153	145.1	145	148.1	148.1
137	PBICR-08-008-#213	155.8	155.8	145.1	144.9	150.2	150.2
138	PBICR-08-008-#214	148.5	148.3	144.8	146.9	146	145.9
139	PBICR-08-008-#215	148.7	148.2	142.5	142.5	145.9	145.7
140	PBICR-08-008-#218	156.2	155.9	146.4	146.5	152.1	152.1
141	PBICR-08-008-#219	148.7	148.7	142.1	142.2	145.7	145.3
142	PBICR-08-008-#221	153.9	154	145.4	144.9	149	148.4
143	PBICR-08-008-#223	154.5	154.6	144.2	144.2	149.6	149.6
144	PBICR-08-008-#225	153.6	153.6	146.8	146	150.3	149.8
145	PBICR-08-008-#227	157.6	158.2	146.8	147	152.8	153.1
146	PBICR-08-008-#228	154.9	155	145.3	145.4	150.8	150.8
147	PBICR-08-008-#229	144.8	144.8	142.5	142.7	144	144
148	PBICR-08-008-#230	159.2	159.3	145.7	145.6	152.9	152.3
149	PBICR-08-008-#231	149.3	149.3	142	141.9	145.3	145.4
150	PBICR-08-008-#232	155.6	155.5	143.4	143.4	150.2	149.8
151	PBICR-08-008-#233	149.6	149.7	142.3	142.1	146.3	146.3
152	PBICR-08-008-#234	157.4	157.5	145.2	144.6	151.1	150.8
153	PBICR-08-008-#235	148.3	148.3	140.9	141.2	144.7	145
154	PBICR-08-008-#236	155.5	155.6	144.2	143.9	150.2	150.2
155	PBICR-08-008-#237	148	148	142.6	143.1	146	146.3
156	PBICR-08-008-#240	156.2	156.3	147.9	148	152.8	152.8
157	PBICR-08-008-#241	154.8	154.7	146.5	146.2	150.4	150.4
158	PBICR-08-008-#242	149.8	149.9	144.1	144.1	147.5	147.5
159	PBICR-08-008-#243	151.6	151.8	146.1	145.6	148.8	148.5
160	PBICR-08-008-#244	146.4	146.2	143.3	143.1	144.8	144.9
161	PBICR-08-008-#247	147.5	147.6	142.8	142.2	146.1	145.5
162	PBICR-08-008-#248	154.5	154.7	146	146.3	150.8	150.4
163	PBICR-08-008-#250	150.1	150.1	143.1	143.1	147.6	147.3
164	PBICR-08-008-#252	156.5	156.6	148.3	148	152.5	152.2
165	PBICR-08-008-#253	161.2	161	148.7	121.4	153.9	140.4
166	PBICR-08-008-#254	152.2	152.2	145.8	145.7	149.8	149.8
167	PBICR-08-008-#255	153.6	153.6	145.7	145.7	149.5	149.5
168	PBICR-08-008-#256	161.7	161.7	149.4	149.2	155.7	155.7
169	PBICR-08-008-#257	150.7	150.8	143.7	143.7	145.9	145.9
170	PBICR-08-008-#258	155.2	155.2	144.9	144.7	150.6	150.6
171	PBICR-08-008-#259	148.9	149	141.8	141.9	145.3	145.3
172	PBICR-08-008-#260	156.4	156.5	146.2	146.1	151.3	151.3
173	PBICR-08-008-#261	153.3	153.4	145.8	145.7	148.7	149.1
174	PBICR-08-008-#262	156	155.9	145.7	145.1	151.3	151
175	PBICR-08-008-#263	145.1	145.2	141.7	141.5	143.3	142.9
176	PBICR-08-008-#267	150.8	150.9	145	143.7	147.8	147.3
177	PBICR-08-008-#268	157.5	157.6	146.8	147.4	152.3	152.5
178	PBICR-08-008-#269	142.9	143	141	140.8	143	143
179	PBICR-08-008-#270	155.5	155.6	145	145.8	150.1	150.3

180	PBICR-08-008-#271	147.2	147.2	141.8	141.8	143.7	143.7
181	PBICR-08-008-#273	156.2	156.1	146.4	146.4	151.1	151.1
182	PBICR-08-008-#274	157.7	157.8	147.3	146.3	152.2	151.7
183	PBICR-08-008-#275	149.9	149.8	144.4	144.3	147.6	147.7
184	PBICR-08-008-#276	153	153	145.2	144.6	149.3	149
185	PBICR-08-008-#278	156.3	157.4	148.9	148.9	152.5	152.9
186	PBICR-08-008-#280	152.1	152.2	144.5	144.7	149.1	149.1
187	PBICR-08-008-#283	152.8	153	145	145.1	149.2	149.2
188	PBICR-08-008-#284	147.1	147.1	140.9	140.9	143.6	143.5
189	PBICR-08-008-#285	147.7	147.8	142.2	142.9	144.1	144.6
190	PBICR-08-008-#289	148.1	148.2	142.7	142.7	144.5	144.5
191	PBICR-08-008-#291	145.9	145.9	142.3	142.5	143.3	143.3
192	PBICR-08-008-#292	149.7	149.7	144.6	144.7	147.2	147.2
193	PBICR-08-008-#293	160.7	160.7	149.2	149	154.7	154.7
194	PBICR-08-008-#294	147.2	147.2	142.3	142.8	145.1	145.7
195	PBICR-08-008-#298	157.3	157.3	148.9	148.2	153.3	153.7
196	PBICR-08-008-#299	155.5	155.6	146.3	146.5	150.9	150.9
197	AUS29529	148.5	148.6	144.1	143.4	146.9	146.5
198	Sunco/Pastor	153.3	153.3	145.7	145.9	150.2	150.2
199	Syn110	154.1	154.1	145.6	145.5	150.5	150.5
200	Suntop	152.9	152.9	145.9	146.2	149.9	150.3
201	Sunguard	154.3	153.2	147	147	150.6	150.1
202	Sunco	153.6	153.6	145.7	145.1	149.5	149.2
203	Spitfire			142.9	143.2		
204	Gregory	156.5	156.7	148.5	148.5	153.4	153
205	Bellaroi	155.5	155.5	144.9	145.6	150.8	151
206	Batavia	155.8	155.4	145.4	144.3	150.6	150.2
207	Wylie	153.8	153.9	146.5	146.6	150.2	150.2
Mean		**152.4**	**152.5**	**144.8**	**144.6**	**148.8**	**148.7**
Minimum		**141.5**	**142.9**	**136.8**	**121.4**	**141.4**	**140.4**
Maximum		**163.2**	**163.4**	**150.6**	**150.5**	**157**	**156.9**
Standard Error of Mean		**0.293**	**0.291**	**0.168**	**0.194**	**0.221**	**0.219**
Standard Error of difference (SED)		**1.72**		**2.23**		**1.64**	
LSD (5%) (Genotype x environment)		**3.39**		**4.37**		**3.21**	
LSD (5%) (Genotype)		**3.37**		**3.44**		**2.34**	

Table 11: Mean for genotype x inoculum of plant height (cm) in 2014, 2015 and across years.

		Plant height (cm)					
		2014		2015		Combined	
Entry	**Genotype**	**Nil**	**Plus**	**Nil**	**Plus**	**Nil**	**Plus**
1	PBICR-08-008-#2	98.5	97.5	105.1	104.1	101.6	100.3
2	PBICR-08-008-#7	93.8	93.7	84.7	78.4	92.2	85.9
3	PBICR-08-008-#8	97.6	97.6	100.9	101.5	100.2	99.7
4	PBICR-08-008-#9	107.9	107.8	111.0	111.3	109.8	109.5
5	PBICR-08-008-#10	63.8	63.7	65.2	63.9	64.0	64.0
6	PBICR-08-008-#11	108.5	106.5	105.9	103.8	106.8	104.6
7	PBICR-08-008-#16	99.0	98.8	102.2	102.1	99.3	98.8
8	PBICR-08-008-#22	91.5	91.3	88.1	86.8	91.3	90.1
9	PBICR-08-008-#23	103.5	103.7	98.0	95.6	100.5	100.0
10	PBICR-08-008-#27	101.6	101.7	82.0	81.1	90.8	90.6
11	PBICR-08-008-#29	98.0	97.8	99.5	98.3	98.9	97.9
12	PBICR-08-008-#37	98.4	98.4	107.2	104.9	102.9	102.4
13	PBICR-08-008-#38	94.7	93.7	99.5	98.6	97.1	96.6
14	PBICR-08-008-#39	99.3	99.3	95.3	96.0	96.5	96.7
15	PBICR-08-008-#44	106.8	105.7	110.7	111.7	110.1	109.1
16	PBICR-08-008-#45	98.2	98.3	98.4	98.0	98.2	97.4
17	PBICR-08-008-#46	90.9	90.4	95.1	93.5	92.9	92.2
18	PBICR-08-008-#47	104.9	105.0	102.0	101.1	103.8	103.6
19	PBICR-08-008-#48	99.5	98.6	102.3	101.9	101.0	100.5
20	PBICR-08-008-#49	93.1	93.2	90.2	85.9	91.5	89.5
21	PBICR-08-008-#50	103.0	101.5	109.0	106.9	105.0	103.7
22	PBICR-08-008-#51	95.0	93.9	98.1	98.4	96.5	96.0
23	PBICR-08-008-#52	96.4	96.5	95.3	94.8	96.5	96.3
24	PBICR-08-008-#53	66.2	67.2	69.3	74.9	65.9	71.4
25	PBICR-08-008-#55	97.6	97.6	98.3	96.6	99.2	98.2
26	PBICR-08-008-#56	100.5	100.5	100.8	97.7	100.7	99.7
27	PBICR-08-008-#57	97.2	96.9	105.9	103.9	101.1	100.3
28	PBICR-08-008-#62	96.6	97.5	97.0	94.6	96.8	96.5
29	PBICR-08-008-#63	95.0	92.8	97.4	96.2	95.6	93.8
30	PBICR-08-008-#64	111.3	111.4	115.4	113.4	113.4	112.4
31	PBICR-08-008-#65	100.9	99.9	102.5	103.2	102.5	102.0
32	PBICR-08-008-#68	91.9	91.9	92.3	90.4	91.9	91.1
33	PBICR-08-008-#69	92.3	91.2	97.2	97.3	94.9	94.1
34	PBICR-08-008-#70	109.5	109.4	112.7	112.2	110.3	110.1
35	PBICR-08-008-#71	91.2	90.6	94.6	94.4	92.6	91.8
36	PBICR-08-008-#72	105.7	105.6	107.6	105.3	106.2	104.7
37	PBICR-08-008-#73	112.2	111.7	114.6	114.0	113.4	112.7
38	PBICR-08-008-#74	112.0	112.0	119.2	120.0	116.2	116.5
39	PBICR-08-008-#75	108.6	108.1	107.8	106.3	108.4	107.4
40	PBICR-08-008-#76	100.0	99.9	104.0	104.0	101.6	101.9
41	PBICR-08-008-#77	92.7	92.7	85.1	84.0	88.6	88.3
42	PBICR-08-008-#80	99.1	97.4	97.6	97.6	98.1	96.9

43	PBICR-08-008-#81	99.5	99.5	100.3	99.1	99.4	98.6
44	PBICR-08-008-#82	95.9	95.8	101.3	99.7	98.9	98.4
45	PBICR-08-008-#83	94.9	95.0	91.5	89.5	92.4	91.7
46	PBICR-08-008-#85	106.3	105.7	107.6	105.6	106.7	105.4
47	PBICR-08-008-#86	95.6	95.5	89.2	88.7	92.6	92.3
48	PBICR-08-008-#89	97.5	95.4	94.5	94.2	95.1	93.8
49	PBICR-08-008-#90	94.6	94.1	91.8	90.9	92.8	92.0
50	PBICR-08-008-#91	86.1	85.9	90.3	87.0	88.4	87.1
51	PBICR-08-008-#94	95.7	95.9	98.4	96.5	96.4	95.1
52	PBICR-08-008-#97	94.9	92.8	93.6	91.4	95.1	93.3
53	PBICR-08-008-#98	90.0	89.2	91.0	86.5	91.9	90.9
54	PBICR-08-008-#99	106.2	105.7	105.2	105.1	105.3	104.8
55	PBICR-08-008-#100	104.7	104.5	101.2	100.3	103.6	103.1
56	PBICR-08-008-#101	96.5	96.4	94.2	92.9	95.0	94.5
57	PBICR-08-008-#103	104.2	104.2	94.8	93.3	99.7	99.2
58	PBICR-08-008-#104	97.1	95.6	113.1	109.5	105.6	103.3
59	PBICR-08-008-#107	91.4	91.4	101.3	100.4	96.2	95.5
60	PBICR-08-008-#108	109.0	109.0	102.2	101.8	105.6	105.1
61	PBICR-08-008-#109	95.4	95.6	100.0	97.0	97.9	96.4
62	PBICR-08-008-#111	84.3	82.1	91.0	90.5	87.6	86.6
63	PBICR-08-008-#112	109.0	109.0	96.5	94.9	102.5	101.7
64	PBICR-08-008-#113	95.2	95.6	106.8	107.1	101.1	100.9
65	PBICR-08-008-#114	89.5	89.7	100.5	99.4	93.9	93.4
66	PBICR-08-008-#115	98.7	98.5	93.9	91.4	95.8	94.8
67	PBICR-08-008-#116	97.7	99.8	93.1	92.2	94.9	95.2
68	PBICR-08-008-#118	99.1	99.4	102.5	103.0	101.3	101.3
69	PBICR-08-008-#119	95.0	96.9	100.5	99.8	98.7	98.9
70	PBICR-08-008-#123	95.3	94.4	100.4	100.0	98.7	97.9
71	PBICR-08-008-#124	97.4	96.9	95.1	95.4	96.0	95.7
72	PBICR-08-008-#125	101.9	101.4	106.6	105.1	104.3	103.3
73	PBICR-08-008-#126	94.5	92.9	98.6	96.2	96.0	94.0
74	PBICR-08-008-#127	100.3	100.2	96.8	95.8	99.1	98.3
75	PBICR-08-008-#129	84.1	84.1	96.3	96.1	89.5	89.0
76	PBICR-08-008-#130	67.2	67.2	69.2	69.0	66.9	66.6
77	PBICR-08-008-#133	101.4	100.0	101.1	101.3	101.9	100.7
78	PBICR-08-008-#134	95.9	95.7	107.7	104.2	101.0	99.5
79	PBICR-08-008-#136	95.8	95.6	102.1	99.9	98.5	97.5
80	PBICR-08-008-#137	101.7	101.8	105.8	103.1	103.9	103.2
81	PBICR-08-008-#138	99.5	93.6	95.7	94.7	97.0	93.5
82	PBICR-08-008-#140	89.4	88.6	85.4	84.0	87.6	86.9
83	PBICR-08-008-#141	98.6	98.6	101.7	100.9	100.8	100.0
84	PBICR-08-008-#145	99.8	100.3	96.0	92.4	98.2	97.4
85	PBICR-08-008-#146	111.6	111.5	123.9	123.5	118.4	118.1
86	PBICR-08-008-#147	93.1	93.4	94.5	94.7	94.2	94.2
87	PBICR-08-008-#148	99.3	99.1	95.8	95.4	97.1	96.6
88	PBICR-08-008-#150	112.0	110.9	118.9	117.6	115.1	114.6

89	PBICR-08-008-#151	102.6	102.4	101.5	100.9	102.2	102.2
90	PBICR-08-008-#153	96.2	96.2	92.2	91.0	94.2	93.5
91	PBICR-08-008-#154	64.2	62.1	65.6	65.1	64.7	63.7
92	PBICR-08-008-#156	90.9	91.0	88.1	84.6	88.9	88.6
93	PBICR-08-008-#157	107.1	107.1	102.4	101.5	104.0	104.0
94	PBICR-08-008-#160	103.0	103.0	106.5	104.0	105.2	103.9
95	PBICR-08-008-#162	99.2	99.1	105.0	101.6	102.0	100.5
96	PBICR-08-008-#163	99.3	99.1	97.8	97.0	98.9	98.2
97	PBICR-08-008-#164	101.6	101.7	93.4	93.2	97.7	97.7
98	PBICR-08-008-#165	86.8	86.8	91.3	90.5	87.4	86.7
99	PBICR-08-008-#166	102.8	102.8	102.3	101.9	102.5	102.5
100	PBICR-08-008-#167	93.9	92.7	92.8	93.0	93.5	93.0
101	PBICR-08-008-#168	99.9	100.0	102.5	102.2	100.9	99.9
102	PBICR-08-008-#169	113.1	112.9	105.1	104.4	109.3	109.0
103	PBICR-08-008-#170	97.0	97.1	99.5	99.1	97.5	97.2
104	PBICR-08-008-#171	94.8	92.7	96.6	95.9	95.9	94.7
105	PBICR-08-008-#173	106.5	106.5	111.3	109.5	108.5	108.5
106	PBICR-08-008-#174	92.4	90.9	101.4	100.7	96.7	95.7
107	PBICR-08-008-#175	94.9	96.9	90.8	92.1	93.6	94.1
108	PBICR-08-008-#176	95.5	94.4	92.5	92.5	94.1	93.6
109	PBICR-08-008-#177	108.8	108.7	110.2	107.5	109.1	108.1
110	PBICR-08-008-#178	101.0	101.0	104.9	102.8	102.8	102.6
111	PBICR-08-008-#180	102.4	100.4	102.9	99.5	102.6	100.1
112	PBICR-08-008-#181	94.0	94.1	84.9	80.2	90.3	90.3
113	PBICR-08-008-#182	100.9	100.8	99.7	98.6	99.9	99.6
114	PBICR-08-008-#183	98.6	97.3	102.7	100.5	101.0	99.5
115	PBICR-08-008-#184	100.1	99.6	103.2	102.2	102.3	101.3
116	PBICR-08-008-#185	110.7	108.3	115.7	112.7	113.6	110.6
117	PBICR-08-008-#186	97.3	96.0	103.4	100.5	101.2	98.9
118	PBICR-08-008-#187	91.7	91.5	98.4	98.8	94.9	94.2
119	PBICR-08-008-#188	86.0	85.9	93.0	89.0	90.1	88.1
120	PBICR-08-008-#189	65.9	65.7	66.9	65.7	65.7	65.7
121	PBICR-08-008-#190	92.8	92.9	94.9	91.4	93.4	91.9
122	PBICR-08-008-#191	105.5	103.7	106.6	107.0	106.7	105.2
123	PBICR-08-008-#193	96.1	97.0	89.2	87.4	92.6	92.1
124	PBICR-08-008-#196	101.2	101.1	98.9	96.4	99.4	98.1
125	PBICR-08-008-#198	95.8	95.7	104.4	99.9	99.3	97.5
126	PBICR-08-008-#199	101.8	101.9	107.6	107.6	104.9	104.7
127	PBICR-08-008-#200	100.9	101.0	101.6	98.2	101.7	100.2
128	PBICR-08-008-#202	104.8	100.8	99.2	98.3	101.7	99.7
129	PBICR-08-008-#203	74.4	74.4	70.6	70.1	73.0	73.0
130	PBICR-08-008-#204	95.3	95.5	96.9	95.4	96.6	95.9
131	PBICR-08-008-#205	109.0	110.8	121.0	111.1	108.5	109.5
132	PBICR-08-008-#206	99.8	101.2	99.5	100.0	100.0	100.3
133	PBICR-08-008-#207	97.1	97.0	94.5	93.8	95.9	95.7
134	PBICR-08-008-#209	99.8	99.7	100.7	101.3	100.2	100.2

135	PBICR-08-008-#210	92.3	89.4	90.7	87.4	90.9	88.4
136	PBICR-08-008-#212	106.1	105.9	103.2	102.0	105.6	105.1
137	PBICR-08-008-#213	106.4	105.8	104.8	102.0	105.6	103.8
138	PBICR-08-008-#214	84.0	83.9	92.7	92.2	86.5	86.7
139	PBICR-08-008-#215	108.0	108.1	113.5	112.9	111.0	110.8
140	PBICR-08-008-#218	103.7	103.7	103.4	103.4	103.9	103.6
141	PBICR-08-008-#219	100.5	100.4	99.9	101.2	100.9	100.6
142	PBICR-08-008-#221	92.5	92.3	95.2	93.6	93.9	93.2
143	PBICR-08-008-#223	92.9	90.6	97.4	96.9	95.6	94.6
144	PBICR-08-008-#225	96.3	96.4	96.8	95.0	96.9	95.9
145	PBICR-08-008-#227	98.7	98.7	96.2	95.9	98.4	97.7
146	PBICR-08-008-#228	99.0	98.9	95.9	96.9	96.9	96.9
147	PBICR-08-008-#229	106.4	106.4	105.2	106.7	106.2	106.0
148	PBICR-08-008-#230	104.5	99.5	101.2	100.8	103.3	100.3
149	PBICR-08-008-#231	108.6	108.5	101.9	102.2	104.8	104.8
150	PBICR-08-008-#232	97.0	97.1	96.8	96.2	97.2	96.9
151	PBICR-08-008-#233	65.5	65.4	63.0	62.7	65.6	65.6
152	PBICR-08-008-#234	99.6	99.3	94.9	92.0	96.2	94.9
153	PBICR-08-008-#235	101.4	100.4	104.1	101.4	101.3	100.6
154	PBICR-08-008-#236	91.5	91.5	94.1	93.1	91.9	91.4
155	PBICR-08-008-#237	95.4	95.2	105.3	104.5	101.1	100.6
156	PBICR-08-008-#240	99.7	99.6	98.7	96.0	99.2	98.7
157	PBICR-08-008-#241	93.3	85.3	93.0	91.4	93.1	88.6
158	PBICR-08-008-#242	123.6	123.6	120.3	120.5	123.0	122.5
159	PBICR-08-008-#243	103.2	103.1	103.8	104.9	104.2	104.2
160	PBICR-08-008-#244	106.9	106.9	121.4	120.8	115.0	115.0
161	PBICR-08-008-#247	107.6	107.5	116.3	116.0	112.2	111.7
162	PBICR-08-008-#248	96.8	96.3	96.9	95.9	97.1	95.6
163	PBICR-08-008-#250	100.6	100.5	102.2	101.5	100.6	99.6
164	PBICR-08-008-#252	98.8	98.7	96.6	96.6	98.8	98.3
165	PBICR-08-008-#253	90.2	90.2	94.8	94.2	92.4	92.4
166	PBICR-08-008-#254	96.4	95.0	95.9	96.7	96.9	96.1
167	PBICR-08-008-#255	96.7	96.3	98.6	96.8	98.0	97.0
168	PBICR-08-008-#256	87.6	87.0	87.9	87.6	87.3	87.1
169	PBICR-08-008-#257	95.4	93.0	91.4	90.2	91.5	90.0
170	PBICR-08-008-#258	99.8	99.7	95.8	95.6	97.0	97.0
171	PBICR-08-008-#259	97.4	97.4	91.6	92.5	94.3	94.0
172	PBICR-08-008-#260	86.0	86.1	95.9	93.7	91.7	91.7
173	PBICR-08-008-#261	93.5	92.3	98.5	97.7	95.2	94.5
174	PBICR-08-008-#262	95.8	94.9	95.8	95.4	95.7	94.9
175	PBICR-08-008-#263	96.7	96.7	99.1	98.2	97.2	97.2
176	PBICR-08-008-#267	98.9	97.0	97.2	94.2	97.4	95.4
177	PBICR-08-008-#268	101.0	101.0	97.7	94.8	99.4	98.2
178	PBICR-08-008-#269	108.7	108.6	114.0	113.3	111.4	111.4
179	PBICR-08-008-#270	106.9	106.9	104.4	101.8	105.5	104.0
180	PBICR-08-008-#271	116.3	116.3	121.7	121.7	119.9	119.6

181	PBICR-08-008-#273	100.1	100.1	93.6	94.0	96.8	96.8
182	PBICR-08-008-#274	104.1	101.0	94.7	92.9	99.7	97.2
183	PBICR-08-008-#275	85.9	85.8	87.9	87.6	87.1	86.8
184	PBICR-08-008-#276	110.2	109.2	112.6	112.3	111.3	110.3
185	PBICR-08-008-#278	96.7	96.6	98.3	95.5	98.3	97.3
186	PBICR-08-008-#280	93.7	93.7	99.1	97.7	96.2	95.4
187	PBICR-08-008-#283	93.9	96.1	95.5	95.8	94.3	95.3
188	PBICR-08-008-#284	109.8	109.8	106.9	104.7	108.3	107.3
189	PBICR-08-008-#285	106.3	106.3	111.3	109.8	109.6	108.9
190	PBICR-08-008-#289	107.5	107.3	111.9	111.9	110.3	110.3
191	PBICR-08-008-#291	120.2	120.1	91.2	91.8	106.0	106.0
192	PBICR-08-008-#292	122.3	122.1	106.7	107.2	114.7	114.4
193	PBICR-08-008-#293	95.7	95.5	90.8	91.1	92.8	92.8
194	PBICR-08-008-#294	95.5	95.3	97.7	95.9	96.6	96.1
195	PBICR-08-008-#298	66.5	66.6	66.5	66.0	65.6	65.6
196	PBICR-08-008-#299	93.8	93.6	95.9	96.0	96.2	95.7
197	AUS29529	97.0	97.0	74.1	101.5	100.6	99.6
198	Sunco/Pastor	88.4	88.4	92.7	90.7	91.0	90.5
199	Syn110	106.6	106.7	99.7	98.4	102.9	101.9
200	Suntop	99.6	99.7	98.0	97.9	99.2	98.7
201	Sunguard	89.0	88.4	91.5	96.5	90.6	92.3
202	Sunco	95.3	95.3	92.2	92.6	93.8	93.8
203	Spitfire			90.4	90.7		
204	Gregory	98.6	102.0	104.8	101.8	101.5	101.7
205	Bellaroi	88.5	88.0	80.6	77.4	83.7	82.2
206	Batavia	102.4	101.4	99.2	97.9	100.0	98.3
207	Wylie	94.9	94.9	93.8	93.4	94.3	94.0
Mean		**97.9**	**97.5**	**98.4**	**97.5**	**98.2**	**97.5**
Minimum		**63.8**	**62.1**	**63.0**	**62.7**	**64.0**	**63.7**
Maximum		**123.6**	**123.5**	**123.9**	**123.5**	**123.0**	**122.5**
Standard Error of Mean		**0.647**	**0.651**	**0.702**	**0.689**	**0.648**	**0.642**
Standard Error of difference (SED)		**4.45**		**5.50**		**4.86**	
LSD (5%) (Genotype x environment)		**7.78**		**10.79**		**9.57**	
LSD (5%) (Genotype)		**8.58**		**9.08**		**7.12**	

Table 12: Mean for genotype x inoculum of % white heads in 2014, 2015 and across years.

		Percent white heads					
		2014		2015		Combined	
Entry	**Genotype**	**Nil**	**Plus**	**Nil**	**Plus**	**Nil**	**Plus**
1	PBICR-08-008-#2	0.7	2.1	2.0	14.2	0.1	5.7
2	PBICR-08-008-#7	2.6	2.8	0.3	30.1	0.6	18.7
3	PBICR-08-008-#8	1.6	3.8	1.9	21.4	0.7	12.1
4	PBICR-08-008-#9	1.5	3.5	0.2	12.4	0.6	9.1
5	PBICR-08-008-#10	0.0	0.3	0.0	20.8	0.6	11.1
6	PBICR-08-008-#11	0.9	3.8	0.0	16.6	0.5	8.8
7	PBICR-08-008-#16	0.0	5.6	4.8	25.9	3.1	15.9
8	PBICR-08-008-#22	1.7	3.9	10.4	54.0	7.1	30.5
9	PBICR-08-008-#23	1.3	2.5	6.6	40.6	3.6	21.6
10	PBICR-08-008-#27	1.4	4.8	0.0	23.5	0.6	14.4
11	PBICR-08-008-#29	0.0	3.6	5.5	37.4	3.6	20.5
12	PBICR-08-008-#37	0.8	0.9	1.2	8.2	0.6	5.7
13	PBICR-08-008-#38	0.2	0.6	1.2	32.8	0.0	15.5
14	PBICR-08-008-#39	0.8	1.7	6.0	48.8	3.1	26.1
15	PBICR-08-008-#44	1.2	4.3	0.2	18.4	0.5	8.9
16	PBICR-08-008-#45	4.6	19.6	4.6	29.9	5.6	25.5
17	PBICR-08-008-#46	1.7	2.1	0.8	16.3	0.5	8.5
18	PBICR-08-008-#47	2.4	4.9	2.3	30.3	3.0	19.2
19	PBICR-08-008-#48	4.3	13.0	1.7	32.3	1.7	21.2
20	PBICR-08-008-#49	1.7	5.1	0.0	32.3	1.1	20.5
21	PBICR-08-008-#50	0.0	0.9	0.1	26.3	0.2	13.5
22	PBICR-08-008-#51	0.0	0.1	0.0	4.6	0.2	3.1
23	PBICR-08-008-#52	1.5	1.9	1.4	22.9	0.6	10.9
24	PBICR-08-008-#53	1.7	4.7	0.0	31.3	0.5	16.8
25	PBICR-08-008-#55	0.1	0.9	0.4	23.8	0.2	13.1
26	PBICR-08-008-#56	0.0	0.0	4.7	9.4	0.6	3.6
27	PBICR-08-008-#57	0.0	0.6	0.2	17.3	0.6	9.0
28	PBICR-08-008-#62	1.5	2.7	0.0	8.9	0.7	6.8
29	PBICR-08-008-#63	1.5	3.6	0.0	7.9	1.0	6.6
30	PBICR-08-008-#64	0.0	0.3	0.9	30.9	0.0	15.3
31	PBICR-08-008-#65	1.9	1.7	0.1	9.7	0.5	6.1
32	PBICR-08-008-#68	6.5	9.0	5.7	49.8	3.8	25.1
33	PBICR-08-008-#69	0.0	0.0	1.1	15.1	1.6	7.0
34	PBICR-08-008-#70	1.9	3.4	3.2	17.6	3.1	11.4
35	PBICR-08-008-#71	0.0	5.4	13.4	55.8	9.1	32.5
36	PBICR-08-008-#72	0.1	1.5	5.5	50.4	2.7	26.0
37	PBICR-08-008-#73	0.0	0.4	0.5	18.4	0.3	11.5
38	PBICR-08-008-#74	0.0	4.4	0.8	21.0	1.1	13.0
39	PBICR-08-008-#75	0.2	3.1	0.0	17.9	0.7	12.0
40	PBICR-08-008-#76	1.1	4.6	3.8	40.8	3.6	23.1
41	PBICR-08-008-#77	1.4	2.6	4.8	37.9	3.1	21.0
42	PBICR-08-008-#80	1.0	3.4	0.0	14.4	0.3	9.0

43	PBICR-08-008-#81	1.3	2.9	0.0	25.4	0.0	13.0
44	PBICR-08-008-#82	0.8	1.9	0.0	35.5	0.0	18.2
45	PBICR-08-008-#83	1.1	6.1	1.2	10.1	1.6	9.7
46	PBICR-08-008-#85	0.2	2.1	7.3	23.8	2.5	11.0
47	PBICR-08-008-#86	0.7	5.3	0.0	13.7	1.1	10.6
48	PBICR-08-008-#89	1.1	2.0	5.1	31.0	3.6	16.7
49	PBICR-08-008-#90	0.0	5.2	4.2	29.7	3.3	18.8
50	PBICR-08-008-#91	5.3	29.8	6.2	40.3	5.6	35.5
51	PBICR-08-008-#94	1.0	2.3	0.0	12.6	0.6	8.6
52	PBICR-08-008-#97	0.1	1.3	3.0	11.4	0.3	5.9
53	PBICR-08-008-#98	2.2	11.4	0.0	11.2	1.1	13.0
54	PBICR-08-008-#99	0.0	0.0	4.7	18.4	2.5	10.5
55	PBICR-08-008-#100	0.0	0.7	0.6	25.8	0.6	13.6
56	PBICR-08-008-#101	5.7	4.2	0.0	32.7	0.6	18.5
57	PBICR-08-008-#103	0.3	2.6	14.6	48.0	7.8	26.2
58	PBICR-08-008-#104	0.7	4.7	0.4	10.5	0.0	6.6
59	PBICR-08-008-#107	0.0	0.5	0.0	21.3	0.0	10.5
60	PBICR-08-008-#108	0.0	6.7	1.1	17.7	0.6	13.0
61	PBICR-08-008-#109	4.2	19.9	8.8	43.4	6.9	31.9
62	PBICR-08-008-#111	8.5	28.8	11.0	40.9	10.6	35.6
63	PBICR-08-008-#112	1.5	2.4	0.2	30.5	0.2	15.8
64	PBICR-08-008-#113	1.0	1.1	6.1	43.8	1.9	19.9
65	PBICR-08-008-#114	0.7	3.0	0.0	26.8	0.6	16.1
66	PBICR-08-008-#115	0.0	2.7	9.7	45.2	5.3	24.1
67	PBICR-08-008-#116	0.9	3.3	0.8	24.5	0.5	14.1
68	PBICR-08-008-#118	0.0	0.0	5.2	10.5	1.9	4.5
69	PBICR-08-008-#119	0.8	4.7	2.0	26.0	0.2	15.9
70	PBICR-08-008-#123	8.3	7.5	0.0	10.5	0.3	6.5
71	PBICR-08-008-#124	1.9	1.8	1.7	26.2	0.2	10.6
72	PBICR-08-008-#125	0.0	1.6	0.0	21.5	0.4	12.1
73	PBICR-08-008-#126	0.0	1.2	0.1	31.0	0.1	17.7
74	PBICR-08-008-#127	0.0	2.4	4.6	19.2	3.1	11.5
75	PBICR-08-008-#129	0.0	0.9	0.4	13.4	0.0	5.9
76	PBICR-08-008-#130	0.0	0.8	4.8	9.7	3.6	8.1
77	PBICR-08-008-#133	3.3	13.8	0.0	26.0	1.6	21.1
78	PBICR-08-008-#134	0.0	2.0	2.0	15.2	1.1	9.0
79	PBICR-08-008-#136	0.5	2.6	0.0	22.2	0.3	11.5
80	PBICR-08-008-#137	0.3	1.2	0.0	39.9	0.2	20.9
81	PBICR-08-008-#138	0.0	2.9	0.0	22.0	0.0	14.5
82	PBICR-08-008-#140	3.1	18.5	5.4	43.8	3.8	28.7
83	PBICR-08-008-#141	0.0	4.2	0.0	27.1	0.5	17.7
84	PBICR-08-008-#145	2.6	9.6	4.4	47.0	4.3	29.9
85	PBICR-08-008-#146	0.7	6.7	6.1	31.5	3.1	18.1
86	PBICR-08-008-#147	3.9	3.3	0.4	20.8	0.0	10.0
87	PBICR-08-008-#148	1.2	6.1	0.0	19.9	0.6	12.4
88	PBICR-08-008-#150	3.0	3.3	0.7	16.6	0.6	9.1

89	PBICR-08-008-#151	0.0	1.0	0.1	17.5	0.6	10.6
90	PBICR-08-008-#153	5.9	8.5	5.3	36.1	3.6	20.6
91	PBICR-08-008-#154	0.0	0.5	5.3	19.0	3.1	10.9
92	PBICR-08-008-#156	0.5	1.8	4.2	35.6	2.4	18.7
93	PBICR-08-008-#157	1.4	2.4	5.3	29.2	3.1	16.0
94	PBICR-08-008-#160	2.8	4.1	3.9	49.3	3.1	26.5
95	PBICR-08-008-#162	0.6	3.5	8.5	24.7	2.7	14.1
96	PBICR-08-008-#163	0.0	3.1	5.2	21.7	3.6	13.1
97	PBICR-08-008-#164	2.0	5.6	0.0	14.2	0.6	8.6
98	PBICR-08-008-#165	0.6	1.1	0.0	2.8	0.6	3.4
99	PBICR-08-008-#166	1.0	1.7	0.6	39.6	0.1	17.9
100	PBICR-08-008-#167	1.8	2.8	0.6	11.4	0.6	6.2
101	PBICR-08-008-#168	0.6	3.7	4.2	27.9	2.7	16.8
102	PBICR-08-008-#169	0.5	1.4	2.1	31.5	0.2	15.5
103	PBICR-08-008-#170	0.0	0.2	0.6	10.8	0.3	6.3
104	PBICR-08-008-#171	1.1	2.0	0.0	4.7	0.0	3.0
105	PBICR-08-008-#173	1.3	2.8	0.0	12.6	0.3	6.2
106	PBICR-08-008-#174	1.1	2.0	0.4	4.0	0.0	3.3
107	PBICR-08-008-#175	2.3	4.5	3.9	9.1	1.1	4.5
108	PBICR-08-008-#176	0.3	1.8	1.9	16.7	2.7	11.0
109	PBICR-08-008-#177	0.0	3.1	0.5	16.6	0.6	9.1
110	PBICR-08-008-#178	0.9	0.9	7.1	22.1	3.1	11.2
111	PBICR-08-008-#180	0.0	5.7	9.8	49.7	6.1	29.1
112	PBICR-08-008-#181	0.4	2.7	9.5	40.5	5.3	21.2
113	PBICR-08-008-#182	4.4	18.7	8.8	36.2	6.6	28.1
114	PBICR-08-008-#183	4.6	8.5	4.1	30.6	4.1	19.0
115	PBICR-08-008-#184	0.0	0.8	0.0	14.2	0.0	8.2
116	PBICR-08-008-#185	1.8	13.9	6.8	44.4	3.7	27.6
117	PBICR-08-008-#186	0.0	1.2	0.0	17.5	0.6	11.0
118	PBICR-08-008-#187	0.0	0.5	0.0	26.9	0.0	15.2
119	PBICR-08-008-#188	2.3	4.5	0.0	15.7	0.6	9.1
120	PBICR-08-008-#189	0.0	0.0	1.2	14.0	1.1	8.1
121	PBICR-08-008-#190	1.1	5.8	1.0	8.6	0.6	8.2
122	PBICR-08-008-#191	0.0	0.1	0.9	4.9	0.0	3.0
123	PBICR-08-008-#193	1.2	3.2	0.0	23.2	0.3	13.9
124	PBICR-08-008-#196	2.4	4.0	5.2	41.0	3.1	22.0
125	PBICR-08-008-#198	1.9	6.8	0.3	23.9	0.7	15.5
126	PBICR-08-008-#199	1.9	4.8	0.0	46.1	1.2	26.4
127	PBICR-08-008-#200	1.9	2.4	0.0	20.9	0.5	13.7
128	PBICR-08-008-#202	0.6	3.5	1.0	14.2	0.2	6.8
129	PBICR-08-008-#203	2.9	4.5	0.0	17.7	0.3	8.8
130	PBICR-08-008-#204	1.0	4.6	1.5	5.8	0.6	3.5
131	PBICR-08-008-#205	0.5	3.2	4.8	22.9	3.6	11.5
132	PBICR-08-008-#206	3.0	16.7	13.5	56.3	6.5	36.3
133	PBICR-08-008-#207	1.5	8.3	0.9	15.5	0.8	11.4
134	PBICR-08-008-#209	0.0	1.5	1.4	5.3	0.0	3.2

135	PBICR-08-008-#210	10.5	26.5	5.2	50.9	8.1	38.0
136	PBICR-08-008-#212	3.3	6.0	0.7	29.6	1.5	18.2
137	PBICR-08-008-#213	1.2	3.3	0.0	30.9	0.2	16.6
138	PBICR-08-008-#214	1.0	5.0	1.2	16.9	1.2	10.6
139	PBICR-08-008-#215	0.0	2.2	0.2	14.8	0.2	8.8
140	PBICR-08-008-#218	0.0	1.0	0.2	22.3	0.6	11.2
141	PBICR-08-008-#219	0.4	3.2	0.6	9.6	0.6	6.9
142	PBICR-08-008-#221	4.8	7.4	3.3	41.4	3.6	25.6
143	PBICR-08-008-#223	2.8	6.3	0.9	10.2	1.2	7.5
144	PBICR-08-008-#225	3.2	12.7	5.0	51.4	4.0	31.2
145	PBICR-08-008-#227	2.0	2.3	0.0	34.6	0.0	18.1
146	PBICR-08-008-#228	0.0	1.3	0.0	5.9	0.6	6.1
147	PBICR-08-008-#229	0.7	0.7	2.3	21.4	0.2	10.2
148	PBICR-08-008-#230	3.4	6.3	2.5	45.0	1.2	25.3
149	PBICR-08-008-#231	2.8	5.8	0.0	32.8	1.6	18.1
150	PBICR-08-008-#232	8.8	21.0	16.0	60.3	12.7	41.0
151	PBICR-08-008-#233	0.4	2.1	0.3	8.9	0.6	6.1
152	PBICR-08-008-#234	2.3	7.8	4.4	49.1	2.7	28.0
153	PBICR-08-008-#235	0.2	0.4	0.0	16.5	0.0	7.8
154	PBICR-08-008-#236	1.0	1.5	5.1	51.0	3.2	26.0
155	PBICR-08-008-#237	0.0	3.3	5.6	12.4	3.1	9.6
156	PBICR-08-008-#240	1.1	2.8	3.1	13.5	0.0	6.0
157	PBICR-08-008-#241	2.3	7.5	4.6	29.8	4.1	19.2
158	PBICR-08-008-#242	2.5	4.6	0.0	20.0	0.6	11.6
159	PBICR-08-008-#243	1.2	3.5	0.2	10.0	1.1	7.0
160	PBICR-08-008-#244	0.7	2.1	0.0	10.4	0.6	6.0
161	PBICR-08-008-#247	0.2	1.7	1.0	17.5	1.1	9.1
162	PBICR-08-008-#248	0.5	4.9	5.6	55.3	3.0	30.2
163	PBICR-08-008-#250	0.0	2.9	0.0	40.4	0.0	21.6
164	PBICR-08-008-#252	0.0	7.5	1.8	22.0	0.5	15.1
165	PBICR-08-008-#253	4.5	10.8	5.0	25.1	4.1	18.2
166	PBICR-08-008-#254	4.9	7.7	10.1	20.7	6.8	13.7
167	PBICR-08-008-#255	3.3	9.8	3.9	34.3	4.3	22.5
168	PBICR-08-008-#256	3.3	6.0	1.7	24.1	1.2	15.2
169	PBICR-08-008-#257	1.6	5.2	1.5	21.9	3.7	15.6
170	PBICR-08-008-#258	6.7	7.0	8.9	45.7	5.7	24.2
171	PBICR-08-008-#259	0.0	1.8	7.9	45.5	5.6	26.1
172	PBICR-08-008-#260	0.5	4.4	0.0	13.3	0.2	9.5
173	PBICR-08-008-#261	0.0	0.4	4.3	23.3	4.1	15.0
174	PBICR-08-008-#262	0.0	2.4	0.0	25.5	0.0	14.1
175	PBICR-08-008-#263	2.6	5.8	0.0	6.2	0.7	4.3
176	PBICR-08-008-#267	0.3	4.8	3.8	42.6	2.7	24.9
177	PBICR-08-008-#268	0.0	1.2	1.5	22.9	0.3	10.9
178	PBICR-08-008-#269	5.4	10.2	0.0	8.7	0.3	5.6
179	PBICR-08-008-#270	0.0	1.9	0.0	28.1	0.6	16.0
180	PBICR-08-008-#271	2.2	3.8	0.0	12.1	1.1	5.9

181	PBICR-08-008-#273	0.0	1.9	0.6	28.7	0.6	16.1
182	PBICR-08-008-#274	2.8	3.7	0.0	19.4	1.1	14.0
183	PBICR-08-008-#275	1.3	5.0	0.2	31.3	0.6	16.5
184	PBICR-08-008-#276	1.2	8.3	9.5	57.3	5.8	34.1
185	PBICR-08-008-#278	2.7	6.5	0.0	6.4	1.1	8.0
186	PBICR-08-008-#280	0.0	1.6	0.0	37.7	0.0	20.8
187	PBICR-08-008-#283	0.1	7.0	1.1	41.8	0.2	23.8
188	PBICR-08-008-#284	2.4	5.1	4.9	22.9	3.5	14.8
189	PBICR-08-008-#285	2.0	1.9	6.3	6.5	3.6	3.5
190	PBICR-08-008-#289	0.6	7.5	0.8	13.7	1.2	8.9
191	PBICR-08-008-#291	3.8	4.3	0.0	11.9	2.2	9.5
192	PBICR-08-008-#292	0.1	5.9	0.0	20.0	0.6	13.5
193	PBICR-08-008-#293	0.3	5.8	0.0	9.9	0.5	10.1
194	PBICR-08-008-#294	2.2	5.8	1.3	21.4	0.5	12.6
195	PBICR-08-008-#298	0.0	1.3	0.0	6.6	0.6	3.5
196	PBICR-08-008-#299	2.4	6.4	0.2	14.8	1.1	10.5
197	AUS29529	2.1	2.4	3.9	31.3	2.1	17.7
198	Sunco/Pastor	10.7	7.1	0.1	13.7	0.8	8.1
199	Syn110	1.4	2.5	6.0	30.6	2.7	15.8
200	Suntop	1.3	4.3	2.1	23.5	0.3	12.0
201	Sunguard		0.0	0.5	12.7	0.5	9.5
202	Sunco	0.5	2.3	0.0	17.8	0.5	12.0
203	Spitfire	0.0		0.9	12.6		
204	Gregory	6.1	11.2	12.3	51.2	10.5	33.3
205	Bellaroi	24.6	40.2	31.0	79.7	28.3	61.2
206	Batavia	1.3	9.7	4.1	58.7	3.0	35.3
207	Wylie	0.0	4.4	5.3	25.3	2.7	14.5
Mean		**1.3**	**4.7**	**2.4**	**25.4**	**2.0**	**15.2**
Minimum		**0**	**0**	**0**	**2.75**	**0**	**2.984**
Maximum		**24.62**	**40.19**	**31.04**	**79.67**	**28.25**	**61.21**
Standard Error of Mean		**0.213**	**0.381**	**0.284**	**0.980**	**0.200**	**0.610**
Standard Error of difference (SED)		**5.87**		**9.34**		**6.68**	
LSD (5%) (Genotype x environment)		**11.58**		**18.31**		**13.11**	
LSD (5%) (Genotype)		**10.87**		**14.78**		**9.29**	

Table 13: Mean for genotype x inoculum of stem browning in 2014, and mean of stem browning 2015.

		Stem browning (0-4 scale)		Stem browning (mm)
		2014		2015
Entry	**Genotype**	**Nil**	**Plus**	**Plus**
1	PBICR-08-008-#2	0.889	1.903	43.33
2	PBICR-08-008-#7	0.965	2.339	43.96
3	PBICR-08-008-#8	0.974	2.136	53.37
4	PBICR-08-008-#9	1.026	1.6	41.33
5	PBICR-08-008-#10	1.199	1.259	75.3
6	PBICR-08-008-#11	0.794	1.865	31.12
7	PBICR-08-008-#16	0.27	1.868	19.48
8	PBICR-08-008-#22	1.847	1.624	63.3
9	PBICR-08-008-#23	1.224	1.689	62.04
10	PBICR-08-008-#27	1.3	2.616	51.72
11	PBICR-08-008-#29	0.033	0.948	27.68
12	PBICR-08-008-#37	1.168	1.398	35.66
13	PBICR-08-008-#38	0.687	1.615	55.67
14	PBICR-08-008-#39	0.822	2.015	44.4
15	PBICR-08-008-#44	1.274	1.878	33.84
16	PBICR-08-008-#45	2.013	2.183	25.45
17	PBICR-08-008-#46	0.747	1.892	57.6
18	PBICR-08-008-#47	0.324	1.759	31.63
19	PBICR-08-008-#48	1.909	1.587	54
20	PBICR-08-008-#49	1.112	2.332	53.37
21	PBICR-08-008-#50	1.798	2.13	42.27
22	PBICR-08-008-#51	0.775	1.597	36.06
23	PBICR-08-008-#52	0.864	2.04	52.19
24	PBICR-08-008-#53	1.01	1.76	70.92
25	PBICR-08-008-#55	1.349	1.338	29.03
26	PBICR-08-008-#56	1.141	1.118	43.05
27	PBICR-08-008-#57	0	1.409	43.85
28	PBICR-08-008-#62	0.738	1.368	13.65
29	PBICR-08-008-#63	0.465	1.963	34.85
30	PBICR-08-008-#64	0.924	2.005	39.6
31	PBICR-08-008-#65	0	0.462	27.47
32	PBICR-08-008-#68	0.575	2.429	63.03
33	PBICR-08-008-#69	1.645	2.493	31.96
34	PBICR-08-008-#70	2.889	1.607	54.65
35	PBICR-08-008-#71	0.63	1.639	49.39
36	PBICR-08-008-#72	0.41	0.749	50
37	PBICR-08-008-#73	0.922	2.283	37.73
38	PBICR-08-008-#74	1.226	2.071	27.22
39	PBICR-08-008-#75	0.853	1.13	64.68
40	PBICR-08-008-#76	0.901	2.498	28.04
41	PBICR-08-008-#77	1.974	1.586	60.6

42	PBICR-08-008-#80	1.758	2.267	21.53
43	PBICR-08-008-#81	1.066	1.626	30
44	PBICR-08-008-#82	0.934	1.253	33.67
45	PBICR-08-008-#83	1.309	2.264	40.53
46	PBICR-08-008-#85	0.903	1.105	43.23
47	PBICR-08-008-#86	1.627	2.403	43.74
48	PBICR-08-008-#89	0.822	2.195	39.46
49	PBICR-08-008-#90	1.019	2.325	59.06
50	PBICR-08-008-#91	0.486	2.028	29.29
51	PBICR-08-008-#94	0.816	1.922	9.48
52	PBICR-08-008-#97	0.657	1.569	23.33
53	PBICR-08-008-#98	1.454	2.387	122.78
54	PBICR-08-008-#99	0.587	1.421	17.1
55	PBICR-08-008-#100	1.051	1.368	51.24
56	PBICR-08-008-#101	0.591	1.298	39.9
57	PBICR-08-008-#103	1.02	1.832	39.38
58	PBICR-08-008-#104	0.777	1.619	25.98
59	PBICR-08-008-#107	0.581	1.234	47.96
60	PBICR-08-008-#108	1.404	2.181	28.6
61	PBICR-08-008-#109	0.828	1.692	76.97
62	PBICR-08-008-#111	0	2.238	56.33
63	PBICR-08-008-#112	0.514	0.861	50.71
64	PBICR-08-008-#113	1.976	0.817	29.08
65	PBICR-08-008-#114	0.597	2.128	57.76
66	PBICR-08-008-#115	0.444	1.421	47.98
67	PBICR-08-008-#116	1.115	1.619	27.4
68	PBICR-08-008-#118	0.825	1.495	14.59
69	PBICR-08-008-#119	0	1.833	47.9
70	PBICR-08-008-#123	1.631	2.006	67.45
71	PBICR-08-008-#124	1.65	0.892	38.2
72	PBICR-08-008-#125	0.583	1.193	25.9
73	PBICR-08-008-#126	0.656	1.612	36.2
74	PBICR-08-008-#127	0.581	1.227	43.16
75	PBICR-08-008-#129	0.274	1.804	33.84
76	PBICR-08-008-#130	2.849	3.021	47.32
77	PBICR-08-008-#133	0.714	1.978	44.14
78	PBICR-08-008-#134	1.051	2.085	27.66
79	PBICR-08-008-#136	0.914	1.111	37.6
80	PBICR-08-008-#137	1.295	1.431	81.41
81	PBICR-08-008-#138	0.093	2.489	70.1
82	PBICR-08-008-#140	0.434	2.086	59.8
83	PBICR-08-008-#141	0.715	2.282	49.69
84	PBICR-08-008-#145	0.33	1.61	18.89
85	PBICR-08-008-#146	0.862	2.17	46.08
86	PBICR-08-008-#147	1.555	3.351	42.98
87	PBICR-08-008-#148	0.868	2.751	59.07

88	PBICR-08-008-#150	0.615	1.089	42.02
89	PBICR-08-008-#151	0.598	1.135	23.94
90	PBICR-08-008-#153	1.246	1.318	71.57
91	PBICR-08-008-#154	1.205	2.281	43.23
92	PBICR-08-008-#156	0.753	2.006	45.66
93	PBICR-08-008-#157	0.898	1.07	46.53
94	PBICR-08-008-#160	0.984	0.96	55
95	PBICR-08-008-#162	1.404	2.274	44.09
96	PBICR-08-008-#163	0.221	1.638	38.35
97	PBICR-08-008-#164	0.47	1.976	13.74
98	PBICR-08-008-#165	0.592	1.217	29.27
99	PBICR-08-008-#166	0.746	1.054	48.1
100	PBICR-08-008-#167	0.713	0.807	52.63
101	PBICR-08-008-#168	0.552	2.479	73.19
102	PBICR-08-008-#169	1.445	2.413	32
103	PBICR-08-008-#170	0.542	1.912	26.11
104	PBICR-08-008-#171	0.745	2.352	47.78
105	PBICR-08-008-#173	0.822	1.158	51.4
106	PBICR-08-008-#174	0.842	1.441	43.51
107	PBICR-08-008-#175	0.52	1.686	35.1
108	PBICR-08-008-#176	0.665	2.302	42.32
109	PBICR-08-008-#177	2.117	2.295	28.18
110	PBICR-08-008-#178	0.598	1.587	24.55
111	PBICR-08-008-#180	0.539	2.529	25.06
112	PBICR-08-008-#181	0.535	1.074	39.8
113	PBICR-08-008-#182	1.528	2.533	45.91
114	PBICR-08-008-#183	0.214	1.463	43.3
115	PBICR-08-008-#184	0.308	2.559	43.85
116	PBICR-08-008-#185	0.545	1.25	17.58
117	PBICR-08-008-#186	0.35	1.707	8.97
118	PBICR-08-008-#187	0.828	1.901	38.09
119	PBICR-08-008-#188	0.861	1.834	51.3
120	PBICR-08-008-#189	1.515	2.516	55.45
121	PBICR-08-008-#190	0.084	2.2	33.44
122	PBICR-08-008-#191	0.813	1.689	51.3
123	PBICR-08-008-#193	0.738	2.16	43.47
124	PBICR-08-008-#196	0.683	2.37	81.16
125	PBICR-08-008-#198	0.761	2.456	51.12
126	PBICR-08-008-#199	0	1.875	32.76
127	PBICR-08-008-#200	0.919	2.155	43.23
128	PBICR-08-008-#202	0.235	1.539	61.9
129	PBICR-08-008-#203	0.872	2.057	60.31
130	PBICR-08-008-#204	0.574	1.689	52.35
131	PBICR-08-008-#205	1.332	1.687	60.85
132	PBICR-08-008-#206	0.562	0.986	57.68
133	PBICR-08-008-#207	0.923	1.078	35.94

134	PBICR-08-008-#209	1.152	1.558	39.9
135	PBICR-08-008-#210	0.776	2.79	59.9
136	PBICR-08-008-#212	0.942	1.113	53
137	PBICR-08-008-#213	0.593	1.752	28.4
138	PBICR-08-008-#214	0.411	1.101	39.2
139	PBICR-08-008-#215	0.951	1.426	43.76
140	PBICR-08-008-#218	0.506	1.832	37.04
141	PBICR-08-008-#219	0.68	1.942	48.59
142	PBICR-08-008-#221	0.803	1.468	79.9
143	PBICR-08-008-#223	0.823	1.367	6.67
144	PBICR-08-008-#225	1.282	0.847	51.72
145	PBICR-08-008-#227	0.852	1.831	111.43
146	PBICR-08-008-#228	2.068	1.415	63.54
147	PBICR-08-008-#229	0.372	1.378	57.5
148	PBICR-08-008-#230	0.871	1.191	64.79
149	PBICR-08-008-#231	2.354	2.416	31.38
150	PBICR-08-008-#232	1.128	1.941	51.72
151	PBICR-08-008-#233	1.246	1.662	9.6
152	PBICR-08-008-#234	0.32	1.982	9.69
153	PBICR-08-008-#235	1.439	2.37	26.28
154	PBICR-08-008-#236	0.571	1.749	46.84
155	PBICR-08-008-#237	0.51	1.431	22.1
156	PBICR-08-008-#240	1.202	1.794	50.2
157	PBICR-08-008-#241	0.078	1.32	61.96
158	PBICR-08-008-#242	0.722	1.719	56.7
159	PBICR-08-008-#243	1.484	1.973	33.83
160	PBICR-08-008-#244	1.622	1.204	38.38
161	PBICR-08-008-#247	0.525	0.685	51.92
162	PBICR-08-008-#248	0.881	2.222	46.52
163	PBICR-08-008-#250	1.094	1.948	65.98
164	PBICR-08-008-#252	1.282	1.345	25.8
165	PBICR-08-008-#253	1.233	1.233	54.41
166	PBICR-08-008-#254	0.394	2.802	61.09
167	PBICR-08-008-#255	0.075	1.588	33.61
168	PBICR-08-008-#256	1.206	1.517	57.27
169	PBICR-08-008-#257	0.3	1.644	49.78
170	PBICR-08-008-#258	0.528	1.602	45.59
171	PBICR-08-008-#259	0.799	1.866	22.37
172	PBICR-08-008-#260	0.629	2.123	79.49
173	PBICR-08-008-#261	1.385	1.375	40.32
174	PBICR-08-008-#262	0.775	2.244	17.47
175	PBICR-08-008-#263	1.85	2.007	84.85
176	PBICR-08-008-#267	0.633	2.264	88.87
177	PBICR-08-008-#268	0.552	1.336	47.84
178	PBICR-08-008-#269	0.883	1.339	37.31
179	PBICR-08-008-#270	0.2	1.483	44.84

180	PBICR-08-008-#271	1.241	1.664	18.66
181	PBICR-08-008-#273	1.411	1.439	37.53
182	PBICR-08-008-#274	2.725	1.82	61.56
183	PBICR-08-008-#275	1.016	0.889	61.75
184	PBICR-08-008-#276	0.757	1.858	63.26
185	PBICR-08-008-#278	2.832	2.574	45.83
186	PBICR-08-008-#280	1.037	1.551	58.41
187	PBICR-08-008-#283	0.411	1.465	64.55
188	PBICR-08-008-#284	1.771	2.106	42.73
189	PBICR-08-008-#285	0.605	2.291	77.17
190	PBICR-08-008-#289	1.771	1.459	20.64
191	PBICR-08-008-#291	1.335	1.622	26.06
192	PBICR-08-008-#292	0.247	1.132	47.3
193	PBICR-08-008-#293	1.085	1.947	78.94
194	PBICR-08-008-#294	1.752	1.539	33.68
195	PBICR-08-008-#298	0.945	1.125	74.9
196	PBICR-08-008-#299	2.382	2.401	33.87
197	AUS29529	0.825	2.242	61.71
198	Sunco/Pastor	0.813	2.255	42.73
199	Syn110	0.313	1.495	71.88
200	Suntop	1.151	2.496	65.51
201	Sunguard	0.914	1.57	37.01
202	Sunco	0.146	1.692	27.1
203	Spitfire			23.9
204	Gregory	1.453	2.195	75.56
205	Bellaroi	1.817	3.761	95.86
206	Batavia	0.282	1.916	40.67
207	Wylie	0.557	1.197	38.78
Mean		**0.926**	**1.769**	**54.82**
Minimum		**0**	**0.462**	**6.67**
Maximum		**2.889**	**3.761**	**122.8**
Standard Error of Mean		**0.039**	**0.036**	**1.277**
Standard Error of difference (SED)		**0.68**		**5.59**
LSD (5%) (Genotype x environment)		**133**		**-**
(LSD 5% , genotype)		**0.97**		**10.95**

Table 14: Mean of % yield loss in 2014, 2015 and across years.

		Percent Yield loss		
Entry	**Genotype**	**2014**	**2015**	**Combined**
1	PBICR-08-008-#2	2.01	6.03	4.02
2	PBICR-08-008-#7	3.31	23.48	13.28
3	PBICR-08-008-#8	8.00	11.63	9.82
4	PBICR-08-008-#9	1.78	2.69	2.12
5	PBICR-08-008-#10	1.78	4.26	2.90
6	PBICR-08-008-#11	1.73	14.35	8.04
7	PBICR-08-008-#16	15.87	10.82	13.23
8	PBICR-08-008-#22	9.70	43.40	26.43
9	PBICR-08-008-#23	14.70	40.30	27.39
10	PBICR-08-008-#27	9.11	21.82	15.35
11	PBICR-08-008-#29	13.16	21.59	17.26
12	PBICR-08-008-#37	1.78	10.74	6.14
13	PBICR-08-008-#38	7.68	22.32	15.00
14	PBICR-08-008-#39	6.74	28.14	17.33
15	PBICR-08-008-#44	1.53	10.63	6.08
16	PBICR-08-008-#45	17.80	11.51	14.54
17	PBICR-08-008-#46	0.00	9.82	4.91
18	PBICR-08-008-#47	2.12	18.49	10.19
19	PBICR-08-008-#48	2.60	18.85	10.72
20	PBICR-08-008-#49	11.70	28.35	19.91
21	PBICR-08-008-#50	1.57	15.18	8.37
22	PBICR-08-008-#51	6.72	9.23	7.98
23	PBICR-08-008-#52	1.78	11.74	6.64
24	PBICR-08-008-#53	2.78	32.17	17.47
25	PBICR-08-008-#55	6.44	17.88	12.16
26	PBICR-08-008-#56	12.12	12.03	11.96
27	PBICR-08-008-#57	6.95	9.49	8.10
28	PBICR-08-008-#62	11.37	6.18	8.78
29	PBICR-08-008-#63	2.54	7.79	5.05
30	PBICR-08-008-#64	0.00	24.61	12.31
31	PBICR-08-008-#65	7.64	12.82	10.12
32	PBICR-08-008-#68	9.00	25.33	17.16
33	PBICR-08-008-#69	9.15	19.29	14.11
34	PBICR-08-008-#70	1.78	16.36	8.95
35	PBICR-08-008-#71	19.38	14.57	16.97
36	PBICR-08-008-#72	1.31	34.66	17.99
37	PBICR-08-008-#73	9.30	19.45	14.37
38	PBICR-08-008-#74	6.83	9.81	8.20
39	PBICR-08-008-#75	6.85	11.59	9.22
40	PBICR-08-008-#76	6.38	19.13	12.64
41	PBICR-08-008-#77	3.82	33.00	18.29
42	PBICR-08-008-#80	5.37	15.30	10.34
43	PBICR-08-008-#81	6.15	22.82	14.49
44	PBICR-08-008-#82	6.27	15.94	11.10
45	PBICR-08-008-#83	21.90	26.87	24.27
46	PBICR-08-008-#85	6.68	15.52	11.10
47	PBICR-08-008-#86	6.40	10.35	8.26
48	PBICR-08-008-#89	2.25	14.64	8.33
49	PBICR-08-008-#90	6.59	21.77	14.18
50	PBICR-08-008-#91	23.90	35.38	29.52
51	PBICR-08-008-#94	3.49	2.53	2.89
52	PBICR-08-008-#97	6.59	13.67	10.13
53	PBICR-08-008-#98	13.22	10.50	11.75

54	PBICR-08-008-#99	0.76	16.84	8.80
55	PBICR-08-008-#100	9.46	15.05	12.14
56	PBICR-08-008-#101	5.81	18.27	11.92
57	PBICR-08-008-#103	5.95	23.27	14.61
58	PBICR-08-008-#104	12.82	7.89	10.35
59	PBICR-08-008-#107	0.29	10.63	5.46
60	PBICR-08-008-#108	1.84	24.16	12.89
61	PBICR-08-008-#109	19.21	21.68	20.56
62	PBICR-08-008-#111	25.77	14.23	19.88
63	PBICR-08-008-#112	4.35	32.69	18.52
64	PBICR-08-008-#113	2.71	17.09	10.02
65	PBICR-08-008-#114	6.44	16.67	11.44
66	PBICR-08-008-#115	0.29	22.37	11.33
67	PBICR-08-008-#116	10.04	9.04	9.54
68	PBICR-08-008-#118	1.71	0.00	0.97
69	PBICR-08-008-#119	20.22	22.62	21.42
70	PBICR-08-008-#123	6.35	9.45	7.90
71	PBICR-08-008-#124	7.05	17.32	12.18
72	PBICR-08-008-#125	0.10	11.20	5.65
73	PBICR-08-008-#126	6.98	26.83	16.90
74	PBICR-08-008-#127	4.92	24.74	14.71
75	PBICR-08-008-#129	6.12	10.75	8.55
76	PBICR-08-008-#130	9.87	18.27	13.96
77	PBICR-08-008-#133	11.23	34.38	22.80
78	PBICR-08-008-#134	6.92	13.21	9.95
79	PBICR-08-008-#136	1.64	13.23	7.44
80	PBICR-08-008-#137	9.64	30.72	20.18
81	PBICR-08-008-#138	15.93	19.39	17.78
82	PBICR-08-008-#140	13.24	16.19	14.71
83	PBICR-08-008-#141	9.01	15.05	12.03
84	PBICR-08-008-#145	9.82	16.32	13.07
85	PBICR-08-008-#146	1.78	25.49	13.52
86	PBICR-08-008-#147	1.41	20.89	11.27
87	PBICR-08-008-#148	10.34	22.66	16.38
88	PBICR-08-008-#150	11.34	0.91	6.01
89	PBICR-08-008-#151	12.33	9.31	10.70
90	PBICR-08-008-#153	13.04	30.18	21.50
91	PBICR-08-008-#154	6.96	20.21	13.47
92	PBICR-08-008-#156	1.48	18.28	9.88
93	PBICR-08-008-#157	2.53	17.29	9.79
94	PBICR-08-008-#160	6.48	22.65	14.45
95	PBICR-08-008-#162	8.56	9.57	9.07
96	PBICR-08-008-#163	1.78	4.44	2.99
97	PBICR-08-008-#164	5.29	7.09	6.07
98	PBICR-08-008-#165	1.94	6.29	4.11
99	PBICR-08-008-#166	4.05	18.84	11.44
100	PBICR-08-008-#167	6.17	16.18	11.06
101	PBICR-08-008-#168	8.22	13.47	10.84
102	PBICR-08-008-#169	0.00	29.28	14.64
103	PBICR-08-008-#170	8.55	9.45	9.00
104	PBICR-08-008-#171	3.82	11.75	7.78
105	PBICR-08-008-#173	1.91	1.34	1.63
106	PBICR-08-008-#174	3.15	15.04	9.09
107	PBICR-08-008-#175	6.73	7.88	7.19
108	PBICR-08-008-#176	5.83	20.12	12.98
109	PBICR-08-008-#177	1.78	29.00	15.27
110	PBICR-08-008-#178	1.78	22.82	12.18

111	PBICR-08-008-#180	29.60	29.04	29.20
112	PBICR-08-008-#181	9.41	22.99	16.20
113	PBICR-08-008-#182	12.98	14.00	13.38
114	PBICR-08-008-#183	14.50	20.40	17.33
115	PBICR-08-008-#184	12.92	14.07	13.50
116	PBICR-08-008-#185	15.94	22.10	19.02
117	PBICR-08-008-#186	17.35	19.72	18.42
118	PBICR-08-008-#187	4.87	17.68	11.27
119	PBICR-08-008-#188	6.86	19.95	13.29
120	PBICR-08-008-#189	25.58	10.26	17.80
121	PBICR-08-008-#190	7.37	17.38	12.26
122	PBICR-08-008-#191	12.44	10.24	11.34
123	PBICR-08-008-#193	10.57	21.94	16.26
124	PBICR-08-008-#196	1.78	23.07	12.31
125	PBICR-08-008-#198	9.39	22.02	15.70
126	PBICR-08-008-#199	1.78	20.42	10.98
127	PBICR-08-008-#200	6.38	21.22	13.69
128	PBICR-08-008-#202	5.55	21.38	13.46
129	PBICR-08-008-#203	5.19	12.99	9.09
130	PBICR-08-008-#204	3.93	40.17	21.93
131	PBICR-08-008-#205	1.78	3.98	2.76
132	PBICR-08-008-#206	12.62	22.98	17.80
133	PBICR-08-008-#207	5.92	15.33	10.62
134	PBICR-08-008-#209	4.43	3.16	3.79
135	PBICR-08-008-#210	1.78	23.55	12.55
136	PBICR-08-008-#212	9.75	28.69	19.11
137	PBICR-08-008-#213	4.25	16.54	10.39
138	PBICR-08-008-#214	2.94	17.32	10.01
139	PBICR-08-008-#215	4.17	9.00	6.59
140	PBICR-08-008-#218	12.06	6.20	9.02
141	PBICR-08-008-#219	14.46	10.55	12.39
142	PBICR-08-008-#221	9.79	30.14	19.85
143	PBICR-08-008-#223	6.15	11.39	8.65
144	PBICR-08-008-#225	6.15	31.18	18.66
145	PBICR-08-008-#227	3.09	30.79	16.94
146	PBICR-08-008-#228	5.08	4.21	4.53
147	PBICR-08-008-#229	0.00	20.96	10.48
148	PBICR-08-008-#230	2.60	23.62	13.11
149	PBICR-08-008-#231	13.54	14.40	13.86
150	PBICR-08-008-#232	10.74	21.75	16.24
151	PBICR-08-008-#233	1.78	7.40	4.47
152	PBICR-08-008-#234	10.87	34.29	22.58
153	PBICR-08-008-#235	4.71	4.71	4.71
154	PBICR-08-008-#236	5.96	16.58	11.15
155	PBICR-08-008-#237	10.71	8.01	9.24
156	PBICR-08-008-#240	11.28	8.20	9.74
157	PBICR-08-008-#241	3.39	14.81	8.98
158	PBICR-08-008-#242	7.82	17.18	12.38
159	PBICR-08-008-#243	1.78	12.44	6.99
160	PBICR-08-008-#244	1.78	0.37	0.96
161	PBICR-08-008-#247	1.78	19.81	10.68
162	PBICR-08-008-#248	10.01	27.94	18.97
163	PBICR-08-008-#250	7.82	23.46	15.64
164	PBICR-08-008-#252	9.10	17.32	13.21
165	PBICR-08-008-#253	19.35	11.18	15.15
166	PBICR-08-008-#254	10.33	7.12	8.73
167	PBICR-08-008-#255	10.68	23.55	17.11

168	PBICR-08-008-#256	1.85	16.73	9.29
169	PBICR-08-008-#257	6.92	18.10	12.40
170	PBICR-08-008-#258	0.00	8.85	4.42
171	PBICR-08-008-#259	5.83	19.53	12.56
172	PBICR-08-008-#260	2.92	5.83	4.37
173	PBICR-08-008-#261	1.78	9.88	5.71
174	PBICR-08-008-#262	9.72	13.73	11.73
175	PBICR-08-008-#263	8.79	2.99	5.89
176	PBICR-08-008-#267	5.96	27.92	16.94
177	PBICR-08-008-#268	6.84	17.35	12.10
178	PBICR-08-008-#269	6.05	16.84	11.44
179	PBICR-08-008-#270	2.26	24.18	13.10
180	PBICR-08-008-#271	9.73	20.31	14.90
181	PBICR-08-008-#273	1.78	16.15	8.85
182	PBICR-08-008-#274	8.76	27.44	17.98
183	PBICR-08-008-#275	6.56	11.37	8.85
184	PBICR-08-008-#276	9.44	20.52	14.98
185	PBICR-08-008-#278	15.72	14.11	14.80
186	PBICR-08-008-#280	6.31	23.03	14.67
187	PBICR-08-008-#283	7.44	25.67	16.56
188	PBICR-08-008-#284	9.13	15.19	12.16
189	PBICR-08-008-#285	19.54	10.69	15.00
190	PBICR-08-008-#289	1.78	4.28	2.91
191	PBICR-08-008-#291	5.37	20.44	12.79
192	PBICR-08-008-#292	1.78	4.96	3.25
193	PBICR-08-008-#293	5.20	17.92	11.44
194	PBICR-08-008-#294	14.91	12.88	13.89
195	PBICR-08-008-#298	1.78	18.89	10.22
196	PBICR-08-008-#299	3.22	17.20	10.09
197	AUS29529	5.13	26.16	15.70
198	Sunco/Pastor	1.78	10.11	5.77
199	Syn110	7.01	19.00	13.01
200	Suntop	6.35	16.62	11.49
201	Sunguard	2.51	10.89	6.70
202	Sunco	7.86	11.07	9.46
203	Spitfire		12.27	
204	Gregory	5.58	29.13	17.35
205	Bellaroi	27.04	43.90	35.47
206	Batavia	14.79	37.94	26.36
207	Wylie	10.04	24.80	17.42
Mean		**7.33**	**17.36**	**12.30**
Minimum		**0**	**0**	**0.96**
Maximum		**29.6**	**43.90**	**35.47**
Standard Error of Mean		**0.390**	**0.945**	**0.390**
Standard Error of difference (SED)		**6.03**	**8.80**	**6.12**
LSD (5%) (Genotype)		**11.90**	**17.24**	**12.02**

Appendix IV

Table 1: List of SNPs significantly associated with various traits in inoculated and un-inoculated environments across years

Environment	Trait	**SNP**	**Chr.**	**Position**	**P-Value**	**-Log$_{10}$(P)**	**MAF**	**R^2 (%)**	**Effect**
Nil	HD	Kukri_rep_c113971_162_1A	1A	117.68	0.000581	3.24	0.437824	3.24	-1.2833
Nil	HD	Kukri_c26168_713_1D	1D	5.47	0.000484	3.32	0.409326	3.33	1.5531
Nil	HD	BobWhite_c359_1026_1D	1D	12.72	0.000294	3.53	0.450777	3.60	-1.7053
Nil	HD	IAAV8700_2A	2A	162.06	0.000665	3.18	0.34715	3.17	1.7148
Nil	HD	D_F1BEJMU02IKD3X_298_2B	2B	75.39	0.000838	3.08	0.414508	3.05	1.1710
Nil	HD	Tdurum_contig18901_188_2B	2B	255.74	0.000543	3.27	0.378238	3.27	1.2110
Nil	HD	Excalibur_c6097_2208_2B	2B	257.74	0.000618	3.21	0.432642	3.21	1.5801
Nil	HD	wsnp_Ku_c34759_44069854_2B	2B	259.03	0.000844	3.07	0.46114	3.04	1.4182
Nil	HD	Excalibur_c43482_196_2B	2B	262.16	0.000756	3.12	0.23057	3.10	1.4131
Nil	HD	BS00067337_51_2B	2B	262.81	0.000813	3.09	0.349741	3.06	-1.5166
Nil	HD	RAC875_c86069_65_2B	2B	263.36	0.000519	3.29	0.321244	3.30	1.4068
Nil	HD	BS00030497_51_2B	2B	263.9	0.000161	3.79	0.391192	3.92	1.6341
Nil	HD	JD_c11869_1300_2B	2B	263.9	0.000642	3.19	0.233161	3.19	1.6161
Nil	HD	Excalibur_rep_c68899_191_2B	2B	264.35	0.000752	3.12	0.388601	3.10	-1.5341
Nil	HD	IAAV1101_2B	2B	264.35	0.000972	3.01	0.393782	2.97	-1.4761
Nil	HD	JD_c11869_1297_2B	2B	264.35	0.000791	3.10	0.396373	3.08	1.5144
Nil	HD	Tdurum_contig47202_1699_2B	2B	264.35	0.000433	3.36	0.393782	3.39	-1.5913
Nil	HD	RFL_Contig996_350_2B	2B	264.46	0.000611	3.21	0.419689	3.21	1.4478
Nil	HD	RFL_Contig996_818_2B	2B	264.46	0.000404	3.39	0.435233	3.43	1.5083
Nil	HD	BS00029713_51_2B	2B	268.72	0.000509	3.29	0.240933	3.31	-1.7018
Nil	HD	BS00038217_51_2B	2B	268.72	0.0005	3.30	0.243523	3.32	-1.6411
Nil	HD	Excalibur_c25430_183_2B	2B	268.72	0.000423	3.37	0.243523	3.40	-1.6493
Nil	HD	Excalibur_c6111_411_2B	2B	268.72	0.00063	3.20	0.220207	3.20	1.4828
Nil	HD	Excalibur_c64276_565_2B	2B	268.72	0.000892	3.05	0.23057	3.01	-1.3935
Nil	HD	RAC875_c26415_350_2B	2B	268.72	0.0006	3.22	0.297927	3.22	1.7541

Nil	HD	RAC875_c3302_1411_2B	2B	268.72	0.0004	3.40	0.253886	3.43	-1.6378
Nil	HD	Tdurum_contig36804_220_2B	2B	268.72	0.000414	3.38	0.233161	3.42	-1.5300
Nil	HD	Tdurum_contig62852_538_2B	2B	268.72	0.000319	3.50	0.240933	3.55	-1.7489
Nil	HD	Tdurum_contig68806_537_2B	2B	268.72	0.000542	3.27	0.256477	3.27	-1.6068
Nil	HD	tplb0045o20_1168_2B	2B	268.72	0.000581	3.24	0.233161	3.24	1.5160
Nil	HD	wsnp_Ex_c741_1456698_2B	2B	268.72	0.000444	3.35	0.233161	3.38	1.5435
Nil	HD	Tdurum_contig30989_79_2B	2B	269.95	0.000442	3.35	0.393782	3.38	1.5912
Nil	HD	Kukri_c5904_80_2B	2B	271.59	0.000932	3.03	0.248705	2.99	1.4746
Nil	HD	Tdurum_contig81323_291_2B	2B	271.59	0.000378	3.42	0.256477	3.46	-1.6738
Nil	HD	wsnp_Ex_rep_c67391_65971023_2B	2B	273.39	0.00061	3.21	0.373057	3.21	-1.5956
Nil	HD	tplb0045o20_699_2B	2B	279.59	0.000452	3.35	0.225389	3.37	-1.6836
Nil	HD	RAC875_c48860_106_3B	3B	578.89	0.000805	3.09	0.406736	3.07	1.3825
Nil	HD	Kukri_c32139_2473_3D	3D	416.72	0.000367	3.44	0.199482	3.48	2.1734
Nil	HD	RAC875_rep_c102042_172_4A	4A	191.56	0.000794	3.10	0.056995	3.07	-3.1567
Nil	HD	BS00065936_51_5A	5A	450.43	0.00075	3.13	0.23057	3.10	-1.4076
Nil	HD	RAC875_c30566_230_5A	5A	450.43	0.000961	3.02	0.204663	2.97	1.3365
Nil	HD	Kukri_c33022_198_5A	5A	453.34	0.000334	3.48	0.15544	3.53	-1.6514
Nil	HD	Tdurum_contig81424_367_5A	5A	453.34	0.000291	3.54	0.233161	3.60	-1.4680
Nil	HD	Excalibur_c31769_793_5A	5A	463.45	0.000577	3.24	0.183938	3.24	1.6786
Nil	HD	wsnp_Ex_rep_c109532_92292121_5A	5A	466.78	0.000787	3.10	0.183938	3.08	1.6418
Nil	HD	Tdurum_contig47120_587_5A	5A	469.39	0.000224	3.65	0.19171	3.74	-1.6164
Nil	HD	Tdurum_contig69612_781_5A	5A	469.39	5.57E-05	4.25	0.199482	4.50	-1.8379
Nil	HD	BobWhite_c17445_83_5A	5A	484.57	9.42E-05	4.03	0.132124	4.21	-2.3612
Nil	HD	Tdurum_contig10086_387_5A	5A	484.57	0.00023	3.64	0.173575	3.73	-1.9405
Nil	HD	Tdurum_contig85105_286_5A	5A	484.57	0.000625	3.20	0.139896	3.20	-1.8810
Nil	HD	wsnp_BF484028B_Td_2_1_5A	5A	484.57	0.000187	3.73	0.15544	3.84	2.0179
Nil	HD	Tdurum_contig54725_586_5A	5A	488	0.000191	3.72	0.15285	3.83	2.0276
Nil	HD	BS00022754_51_5A	5A	492.85	0.000234	3.63	0.199482	3.72	-1.7118
Nil	HD	BS00063973_51_5A	5A	492.85	0.000535	3.27	0.204663	3.28	-1.6703
Nil	HD	Jagger_c6618_144_5A	5A	492.85	3.10E-05	4.51	0.181347	4.82	-2.1864

Nil	HD	wsnp_CAP11_c1506_840938_5A	5A	492.85	0.000648	3.19	0.199482	3.18	-1.6845
Nil	HD	wsnp_Ku_c42416_50159250_5A	5A	492.85	0.000804	3.09	0.196891	3.07	-1.6456
Nil	HD	wsnp_Ku_c42416_50159402_5A	5A	492.85	0.000791	3.10	0.212435	3.08	-1.6771
Nil	HD	BS00022098_51_5A	5A	493.65	2.13E-05	4.67	0.238342	5.03	1.8492
Nil	HD	BS00041911_51_5A	5A	494.25	0.000128	3.89	0.168394	4.05	2.0412
Nil	HD	BS00067150_51_5A	5A	494.25	0.000444	3.35	0.168394	3.38	1.8077
Nil	HD	RAC875_c7132_134_5A	5A	494.25	0.000725	3.14	0.15544	3.12	-1.8182
Nil	HD	BobWhite_c14689_172_5A	5A	495.18	0.000327	3.49	0.186528	3.54	1.6308
Nil	HD	wsnp_BG607308A_Ta_2_1_5A	5A	498.48	0.00012	3.92	0.194301	4.08	1.7514
Nil	HD	wsnp_BG607308A_Ta_2_2_5A	5A	498.48	0.000186	3.73	0.15544	3.84	-2.0653
Nil	HD	BS00069739_51_5A	5A	500.09	0.000453	3.34	0.137306	3.37	-1.8427
Nil	HD	D_GB5Y7FA02IZ73U_152_5D	5D	338.67	1.06E-10	9.97	0.160622	12.38	-3.8780
Nil	HD	D_contig14133_180_5D	5D	344.94	2.95E-10	9.53	0.158031	11.72	3.7899
Nil	HD	D_contig62661_72_5D	5D	349.65	6.09E-08	7.22	0.176166	8.42	-2.9854
Nil	HD	RFL_Contig1091_1538_5D	5D	354.06	1.35E-09	8.87	0.189119	10.76	3.3560
Nil	HD	BobWhite_c20106_377_5D	5D	357.85	9.40E-09	8.03	0.142487	9.55	2.9713
Nil	HD	BobWhite_c27870_103_5D	5D	357.85	9.65E-09	8.02	0.139896	9.54	3.0169
Nil	HD	D_GBB4FNX02GXFL1_268_5D	5D	357.85	9.79E-10	9.01	0.160622	10.96	3.6845
Nil	HD	D_GDS7LZN01DW87V_234_5D	5D	357.85	5.77E-07	6.24	0.183938	7.08	2.4920
Nil	HD	tplb0055c05_1689_5D	5D	357.85	2.42E-10	9.62	0.160622	11.85	3.9300
Nil	HD	wsnp_RFL_Contig2346_1854360_5D	5D	357.85	2.78E-06	5.56	0.189119	6.17	2.3805
Nil	HD	D_F5XZDLF02IP5IR_228_5D	5D	365.23	8.63E-05	4.06	0.186528	4.26	1.6902
Nil	HD	Ku_c19010_273_5D	5D	365.23	7.68E-08	7.11	0.119171	8.28	-2.8252
Nil	HD	Excalibur_c76347_77_5D	5D	371.54	1.92E-09	8.72	0.160622	10.54	3.8330
Nil	HD	Tdurum_contig11553_534_5D	5D	371.54	4.07E-09	8.39	0.163212	10.07	3.6182
Nil	HD	IACX3123_5D	5D	377.86	5.38E-05	4.27	0.178756	4.52	1.8051
Nil	HD	Jagger_c754_272_5D	5D	377.86	1.56E-07	6.81	0.132124	7.85	3.4492
Nil	HD	Ku_c6176_938_5D	5D	377.86	1.05E-06	5.98	0.142487	6.74	-2.8761
Nil	HD	Kukri_c41787_141_5D	5D	387.6	0.000971	3.01	0.111399	2.97	-1.8444
Nil	HD	RAC875_c24411_889_7A	7A	466.45	0.000258	3.59	0.303109	3.67	-1.4653

Nil	HD	wsnp_CAP8_c334_304253_7B	7B	94.4	0.000343	3.47	0.492228	3.52	-1.4325
Nil	HD	IAAV4510_7D	7D	332.77	0.000988	3.01	0.246114	2.96	-1.2605
Plus	HD	wsnp_CAP11_c710_458019_1A	1A	75.37	0.000466	3.33	0.38601	3.58	1.3581
Plus	HD	RAC875_c97040_104_1A	1A	90.01	0.00096	3.02	0.334197	3.17	1.3162
Plus	HD	Kukri_rep_c113971_162_1A	1A	117.68	0.000458	3.34	0.437824	3.59	-1.4038
Plus	HD	GENE-0014_822_1D	1D	5.47	0.000643	3.19	0.398964	3.40	-1.4496
Plus	HD	Kukri_c26168_713_1D	1D	5.47	0.000164	3.79	0.409326	4.17	1.6913
Plus	HD	BobWhite_c359_1026_1D	1D	12.72	0.000345	3.46	0.450777	3.75	-1.6550
Plus	HD	IAAV8700_2A	2A	162.06	0.000472	3.33	0.34715	3.57	1.8186
Plus	HD	Excalibur_c12916_123_2A	2A	590.4	0.000501	3.30	0.313472	3.54	1.6546
Plus	HD	D_F1BEJMU02IKD3X_298_2B	2B	75.39	0.000464	3.33	0.414508	3.58	1.3261
Plus	HD	CAP12_rep_c5926_115_2B	2B	255.74	0.000456	3.34	0.409326	3.59	-1.5370
Plus	HD	CAP12_rep_c5926_51_2B	2B	255.74	0.000582	3.23	0.401554	3.45	-1.4942
Plus	HD	D_contig36671_269_2B	2B	255.74	0.000712	3.15	0.448187	3.34	-1.5099
Plus	HD	Excalibur_c27557_381_2B	2B	255.74	0.000367	3.43	0.417098	3.71	1.5428
Plus	HD	Excalibur_c53027_302_2B	2B	255.74	0.000511	3.29	0.440415	3.53	1.5994
Plus	HD	Excalibur_c53027_323_2B	2B	255.74	0.000337	3.47	0.437824	3.76	-1.6271
Plus	HD	Excalibur_rep_c101660_546_2B	2B	255.74	0.000566	3.25	0.414508	3.47	1.6167
Plus	HD	Jagger_c8098_88_2B	2B	255.74	0.000716	3.14	0.443005	3.34	1.5612
Plus	HD	Kukri_c12616_844_2B	2B	255.74	0.000684	3.17	0.409326	3.36	-1.4367
Plus	HD	Kukri_c27574_725_2B	2B	255.74	0.000446	3.35	0.432642	3.60	1.6280
Plus	HD	Kukri_c29272_363_2B	2B	255.74	0.000755	3.12	0.448187	3.31	1.5308
Plus	HD	Kukri_c43403_346_2B	2B	255.74	0.000733	3.14	0.419689	3.33	1.5824
Plus	HD	Kukri_c43403_412_2B	2B	255.74	0.000571	3.24	0.409326	3.46	-1.4503
Plus	HD	Kukri_c43403_594_2B	2B	255.74	0.000274	3.56	0.411917	3.88	-1.7072
Plus	HD	Kukri_c67627_393_2B	2B	255.74	0.000933	3.03	0.411917	3.19	-1.4394
Plus	HD	RAC875_c8780_441_2B	2B	255.74	0.000531	3.28	0.450777	3.51	1.5792
Plus	HD	TA001567-0999_2B	2B	255.74	0.000906	3.04	0.398964	3.21	-1.5876
Plus	HD	TA005827-0874_2B	2B	255.74	0.000286	3.54	0.414508	3.86	1.6978
Plus	HD	Tdurum_contig18901_188_2B	2B	255.74	0.00024	3.62	0.378238	3.96	1.4129

Plus	HD	Tdurum_contig19415_271_2B	2B	255.74	0.000457	3.34	0.406736	3.59	-1.5102
Plus	HD	Tdurum_contig29620_125_2B	2B	255.74	0.000393	3.41	0.411917	3.68	1.6641
Plus	HD	Tdurum_contig61293_131_2B	2B	255.74	0.000675	3.17	0.435233	3.37	1.5644
Plus	HD	Tdurum_contig74936_264_2B	2B	255.74	0.000608	3.22	0.440415	3.43	-1.5859
Plus	HD	Tdurum_contig74936_387_2B	2B	255.74	0.000925	3.03	0.365285	3.19	1.2571
Plus	HD	Tdurum_contig7526_301_2B	2B	255.74	0.000411	3.39	0.417098	3.65	-1.6526
Plus	HD	wsnp_Ex_c66052_64232430_2B	2B	255.74	0.00039	3.41	0.396373	3.68	-1.5160
Plus	HD	wsnp_Ku_c23305_33210628_2B	2B	255.74	0.000343	3.46	0.450777	3.75	-1.6310
Plus	HD	Excalibur_c6097_2208_2B	2B	257.74	0.000306	3.51	0.432642	3.82	1.7434
Plus	HD	wsnp_Ku_c31_62657_2B	2B	259.03	0.000725	3.14	0.427461	3.33	1.5803
Plus	HD	wsnp_Ku_c34759_44069854_2B	2B	259.03	0.000175	3.76	0.46114	4.14	1.6684
Plus	HD	Excalibur_c43482_196_2B	2B	262.16	0.000138	3.86	0.23057	4.27	1.7132
Plus	HD	BobWhite_c30112_275_2B	2B	262.81	0.000332	3.48	0.30829	3.77	-1.5595
Plus	HD	BS00067337_51_2B	2B	262.81	0.000109	3.96	0.349741	4.41	-1.8739
Plus	HD	RAC875_c37837_889_2B	2B	262.81	0.000208	3.68	0.316062	4.04	1.5054
Plus	HD	Excalibur_rep_c68899_1400_2B	2B	263.36	0.000729	3.14	0.334197	3.33	1.6151
Plus	HD	IACX6223_2B	2B	263.36	0.00035	3.46	0.349741	3.74	-1.6915
Plus	HD	RAC875_c86069_65_2B	2B	263.36	0.000151	3.82	0.321244	4.22	1.6552
Plus	HD	BS00030497_51_2B	2B	263.9	4.07E-05	4.39	0.391192	4.98	1.8944
Plus	HD	JD_c11869_1300_2B	2B	263.9	0.000386	3.41	0.233161	3.69	1.8281
Plus	HD	BobWhite_c30622_180_2B	2B	264.35	0.000244	3.61	0.321244	3.94	1.6725
Plus	HD	Excalibur_rep_c68899_191_2B	2B	264.35	0.00012	3.92	0.388601	4.35	-1.8505
Plus	HD	IAAV1101_2B	2B	264.35	0.000164	3.78	0.393782	4.17	-1.7781
Plus	HD	JD_c11869_1297_2B	2B	264.35	0.000136	3.87	0.396373	4.28	1.8171
Plus	HD	Tdurum_contig47202_1699_2B	2B	264.35	6.51E-05	4.19	0.393782	4.71	-1.9065
Plus	HD	Kukri_rep_c76670_262_2B	2B	264.46	0.000351	3.45	0.360104	3.74	-1.4693
Plus	HD	RFL_Contig996_350_2B	2B	264.46	0.000114	3.94	0.419689	4.38	1.7070
Plus	HD	RFL_Contig996_818_2B	2B	264.46	7.08E-05	4.15	0.435233	4.66	1.7754
Plus	HD	Tdurum_contig62458_179_2B	2B	264.46	0.000192	3.72	0.398964	4.08	-1.7763
Plus	HD	Tdurum_contig60978_352_2B	2B	267.43	0.000204	3.69	0.409326	4.05	1.6912

Plus	HD	BS00029713_51_2B	2B	268.72	6.69E-05	4.17	0.240933	4.69	-2.0822
Plus	HD	BS00038217_51_2B	2B	268.72	5.17E-05	4.29	0.243523	4.84	-2.0515
Plus	HD	BS00079213_51_2B	2B	268.72	0.000383	3.42	0.259067	3.69	-1.7267
Plus	HD	BS00103461_51_2B	2B	268.72	0.000887	3.05	0.238342	3.22	1.5895
Plus	HD	Excalibur_c25430_183_2B	2B	268.72	4.44E-05	4.35	0.243523	4.93	-2.0503
Plus	HD	Excalibur_c6111_411_2B	2B	268.72	9.50E-05	4.02	0.220207	4.49	1.8239
Plus	HD	Excalibur_c64276_565_2B	2B	268.72	0.000159	3.80	0.23057	4.19	-1.6961
Plus	HD	Kukri_c15043_326_2B	2B	268.72	0.000957	3.02	0.279793	3.18	-1.4535
Plus	HD	RAC875_c26415_350_2B	2B	268.72	0.00018	3.74	0.297927	4.12	1.9697
Plus	HD	RAC875_c3302_1411_2B	2B	268.72	4.15E-05	4.38	0.253886	4.97	-2.0316
Plus	HD	RAC875_c76533_442_2B	2B	268.72	0.000312	3.51	0.246114	3.81	1.6875
Plus	HD	Tdurum_contig36804_220_2B	2B	268.72	6.29E-05	4.20	0.233161	4.73	-1.8671
Plus	HD	Tdurum_contig62852_538_2B	2B	268.72	3.76E-05	4.42	0.240933	5.03	-2.1338
Plus	HD	Tdurum_contig62852_592_2B	2B	268.72	0.000138	3.86	0.251295	4.27	-1.9002
Plus	HD	Tdurum_contig68806_537_2B	2B	268.72	5.76E-05	4.24	0.256477	4.78	-2.0031
Plus	HD	tplb0045o20_1168_2B	2B	268.72	9.06E-05	4.04	0.233161	4.52	1.8633
Plus	HD	wsnp_Ex_c741_1456698_2B	2B	268.72	6.74E-05	4.17	0.233161	4.69	1.8909
Plus	HD	Jagger_c36_213_2B	2B	269.95	0.000675	3.17	0.393782	3.37	1.5317
Plus	HD	Tdurum_contig30989_79_2B	2B	269.95	6.79E-05	4.17	0.393782	4.68	1.9038
Plus	HD	Kukri_c5904_80_2B	2B	271.59	0.000137	3.86	0.248705	4.28	1.8301
Plus	HD	Tdurum_contig28227_304_2B	2B	271.59	0.000672	3.17	0.354922	3.37	-1.5306
Plus	HD	Tdurum_contig62852_302_2B	2B	271.59	0.000208	3.68	0.243523	4.04	1.8382
Plus	HD	Tdurum_contig81323_291_2B	2B	271.59	3.49E-05	4.46	0.256477	5.07	-2.0937
Plus	HD	wsnp_Ex_c5239_9272511_2B	2B	271.59	0.000264	3.58	0.261658	3.90	-1.7718
Plus	HD	wsnp_Ex_rep_c67391_65971023_2B	2B	273.39	9.88E-05	4.01	0.373057	4.46	-1.9209
Plus	HD	BS00110319_51_2B	2B	279.59	0.000265	3.58	0.238342	3.90	1.6755
Plus	HD	BS00110442_51_2B	2B	279.59	0.000462	3.34	0.243523	3.58	1.5844
Plus	HD	tplb0045o20_699_2B	2B	279.59	5.82E-05	4.24	0.225389	4.77	-2.0523
Plus	HD	Excalibur_c2496_1141_2B	2B	280.05	0.000319	3.50	0.217617	3.79	1.8660
Plus	HD	RAC875_c55059_202_2B	2B	280.05	0.000765	3.12	0.26943	3.30	-1.2859

Plus	HD	Kukri_c40637_223_2B	2B	280.39	0.000956	3.02	0.199482	3.18	1.7677
Plus	HD	BS00088575_51_2B	2B	283.61	0.00082	3.09	0.349741	3.26	1.6661
Plus	HD	Excalibur_c1305_662_2B	2B	283.61	0.000281	3.55	0.352332	3.87	1.8205
Plus	HD	RAC875_rep_c113555_122_2B	2B	283.61	0.000997	3.00	0.326425	3.15	-1.4355
Plus	HD	wsnp_Ra_c11493_18637928_2B	2B	285.18	0.000658	3.18	0.233161	3.39	-1.6348
Plus	HD	JD_c39990_130_2B	2B	292.15	0.000662	3.18	0.352332	3.38	-1.7080
Plus	HD	Kukri_c106282_114_2B	2B	292.15	0.000321	3.49	0.352332	3.79	-1.7250
Plus	HD	wsnp_Ex_c57_116914_2B	2B	292.15	0.000639	3.19	0.34456	3.40	-1.4657
Plus	HD	RAC875_c48860_106_3B	3B	578.89	0.000732	3.14	0.406736	3.33	1.4455
Plus	HD	Kukri_c32139_2473_3D	3D	416.72	0.000304	3.52	0.199482	3.82	2.1636
Plus	HD	RAC875_rep_c102042_172_4A	4A	191.56	0.000938	3.03	0.056995	3.19	-3.0575
Plus	HD	BS00110365_51_4B	4B	182.55	0.000938	3.03	0.246114	3.19	-1.4121
Plus	HD	Excalibur_c7729_144_5A	5A	448.42	0.000881	3.05	0.202073	3.22	-1.6235
Plus	HD	wsnp_Ex_c31799_40545376_5A	5A	448.42	0.000641	3.19	0.199482	3.40	1.6547
Plus	HD	BS00065936_51_5A	5A	450.43	0.000304	3.52	0.23057	3.82	-1.6235
Plus	HD	RAC875_c13931_205_5A	5A	450.43	0.000643	3.19	0.220207	3.40	1.5694
Plus	HD	RAC875_c30566_230_5A	5A	450.43	0.0003	3.52	0.204663	3.83	1.5956
Plus	HD	Kukri_c33022_198_5A	5A	453.34	0.00012	3.92	0.15544	4.35	-1.9105
Plus	HD	Tdurum_contig81424_367_5A	5A	453.34	0.000224	3.65	0.233161	3.99	-1.5939
Plus	HD	Kukri_c6669_145_5A	5A	457.14	0.00046	3.34	0.158031	3.59	-1.7220
Plus	HD	Excalibur_c31769_793_5A	5A	463.45	0.000202	3.69	0.183938	4.05	1.9250
Plus	HD	Excalibur_c24051_502_5A	5A	463.65	0.000633	3.20	0.176166	3.41	1.6366
Plus	HD	Kukri_c865_59_5A	5A	463.65	0.000261	3.58	0.170984	3.91	1.3910
Plus	HD	wsnp_Ex_c44164_50292954_5A	5A	463.65	0.000847	3.07	0.181347	3.24	-1.3647
Plus	HD	wsnp_RFL_Contig2265_1693968_5A	5A	463.65	0.0003	3.52	0.165803	3.83	-1.6486
Plus	HD	Excalibur_c41710_417_5A	5A	464.98	0.000632	3.20	0.181347	3.41	-1.5686
Plus	HD	GENE-2794_70_5A	5A	464.98	0.000416	3.38	0.176166	3.64	-1.6278
Plus	HD	wsnp_Ex_c2185_4094843_5A	5A	464.98	0.000876	3.06	0.160622	3.23	-1.5309
Plus	HD	BobWhite_c658_377_5A	5A	466.78	0.000612	3.21	0.189119	3.43	-1.4082
Plus	HD	BS00041063_51_5A	5A	466.78	0.000431	3.37	0.170984	3.62	1.7299

Plus	HD	Tdurum_contig10843_745_5A	5A	466.78	0.000598	3.22	0.181347	3.44	1.6841
Plus	HD	Tdurum_contig50175_875_5A	5A	466.78	0.000653	3.19	0.183938	3.39	-1.4089
Plus	HD	wsnp_Ex_c55777_58153636_5A	5A	466.78	0.000943	3.03	0.173575	3.18	-1.5495
Plus	HD	wsnp_Ex_rep_c109532_92292121_5A	5A	466.78	0.000278	3.56	0.183938	3.87	1.8895
Plus	HD	wsnp_Ex_c8543_14357385_5A	5A	466.81	0.000898	3.05	0.145078	3.21	-1.7801
Plus	HD	Tdurum_contig47120_587_5A	5A	469.39	5.50E-05	4.26	0.19171	4.81	-1.8786
Plus	HD	Tdurum_contig69612_781_5A	5A	469.39	2.39E-05	4.62	0.199482	5.30	-2.0552
Plus	HD	BobWhite_c17445_83_5A	5A	484.57	3.87E-05	4.41	0.132124	5.01	-2.6266
Plus	HD	Tdurum_contig10086_387_5A	5A	484.57	0.00033	3.48	0.173575	3.77	-1.9205
Plus	HD	Tdurum_contig85105_286_5A	5A	484.57	0.000479	3.32	0.139896	3.56	-2.0304
Plus	HD	wsnp_BF484028B_Td_2_1_5A	5A	484.57	8.95E-05	4.05	0.15544	4.52	2.1993
Plus	HD	Tdurum_contig54725_586_5A	5A	488	0.000158	3.80	0.15285	4.20	2.1231
Plus	HD	BS00022754_51_5A	5A	492.85	0.000328	3.48	0.199482	3.78	-1.7608
Plus	HD	BS00063973_51_5A	5A	492.85	0.000726	3.14	0.204663	3.33	-1.6860
Plus	HD	Jagger_c6618_144_5A	5A	492.85	2.56E-05	4.59	0.181347	5.25	-2.2432
Plus	HD	wsnp_CAP11_c1506_840938_5A	5A	492.85	0.00088	3.06	0.199482	3.22	-1.7031
Plus	HD	BS00022098_51_5A	5A	493.65	6.33E-05	4.20	0.238342	4.72	1.7905
Plus	HD	BS00041911_51_5A	5A	494.25	0.000111	3.96	0.168394	4.40	2.1241
Plus	HD	BS00067150_51_5A	5A	494.25	0.000363	3.44	0.168394	3.72	1.9149
Plus	HD	RAC875_c7132_134_5A	5A	494.25	0.000669	3.17	0.15544	3.38	-1.8903
Plus	HD	BobWhite_c14689_172_5A	5A	495.18	0.000839	3.08	0.186528	3.25	1.6081
Plus	HD	wsnp_BG607308A_Ta_2_1_5A	5A	498.48	0.000277	3.56	0.194301	3.87	1.6964
Plus	HD	wsnp_BG607308A_Ta_2_2_5A	5A	498.48	0.000154	3.81	0.15544	4.21	-2.1653
Plus	HD	BS00069739_51_5A	5A	500.09	0.000723	3.14	0.137306	3.33	-1.8677
Plus	HD	D_GB5Y7FA02IZ73U_152_5D	5D	338.67	6.22E-11	10.21	0.160622	13.58	-3.9686
Plus	HD	D_contig14133_180_5D	5D	344.94	1.66E-10	9.78	0.158031	12.91	3.8860
Plus	HD	D_contig62661_72_5D	5D	349.65	1.66E-08	7.78	0.176166	9.82	-3.1911
Plus	HD	RFL_Contig1091_1538_5D	5D	354.06	5.22E-10	9.28	0.189119	12.12	3.5139
Plus	HD	BobWhite_c20106_377_5D	5D	357.85	1.66E-09	8.78	0.142487	11.34	3.2569
Plus	HD	BobWhite_c27870_103_5D	5D	357.85	1.57E-09	8.80	0.139896	11.38	3.3212

Plus	HD	D_GBB4FNX02GXFL1_268_5D	5D	357.85	5.77E-10	9.24	0.160622	12.05	3.7766
Plus	HD	D_GDS7LZN01DW87V_234_5D	5D	357.85	1.59E-07	6.80	0.183938	8.37	2.7270
Plus	HD	tplb0055c05_1689_5D	5D	357.85	1.36E-10	9.87	0.160622	13.04	4.0344
Plus	HD	wsnp_RFL_Contig2346_1854360_5D	5D	357.85	6.68E-07	6.18	0.189119	7.47	2.6133
Plus	HD	D_F5XZDLF02IP5IR_228_5D	5D	365.23	1.06E-05	4.97	0.186528	5.78	2.0240
Plus	HD	Ku_c19010_273_5D	5D	365.23	1.04E-08	7.98	0.119171	10.13	-3.1928
Plus	HD	Excalibur_c76347_77_5D	5D	371.54	1.24E-09	8.91	0.160622	11.54	3.9259
Plus	HD	Tdurum_contig11553_534_5D	5D	371.54	2.76E-09	8.56	0.163212	11.00	3.6964
Plus	HD	BS00000929_51_5D	5D	377.86	0.000288	3.54	0.147668	3.85	2.0510
Plus	HD	IACX3123_5D	5D	377.86	8.46E-06	5.07	0.178756	5.92	2.1327
Plus	HD	Jagger_c754_272_5D	5D	377.86	8.38E-08	7.08	0.132124	8.78	3.5756
Plus	HD	Ku_c6176_938_5D	5D	377.86	1.87E-07	6.73	0.142487	8.27	-3.2067
Plus	HD	Kukri_c41787_141_5D	5D	387.6	0.000249	3.60	0.111399	3.93	-2.2018
Plus	HD	Kukri_rep_c110911_477_5D	5D	391.59	0.000498	3.30	0.440415	3.54	1.2577
Plus	HD	Ex_c2978_640_6B	6B	79.63	0.000604	3.22	0.313472	3.43	-1.4103
Plus	HD	GENE-4897_105_7A	7A	382.54	0.00093	3.03	0.34715	3.19	1.5113
Plus	HD	Ra_c16930_416_7A	7A	385.01	0.000732	3.14	0.365285	3.33	-1.3928
Plus	HD	wsnp_Ex_c8692_14557179_7A	7A	394	0.000498	3.30	0.339378	3.54	1.4367
Plus	HD	RAC875_c24411_889_7A	7A	466.45	0.000931	3.03	0.303109	3.19	-1.3918
Plus	HD	wsnp_CAP8_c334_304253_7B	7B	94.4	0.000274	3.56	0.492228	3.88	-1.4890
Nil	NDVI	Kukri_c36026_68_2B	2B	298.27	0.000968	3.01	0.145078	5.79	0.0514
Nil	NDVI	RAC875_c57584_240_3A	2D	47.94	0.000899	3.05	0.222798	5.86	0.0410
Nil	NDVI	BS00065453_51_7A	7A	624.47	0.000336	3.47	0.292746	6.87	0.0622
Plus	NDVI	BobWhite_rep_c49768_768_2A	2A	408.38	0.000833	3.08	0.170984	5.44	-0.0922
Plus	NDVI	RAC875_c52566_447_2B	2B	291.73	0.000869	3.06	0.259067	5.40	-0.0869
Plus	NDVI	Tdurum_contig74936_456_2B	2B	255.74	0.000917	3.04	0.466321	5.35	-0.0669
Plus	NDVI	D_GCE8AKX02I8TJ5_334_2Dx	2B	190.58	0.000433	3.36	0.34456	6.06	0.0773
Plus	NDVI	Excalibur_c34581_339_3B	3B	280.43	0.00082	3.09	0.34456	5.46	0.0492
Plus	NDVI	Excalibur_c35491_788_3B	3B	250.63	0.000905	3.04	0.111399	5.37	-0.0913
Plus	NDVI	wsnp_Ex_c4125_7456528_4B	4B	335.17	0.000774	3.11	0.067358	5.51	-0.1214

Plus	NDVI	GENE-4579_108_5B	5B	212.38	0.000116	3.93	0.126943	7.31	-0.0737
Plus	NDVI	CAP11_c5629_55_5B	5B	212.38	0.000824	3.08	0.189119	5.45	0.0975
Plus	NDVI	Kukri_c15912_2019_7D	7D	386.67	0.000588	3.23	0.489637	5.77	0.0411
Nil	PH	BS00023419_51_1A	1A	477.23	0.000812	3.09	0.282383	3.05	-3.2159
Nil	PH	Excalibur_c12819_216_1A	1A	477.23	0.000928	3.03	0.284974	2.98	-3.2458
Nil	PH	wsnp_Ex_rep_c107564_91144523_4D	4D	122.12	1.05E-05	4.98	0.160622	5.39	5.3100
Nil	PH	TA005330-0793_6A	6A	332.16	0.000727	3.14	0.290155	3.10	-2.8362
Nil	PH	Excalibur_c15109_942_6A	6A	338.95	0.000929	3.03	0.30829	2.98	2.7550
Nil	PH	Excalibur_c31035_805_6A	6A	338.95	0.00078	3.11	0.264249	3.07	-2.6842
Nil	PH	Tdurum_contig17378_299_6A	6A	384.11	0.000844	3.07	0.272021	3.03	2.7528
Nil	PH	Excalibur_c35871_596_6A	6A	385.69	0.000302	3.52	0.243523	3.57	-3.0274
Nil	PH	Excalibur_c58410_729_6B	6B	327.16	0.000919	3.04	0.23057	2.98	-2.6453
Nil	PH	Tdurum_contig8741_194_6D	6D	352.32	0.000722	3.14	0.365285	3.11	-2.4675
Plus	PH	Tdurum_contig42229_113_4B	4B	162.07	0.000653	3.19	0.357513	3.20	2.7484
Plus	PH	RAC875_rep_c105922_169_4D	4D	119.73	0.000603	3.22	0.378238	3.24	-2.2801
Plus	PH	wsnp_Ex_rep_c107564_91144523_4D	4D	122.12	2.99E-05	4.52	0.160622	4.88	4.9238
Plus	PH	Excalibur_c35871_596_6A	6A	385.69	0.000729	3.14	0.243523	3.14	-2.8133
Plus	PH	wsnp_Ex_rep_c68169_66940235_6B	6B	221.38	0.000783	3.11	0.19171	3.11	-3.0614
Nil	PM	BS00066092_51_1B	1B	129.09	0.000131	3.88	0.305699	4.42	0.9884
Nil	PM	GENE-0014_822_1D	1D	5.47	0.000225	3.65	0.398964	4.11	-1.0254
Nil	PM	Kukri_c26168_713_1D	1D	5.47	0.000145	3.84	0.409326	4.36	1.1164
Nil	PM	BobWhite_c359_1026_1D	1D	12.72	0.000164	3.78	0.450777	4.29	-1.0707
Nil	PM	Jagger_c3179_499_1D	1D	35.05	0.000975	3.01	0.378238	3.26	0.7556
Nil	PM	wsnp_JD_rep_c48890_33141899_1D	1D	35.05	0.000451	3.35	0.321244	3.70	0.8110
Nil	PM	RFL_Contig5625_2578_2A	2A	86.88	0.000283	3.55	0.129534	3.97	-1.3595
Nil	PM	Tdurum_contig15156_730_2A	2A	86.88	0.000543	3.27	0.165803	3.59	1.2017
Nil	PM	D_F1BEJMU02IKD3X_298_2B	2B	75.39	0.000251	3.60	0.414508	4.04	0.9695
Nil	PM	wsnp_JD_c29939_23694256_2B	2B	212.28	4.44E-06	5.35	0.15285	6.48	-1.6606
Nil	PM	Excalibur_c27557_381_2B	2B	255.74	0.000764	3.12	0.417098	3.39	1.0200
Nil	PM	Excalibur_c53027_323_2B	2B	255.74	0.000845	3.07	0.437824	3.34	-1.0596

Nil	PM	Kukri_c43403_594_2B	2B	255.74	0.000914	3.04	0.411917	3.29	-1.0945
Nil	PM	Tdurum_contig12293_1003_2B	2B	255.74	0.000719	3.14	0.437824	3.43	0.8699
Nil	PM	Tdurum_contig18901_188_2B	2B	255.74	0.000221	3.65	0.378238	4.11	1.0748
Nil	PM	Tdurum_contig19415_271_2B	2B	255.74	0.000902	3.04	0.406736	3.30	-1.0231
Nil	PM	Tdurum_contig74936_387_2B	2B	255.74	0.000377	3.42	0.365285	3.80	1.0384
Nil	PM	wsnp_Ku_c34759_44069854_2B	2B	259.03	0.000279	3.55	0.46114	3.98	1.0932
Nil	PM	BobWhite_c40418_289_2B	2B	262.16	0.000898	3.05	0.297927	3.30	0.8892
Nil	PM	Excalibur_c43482_196_2B	2B	262.16	0.000744	3.13	0.23057	3.41	1.0546
Nil	PM	BobWhite_c30112_275_2B	2B	262.81	0.000325	3.49	0.30829	3.89	-1.0091
Nil	PM	BS00067337_51_2B	2B	262.81	0.000363	3.44	0.349741	3.82	-1.1952
Nil	PM	RAC875_c37837_889_2B	2B	262.81	0.000608	3.22	0.316062	3.53	0.9904
Nil	PM	IACX6223_2B	2B	263.36	0.000452	3.34	0.349741	3.70	-1.1481
Nil	PM	RAC875_c86069_65_2B	2B	263.36	0.000411	3.39	0.321244	3.75	1.0735
Nil	PM	BS00030497_51_2B	2B	263.9	0.000484	3.32	0.391192	3.66	1.1371
Nil	PM	JD_c11869_1300_2B	2B	263.9	0.000499	3.30	0.233161	3.64	1.2417
Nil	PM	BobWhite_c30622_180_2B	2B	264.35	0.000502	3.30	0.321244	3.64	1.0441
Nil	PM	Excalibur_rep_c68899_191_2B	2B	264.35	0.000251	3.60	0.388601	4.04	-1.1993
Nil	PM	IAAV1101_2B	2B	264.35	0.00071	3.15	0.393782	3.44	-1.1059
Nil	PM	JD_c11869_1297_2B	2B	264.35	0.000303	3.52	0.396373	3.93	1.1716
Nil	PM	Tdurum_contig47202_1699_2B	2B	264.35	0.000193	3.71	0.393782	4.19	-1.2093
Nil	PM	Kukri_rep_c76670_262_2B	2B	264.46	0.000824	3.08	0.360104	3.35	-0.8828
Nil	PM	RFL_Contig996_350_2B	2B	264.46	0.000344	3.46	0.419689	3.86	1.0585
Nil	PM	RFL_Contig996_818_2B	2B	264.46	0.000135	3.87	0.435233	4.41	1.0608
Nil	PM	Tdurum_contig62458_179_2B	2B	264.46	0.000371	3.43	0.398964	3.81	-1.1553
Nil	PM	Tdurum_contig60978_352_2B	2B	267.43	0.000859	3.07	0.409326	3.33	1.0610
Nil	PM	BS00029713_51_2B	2B	268.72	0.000228	3.64	0.240933	4.10	-1.2135
Nil	PM	BS00038217_51_2B	2B	268.72	0.000237	3.63	0.243523	4.07	-1.3430
Nil	PM	BS00079213_51_2B	2B	268.72	0.000146	3.84	0.259067	4.36	-1.3188
Nil	PM	Excalibur_c25430_183_2B	2B	268.72	0.000258	3.59	0.243523	4.02	-1.3185
Nil	PM	Excalibur_c6111_411_2B	2B	268.72	0.000418	3.38	0.220207	3.74	1.0775

Nil	PM	Excalibur_c64276_565_2B	2B	268.72	0.000369	3.43	0.23057	3.81	-1.0219
Nil	PM	Kukri_c15043_326_2B	2B	268.72	8.81E-05	4.05	0.279793	4.66	-1.2648
Nil	PM	RAC875_c26415_350_2B	2B	268.72	0.000141	3.85	0.297927	4.38	1.2112
Nil	PM	RAC875_c3302_1411_2B	2B	268.72	0.000166	3.78	0.253886	4.28	-1.2897
Nil	PM	Tdurum_contig36804_220_2B	2B	268.72	0.000163	3.79	0.233161	4.29	-1.1493
Nil	PM	Tdurum_contig62852_538_2B	2B	268.72	0.000139	3.86	0.240933	4.39	-1.2455
Nil	PM	Tdurum_contig62852_592_2B	2B	268.72	0.00041	3.39	0.251295	3.75	-1.2676
Nil	PM	Tdurum_contig68806_537_2B	2B	268.72	0.000311	3.51	0.256477	3.91	-1.2889
Nil	PM	tplb0045o20_1168_2B	2B	268.72	0.000421	3.38	0.233161	3.74	1.1087
Nil	PM	wsnp_Ex_c741_1456698_2B	2B	268.72	0.000294	3.53	0.233161	3.95	1.1353
Nil	PM	Tdurum_contig30989_79_2B	2B	269.95	0.000101	4.00	0.393782	4.58	1.1798
Nil	PM	Kukri_c5904_80_2B	2B	271.59	0.000401	3.40	0.248705	3.77	1.2371
Nil	PM	Tdurum_contig62852_302_2B	2B	271.59	0.000565	3.25	0.243523	3.57	1.2274
Nil	PM	Tdurum_contig81323_291_2B	2B	271.59	7.52E-05	4.12	0.256477	4.75	-1.4051
Nil	PM	wsnp_Ex_c5239_9272511_2B	2B	271.59	0.000415	3.38	0.261658	3.75	-1.1206
Nil	PM	wsnp_Ex_rep_c67391_65971023_2B	2B	273.39	0.000257	3.59	0.373057	4.03	-1.1442
Nil	PM	BS00110319_51_2B	2B	279.59	0.000993	3.00	0.238342	3.24	1.1247
Nil	PM	tplb0045o20_699_2B	2B	279.59	0.000313	3.51	0.225389	3.91	-1.1317
Nil	PM	Excalibur_c1305_662_2B	2B	283.61	0.000499	3.30	0.352332	3.64	1.1315
Nil	PM	Kukri_c106282_114_2B	2B	292.15	0.000988	3.01	0.352332	3.25	-1.0452
Nil	PM	Excalibur_c94336_103_2Dx	2D	18.13	0.000698	3.16	0.11658	3.45	1.3128
Nil	PM	Excalibur_c94336_68_2Dx	2D	18.13	0.000981	3.01	0.129534	3.25	-1.3242
Nil	PM	Kukri_c23961_636_2Dx	2D	18.13	0.00047	3.33	0.139896	3.67	1.3416
Nil	PM	Excalibur_rep_c106461_262_3B	3B	143.05	0.000304	3.52	0.170984	3.93	-1.4687
Nil	PM	IAAV8683_4A	4A	392.59	0.000752	3.12	0.484456	3.40	1.0564
Nil	PM	Ku_c1125_814_4A	4A	392.59	0.000952	3.02	0.484456	3.27	1.0213
Nil	PM	Ex_c27046_3425_5A	5A	440.73	0.00062	3.21	0.204663	3.51	-1.0513
Nil	PM	Excalibur_c11656_1760_5A	5A	440.73	0.000221	3.66	0.207254	4.12	-1.1992
Nil	PM	IAAV2473_5A	5A	440.73	0.000498	3.30	0.251295	3.64	-1.0402
Nil	PM	wsnp_Ex_c17523_26244256_5A	5A	440.73	0.000381	3.42	0.253886	3.80	-1.0513

Nil	PM	wsnp_Ex_c27046_36265198_5A	5A	440.73	0.000678	3.17	0.227979	3.46	-1.0449
Nil	PM	wsnp_Ku_c40349_48594583_5A	5A	440.73	0.000379	3.42	0.212435	3.80	-1.1517
Nil	PM	BS00065481_51_5A	5A	445.69	0.000206	3.69	0.227979	4.16	-1.1525
Nil	PM	Excalibur_c37943_221_5A	5A	445.69	0.000657	3.18	0.207254	3.48	-1.1074
Nil	PM	wsnp_Ex_c11120_18022932_5A	5A	445.69	0.000867	3.06	0.256477	3.32	0.9864
Nil	PM	wsnp_Ex_c37943_45584325_5A	5A	445.69	0.000507	3.30	0.212435	3.63	-1.1234
Nil	PM	wsnp_Ku_c20011_29589514_5A	5A	445.69	0.000375	3.43	0.212435	3.81	-1.1752
Nil	PM	wsnp_Ku_c3684_6789632_5A	5A	446.53	3.28E-05	4.48	0.199482	5.25	1.4110
Nil	PM	Excalibur_c7729_144_5A	5A	448.42	9.69E-05	4.01	0.202073	4.60	-1.3086
Nil	PM	Excalibur_rep_c103747_193_5A	5A	448.42	0.000553	3.26	0.15544	3.58	-1.2037
Nil	PM	IAAV1650_5A	5A	448.42	0.000514	3.29	0.15285	3.62	-1.2018
Nil	PM	IACX9023_5A	5A	448.42	0.000928	3.03	0.186528	3.28	-0.9789
Nil	PM	wsnp_Ex_c13942_21820758_5A	5A	448.42	0.000584	3.23	0.15285	3.55	1.1655
Nil	PM	wsnp_Ex_c31799_40545376_5A	5A	448.42	7.19E-05	4.14	0.199482	4.78	1.3229
Nil	PM	wsnp_Ex_rep_c66689_65011117_5A	5A	448.42	0.000159	3.80	0.196891	4.31	1.2505
Nil	PM	BS00065936_51_5A	5A	450.43	0.000218	3.66	0.23057	4.12	-1.1380
Nil	PM	RAC875_c30566_230_5A	5A	450.43	0.000314	3.50	0.204663	3.91	1.0808
Nil	PM	Excalibur_c30482_898_5A	5A	453.34	0.000158	3.80	0.204663	4.31	1.2596
Nil	PM	Kukri_c33022_198_5A	5A	453.34	1.78E-05	4.75	0.15544	5.62	-1.5814
Nil	PM	Tdurum_contig81424_367_5A	5A	453.34	0.000283	3.55	0.233161	3.97	-1.1510
Nil	PM	Kukri_c6669_145_5A	5A	457.14	6.17E-05	4.21	0.158031	4.87	-1.4561
Nil	PM	RAC875_rep_c76193_513_5A	5A	460.6	8.60E-05	4.07	0.158031	4.67	1.5283
Nil	PM	Excalibur_c31769_793_5A	5A	463.45	8.14E-06	5.09	0.183938	6.11	1.6827
Nil	PM	Excalibur_c24051_502_5A	5A	463.65	2.59E-05	4.59	0.176166	5.40	1.5148
Nil	PM	Kukri_c865_59_5A	5A	463.65	0.000124	3.91	0.170984	4.46	1.1227
Nil	PM	wsnp_Ex_c44164_50292954_5A	5A	463.65	0.000236	3.63	0.181347	4.08	-1.1535
Nil	PM	wsnp_RFL_Contig2265_1693968_5A	5A	463.65	1.79E-05	4.75	0.165803	5.62	-1.4763
Nil	PM	Excalibur_c41710_417_5A	5A	464.98	0.0001	4.00	0.181347	4.58	-1.3491
Nil	PM	GENE-2794_70_5A	5A	464.98	9.31E-05	4.03	0.176166	4.63	-1.3627
Nil	PM	wsnp_Ex_c2185_4094843_5A	5A	464.98	0.000109	3.96	0.160622	4.53	-1.3492

Nil	PM	BobWhite_c15758_79_5A	5A	466.78	0.00011	3.96	0.139896	4.53	-1.4522
Nil	PM	BobWhite_c658_377_5A	5A	466.78	0.000355	3.45	0.189119	3.84	-1.1244
Nil	PM	BS00041063_51_5A	5A	466.78	2.10E-05	4.68	0.170984	5.52	1.5823
Nil	PM	JD_c15758_288_5A	5A	466.78	0.000567	3.25	0.170984	3.57	1.1542
Nil	PM	RFL_Contig316_572_5A	5A	466.78	0.000842	3.07	0.15544	3.34	-1.1550
Nil	PM	Tdurum_contig10843_745_5A	5A	466.78	6.10E-06	5.21	0.181347	6.29	1.6365
Nil	PM	Tdurum_contig50175_875_5A	5A	466.78	0.000267	3.57	0.183938	4.00	-1.1574
Nil	PM	wsnp_Ex_c55777_58153636_5A	5A	466.78	0.000235	3.63	0.173575	4.08	-1.3100
Nil	PM	wsnp_Ex_c8424_14192191_5A	5A	466.78	0.000369	3.43	0.160622	3.82	1.2643
Nil	PM	wsnp_Ex_rep_c109532_92292121_5A	5A	466.78	1.06E-05	4.98	0.183938	5.95	1.6701
Nil	PM	wsnp_Ex_c8543_14357385_5A	5A	466.81	3.53E-05	4.45	0.145078	5.21	-1.6350
Nil	PM	Tdurum_contig47120_587_5A	5A	469.39	1.25E-05	4.90	0.19171	5.84	-1.4866
Nil	PM	Tdurum_contig69612_781_5A	5A	469.39	5.69E-06	5.24	0.199482	6.33	-1.6045
Nil	PM	wsnp_Ex_c5978_10478584_5A	5A	473.13	0.000452	3.35	0.147668	3.70	-1.2328
Nil	PM	BobWhite_c17445_83_5A	5A	484.57	2.38E-05	4.62	0.132124	5.45	-1.8283
Nil	PM	Kukri_c67527_89_5A	5A	484.57	0.000675	3.17	0.178756	3.47	0.9258
Nil	PM	Tdurum_contig10086_387_5A	5A	484.57	0.000528	3.28	0.173575	3.61	-1.0897
Nil	PM	Tdurum_contig54543_888_5A	5A	484.57	0.000668	3.18	0.19171	3.47	-0.9265
Nil	PM	Tdurum_contig85105_286_5A	5A	484.57	3.10E-05	4.51	0.139896	5.29	-1.6745
Nil	PM	wsnp_BF484028B_Td_2_1_5A	5A	484.57	6.05E-05	4.22	0.15544	4.88	1.4852
Nil	PM	RAC875_c104483_394_5A	5A	488	0.0003	3.52	0.147668	3.94	-1.2917
Nil	PM	Tdurum_contig54725_586_5A	5A	488	4.65E-05	4.33	0.15285	5.04	1.5235
Nil	PM	wsnp_BG606780A_Td_2_1_5A	5A	488	0.000544	3.26	0.165803	3.59	1.2254
Nil	PM	wsnp_Ex_c790_1554988_5A	5A	490.41	0.000888	3.05	0.406736	3.31	-0.8841
Nil	PM	BS00022754_51_5A	5A	492.85	0.00022	3.66	0.199482	4.12	-1.2685
Nil	PM	BS00063973_51_5A	5A	492.85	0.000565	3.25	0.204663	3.57	-1.1680
Nil	PM	Jagger_c6618_144_5A	5A	492.85	1.10E-06	5.96	0.181347	7.36	-1.6455
Nil	PM	wsnp_CAP11_c1506_840938_5A	5A	492.85	0.000632	3.20	0.199482	3.50	-1.1910
Nil	PM	wsnp_CAP11_c1506_840951_5A	5A	492.85	0.000962	3.02	0.170984	3.26	1.0994
Nil	PM	wsnp_Ku_c42416_50159250_5A	5A	492.85	0.000571	3.24	0.196891	3.56	-1.1939

Nil	PM	wsnp_Ku_c42416_50159402_5A	5A	492.85	0.000319	3.50	0.212435	3.90	-1.1111
Nil	PM	BS00022098_51_5A	5A	493.65	1.06E-05	4.98	0.238342	5.95	1.2517
Nil	PM	BS00074855_51_5A	5A	493.65	0.000888	3.05	0.19171	3.31	1.1796
Nil	PM	BS00041911_51_5A	5A	494.25	1.99E-05	4.70	0.168394	5.56	1.5827
Nil	PM	BS00067150_51_5A	5A	494.25	1.24E-05	4.91	0.168394	5.85	1.6039
Nil	PM	RAC875_c7132_134_5A	5A	494.25	4.22E-05	4.37	0.15544	5.10	-1.5436
Nil	PM	BobWhite_c14689_172_5A	5A	495.18	0.00013	3.89	0.186528	4.43	1.3166
Nil	PM	BobWhite_rep_c64315_180_5A	5A	496.4	0.000102	3.99	0.186528	4.57	-1.3558
Nil	PM	Excalibur_c92705_94_5A	5A	496.4	0.000982	3.01	0.165803	3.25	-1.1046
Nil	PM	wsnp_BG607308A_Ta_2_1_5A	5A	498.48	2.78E-05	4.56	0.194301	5.35	1.2575
Nil	PM	wsnp_BG607308A_Ta_2_2_5A	5A	498.48	3.81E-05	4.42	0.15544	5.16	-1.5959
Nil	PM	BS00069739_51_5A	5A	500.09	3.66E-06	5.44	0.137306	6.60	-1.7033
Nil	PM	D_GB5Y7FA02IZ73U_152_5D	5D	338.67	4.85E-06	5.31	0.160622	6.43	-1.7773
Nil	PM	D_contig14133_180_5D	5D	344.94	1.53E-05	4.82	0.158031	5.72	1.6588
Nil	PM	D_contig62661_72_5D	5D	349.65	2.02E-05	4.69	0.176166	5.55	-1.5739
Nil	PM	RFL_Contig1091_1538_5D	5D	354.06	1.11E-05	4.96	0.189119	5.92	1.6029
Nil	PM	BobWhite_c20106_377_5D	5D	357.85	3.71E-05	4.43	0.142487	5.18	1.5070
Nil	PM	BobWhite_c27870_103_5D	5D	357.85	1.23E-05	4.91	0.139896	5.85	1.6123
Nil	PM	D_GBB4FNX02GXFL1_268_5D	5D	357.85	1.19E-05	4.93	0.160622	5.87	1.7161
Nil	PM	D_GDS7LZN01DW87V_234_5D	5D	357.85	0.000247	3.61	0.183938	4.05	1.3172
Nil	PM	tplb0055c05_1689_5D	5D	357.85	2.45E-05	4.61	0.160622	5.43	1.6930
Nil	PM	Ku_c19010_273_5D	5D	365.23	6.33E-05	4.20	0.119171	4.86	-1.5466
Nil	PM	Excalibur_c76347_77_5D	5D	371.54	2.94E-05	4.53	0.160622	5.32	1.7013
Nil	PM	Tdurum_contig11553_534_5D	5D	371.54	3.71E-05	4.43	0.163212	5.18	1.6231
Nil	PM	IACX3123_5D	5D	377.86	0.000456	3.34	0.178756	3.69	1.1086
Nil	PM	Jagger_c754_272_5D	5D	377.86	0.000234	3.63	0.132124	4.08	1.5527
Nil	PM	Ku_c6176_938_5D	5D	377.86	0.000106	3.98	0.142487	4.55	-1.5884
Nil	PM	BS00049887_51_7B	7B	228.36	0.000178	3.75	0.287565	4.24	-1.2834
Nil	PM	BS00068071_51_7B	7B	228.36	0.000644	3.19	0.240933	3.49	1.1339
Nil	PM	RAC875_c11731_112_7B	7B	228.36	0.000345	3.46	0.264249	3.85	-1.4616

Nil	PM	TA003961-0636_7B	7B	228.36	0.000611	3.21	0.272021	3.52	-1.3566
Plus	PM	BS00066092_51_1B	1B	129.09	9.86E-05	4.01	0.305699	4.70	1.0113
Plus	PM	GENE-0014_822_1D	1D	5.47	0.000173	3.76	0.398964	4.36	-1.0251
Plus	PM	Kukri_c26168_713_1D	1D	5.47	3.74E-05	4.43	0.409326	5.30	1.1855
Plus	PM	BobWhite_c359_1026_1D	1D	12.72	6.85E-05	4.16	0.450777	4.93	-1.1070
Plus	PM	wsnp_JD_rep_c48890_33141899_1D	1D	35.05	0.000787	3.10	0.321244	3.46	0.7736
Plus	PM	Tdurum_contig15156_730_2A	2A	86.88	0.00046	3.34	0.165803	3.78	1.2042
Plus	PM	D_F1BEJMU02IKD3X_298_2B	2B	75.39	0.00016	3.80	0.414508	4.41	1.0005
Plus	PM	wsnp_JD_c29939_23694256_2B	2B	212.28	7.26E-06	5.14	0.15285	6.33	-1.5976
Plus	PM	CAP12_rep_c5926_115_2B	2B	255.74	0.000476	3.32	0.409326	3.76	-1.1032
Plus	PM	CAP12_rep_c5926_51_2B	2B	255.74	0.000373	3.43	0.401554	3.90	-1.1010
Plus	PM	D_contig36671_269_2B	2B	255.74	0.000565	3.25	0.448187	3.65	-1.0794
Plus	PM	Excalibur_c27557_381_2B	2B	255.74	0.000324	3.49	0.417098	3.98	1.0805
Plus	PM	Excalibur_c53027_302_2B	2B	255.74	0.00061	3.21	0.440415	3.61	1.0967
Plus	PM	Excalibur_c53027_323_2B	2B	255.74	0.000241	3.62	0.437824	4.16	-1.1544
Plus	PM	Excalibur_rep_c101660_546_2B	2B	255.74	0.000542	3.27	0.414508	3.68	1.1308
Plus	PM	Jagger_c8098_88_2B	2B	255.74	0.000702	3.15	0.443005	3.53	1.1074
Plus	PM	Kukri_c12616_844_2B	2B	255.74	0.000437	3.36	0.409326	3.81	-1.0520
Plus	PM	Kukri_c17483_568_2B	2B	255.74	0.000845	3.07	0.443005	3.42	-0.9864
Plus	PM	Kukri_c27574_725_2B	2B	255.74	0.000688	3.16	0.432642	3.54	1.0942
Plus	PM	Kukri_c29272_363_2B	2B	255.74	0.000692	3.16	0.448187	3.53	1.0848
Plus	PM	Kukri_c43403_412_2B	2B	255.74	0.000525	3.28	0.409326	3.70	-1.0296
Plus	PM	Kukri_c43403_594_2B	2B	255.74	0.000259	3.59	0.411917	4.12	-1.1947
Plus	PM	RAC875_c8780_441_2B	2B	255.74	0.00062	3.21	0.450777	3.60	1.1004
Plus	PM	TA005827-0874_2B	2B	255.74	0.000321	3.49	0.414508	3.99	1.1725
Plus	PM	Tdurum_contig12293_1003_2B	2B	255.74	0.000251	3.60	0.437824	4.14	0.9420
Plus	PM	Tdurum_contig18901_188_2B	2B	255.74	8.58E-05	4.07	0.378238	4.79	1.1451
Plus	PM	Tdurum_contig19415_271_2B	2B	255.74	0.000311	3.51	0.406736	4.01	-1.1052
Plus	PM	Tdurum_contig29620_125_2B	2B	255.74	0.000455	3.34	0.411917	3.78	1.1468
Plus	PM	Tdurum_contig74936_264_2B	2B	255.74	0.000763	3.12	0.440415	3.48	-1.1021

Plus	PM	Tdurum_contig74936_387_2B	2B	255.74	0.000134	3.87	0.365285	4.52	1.1234
Plus	PM	Tdurum_contig7526_301_2B	2B	255.74	0.000381	3.42	0.417098	3.89	-1.1579
Plus	PM	wsnp_Ex_c66052_64232430_2B	2B	255.74	0.000388	3.41	0.396373	3.88	-1.0758
Plus	PM	wsnp_Ku_c23305_33210628_2B	2B	255.74	0.000514	3.29	0.450777	3.71	-1.1153
Plus	PM	wsnp_Ku_c23305_33210841_2B	2B	255.74	0.00057	3.24	0.432642	3.65	1.0492
Plus	PM	Kukri_rep_c69288_529_2B	2B	257.74	0.000792	3.10	0.401554	3.46	1.0759
Plus	PM	wsnp_Ku_c31_62657_2B	2B	259.03	0.000735	3.13	0.427461	3.50	1.1005
Plus	PM	wsnp_Ku_c34759_44069854_2B	2B	259.03	0.000103	3.99	0.46114	4.68	1.1552
Plus	PM	BobWhite_c40418_289_2B	2B	262.16	0.000564	3.25	0.297927	3.66	0.9351
Plus	PM	Excalibur_c43482_196_2B	2B	262.16	0.000385	3.41	0.23057	3.88	1.1043
Plus	PM	BobWhite_c30112_275_2B	2B	262.81	0.000209	3.68	0.30829	4.25	-1.0464
Plus	PM	BS00067337_51_2B	2B	262.81	0.000129	3.89	0.349741	4.54	-1.2766
Plus	PM	RAC875_c37837_889_2B	2B	262.81	0.000273	3.56	0.316062	4.09	1.0531
Plus	PM	IACX6223_2B	2B	263.36	0.000199	3.70	0.349741	4.28	-1.2095
Plus	PM	RAC875_c86069_65_2B	2B	263.36	0.000216	3.67	0.321244	4.23	1.1222
Plus	PM	BS00030497_51_2B	2B	263.9	0.00021	3.68	0.391192	4.25	1.1960
Plus	PM	JD_c11869_1300_2B	2B	263.9	0.000435	3.36	0.233161	3.81	1.2639
Plus	PM	BobWhite_c30622_180_2B	2B	264.35	0.00028	3.55	0.321244	4.07	1.0916
Plus	PM	Excalibur_rep_c68899_191_2B	2B	264.35	0.000109	3.96	0.388601	4.64	-1.2550
Plus	PM	IAAV1101_2B	2B	264.35	0.000286	3.54	0.393782	4.06	-1.1699
Plus	PM	JD_c11869_1297_2B	2B	264.35	0.000125	3.90	0.396373	4.56	1.2321
Plus	PM	Tdurum_contig47202_1699_2B	2B	264.35	8.02E-05	4.10	0.393782	4.83	-1.2667
Plus	PM	Kukri_rep_c76670_262_2B	2B	264.46	0.000523	3.28	0.360104	3.70	-0.9151
Plus	PM	RFL_Contig996_350_2B	2B	264.46	0.000148	3.83	0.419689	4.46	1.1111
Plus	PM	RFL_Contig996_818_2B	2B	264.46	6.53E-05	4.19	0.435233	4.95	1.1085
Plus	PM	Tdurum_contig62458_179_2B	2B	264.46	0.000159	3.80	0.398964	4.41	-1.2136
Plus	PM	Tdurum_contig60978_352_2B	2B	267.43	0.000339	3.47	0.409326	3.96	1.1347
Plus	PM	BS00029713_51_2B	2B	268.72	0.000109	3.96	0.240933	4.64	-1.2751
Plus	PM	BS00038217_51_2B	2B	268.72	6.15E-05	4.21	0.243523	4.99	-1.4500
Plus	PM	BS00079213_51_2B	2B	268.72	3.78E-05	4.42	0.259067	5.29	-1.4244

Plus	PM	BS00103461_51_2B	2B	268.72	0.000652	3.19	0.238342	3.57	1.1881
Plus	PM	Excalibur_c25430_183_2B	2B	268.72	7.30E-05	4.14	0.243523	4.89	-1.4164
Plus	PM	Excalibur_c6111_411_2B	2B	268.72	0.000291	3.54	0.220207	4.05	1.1085
Plus	PM	Excalibur_c64276_565_2B	2B	268.72	0.00022	3.66	0.23057	4.22	-1.0640
Plus	PM	Kukri_c15043_326_2B	2B	268.72	1.88E-05	4.73	0.279793	5.73	-1.3750
Plus	PM	RAC875_c26415_350_2B	2B	268.72	0.000102	3.99	0.297927	4.68	1.2272
Plus	PM	RAC875_c3302_1411_2B	2B	268.72	5.10E-05	4.29	0.253886	5.11	-1.3795
Plus	PM	RAC875_c76533_442_2B	2B	268.72	0.000974	3.01	0.246114	3.33	1.0847
Plus	PM	Tdurum_contig36804_220_2B	2B	268.72	0.000102	3.99	0.233161	4.68	-1.1865
Plus	PM	Tdurum_contig62852_538_2B	2B	268.72	6.12E-05	4.21	0.240933	4.99	-1.3103
Plus	PM	Tdurum_contig62852_592_2B	2B	268.72	0.000122	3.91	0.251295	4.57	-1.3639
Plus	PM	Tdurum_contig68806_537_2B	2B	268.72	9.09E-05	4.04	0.256477	4.75	-1.3841
Plus	PM	tplb0045o20_1168_2B	2B	268.72	0.000211	3.68	0.233161	4.24	1.1673
Plus	PM	wsnp_Ex_c741_1456698_2B	2B	268.72	0.000147	3.83	0.233161	4.46	1.1931
Plus	PM	Jagger_c36_213_2B	2B	269.95	0.000823	3.08	0.393782	3.43	1.0545
Plus	PM	Tdurum_contig30989_79_2B	2B	269.95	4.77E-05	4.32	0.393782	5.15	1.2308
Plus	PM	Kukri_c5904_80_2B	2B	271.59	0.000125	3.90	0.248705	4.56	1.3291
Plus	PM	Tdurum_contig62852_302_2B	2B	271.59	0.0002	3.70	0.243523	4.27	1.3089
Plus	PM	Tdurum_contig81323_291_2B	2B	271.59	2.33E-05	4.63	0.256477	5.59	-1.4917
Plus	PM	wsnp_Ex_c5239_9272511_2B	2B	271.59	0.00016	3.80	0.261658	4.41	-1.2022
Plus	PM	wsnp_Ex_rep_c67391_65971023_2B	2B	273.39	0.000139	3.86	0.373057	4.49	-1.1917
Plus	PM	BS00110319_51_2B	2B	279.59	0.00037	3.43	0.238342	3.91	1.2139
Plus	PM	BS00110442_51_2B	2B	279.59	0.000297	3.53	0.243523	4.04	1.2328
Plus	PM	tplb0045o20_699_2B	2B	279.59	0.000188	3.73	0.225389	4.31	-1.1753
Plus	PM	Excalibur_c1305_662_2B	2B	283.61	0.000298	3.53	0.352332	4.04	1.1730
Plus	PM	Ex_c12004_1006_2B	2B	292.15	0.000933	3.03	0.375648	3.36	-0.9530
Plus	PM	Kukri_c106282_114_2B	2B	292.15	0.000652	3.19	0.352332	3.57	-1.0809
Plus	PM	Excalibur_rep_c106461_262_3B	3B	143.05	0.00033	3.48	0.170984	3.97	-1.4815
Plus	PM	IAAV8683_4A	4A	392.59	0.000693	3.16	0.484456	3.53	1.0320
Plus	PM	Ku_c1125_814_4A	4A	392.59	0.000904	3.04	0.484456	3.38	0.9955

Plus	PM	BS00110365_51_4B	4B	182.55	0.000514	3.29	0.246114	3.71	-1.0027
Plus	PM	Kukri_c64744_1087_4D	4D	30.61	0.000785	3.11	0.432642	3.46	0.7232
Plus	PM	Tdurum_contig10759_260_5A	5A	421.21	0.000927	3.03	0.178756	3.36	1.1546
Plus	PM	Tdurum_contig67291_367_5A	5A	421.21	0.000317	3.50	0.183938	4.00	1.2554
Plus	PM	Ex_c27046_1362_5A	5A	440.73	0.000543	3.27	0.23057	3.68	-1.0425
Plus	PM	Ex_c27046_3425_5A	5A	440.73	0.000274	3.56	0.204663	4.08	-1.1165
Plus	PM	Ex_c898_1319_5A	5A	440.73	0.000812	3.09	0.235751	3.44	-1.0273
Plus	PM	Excalibur_c11656_1760_5A	5A	440.73	0.000122	3.91	0.207254	4.57	-1.2452
Plus	PM	IAAV2473_5A	5A	440.73	0.000181	3.74	0.251295	4.33	-1.1132
Plus	PM	RAC875_c3046_1764_5A	5A	440.73	0.000864	3.06	0.240933	3.40	-0.9989
Plus	PM	wsnp_Ex_c17523_26244256_5A	5A	440.73	0.000133	3.88	0.253886	4.52	-1.1249
Plus	PM	wsnp_Ex_c27046_36265198_5A	5A	440.73	0.000428	3.37	0.227979	3.82	-1.0807
Plus	PM	wsnp_Ex_c898_1738424_5A	5A	440.73	0.000853	3.07	0.23057	3.41	-1.0283
Plus	PM	wsnp_Ku_c40349_48594583_5A	5A	440.73	0.000222	3.65	0.212435	4.21	-1.1943
Plus	PM	BS00044408_51_5A	5A	445.69	0.000678	3.17	0.204663	3.55	1.1126
Plus	PM	BS00065481_51_5A	5A	445.69	0.000165	3.78	0.227979	4.39	-1.1739
Plus	PM	Excalibur_c37943_221_5A	5A	445.69	0.000372	3.43	0.207254	3.90	-1.1552
Plus	PM	wsnp_Ex_c11120_18022932_5A	5A	445.69	0.000486	3.31	0.256477	3.74	1.0244
Plus	PM	wsnp_Ex_c37943_45584325_5A	5A	445.69	0.000304	3.52	0.212435	4.02	-1.1668
Plus	PM	wsnp_Ex_c62818_62296773_5A	5A	445.69	0.000675	3.17	0.220207	3.55	-1.0435
Plus	PM	wsnp_Ku_c20011_29589289_5A	5A	445.69	0.000719	3.14	0.202073	3.51	-1.0404
Plus	PM	wsnp_Ku_c20011_29589514_5A	5A	445.69	0.000244	3.61	0.212435	4.15	-1.2070
Plus	PM	wsnp_Ku_c3684_6789632_5A	5A	446.53	2.01E-05	4.70	0.199482	5.68	1.4442
Plus	PM	Excalibur_c7729_144_5A	5A	448.42	7.19E-05	4.14	0.202073	4.90	-1.3302
Plus	PM	Excalibur_rep_c103747_193_5A	5A	448.42	0.000438	3.36	0.15544	3.80	-1.2280
Plus	PM	IAAV1650_5A	5A	448.42	0.000416	3.38	0.15285	3.84	-1.2232
Plus	PM	IACX9023_5A	5A	448.42	0.000369	3.43	0.186528	3.91	-1.0527
Plus	PM	wsnp_Ex_c13942_21820758_5A	5A	448.42	0.000482	3.32	0.15285	3.75	1.1836
Plus	PM	wsnp_Ex_c31799_40545376_5A	5A	448.42	5.42E-05	4.27	0.199482	5.07	1.3424
Plus	PM	wsnp_Ex_rep_c66689_65011117_5A	5A	448.42	0.000132	3.88	0.196891	4.52	1.2663

Plus	PM	BS00065936_51_5A	5A	450.43	0.000115	3.94	0.23057	4.61	-1.1872
Plus	PM	RAC875_c13931_205_5A	5A	450.43	0.000777	3.11	0.220207	3.47	1.0220
Plus	PM	RAC875_c30566_230_5A	5A	450.43	0.000196	3.71	0.204663	4.29	1.1240
Plus	PM	Excalibur_c30482_898_5A	5A	453.34	0.000113	3.95	0.204663	4.62	1.2845
Plus	PM	Kukri_c33022_198_5A	5A	453.34	7.18E-06	5.14	0.15544	6.33	-1.6445
Plus	PM	Tdurum_contig81424_367_5A	5A	453.34	0.000143	3.84	0.233161	4.47	-1.1893
Plus	PM	wsnp_BF293620A_Ta_2_3_5A	5A	453.34	0.000533	3.27	0.209845	3.69	1.0358
Plus	PM	Kukri_c6669_145_5A	5A	457.14	1.75E-05	4.76	0.158031	5.77	-1.5451
Plus	PM	RAC875_rep_c76193_513_5A	5A	460.6	0.000133	3.87	0.158031	4.52	1.4796
Plus	PM	Excalibur_c31769_793_5A	5A	463.45	1.17E-05	4.93	0.183938	6.03	1.6264
Plus	PM	Excalibur_c24051_502_5A	5A	463.65	3.98E-05	4.40	0.176166	5.26	1.4626
Plus	PM	Kukri_c865_59_5A	5A	463.65	1.46E-05	4.84	0.170984	5.89	1.2693
Plus	PM	wsnp_Ex_c44164_50292954_5A	5A	463.65	0.000196	3.71	0.181347	4.29	-1.1647
Plus	PM	wsnp_RFL_Contig2265_1693968_5A	5A	463.65	2.60E-05	4.59	0.165803	5.52	-1.4323
Plus	PM	Excalibur_c41710_417_5A	5A	464.98	8.87E-05	4.05	0.181347	4.77	-1.3475
Plus	PM	GENE-2794_70_5A	5A	464.98	0.00011	3.96	0.176166	4.64	-1.3365
Plus	PM	wsnp_Ex_c2185_4094843_5A	5A	464.98	0.000153	3.81	0.160622	4.43	-1.3077
Plus	PM	BobWhite_c15758_79_5A	5A	466.78	0.000146	3.83	0.139896	4.46	-1.4183
Plus	PM	BobWhite_c658_377_5A	5A	466.78	0.000239	3.62	0.189119	4.17	-1.1533
Plus	PM	BS00041063_51_5A	5A	466.78	2.95E-05	4.53	0.170984	5.45	1.5386
Plus	PM	JD_c15758_288_5A	5A	466.78	0.000596	3.22	0.170984	3.62	1.1379
Plus	PM	RFL_Contig316_572_5A	5A	466.78	0.000635	3.20	0.15544	3.59	-1.1759
Plus	PM	Tdurum_contig10843_745_5A	5A	466.78	9.63E-06	5.02	0.181347	6.15	1.5786
Plus	PM	Tdurum_contig50175_875_5A	5A	466.78	0.000192	3.72	0.183938	4.30	-1.1814
Plus	PM	wsnp_Ex_c55777_58153636_5A	5A	466.78	0.000261	3.58	0.173575	4.11	-1.2900
Plus	PM	wsnp_Ex_c8424_14192191_5A	5A	466.78	0.000514	3.29	0.160622	3.71	1.2156
Plus	PM	wsnp_Ex_rep_c109532_92292121_5A	5A	466.78	1.64E-05	4.79	0.183938	5.81	1.6071
Plus	PM	wsnp_Ex_c8543_14357385_5A	5A	466.81	4.27E-05	4.37	0.145078	5.22	-1.5966
Plus	PM	Tdurum_contig47120_587_5A	5A	469.39	1.08E-05	4.97	0.19171	6.08	-1.4732
Plus	PM	Tdurum_contig69612_781_5A	5A	469.39	6.35E-06	5.20	0.199482	6.41	-1.5761

Plus	PM	wsnp_Ex_c5978_10478584_5A	5A	473.13	0.000484	3.31	0.147668	3.75	-1.2241
Plus	PM	wsnp_Ex_c23787_33024604_5A	5A	475.36	0.000875	3.06	0.145078	3.40	0.9652
Plus	PM	BobWhite_c17445_83_5A	5A	484.57	3.33E-05	4.48	0.132124	5.37	-1.7792
Plus	PM	Kukri_c36397_149_5A	5A	484.57	0.000363	3.44	0.398964	3.92	0.8323
Plus	PM	Tdurum_contig10086_387_5A	5A	484.57	0.000877	3.06	0.173575	3.40	-1.0409
Plus	PM	Tdurum_contig85105_286_5A	5A	484.57	5.86E-05	4.23	0.139896	5.02	-1.6002
Plus	PM	wsnp_BF484028B_Td_2_1_5A	5A	484.57	7.31E-05	4.14	0.15544	4.89	1.4506
Plus	PM	RAC875_c104483_394_5A	5A	488	0.00049	3.31	0.147668	3.74	-1.2335
Plus	PM	Tdurum_contig54725_586_5A	5A	488	8.99E-05	4.05	0.15285	4.76	1.4419
Plus	PM	wsnp_BG606780A_Td_2_1_5A	5A	488	0.000924	3.03	0.165803	3.36	1.1678
Plus	PM	wsnp_Ex_c790_1554988_5A	5A	490.41	0.000453	3.34	0.406736	3.78	-0.9278
Plus	PM	BS00022754_51_5A	5A	492.85	0.000416	3.38	0.199482	3.84	-1.1943
Plus	PM	BS00063973_51_5A	5A	492.85	0.000792	3.10	0.204663	3.46	-1.1162
Plus	PM	Jagger_c6618_144_5A	5A	492.85	2.00E-06	5.70	0.181347	7.15	-1.5799
Plus	PM	wsnp_CAP11_c1506_840938_5A	5A	492.85	0.000962	3.02	0.199482	3.34	-1.1304
Plus	PM	wsnp_Ku_c42416_50159250_5A	5A	492.85	0.000861	3.06	0.196891	3.41	-1.1346
Plus	PM	wsnp_Ku_c42416_50159402_5A	5A	492.85	0.000785	3.10	0.212435	3.46	-1.0224
Plus	PM	BS00022098_51_5A	5A	493.65	3.32E-05	4.48	0.238342	5.37	1.1666
Plus	PM	BS00041911_51_5A	5A	494.25	2.69E-05	4.57	0.168394	5.50	1.5291
Plus	PM	BS00067150_51_5A	5A	494.25	2.07E-05	4.68	0.168394	5.67	1.5407
Plus	PM	RAC875_c7132_134_5A	5A	494.25	7.00E-05	4.16	0.15544	4.91	-1.4718
Plus	PM	BobWhite_c14689_172_5A	5A	495.18	0.000312	3.51	0.186528	4.01	1.2250
Plus	PM	BobWhite_rep_c64315_180_5A	5A	496.4	0.000212	3.67	0.186528	4.24	-1.2724
Plus	PM	wsnp_BG607308A_Ta_2_1_5A	5A	498.48	0.000265	3.58	0.194301	4.10	1.0758
Plus	PM	wsnp_BG607308A_Ta_2_2_5A	5A	498.48	8.92E-05	4.05	0.15544	4.76	-1.4908
Plus	PM	BS00069739_51_5A	5A	500.09	1.62E-05	4.79	0.137306	5.82	-1.5737
Plus	PM	D_GB5Y7FA02IZ73U_152_5D	5D	338.67	1.34E-06	5.87	0.160622	7.41	-1.8494
Plus	PM	D_contig14133_180_5D	5D	344.94	3.79E-06	5.42	0.158031	6.74	1.7490
Plus	PM	D_contig62661_72_5D	5D	349.65	7.26E-06	5.14	0.176166	6.33	-1.6346
Plus	PM	RFL_Contig1091_1538_5D	5D	354.06	1.06E-05	4.98	0.189119	6.09	1.5778

Plus	PM	BobWhite_c20106_377_5D	5D	357.85	3.79E-05	4.42	0.142487	5.29	1.4843
Plus	PM	BobWhite_c27870_103_5D	5D	357.85	1.46E-05	4.83	0.139896	5.88	1.5791
Plus	PM	D_GBB4FNX02GXFL1_268_5D	5D	357.85	1.46E-05	4.84	0.160622	5.88	1.6648
Plus	PM	D_GDS7LZN01DW87V_234_5D	5D	357.85	7.87E-05	4.10	0.183938	4.84	1.4004
Plus	PM	tplb0055c05_1689_5D	5D	357.85	4.97E-06	5.30	0.160622	6.57	1.8050
Plus	PM	wsnp_RFL_Contig2346_1854360_5D	5D	357.85	0.000631	3.20	0.189119	3.59	1.1450
Plus	PM	Ku_c19010_273_5D	5D	365.23	3.90E-05	4.41	0.119171	5.27	-1.5766
Plus	PM	Excalibur_c76347_77_5D	5D	371.54	5.44E-05	4.26	0.160622	5.07	1.6119
Plus	PM	Tdurum_contig11553_534_5D	5D	371.54	6.70E-05	4.17	0.163212	4.94	1.5383
Plus	PM	IACX3123_5D	5D	377.86	0.000746	3.13	0.178756	3.49	1.0676
Plus	PM	Jagger_c754_272_5D	5D	377.86	0.000359	3.44	0.132124	3.92	1.4785
Plus	PM	Ku_c6176_938_5D	5D	377.86	0.000156	3.81	0.142487	4.43	-1.5307
Plus	PM	wsnp_Ex_c8692_14557179_7A	7A	394	0.000634	3.20	0.339378	3.59	1.0089
Plus	PM	TA005578-0927_7A	7A	398	0.000871	3.06	0.329016	3.40	-1.0125
Plus	PM	wsnp_CAP7_c949_486485_7A	7A	400.61	0.000808	3.09	0.365285	3.44	-1.0858
Plus	PM	BS00049887_51_7B	7B	228.36	0.000423	3.37	0.287565	3.83	-1.1979
Plus	PM	RAC875_c11731_112_7B	7B	228.36	0.000763	3.12	0.264249	3.48	-1.3411
Nil	Screenings	RFL_Contig2443_255_1B	1B	202.41	0.000938	3.03	0.476684	3.68	1.1849
Nil	Screenings	Kukri_c38065_217_3B	3B	545.17	0.000455	3.34	0.142487	4.15	2.1974
Nil	Screenings	IACX1162_6B	6B	245.8	0.000608	3.22	0.106218	3.96	2.2481
Plus	Screenings	RAC875_c744_1935_1A	1A	55.22	4.56E-05	4.34	0.367876	4.97	2.3509
Plus	Screenings	Tdurum_contig43475_978_1A	1A	66.54	0.000791	3.10	0.440415	3.32	-2.0299
Plus	Screenings	Kukri_rep_c76691_483_2A	2A	413.64	0.00085	3.07	0.38342	3.28	1.4649
Plus	Screenings	BobWhite_c30009_285_3A	3A	269.13	0.000458	3.34	0.158031	3.63	2.3604
Plus	Screenings	Excalibur_c41477_1272_3A	3A	269.13	0.000437	3.36	0.194301	3.66	2.1673
Plus	Screenings	Excalibur_rep_c68583_689_3A	3A	269.13	0.000412	3.39	0.207254	3.69	-2.2900
Plus	Screenings	BobWhite_c35303_192_3A	3A	273.07	0.000475	3.32	0.339378	3.61	-2.0366
Plus	Screenings	Ku_c1638_648_3A	3A	280.36	0.000257	3.59	0.274611	3.96	-2.1778
Plus	Screenings	IAAV8768_3A	3A	288.25	0.000932	3.03	0.334197	3.23	2.1592
Plus	Screenings	wsnp_Ex_rep_c69034_67934852_3A	3A	288.43	0.000972	3.01	0.331606	3.20	2.1662

Plus	Screenings	Kukri_c52733_358_5A	5A	78.82	0.000361	3.44	0.274611	3.77	1.8871
Plus	Screenings	BS00062996_51_5A	5A	132.71	0.000973	3.01	0.274611	3.20	1.7089
Plus	Screenings	Kukri_c12738_882_5A	5A	214.57	0.000611	3.21	0.303109	3.47	1.7127
Plus	Screenings	wsnp_Ex_c7841_13337935_5A	5A	214.57	0.000611	3.21	0.303109	3.47	1.7127
Plus	Screenings	Excalibur_c17553_84_5A	5A	216.63	0.000851	3.07	0.290155	3.28	-1.8111
Plus	Screenings	RAC875_rep_c106044_137_5A	5A	216.63	0.000487	3.31	0.303109	3.60	1.7773
Plus	Screenings	wsnp_BE426080A_Ta_2_1_5A	5A	216.63	0.000846	3.07	0.34456	3.28	1.4601
Plus	Screenings	BS00022162_51_7B	7B	482.15	0.000974	3.01	0.217617	3.20	-1.6383
Nil	TKW	RAC875_c744_1935_1A	1A	55.22	0.000168	3.77	0.367876	0.03	-1.7967
Nil	TKW	BS00021942_51_1A	1A	192.55	0.000574	3.24	0.380829	0.03	-1.4432
Nil	TKW	tplb0050c03_1003_1B	1B	209.09	0.000381	3.42	0.336787	0.03	0.9631
Nil	TKW	wsnp_CAP11_c8597_3709328_1D	1D	45.36	0.000375	3.43	0.487047	0.03	1.2094
Nil	TKW	Kukri_c17177_1575_1D	1D	46.92	0.000924	3.03	0.440415	0.03	1.0426
Nil	TKW	BobWhite_c2988_2161_2B	2B	180.45	0.000764	3.12	0.476684	0.03	1.0142
Nil	TKW	BobWhite_c30009_285_3A	3A	269.13	0.000473	3.32	0.158031	0.03	-1.7671
Nil	TKW	Excalibur_rep_c68583_689_3A	3A	269.13	0.000597	3.22	0.207254	0.03	1.6626
Nil	TKW	Tdurum_contig15529_135_3A	3A	296.36	0.00098	3.01	0.072539	0.03	-1.5087
Nil	TKW	BS00110365_51_4B	4B	182.55	8.70E-05	4.06	0.246114	0.04	1.4135
Nil	TKW	Excalibur_c34426_723_5A	5A	193.73	0.00026	3.58	0.365285	0.03	1.2991
Nil	TKW	wsnp_RFL_Contig4136_4696148_5A	5A	216.63	0.000713	3.15	0.310881	0.03	1.2411
Nil	TKW	Tdurum_contig10759_260_5A	5A	421.21	0.000274	3.56	0.178756	0.03	-1.4631
Nil	TKW	Tdurum_contig67291_367_5A	5A	421.21	0.000275	3.56	0.183938	0.03	-1.4384
Nil	TKW	BS00089795_51_5A	5A	440.73	0.000208	3.68	0.233161	0.03	1.4556
Nil	TKW	Ex_c27046_1362_5A	5A	440.73	0.000472	3.33	0.23057	0.03	1.3510
Nil	TKW	Ex_c27046_3425_5A	5A	440.73	0.000964	3.02	0.204663	0.03	1.2818
Nil	TKW	Ex_c898_1319_5A	5A	440.73	0.000857	3.07	0.235751	0.03	1.3008
Nil	TKW	Excalibur_c11656_1760_5A	5A	440.73	0.000983	3.01	0.207254	0.03	1.3792
Nil	TKW	IAAV2473_5A	5A	440.73	0.00015	3.82	0.251295	0.03	1.4095
Nil	TKW	RAC875_c3046_1764_5A	5A	440.73	0.000326	3.49	0.240933	0.03	1.3707
Nil	TKW	RFL_Contig3739_2135_5A	5A	440.73	0.000484	3.32	0.235751	0.03	1.3482

Nil	TKW	wsnp_Ex_c17523_26244256_5A	5A	440.73	0.000121	3.92	0.253886	0.04	1.4114
Nil	TKW	wsnp_Ex_c27046_36265198_5A	5A	440.73	0.000932	3.03	0.227979	0.03	1.2017
Nil	TKW	wsnp_Ex_c898_1738424_5A	5A	440.73	0.000446	3.35	0.23057	0.03	1.3822
Nil	TKW	wsnp_Ku_c40349_48594583_5A	5A	440.73	0.000356	3.45	0.212435	0.03	1.4989
Nil	TKW	BS00044408_51_5A	5A	445.69	0.000597	3.22	0.204663	0.03	-1.4074
Nil	TKW	Excalibur_c37943_221_5A	5A	445.69	0.000335	3.48	0.207254	0.03	1.4282
Nil	TKW	Kukri_c29560_455_5A	5A	445.69	0.000212	3.67	0.227979	0.03	-1.4148
Nil	TKW	wsnp_Ex_c11120_18022932_5A	5A	445.69	0.000219	3.66	0.256477	0.03	-1.3352
Nil	TKW	wsnp_Ex_c13258_20911706_5A	5A	445.69	0.000526	3.28	0.23057	0.03	-1.3509
Nil	TKW	wsnp_Ex_c37943_45584325_5A	5A	445.69	0.000564	3.25	0.212435	0.03	1.3782
Nil	TKW	wsnp_Ex_c62818_62296773_5A	5A	445.69	0.000946	3.02	0.220207	0.03	1.2883
Nil	TKW	wsnp_Ku_c20011_29589089_5A	5A	445.69	0.000336	3.47	0.227979	0.03	-1.4087
Nil	TKW	wsnp_Ku_c20011_29589289_5A	5A	445.69	0.000596	3.22	0.202073	0.03	1.2221
Nil	TKW	wsnp_Ku_c20011_29589514_5A	5A	445.69	0.000605	3.22	0.212435	0.03	1.3973
Nil	TKW	wsnp_Ra_c12183_19587379_5A	5A	445.69	0.000346	3.46	0.23057	0.03	-1.3912
Nil	TKW	wsnp_Ku_c3684_6789632_5A	5A	446.53	0.000339	3.47	0.199482	0.03	-1.5001
Nil	TKW	Excalibur_c7729_144_5A	5A	448.42	7.49E-05	4.13	0.202073	0.04	1.6329
Nil	TKW	Excalibur_rep_c103747_193_5A	5A	448.42	0.00096	3.02	0.15544	0.03	1.4272
Nil	TKW	IACX9023_5A	5A	448.42	0.000902	3.04	0.186528	0.03	1.1982
Nil	TKW	Tdurum_contig55097_601_5A	5A	448.42	0.000814	3.09	0.207254	0.03	-1.2645
Nil	TKW	wsnp_Ex_c31799_40545376_5A	5A	448.42	0.000107	3.97	0.199482	0.04	-1.5804
Nil	TKW	wsnp_Ex_rep_c66689_65011117_5A	5A	448.42	0.000217	3.66	0.196891	0.03	-1.4185
Nil	TKW	BS00065936_51_5A	5A	450.43	2.87E-06	5.54	0.23057	0.05	1.7753
Nil	TKW	RAC875_c13931_205_5A	5A	450.43	0.00059	3.23	0.220207	0.03	-1.3110
Nil	TKW	Excalibur_c30482_898_5A	5A	453.34	0.000129	3.89	0.204663	0.04	-1.5668
Nil	TKW	Kukri_c33022_198_5A	5A	453.34	1.36E-06	5.87	0.15544	0.06	2.0948
Nil	TKW	Tdurum_contig81424_367_5A	5A	453.34	2.97E-06	5.53	0.233161	0.05	1.6166
Nil	TKW	Kukri_c6669_145_5A	5A	457.14	2.33E-05	4.63	0.158031	0.04	1.7507
Nil	TKW	RAC875_rep_c76193_513_5A	5A	460.6	0.000159	3.80	0.158031	0.03	-1.5962
Nil	TKW	Excalibur_c31769_793_5A	5A	463.45	7.39E-05	4.13	0.183938	0.04	-1.7102

Nil	TKW	Excalibur_c24051_502_5A	5A	463.65	0.000119	3.92	0.176166	0.04	-1.5597
Nil	TKW	Kukri_c865_59_5A	5A	463.65	0.000214	3.67	0.170984	0.03	-1.2383
Nil	TKW	wsnp_Ex_c44164_50292954_5A	5A	463.65	0.00027	3.57	0.181347	0.03	1.2702
Nil	TKW	wsnp_RFL_Contig2265_1693968_5A	5A	463.65	0.000126	3.90	0.165803	0.04	1.4738
Nil	TKW	Excalibur_c41710_417_5A	5A	464.98	9.77E-06	5.01	0.181347	0.05	1.7332
Nil	TKW	GENE-2794_70_5A	5A	464.98	1.96E-05	4.71	0.176166	0.04	1.6787
Nil	TKW	wsnp_Ex_c2185_4094843_5A	5A	464.98	1.65E-05	4.78	0.160622	0.05	1.6937
Nil	TKW	BobWhite_c15758_79_5A	5A	466.78	0.00018	3.75	0.139896	0.03	1.6125
Nil	TKW	BobWhite_c658_377_5A	5A	466.78	8.18E-05	4.09	0.189119	0.04	1.3847
Nil	TKW	BS00041063_51_5A	5A	466.78	3.56E-06	5.45	0.170984	0.05	-1.9593
Nil	TKW	Tdurum_contig10843_745_5A	5A	466.78	0.000187	3.73	0.181347	0.03	-1.5337
Nil	TKW	Tdurum_contig50175_875_5A	5A	466.78	0.000115	3.94	0.183938	0.04	1.3653
Nil	TKW	wsnp_Ex_c55777_58153636_5A	5A	466.78	3.43E-05	4.46	0.173575	0.04	1.6654
Nil	TKW	wsnp_Ex_c8424_14192191_5A	5A	466.78	8.42E-05	4.07	0.160622	0.04	-1.5142
Nil	TKW	wsnp_Ex_rep_c109532_92292121_5A	5A	466.78	0.000295	3.53	0.183938	0.03	-1.5661
Nil	TKW	wsnp_Ex_c8543_14357385_5A	5A	466.81	0.000311	3.51	0.145078	0.03	1.6306
Nil	TKW	Tdurum_contig47120_587_5A	5A	469.39	3.12E-07	6.51	0.19171	0.07	1.9504
Nil	TKW	Tdurum_contig69612_781_5A	5A	469.39	1.67E-05	4.78	0.199482	0.05	1.7426
Nil	TKW	wsnp_Ex_c5978_10478584_5A	5A	473.13	8.93E-07	6.05	0.147668	0.06	2.0487
Nil	TKW	wsnp_Ra_c3966_7286546_5A	5A	473.13	6.64E-06	5.18	0.142487	0.05	1.7396
Nil	TKW	IAAV4799_5A	5A	475.36	1.91E-05	4.72	0.15285	0.04	-1.7356
Nil	TKW	IAAV108_5A	5A	478.4	0.000158	3.80	0.354922	0.03	1.2260
Nil	TKW	BobWhite_c17445_83_5A	5A	484.57	3.14E-07	6.50	0.132124	0.07	2.7120
Nil	TKW	Kukri_c67527_89_5A	5A	484.57	1.13E-05	4.95	0.178756	0.05	-1.4509
Nil	TKW	Tdurum_contig10086_387_5A	5A	484.57	3.76E-06	5.43	0.173575	0.05	1.8875
Nil	TKW	Tdurum_contig54543_888_5A	5A	484.57	1.53E-05	4.82	0.19171	0.05	1.4282
Nil	TKW	Tdurum_contig85105_286_5A	5A	484.57	1.06E-05	4.97	0.139896	0.05	2.1744
Nil	TKW	wsnp_BF484028B_Td_2_1_5A	5A	484.57	6.85E-06	5.16	0.15544	0.05	-2.0272
Nil	TKW	RAC875_c104483_394_5A	5A	488	7.11E-05	4.15	0.147668	0.04	1.6992
Nil	TKW	Tdurum_contig54725_586_5A	5A	488	5.97E-05	4.22	0.15285	0.04	-1.8411

Nil	TKW	wsnp_BG606780A_Td_2_1_5A	5A	488	1.47E-05	4.83	0.165803	0.05	-1.8540
Nil	TKW	wsnp_Ex_c790_1554988_5A	5A	490.41	9.91E-05	4.00	0.406736	0.04	1.2754
Nil	TKW	BobWhite_c3675_788_5A	5A	492.85	0.000452	3.35	0.199482	0.03	-1.2736
Nil	TKW	BS00022753_51_5A	5A	492.85	0.000598	3.22	0.204663	0.03	1.4248
Nil	TKW	BS00022754_51_5A	5A	492.85	0.000646	3.19	0.199482	0.03	1.3693
Nil	TKW	BS00063973_51_5A	5A	492.85	9.51E-05	4.02	0.204663	0.04	1.5726
Nil	TKW	Jagger_c6618_144_5A	5A	492.85	1.60E-05	4.80	0.181347	0.05	1.7861
Nil	TKW	RAC875_c3964_752_5A	5A	492.85	0.000639	3.19	0.207254	0.03	1.2404
Nil	TKW	wsnp_CAP11_c1506_840938_5A	5A	492.85	0.00034	3.47	0.199482	0.03	1.4851
Nil	TKW	wsnp_CAP11_c1506_840951_5A	5A	492.85	0.000385	3.41	0.170984	0.03	-1.3826
Nil	TKW	wsnp_Ku_c42416_50159250_5A	5A	492.85	0.000151	3.82	0.196891	0.03	1.5635
Nil	TKW	wsnp_Ku_c42416_50159402_5A	5A	492.85	0.0003	3.52	0.212435	0.03	1.3758
Nil	TKW	BS00022098_51_5A	5A	493.65	5.56E-06	5.26	0.238342	0.05	-1.5693
Nil	TKW	BS00074855_51_5A	5A	493.65	0.000197	3.71	0.19171	0.03	-1.5779
Nil	TKW	BS00041911_51_5A	5A	494.25	1.52E-05	4.82	0.168394	0.05	-1.9345
Nil	TKW	BS00067150_51_5A	5A	494.25	9.64E-05	4.02	0.168394	0.04	-1.7609
Nil	TKW	RAC875_c7132_134_5A	5A	494.25	6.68E-05	4.18	0.15544	0.04	1.8110
Nil	TKW	RAC875_rep_c112818_307_5A	5A	495.18	0.000328	3.48	0.189119	0.03	-1.5231
Nil	TKW	BobWhite_rep_c64315_180_5A	5A	496.4	0.000458	3.34	0.186528	0.03	1.4614
Nil	TKW	wsnp_BG607308A_Ta_2_1_5A	5A	498.48	5.87E-05	4.23	0.194301	0.04	-1.4350
Nil	TKW	wsnp_BG607308A_Ta_2_2_5A	5A	498.48	3.86E-05	4.41	0.15544	0.04	1.9352
Nil	TKW	BS00069739_51_5A	5A	500.09	0.000263	3.58	0.137306	0.03	1.6356
Nil	TKW	RAC875_c60453_122_5A	5A	505.2	0.000651	3.19	0.129534	0.03	1.6781
Nil	TKW	RAC875_c62807_251_5A	5A	505.2	0.000562	3.25	0.137306	0.03	1.5030
Nil	TKW	TA006037-0261_5A	5A	505.2	0.00016	3.80	0.124352	0.03	-1.9221
Nil	TKW	Tdurum_contig45823_821_5A	5A	505.2	0.000206	3.69	0.126943	0.03	1.8311
Nil	TKW	wsnp_BE403211A_Td_2_1_5A	5A	505.2	0.000909	3.04	0.139896	0.03	-1.5579
Nil	TKW	wsnp_CD454152A_Ta_2_1_5A	5A	506.47	0.000561	3.25	0.11399	0.03	1.6373
Nil	TKW	wsnp_Ex_c1880_3545329_5A	5A	525.04	0.000575	3.24	0.137306	0.03	1.7456
Nil	TKW	BS00109908_51_5A	5A	525.3	0.000942	3.03	0.150259	0.03	1.4288

Nil	TKW	wsnp_Ex_c18107_26909127_5A	5A	530.67	0.000683	3.17	0.357513	0.03	1.2271
Nil	TKW	Kukri_c41787_141_5D	5D	387.6	0.00092	3.04	0.111399	0.03	1.5897
Nil	TKW	wsnp_Ex_c9428_15641609_7A	7A	466.45	0.000697	3.16	0.357513	0.03	1.1985
Nil	TKW	RAC875_c30123_913_7B	7B	182.1	0.000968	3.01	0.181347	0.03	-1.6208
Plus	TKW	RAC875_c744_1935_1A	1A	55.22	0.000157	3.80	0.367876	4.17	-1.8483
Plus	TKW	RAC875_c41145_189_1A	1A	91.64	0.000493	3.31	0.479275	3.52	-1.1300
Plus	TKW	BS00021942_51_1A	1A	192.55	0.000319	3.50	0.380829	3.77	-1.5570
Plus	TKW	tplb0050c03_1003_1B	1B	209.09	0.000441	3.36	0.336788	3.58	1.0803
Plus	TKW	wsnp_JD_c5316_6447231_1D	1D	5.47	0.000543	3.27	0.352332	3.47	1.2292
Plus	TKW	BobWhite_c1715_887_1D	1D	35.05	0.0009	3.05	0.494819	3.19	-1.1211
Plus	TKW	wsnp_CAP11_c8597_3709328_1D	1D	45.36	0.00052	3.28	0.487047	3.49	1.2058
Plus	TKW	BS00022382_51_2A	2A	219.62	0.000628	3.20	0.07772	3.39	2.1914
Plus	TKW	Tdurum_contig29620_285_2B	2B	255.74	0.000815	3.09	0.414508	3.24	1.2860
Plus	TKW	Excalibur_rep_c68583_689_3A	3A	269.13	0.000368	3.43	0.207254	3.69	1.7609
Plus	TKW	Tdurum_contig93364_355_3A	3A	271.98	0.000657	3.18	0.300518	3.36	-1.7616
Plus	TKW	BS00098840_51_3A	3A	273.07	0.000776	3.11	0.326425	3.27	-1.8044
Plus	TKW	wsnp_Ku_c44089_51445136_3A	3A	274.44	0.000465	3.33	0.310881	3.56	1.6028
Plus	TKW	Tdurum_contig15529_135_3A	3A	296.36	0.000455	3.34	0.072539	3.57	-1.7776
Plus	TKW	BS00110365_51_4B	4B	182.55	3.95E-05	4.40	0.246114	4.97	1.5784
Plus	TKW	Excalibur_c34426_723_5A	5A	193.73	0.000694	3.16	0.365285	3.33	1.2484
Plus	TKW	Tdurum_contig10759_260_5A	5A	421.21	0.000223	3.65	0.178756	3.97	-1.5540
Plus	TKW	Tdurum_contig67291_367_5A	5A	421.21	0.000178	3.75	0.183938	4.10	-1.5507
Plus	TKW	BS00089795_51_5A	5A	440.73	0.00013	3.89	0.233161	4.28	1.5695
Plus	TKW	Ex_c27046_1362_5A	5A	440.73	0.000138	3.86	0.23057	4.24	1.5411
Plus	TKW	Ex_c27046_3425_5A	5A	440.73	9.81E-05	4.01	0.204663	4.44	1.5886
Plus	TKW	Ex_c898_1319_5A	5A	440.73	0.000235	3.63	0.235751	3.94	1.5030
Plus	TKW	Excalibur_c11656_1760_5A	5A	440.73	0.00028	3.55	0.207254	3.84	1.5857
Plus	TKW	IAAV2473_5A	5A	440.73	1.94E-05	4.71	0.251295	5.38	1.6606
Plus	TKW	RAC875_c3046_1764_5A	5A	440.73	8.88E-05	4.05	0.240933	4.50	1.5623
Plus	TKW	RFL_Contig3739_2135_5A	5A	440.73	0.000143	3.85	0.235751	4.22	1.5365

Plus	TKW	wsnp_Ex_c17523_26244256_5A	5A	440.73	2.00E-05	4.70	0.253886	5.36	1.6355
Plus	TKW	wsnp_Ex_c27046_36265198_5A	5A	440.73	0.000181	3.74	0.227979	4.09	1.4464
Plus	TKW	wsnp_Ex_c898_1738424_5A	5A	440.73	0.000118	3.93	0.23057	4.33	1.5873
Plus	TKW	wsnp_Ku_c40349_48594583_5A	5A	440.73	0.000251	3.60	0.212435	3.90	1.5985
Plus	TKW	BS00044408_51_5A	5A	445.69	0.000483	3.32	0.204663	3.53	-1.4988
Plus	TKW	Excalibur_c37943_221_5A	5A	445.69	0.000136	3.87	0.207254	4.25	1.6038
Plus	TKW	Kukri_c29560_455_5A	5A	445.69	5.55E-05	4.26	0.227979	4.77	-1.6208
Plus	TKW	wsnp_Ex_c11120_18022932_5A	5A	445.69	5.13E-05	4.29	0.256477	4.81	-1.5248
Plus	TKW	wsnp_Ex_c13258_20911706_5A	5A	445.69	0.000144	3.84	0.23057	4.22	-1.5503
Plus	TKW	wsnp_Ex_c37943_45584325_5A	5A	445.69	0.00015	3.82	0.212435	4.20	1.6014
Plus	TKW	wsnp_Ex_c62818_62296773_5A	5A	445.69	0.000243	3.62	0.220207	3.92	1.4974
Plus	TKW	wsnp_Ku_c20011_29589089_5A	5A	445.69	7.32E-05	4.14	0.227979	4.61	-1.6320
Plus	TKW	wsnp_Ku_c20011_29589289_5A	5A	445.69	0.000113	3.95	0.202073	4.35	1.4719
Plus	TKW	wsnp_Ku_c20011_29589514_5A	5A	445.69	0.000103	3.99	0.212435	4.41	1.6620
Plus	TKW	wsnp_Ra_c12183_19587379_5A	5A	445.69	8.70E-05	4.06	0.23057	4.51	-1.5965
Plus	TKW	wsnp_Ku_c3684_6789632_5A	5A	446.53	0.00014	3.85	0.199482	4.23	-1.6738
Plus	TKW	Kukri_c20011_147_5A	5A	447.33	0.000172	3.76	0.284974	4.12	1.2937
Plus	TKW	Excalibur_c7729_144_5A	5A	448.42	5.32E-05	4.27	0.202073	4.79	1.7572
Plus	TKW	IACX9023_5A	5A	448.42	0.000967	3.01	0.186528	3.15	1.2566
Plus	TKW	Tdurum_contig55097_601_5A	5A	448.42	0.000244	3.61	0.207254	3.92	-1.4740
Plus	TKW	wsnp_Ex_c31799_40545376_5A	5A	448.42	7.60E-05	4.12	0.199482	4.58	-1.7016
Plus	TKW	wsnp_Ex_rep_c66689_65011117_5A	5A	448.42	0.000132	3.88	0.196891	4.27	-1.5738
Plus	TKW	BS00065936_51_5A	5A	450.43	2.06E-06	5.69	0.23057	6.73	1.9037
Plus	TKW	RAC875_c13931_205_5A	5A	450.43	0.000187	3.73	0.220207	4.07	-1.5014
Plus	TKW	RAC875_c30566_230_5A	5A	450.43	0.000568	3.25	0.204663	3.44	-1.3706
Plus	TKW	Excalibur_c30482_898_5A	5A	453.34	0.000108	3.97	0.204663	4.38	-1.6695
Plus	TKW	Kukri_c33022_198_5A	5A	453.34	2.13E-06	5.67	0.15544	6.70	2.1555
Plus	TKW	Tdurum_contig81424_367_5A	5A	453.34	4.48E-06	5.35	0.233161	6.26	1.6751
Plus	TKW	wsnp_BF293620A_Ta_2_3_5A	5A	453.34	0.000754	3.12	0.209845	3.29	-1.3264
Plus	TKW	Kukri_c6669_145_5A	5A	457.14	4.45E-06	5.35	0.158031	6.26	1.9990

Plus	TKW	RAC875_rep_c76193_513_5A	5A	460.6	8.09E-05	4.09	0.158031	4.55	-1.7957
Plus	TKW	Excalibur_c31769_793_5A	5A	463.45	4.23E-05	4.37	0.183938	4.92	-1.8417
Plus	TKW	Excalibur_c24051_502_5A	5A	463.65	3.59E-05	4.45	0.176166	5.02	-1.7737
Plus	TKW	Kukri_c865_59_5A	5A	463.65	2.72E-05	4.57	0.170984	5.18	-1.4991
Plus	TKW	wsnp_Ex_c44164_50292954_5A	5A	463.65	4.23E-05	4.37	0.181347	4.92	1.5376
Plus	TKW	wsnp_RFL_Contig2265_1693968_5A	5A	463.65	9.13E-06	5.04	0.165803	5.83	1.8166
Plus	TKW	Excalibur_c41710_417_5A	5A	464.98	8.80E-06	5.06	0.181347	5.85	1.8460
Plus	TKW	GENE-2794_70_5A	5A	464.98	3.27E-06	5.48	0.176166	6.44	1.9484
Plus	TKW	wsnp_Ex_c2185_4094843_5A	5A	464.98	2.29E-05	4.64	0.160622	5.29	1.7645
Plus	TKW	BobWhite_c15758_79_5A	5A	466.78	0.000172	3.77	0.139896	4.12	1.7190
Plus	TKW	BobWhite_c658_377_5A	5A	466.78	1.39E-05	4.86	0.189119	5.58	1.6449
Plus	TKW	BS00041063_51_5A	5A	466.78	3.01E-06	5.52	0.170984	6.49	-2.0892
Plus	TKW	RFL_Contig316_572_5A	5A	466.78	0.000778	3.11	0.15544	3.27	1.4013
Plus	TKW	Tdurum_contig10843_745_5A	5A	466.78	4.55E-05	4.34	0.181347	4.88	-1.7595
Plus	TKW	Tdurum_contig50175_875_5A	5A	466.78	1.81E-05	4.74	0.183938	5.42	1.6360
Plus	TKW	wsnp_Ex_c55777_58153636_5A	5A	466.78	1.64E-05	4.78	0.173575	5.48	1.8431
Plus	TKW	wsnp_Ex_c8424_14192191_5A	5A	466.78	1.28E-05	4.89	0.160622	5.63	-1.7881
Plus	TKW	wsnp_Ex_rep_c109532_92292121_5A	5A	466.78	0.000234	3.63	0.183938	3.94	-1.6585
Plus	TKW	wsnp_Ex_c8543_14357385_5A	5A	466.81	0.000442	3.35	0.145078	3.58	1.6598
Plus	TKW	Tdurum_contig47120_587_5A	5A	469.39	1.54E-07	6.81	0.19171	8.33	2.1000
Plus	TKW	Tdurum_contig69612_781_5A	5A	469.39	6.01E-06	5.22	0.199482	6.08	1.9215
Plus	TKW	wsnp_Ex_c5978_10478584_5A	5A	473.13	4.33E-06	5.36	0.147668	6.28	2.0291
Plus	TKW	wsnp_Ra_c3966_7286546_5A	5A	473.13	1.51E-05	4.82	0.142487	5.53	1.7648
Plus	TKW	IAAV4799_5A	5A	475.36	6.85E-06	5.16	0.15285	6.00	-1.9607
Plus	TKW	wsnp_Ex_c23787_33024604_5A	5A	475.36	0.000235	3.63	0.145078	3.94	-1.3790
Plus	TKW	IAAV108_5A	5A	478.4	0.000702	3.15	0.354922	3.33	1.1594
Plus	TKW	BobWhite_c17445_83_5A	5A	484.57	8.47E-07	6.07	0.132124	7.27	2.7075
Plus	TKW	Kukri_c67527_89_5A	5A	484.57	3.89E-05	4.41	0.178756	4.97	-1.4316
Plus	TKW	Tdurum_contig10086_387_5A	5A	484.57	1.55E-05	4.81	0.173575	5.51	1.8111
Plus	TKW	Tdurum_contig54543_888_5A	5A	484.57	1.08E-05	4.97	0.19171	5.73	1.5417

Plus	TKW	Tdurum_contig85105_286_5A	5A	484.57	0.000129	3.89	0.139896	4.28	1.9491
Plus	TKW	wsnp_BF484028B_Td_2_1_5A	5A	484.57	1.10E-05	4.96	0.15544	5.72	-2.0439
Plus	TKW	RAC875_c104483_394_5A	5A	488	5.25E-05	4.28	0.147668	4.80	1.8070
Plus	TKW	Tdurum_contig54725_586_5A	5A	488	0.000181	3.74	0.15285	4.09	-1.7535
Plus	TKW	wsnp_Ex_c790_1554988_5A	5A	490.41	5.30E-05	4.28	0.406736	4.79	1.3785
Plus	TKW	BS00063973_51_5A	5A	492.85	0.000446	3.35	0.204663	3.58	1.4490
Plus	TKW	Jagger_c6618_144_5A	5A	492.85	3.48E-05	4.46	0.181347	5.04	1.7476
Plus	TKW	wsnp_CAP11_c1506_840938_5A	5A	492.85	0.000767	3.12	0.199482	3.28	1.4320
Plus	TKW	wsnp_Ku_c42416_50159250_5A	5A	492.85	0.000904	3.04	0.196891	3.19	1.4027
Plus	TKW	wsnp_Ku_c42416_50159402_5A	5A	492.85	0.000667	3.18	0.212435	3.35	1.3275
Plus	TKW	BS00022098_51_5A	5A	493.65	8.36E-05	4.08	0.238342	4.53	-1.4025
Plus	TKW	BS00041911_51_5A	5A	494.25	5.39E-05	4.27	0.168394	4.78	-1.8416
Plus	TKW	RAC875_c7132_134_5A	5A	494.25	0.000364	3.44	0.15544	3.69	1.6505
Plus	TKW	wsnp_BG607308A_Ta_2_1_5A	5A	498.48	0.000252	3.60	0.194301	3.90	-1.3497
Plus	TKW	wsnp_BG607308A_Ta_2_2_5A	5A	498.48	0.000159	3.80	0.15544	4.16	1.8125
Plus	TKW	BS00069739_51_5A	5A	500.09	7.43E-05	4.13	0.137306	4.60	1.8583
Plus	TKW	BS00109908_51_5A	5A	525.3	0.000921	3.04	0.150259	3.18	1.4761
Plus	TKW	wsnp_Ex_c18107_26909127_5A	5A	530.67	0.000528	3.28	0.357513	3.48	1.2982
Plus	TKW	D_GDS7LZN01DW87V_234_5D	5D	357.85	0.000291	3.54	0.183938	3.82	-1.5117
Plus	TKW	wsnp_RFL_Contig2346_1854360_5D	5D	357.85	0.000218	3.66	0.189119	3.98	-1.5538
Plus	TKW	D_F5XZDLF02IP5IR_228_5D	5D	365.23	3.02E-05	4.52	0.186528	5.12	-1.6375
Plus	TKW	Jagger_c754_272_5D	5D	377.86	0.000879	3.06	0.132124	3.20	-1.6840
Plus	TKW	Kukri_c41787_141_5D	5D	387.6	0.000464	3.33	0.111399	3.56	1.7921
Plus	TKW	D_contig79410_237_5D	5D	489.95	0.000531	3.27	0.266839	3.48	-1.2953
Plus	TKW	wsnp_Ku_c10877_17896883_5D	5D	489.95	0.000269	3.57	0.264249	3.86	-1.3669
Plus	TKW	RAC875_c30123_913_7B	7B	182.1	0.000728	3.14	0.181347	3.31	-1.6777
Plus	TKW	wsnp_Ex_c12535_19963035_7B	7B	224.57	0.000864	3.06	0.142487	3.21	1.7291
Plus	WH	Excalibur_c18966_1008_2B	2B	417.82	5.59E-05	4.25	0.101036	7.56	9.1952
Plus	WH	BS00034147_51_4B	4B	333.52	0.00084	3.08	0.297927	5.12	-5.7320
Plus	WH	RAC875_c39339_400_4B	4B	333.52	0.00089	3.05	0.30829	5.07	-5.1995

Plus	WH	Ex_c16174_681_4D	4D	36.87	0.000813	3.09	0.481865	5.15	-4.0509
Plus	WH	Excalibur_c23452_352_5B	5B	551.78	0.000761	3.12	0.406736	5.21	4.3066
Plus	WH	BS00067074_51_5B	5B	568.44	3.87E-05	4.41	0.207254	7.90	-7.3999
Plus	WH	CAP7_c8713_356_5B	5B	568.44	0.000321	3.49	0.212435	5.98	6.0916
Plus	WH	RAC875_c14732_461_5B	5B	568.44	3.71E-05	4.43	0.196891	7.94	7.2579
Plus	WH	RAC875_c82589_246_5B	5B	568.44	0.000187	3.73	0.194301	6.46	6.7088
Plus	WH	Tdurum_contig60165_722_5B	5B	568.44	4.40E-05	4.36	0.202073	7.78	6.9313
Plus	WH	BobWhite_c46416_247_5B	5B	568.98	2.02E-05	4.70	0.202073	8.51	7.2652
Plus	WH	BobWhite_s66049_223_5B	5B	568.98	5.27E-05	4.28	0.253886	7.62	5.9825
Plus	WH	Kukri_c18410_193_5B	5B	568.98	7.53E-05	4.12	0.189119	7.29	-6.9104
Plus	WH	Kukri_c18410_349_5B	5B	568.98	0.000316	3.50	0.183938	5.99	5.9805
Plus	WH	Kukri_c18410_409_5B	5B	568.98	6.67E-05	4.18	0.212435	7.40	-6.0387
Plus	WH	Kukri_c4594_825_5B	5B	568.98	0.000104	3.98	0.217617	6.99	6.8970
Plus	WH	RAC875_c1035_65_5B	5B	568.98	7.69E-06	5.11	0.204663	9.42	7.3273
Plus	WH	RAC875_rep_c106982_82_5B	5B	568.98	2.74E-05	4.56	0.233161	8.22	-6.0995
Plus	WH	RAC875_rep_c109540_64_5B	5B	568.98	0.000138	3.86	0.220207	6.74	6.4569
Plus	WH	Tdurum_contig60189_192_5B	5B	568.98	0.000239	3.62	0.220207	6.24	5.5942
Plus	WH	Tdurum_contig60189_263_5B	5B	568.98	0.000265	3.58	0.243523	6.15	5.3009
Plus	WH	BobWhite_c15406_510_5B	5B	585.04	0.000604	3.22	0.170984	5.41	5.6535
Plus	WH	RAC875_c12879_176_6B	6B	220.52	0.000904	3.04	0.134715	5.06	-7.5234
Plus	WH	Kukri_c28160_2017_7B	7B	470.16	0.000869	3.06	0.282383	5.09	-5.4178
Plus	WH	IACX9217_7B	7B	475.92	0.000156	3.81	0.233161	6.62	-6.8057
Plus	WH	JD_c17199_230_7B	7B	475.92	0.00053	3.28	0.272021	5.53	-5.1719
Plus	WH	Excalibur_c1070_2327_7B	7B	490.67	0.000548	3.26	0.261658	5.50	6.1880
Plus	WH	wsnp_Ex_c4484_8065800_7B	7B	502.72	0.000455	3.34	0.253886	5.67	-5.9391
Plus	WSB	Tdurum_contig83066_276_2B	2B	292.15	0.000843	3.07	0.42487	6.12	-6.9656
Plus	WSB	Ku_c21490_472_6A	6A	188.89	0.000593	3.23	0.056995	6.49	-11.1742
Plus	WSB	Ra_c8185_676_6A	6A	188.89	0.000974	3.01	0.054404	5.96	11.1324
Plus	WSB	Tdurum_contig14544_1550_6A	6A	190.27	0.000437	3.36	0.101036	6.81	8.0869
Nil	Yield	BS00067024_51_1B	1B	306.49	0.000182	3.74	0.054404	6.51	-0.3998

Nil	Yield	IAAV7856_1D	1D	60.7	0.000651	3.19	0.147668	5.37	0.2221
Nil	Yield	Kukri_c136_150_2A	2A	413.06	0.000877	3.06	0.142487	5.10	0.2096
Nil	Yield	RAC875_c64377_350_2A	2A	413.64	0.000828	3.08	0.064767	5.15	-0.2872
Nil	Yield	RAC875_rep_c72517_1215_2A	2A	614.77	0.000537	3.27	0.196891	5.54	0.2704
Nil	Yield	Kukri_c3507_158_2B	2B	78.23	0.000231	3.64	0.145078	6.29	0.2305
Nil	Yield	BS00007901_51_2B	2B	314.41	0.000478	3.32	0.051813	5.64	0.3771
Nil	Yield	BobWhite_rep_c48966_570_2Dx	2D	267.98	0.000253	3.60	0.147668	6.21	-0.3351
Nil	Yield	D_contig64400_391_3B	3B	269.78	0.000951	3.02	0.07772	5.03	0.3043
Nil	Yield	RAC875_c35672_136_3B	3B	539.26	0.000233	3.63	0.059585	6.28	0.4087
Nil	Yield	RAC875_c35672_73_3B	3B	539.26	0.000542	3.27	0.056995	5.53	-0.3973
Nil	Yield	RAC875_c68392_137_3B	3B	539.26	0.000542	3.27	0.056995	5.53	-0.3973
Nil	Yield	BS00011605_51_3B	3B	545.17	0.000265	3.58	0.051813	6.17	0.4787
Nil	Yield	RAC875_rep_c74926_682_3D	3D	276.85	9.17E-05	4.04	0.054404	7.13	-0.4035
Nil	Yield	Kukri_c5252_107_3D	3D	280.71	1.94E-05	4.71	0.051813	8.58	0.5166
Nil	Yield	D_GBB4FNX02JKG8H_167_3D	3D	283.69	0.000135	3.87	0.056995	6.78	0.4309
Nil	Yield	BS00023217_51_3D	3D	284.57	0.000516	3.29	0.062176	5.57	0.3441
Nil	Yield	CAP12_c470_361_3D	3D	284.57	3.24E-05	4.49	0.059585	8.10	-0.4638
Nil	Yield	D_contig09222_937_3D	3D	284.57	0.000361	3.44	0.059585	5.89	-0.3891
Nil	Yield	D_contig11810_446_3D	3D	284.57	0.000203	3.69	0.062176	6.41	-0.3811
Nil	Yield	Excalibur_c40068_522_3D	3D	284.57	2.44E-05	4.61	0.051813	8.36	0.4819
Nil	Yield	Kukri_c17342_231_3D	3D	284.57	1.94E-05	4.71	0.051813	8.58	-0.5166
Nil	Yield	Kukri_c5411_1312_3D	3D	284.57	0.000208	3.68	0.056995	6.39	0.4201
Nil	Yield	RAC875_c24641_720_3D	3D	284.57	3.57E-05	4.45	0.051813	8.01	-0.4767
Nil	Yield	wsnp_CAP7_rep_c5643_2537213_3D	3D	284.57	8.28E-05	4.08	0.054404	7.23	-0.4591
Nil	Yield	Kukri_c19263_346_3D	3D	290.37	0.000249	3.60	0.056995	6.23	0.4094
Nil	Yield	Kukri_c22857_496_3D	3D	290.37	0.000196	3.71	0.051813	6.44	-0.4315
Nil	Yield	Tdurum_contig1015_131_3D	3D	292.51	9.31E-05	4.03	0.051813	7.12	-0.4186
Nil	Yield	IAAV163_4B	4B	203.85	0.000897	3.05	0.098446	5.08	-0.2363
Nil	Yield	Kukri_c32064_629_4B	4B	203.85	0.000773	3.11	0.103627	5.21	0.2313
Nil	Yield	RAC875_c104414_76_4B	4B	203.85	0.000897	3.05	0.098446	5.08	-0.2363

Nil	Yield	wsnp_Ex_c296_573976_4B	4B	203.85	0.0009	3.05	0.095855	5.08	0.2407
Nil	Yield	Tdurum_contig93160_155_4B	4B	205.73	0.000614	3.21	0.106218	5.42	-0.2319
Nil	Yield	tplb0034b12_591_4B	4B	206.89	0.000897	3.05	0.098446	5.08	-0.2363
Nil	Yield	wsnp_Ku_rep_c104382_90867406_4B	4B	206.89	0.000981	3.01	0.101036	5.01	0.2253
Nil	Yield	wsnp_Ra_c22945_32440611_4B	4B	206.89	0.000804	3.09	0.080311	5.18	-0.2443
Nil	Yield	RAC875_c23144_1560_4B	4B	208.51	0.000534	3.27	0.101036	5.54	0.2418
Nil	Yield	wsnp_Ex_c50195_54565006_4B	4B	208.51	0.000807	3.09	0.095855	5.18	0.2501
Nil	Yield	wsnp_Ex_c16825_25387841_4B	4B	215.45	0.000368	3.43	0.11658	5.87	-0.2315
Nil	Yield	wsnp_Ex_c35910_43971560_4B	4B	215.51	0.000213	3.67	0.090674	6.37	0.2678
Nil	Yield	Kukri_c12814_763_4B	4B	220.72	0.000942	3.03	0.137306	5.04	-0.2015
Nil	Yield	Tdurum_contig10466_87_4B	4B	226.2	4.66E-05	4.33	0.062176	7.76	-0.4718
Nil	Yield	BS00022830_51_4B	4B	230.39	0.000599	3.22	0.067358	5.44	-0.4041
Nil	Yield	Excalibur_c19547_75_4B	4B	230.39	0.000634	3.20	0.059585	5.39	-0.4439
Nil	Yield	IACX6482_4B	4B	230.39	0.000781	3.11	0.056995	5.21	-0.4437
Nil	Yield	Excalibur_c19547_1012_4B	4B	232.66	0.000117	3.93	0.069948	6.91	-0.4159
Nil	Yield	Ku_c103450_879_4B	4B	262.81	0.000297	3.53	0.054404	6.07	-0.3836
Nil	Yield	Kukri_c2148_137_4B	4B	262.81	0.000277	3.56	0.054404	6.13	-0.3699
Nil	Yield	GENE-1584_692_4B	4B	264.66	0.000259	3.59	0.430052	6.19	-0.1585
Nil	Yield	RFL_Contig727_736_5A	5A	260.89	9.10E-05	4.04	0.054404	7.14	-0.5205
Nil	Yield	wsnp_Ku_rep_c103274_90057407_5B	5B	36.44	0.000441	3.36	0.225389	5.71	-0.2109
Nil	Yield	wsnp_Ex_rep_c68504_67334656_5B	5B	40.09	0.000949	3.02	0.189119	5.03	-0.2043
Nil	Yield	D_GB5Y7FA02IZ73U_152_5D	5D	338.67	0.000222	3.65	0.160622	6.33	0.2096
Nil	Yield	D_contig14133_180_5D	5D	344.94	8.60E-05	4.07	0.158031	7.19	-0.2248
Nil	Yield	D_contig62661_72_5D	5D	349.65	0.000138	3.86	0.176166	6.76	0.2117
Nil	Yield	RFL_Contig1091_1538_5D	5D	354.06	1.86E-05	4.73	0.189119	8.62	-0.2336
Nil	Yield	BobWhite_c20106_377_5D	5D	357.85	0.000768	3.11	0.142487	5.22	-0.1846
Nil	Yield	BobWhite_c27870_103_5D	5D	357.85	0.00025	3.60	0.139896	6.22	-0.2069
Nil	Yield	D_GBB4FNX02GXFL1_268_5D	5D	357.85	0.000502	3.30	0.160622	5.60	-0.2005
Nil	Yield	D_GDS7LZN01DW87V_234_5D	5D	357.85	0.00015	3.82	0.183938	6.68	-0.2055
Nil	Yield	tplb0055c05_1689_5D	5D	357.85	0.000104	3.98	0.160622	7.02	-0.2308

Nil	Yield	wsnp_RFL_Contig2346_1854360_5D	5D	357.85	0.00017	3.77	0.189119	6.57	-0.2024
Nil	Yield	Ku_c19010_273_5D	5D	365.23	0.000255	3.59	0.119171	6.20	0.2187
Nil	Yield	Excalibur_c76347_77_5D	5D	371.54	0.000177	3.75	0.160622	6.54	-0.2294
Nil	Yield	Tdurum_contig11553_534_5D	5D	371.54	0.000413	3.38	0.163212	5.77	-0.2076
Nil	Yield	BS00000929_51_5D	5D	377.86	9.27E-07	6.03	0.147668	11.50	-0.3085
Nil	Yield	IACX3123_5D	5D	377.86	2.14E-06	5.67	0.178756	10.68	-0.2655
Nil	Yield	Jagger_c754_272_5D	5D	377.86	0.000479	3.32	0.132124	5.64	-0.2276
Nil	Yield	Ku_c6176_938_5D	5D	377.86	0.000625	3.20	0.142487	5.40	0.2172
Nil	Yield	Kukri_c41787_141_5D	5D	387.6	0.000676	3.17	0.111399	5.33	0.2467
Nil	Yield	BS00037002_51_6A	6A	9.88	1.85E-05	4.73	0.064767	8.62	0.5211
Nil	Yield	BS00037003_51_6B	6B	1.28	4.68E-05	4.33	0.07513	7.75	0.4116
Nil	Yield	BobWhite_c3506_1559_6B	6B	377.2	0.00055	3.26	0.056995	5.52	0.4544
Nil	Yield	TA003403-0617_6B	6B	377.2	0.000852	3.07	0.134715	5.13	0.2318
Nil	Yield	Excalibur_c109258_1038_7A	7A	382.54	0.000984	3.01	0.095855	5.00	-0.2289
Nil	Yield	RAC875_c13300_139_7A	7A	382.54	0.001011	3.00	0.119171	4.98	-0.2048
Nil	Yield	RAC875_c28144_448_7A	7A	382.54	0.000709	3.15	0.095855	5.29	-0.2327
Nil	Yield	wsnp_Ex_c2277_4267788_7A	7A	382.54	0.000202	3.69	0.134715	6.41	-0.2077
Nil	Yield	BS00076379_51_7A	7A	386.33	0.000697	3.16	0.378238	5.31	0.1657
Nil	Yield	RAC875_c114809_130_7A	7A	386.33	0.000375	3.43	0.132124	5.86	0.2092
Nil	Yield	BobWhite_c156_381_7A	7A	398.79	0.000714	3.15	0.121762	5.28	-0.1874
Nil	Yield	Ra_c4601_2417_7A	7A	398.79	0.000467	3.33	0.121762	5.66	-0.1926
Nil	Yield	Tdurum_contig76683_147_7B	7B	236.25	0.000506	3.30	0.054404	5.59	-0.3967
Nil	Yield	Excalibur_c13912_587_7B	7B	247.05	0.000506	3.30	0.054404	5.59	-0.3967
Nil	Yield	Tdurum_contig19852_242_7B	7B	251.12	0.000206	3.69	0.051813	6.40	0.4374
Nil	Yield	Kukri_c64387_218_7B	7B	258.64	0.000723	3.14	0.204663	5.27	-0.1960
Nil	Yield	Kukri_c50384_371_7B	7B	378.06	0.000972	3.01	0.471503	5.01	-0.1470
Plus	Yield	BobWhite_c17044_155_1B	1B	102.58	0.000729	3.14	0.129534	5.48	-0.2194
Plus	Yield	BS00067024_51_1B	1B	306.49	0.000127	3.90	0.054404	7.12	-0.4105
Plus	Yield	Excalibur_c1453_1310_1B	1B	356.34	0.000319	3.50	0.062176	6.25	-0.3419
Plus	Yield	Tdurum_contig56157_1595_2A	2A	20.21	0.000313	3.51	0.059585	6.27	-0.3587

Plus	Yield	RAC875_rep_c111906_144_2A	2A	173.96	0.00066	3.18	0.093264	5.58	-0.2566
Plus	Yield	RAC875_c64377_350_2A	2A	413.64	0.000704	3.15	0.064767	5.52	-0.2971
Plus	Yield	Excalibur_c1999_1130_2A	2A	617.93	0.000889	3.05	0.468912	5.30	0.1723
Plus	Yield	Kukri_c3507_158_2B	2B	78.23	9.92E-05	4.00	0.145078	7.35	0.2466
Plus	Yield	Excalibur_c4748_360_2B	2B	87.22	0.000628	3.20	0.056995	5.62	0.3419
Plus	Yield	Excalibur_c2454_333_2B	2B	137.62	0.000886	3.05	0.069948	5.30	-0.3862
Plus	Yield	wsnp_Ex_rep_c101349_86725007_2B	2B	327.82	0.000516	3.29	0.051813	5.80	-0.3825
Plus	Yield	wsnp_Ex_c47157_52450090_2B	2B	356.43	8.79E-05	4.06	0.051813	7.47	0.3972
Plus	Yield	Kukri_c29052_75_2B	2B	413.94	0.000645	3.19	0.059585	5.60	-0.2823
Plus	Yield	GENE-0862_110_2B	2B	417.82	0.00063	3.20	0.054404	5.62	0.3757
Plus	Yield	BS00063589_51_2B	2B	439.24	2.48E-05	4.60	0.069948	8.69	-0.2882
Plus	Yield	D_contig17313_245_2Dx	2D	6.13	0.000508	3.29	0.098446	5.82	-0.2374
Plus	Yield	BobWhite_rep_c48966_570_2Dx	2D	267.98	0.000882	3.05	0.147668	5.31	-0.3070
Plus	Yield	IAAV4641_3B	3B	539.26	0.000887	3.05	0.062176	5.30	0.3957
Plus	Yield	Kukri_c22748_211_3B	3B	539.26	0.000526	3.28	0.067358	5.78	-0.3557
Plus	Yield	RAC875_c17373_848_3B	3B	539.26	0.000173	3.76	0.062176	6.82	-0.3979
Plus	Yield	RAC875_c23665_68_3B	3B	539.26	0.00027	3.57	0.062176	6.40	-0.3878
Plus	Yield	RAC875_c31133_533_3B	3B	539.26	0.000991	3.00	0.062176	5.20	-0.3140
Plus	Yield	RAC875_c35672_136_3B	3B	539.26	0.000112	3.95	0.059585	7.24	0.4260
Plus	Yield	RAC875_c35672_205_3B	3B	539.26	0.000677	3.17	0.062176	5.55	-0.3584
Plus	Yield	RAC875_c35672_73_3B	3B	539.26	0.000163	3.79	0.056995	6.88	-0.4286
Plus	Yield	RAC875_c68392_137_3B	3B	539.26	0.000163	3.79	0.056995	6.88	-0.4286
Plus	Yield	BS00011605_51_3B	3B	545.17	0.000365	3.44	0.051813	6.12	0.4580
Plus	Yield	D_contig79290_372_3D	3D	276.85	0.000921	3.04	0.067358	5.27	0.3198
Plus	Yield	RAC875_rep_c74926_682_3D	3D	276.85	8.61E-05	4.07	0.054404	7.49	-0.4050
Plus	Yield	Kukri_c5252_107_3D	3D	280.71	1.81E-05	4.74	0.051813	9.00	0.5095
Plus	Yield	D_GBB4FNX02JKG8H_167_3D	3D	283.69	0.000142	3.85	0.056995	7.01	0.4246
Plus	Yield	BS00023217_51_3D	3D	284.57	0.000156	3.81	0.062176	6.92	0.3783
Plus	Yield	CAP12_c470_361_3D	3D	284.57	1.18E-05	4.93	0.059585	9.42	-0.4844
Plus	Yield	D_contig09222_937_3D	3D	284.57	0.000179	3.75	0.059585	6.79	-0.4073

Plus	Yield	D_contig11810_446_3D	3D	284.57	0.00012	3.92	0.062176	7.17	-0.3949
Plus	Yield	D_F5XZDLF02HWOJZ_227_3D	3D	284.57	0.000724	3.14	0.129534	5.49	-0.2439
Plus	Yield	Excalibur_c40068_522_3D	3D	284.57	3.70E-06	5.43	0.051813	10.57	0.5273
Plus	Yield	Kukri_c17342_231_3D	3D	284.57	1.81E-05	4.74	0.051813	9.00	-0.5095
Plus	Yield	Kukri_c5411_1312_3D	3D	284.57	8.43E-05	4.07	0.056995	7.51	0.4419
Plus	Yield	RAC875_c24641_720_3D	3D	284.57	3.69E-05	4.43	0.051813	8.30	-0.4717
Plus	Yield	wsnp_CAP7_rep_c5643_2537213_3D	3D	284.57	2.70E-05	4.57	0.054404	8.61	-0.4843
Plus	Yield	Kukri_c19263_346_3D	3D	290.37	0.000279	3.55	0.056995	6.38	0.4022
Plus	Yield	Kukri_c22857_496_3D	3D	290.37	0.000129	3.89	0.051813	7.10	-0.4399
Plus	Yield	Tdurum_contig1015_131_3D	3D	292.51	7.83E-05	4.11	0.051813	7.58	-0.4207
Plus	Yield	RAC875_c15807_669_4B	4B	203.6	0.000454	3.34	0.108808	5.92	0.2411
Plus	Yield	wsnp_Ex_c296_574790_4B	4B	203.6	0.000332	3.48	0.090674	6.21	0.2752
Plus	Yield	Excalibur_c38012_393_4B	4B	203.85	0.00058	3.24	0.119171	5.69	0.2242
Plus	Yield	IAAV163_4B	4B	203.85	0.00018	3.74	0.098446	6.79	-0.2673
Plus	Yield	Kukri_c15910_159_4B	4B	203.85	0.000187	3.73	0.101036	6.75	0.2620
Plus	Yield	Kukri_c32064_629_4B	4B	203.85	0.00011	3.96	0.103627	7.26	0.2676
Plus	Yield	RAC875_c104414_76_4B	4B	203.85	0.00018	3.74	0.098446	6.79	-0.2673
Plus	Yield	wsnp_Ex_c296_573976_4B	4B	203.85	0.000198	3.70	0.095855	6.70	0.2710
Plus	Yield	Tdurum_contig93160_155_4B	4B	205.73	0.000209	3.68	0.106218	6.65	-0.2529
Plus	Yield	BS00087144_51_4B	4B	206.89	0.00054	3.27	0.106218	5.76	-0.2405
Plus	Yield	Excalibur_c5769_798_4B	4B	206.89	0.000187	3.73	0.101036	6.75	-0.2620
Plus	Yield	Kukri_c26900_996_4B	4B	206.89	0.000257	3.59	0.085492	6.45	-0.2588
Plus	Yield	RAC875_rep_c109069_89_4B	4B	206.89	0.000808	3.09	0.111399	5.39	-0.2159
Plus	Yield	RFL_Contig3363_1294_4B	4B	206.89	0.000386	3.41	0.103627	6.07	0.2436
Plus	Yield	Tdurum_contig47552_957_4B	4B	206.89	0.000349	3.46	0.103627	6.17	0.2494
Plus	Yield	Tdurum_contig86933_317_4B	4B	206.89	0.000671	3.17	0.108808	5.56	-0.2245
Plus	Yield	tplb0034b12_591_4B	4B	206.89	0.00018	3.74	0.098446	6.79	-0.2673
Plus	Yield	wsnp_Ex_c40815_47789152_4B	4B	206.89	0.00054	3.27	0.106218	5.76	-0.2405
Plus	Yield	wsnp_Ex_c5769_10136243_4B	4B	206.89	0.000321	3.49	0.103627	6.24	-0.2499
Plus	Yield	wsnp_Ex_c5769_10136788_4B	4B	206.89	0.000187	3.73	0.101036	6.75	0.2620

Plus	Yield	wsnp_Ku_c7453_12833586_4B	4B	206.89	0.000783	3.11	0.090674	5.42	-0.2436
Plus	Yield	wsnp_Ku_rep_c104382_90867406_4B	4B	206.89	0.000515	3.29	0.101036	5.80	0.2386
Plus	Yield	wsnp_Ra_c22945_32440611_4B	4B	206.89	0.000145	3.84	0.080311	6.99	-0.2785
Plus	Yield	CAP7_c10839_300_4B	4B	208.51	0.000263	3.58	0.103627	6.43	-0.2564
Plus	Yield	Excalibur_rep_c108293_345_4B	4B	208.51	0.000418	3.38	0.108808	6.00	-0.2390
Plus	Yield	GENE-2636_193_4B	4B	208.51	0.000292	3.54	0.093264	6.33	0.2628
Plus	Yield	Kukri_c5502_2513_4B	4B	208.51	0.000676	3.17	0.134715	5.55	-0.2195
Plus	Yield	RAC875_c23144_1560_4B	4B	208.51	0.000125	3.90	0.101036	7.13	0.2687
Plus	Yield	wsnp_Ex_c50195_54565006_4B	4B	208.51	0.00019	3.72	0.095855	6.74	0.2784
Plus	Yield	wsnp_Ku_c5502_9765942_4B	4B	208.51	0.000187	3.73	0.101036	6.75	-0.2620
Plus	Yield	wsnp_Ra_rep_c69724_67278233_4B	4B	208.51	0.000877	3.06	0.101036	5.31	0.2338
Plus	Yield	Ku_c13328_1228_4B	4B	210.85	0.00046	3.34	0.067358	5.91	0.3283
Plus	Yield	wsnp_Ex_c16825_25387841_4B	4B	215.45	0.000122	3.91	0.11658	7.15	-0.2518
Plus	Yield	CAP8_c1408_167_4B	4B	215.51	0.000525	3.28	0.098446	5.79	-0.2448
Plus	Yield	GENE-2422_208_4B	4B	215.51	0.000376	3.43	0.101036	6.10	-0.2465
Plus	Yield	IAAV6327_4B	4B	215.51	0.000956	3.02	0.093264	5.23	0.2413
Plus	Yield	RAC875_c89195_138_4B	4B	215.51	0.000309	3.51	0.095855	6.28	0.2573
Plus	Yield	wsnp_Ex_c35910_43971560_4B	4B	215.51	5.33E-05	4.27	0.090674	7.95	0.2936
Plus	Yield	wsnp_Ex_c37437_45183236_4B	4B	215.51	0.000908	3.04	0.085492	5.28	0.2433
Plus	Yield	wsnp_Ex_c37437_45184851_4B	4B	215.51	0.000525	3.28	0.098446	5.79	-0.2448
Plus	Yield	wsnp_Ex_c72198_70679871_4B	4B	215.51	0.000309	3.51	0.095855	6.28	-0.2573
Plus	Yield	BobWhite_c11005_236_4B	4B	220.72	0.000418	3.38	0.103627	6.00	-0.2443
Plus	Yield	Excalibur_c12925_510_4B	4B	220.72	0.000787	3.10	0.106218	5.41	-0.2188
Plus	Yield	Excalibur_c24563_339_4B	4B	220.72	0.00013	3.88	0.106218	7.09	-0.2690
Plus	Yield	Kukri_c12814_763_4B	4B	220.72	0.000127	3.90	0.137306	7.12	-0.2380
Plus	Yield	RAC875_c62816_54_4B	4B	220.72	0.000247	3.61	0.101036	6.49	-0.2562
Plus	Yield	RAC875_c77652_348_4B	4B	220.72	0.00036	3.44	0.098446	6.14	0.2523
Plus	Yield	Tdurum_contig42107_1978_4B	4B	220.72	0.000886	3.05	0.106218	5.30	-0.2308
Plus	Yield	Tdurum_contig42107_2206_4B	4B	220.72	0.000885	3.05	0.093264	5.31	0.2300
Plus	Yield	Tdurum_contig48088_463_4B	4B	220.72	0.000269	3.57	0.101036	6.41	-0.2526

Plus	Yield	Tdurum_contig10466_87_4B	4B	226.2	0.000101	3.99	0.062176	7.33	-0.4380
Plus	Yield	BS00022830_51_4B	4B	230.39	0.000426	3.37	0.067358	5.98	-0.4055
Plus	Yield	Excalibur_c19547_128_4B	4B	230.39	0.000947	3.02	0.072539	5.24	0.3540
Plus	Yield	Excalibur_c19547_75_4B	4B	230.39	0.00036	3.44	0.059585	6.14	-0.4478
Plus	Yield	IACX6482_4B	4B	230.39	0.000554	3.26	0.056995	5.74	-0.4398
Plus	Yield	Excalibur_c19547_1012_4B	4B	232.66	0.000215	3.67	0.069948	6.62	-0.3917
Plus	Yield	Ku_c103450_879_4B	4B	262.81	9.32E-05	4.03	0.054404	7.41	-0.4168
Plus	Yield	Kukri_c2148_137_4B	4B	262.81	5.35E-05	4.27	0.054404	7.95	-0.4143
Plus	Yield	Kukri_rep_c103450_1504_4B	4B	262.81	0.000861	3.06	0.051813	5.33	0.3488
Plus	Yield	RAC875_c103017_302_4B	4B	263.93	0.00082	3.09	0.147668	5.38	-0.2135
Plus	Yield	GENE-1584_692_4B	4B	264.66	7.20E-05	4.14	0.430052	7.66	-0.1737
Plus	Yield	Kukri_c21787_283_4B	4B	305.75	0.000489	3.31	0.129534	5.85	0.2960
Plus	Yield	wsnp_Ex_c4148_7495656_4B	4B	305.75	0.000351	3.45	0.121762	6.16	0.3201
Plus	Yield	RFL_Contig727_736_5A	5A	260.89	0.000176	3.76	0.054404	6.81	-0.4837
Plus	Yield	D_GB5Y7FA02IZ73U_152_5D	5D	338.67	0.000927	3.03	0.160622	5.26	0.1908
Plus	Yield	D_contig14133_180_5D	5D	344.94	0.000426	3.37	0.158031	5.98	-0.2046
Plus	Yield	D_contig62661_72_5D	5D	349.65	0.000197	3.71	0.176166	6.70	0.2102
Plus	Yield	RFL_Contig1091_1538_5D	5D	354.06	1.43E-05	4.84	0.189119	9.23	-0.2396
Plus	Yield	BobWhite_c20106_377_5D	5D	357.85	0.000524	3.28	0.142487	5.79	-0.1947
Plus	Yield	BobWhite_c27870_103_5D	5D	357.85	0.000171	3.77	0.139896	6.84	-0.2168
Plus	Yield	D_GBB4FNX02GXFL1_268_5D	5D	357.85	0.000624	3.21	0.160622	5.63	-0.2006
Plus	Yield	D_GDS7LZN01DW87V_234_5D	5D	357.85	0.000241	3.62	0.183938	6.51	-0.2028
Plus	Yield	tplb0055c05_1689_5D	5D	357.85	0.000181	3.74	0.160622	6.78	-0.2259
Plus	Yield	wsnp_RFL_Contig2346_1854360_5D	5D	357.85	0.00053	3.28	0.189119	5.78	-0.1897
Plus	Yield	D_F5XZDLF02IP5IR_228_5D	5D	365.23	0.000287	3.54	0.186528	6.35	-0.1949
Plus	Yield	Ku_c19010_273_5D	5D	365.23	9.75E-05	4.01	0.119171	7.37	0.2380
Plus	Yield	Excalibur_c76347_77_5D	5D	371.54	0.000534	3.27	0.160622	5.77	-0.2139
Plus	Yield	Tdurum_contig11553_534_5D	5D	371.54	0.000639	3.19	0.163212	5.60	-0.2034
Plus	Yield	BS00000929_51_5D	5D	377.86	1.58E-06	5.80	0.147668	11.43	-0.3090
Plus	Yield	IACX3123_5D	5D	377.86	5.34E-06	5.27	0.178756	10.20	-0.2586

Plus	Yield	Jagger_c754_272_5D	5D	377.86	0.000141	3.85	0.132124	7.02	-0.2508
Plus	Yield	Ku_c6176_938_5D	5D	377.86	0.000487	3.31	0.142487	5.86	0.2257
Plus	Yield	Kukri_c41787_141_5D	5D	387.6	0.000632	3.20	0.111399	5.62	0.2514
Plus	Yield	BS00037002_51_6A	6A	9.88	3.92E-05	4.41	0.064767	8.25	0.4902
Plus	Yield	IAAV5346_6A	6A	173.19	0.000581	3.24	0.072539	5.69	0.2669
Plus	Yield	BS00065852_51_6A	6A	175.85	0.000803	3.10	0.056995	5.39	-0.2844
Plus	Yield	BS00037003_51_6B	6B	1.28	7.73E-05	4.11	0.07513	7.59	0.3949
Plus	Yield	wsnp_Ex_c24927_34181611_6B	6B	259.52	0.000743	3.13	0.056995	5.47	-0.3690
Plus	Yield	BobWhite_c3506_1559_6B	6B	377.2	0.000395	3.40	0.056995	6.05	0.4492
Plus	Yield	Kukri_c27662_675_6B	6B	377.2	0.000418	3.38	0.064767	6.00	-0.4054
Plus	Yield	RAC875_c31299_1215_6B	6B	377.2	0.000303	3.52	0.062176	6.30	-0.4224
Plus	Yield	TA003403-0617_6B	6B	377.2	0.000437	3.36	0.134715	5.96	0.2509
Plus	Yield	RAC875_c45987_132_6B	6B	388.21	0.000418	3.38	0.064767	6.00	0.4054
Plus	Yield	RAC875_rep_c72984_1417_7A	7A	332.69	7.38E-05	4.13	0.056995	7.64	-0.3776
Plus	Yield	wsnp_Ex_c2360_4422599_7A	7A	371.18	0.000266	3.57	0.054404	6.42	-0.3796
Plus	Yield	Tdurum_contig76683_147_7B	7B	236.25	0.000415	3.38	0.054404	6.01	-0.3979
Plus	Yield	Excalibur_c13912_587_7B	7B	247.05	0.000415	3.38	0.054404	6.01	-0.3979
Plus	Yield	Tdurum_contig19852_242_7B	7B	251.12	0.000144	3.84	0.051813	7.00	0.4409

Note: Chro, chromosome; Pos (cM), the marker position; MAF, minor allele frequency, R^2, variance explained by marker on specific trait; QTL, name of the QTL; Yield, grain yield; TKW, thousand kernel weight; WH, % white heads; Screening, Percent screenings; WSB, Weighted stem browning; NDVI = Normalized difference vegetation index; PH = Plant height (cm); HD = Heading days; PMD = Physiological maturity days.

Appendix V

Table 1: Mean of stem browning (mm) in MARS population 1.

		Stem browning	
Entry	**Line name**	**Marker combined**	**Stem browning (mm)**
1	MARS4 DH2-3-1	19	8
2	MARS4 DH2-3-2	19	27.19
3	MARS4 DH2-3-3	19	13.32
4	MARS4 DH2-3-4	19	17.89
5	MARS4 DH2-3-5	19	27.68
6	MARS4 DH2-11-1	18	10.85
7	MARS4 DH2-11-2	18	20.85
8	MARS4 DH2-11-3	18	14.7
9	MARS4 DH2-11-4	18	37.92
10	MARS4 DH2-21-1	19	14.66
11	MARS4 DH2-21-2	19	5.03
12	MARS4 DH2-21-3	19	15.26
13	MARS4 DH2-21-4	19	9.2
14	MARS4 DH2-21-5	19	34.83
15	MARS4 DH2-21-6	19	27.51
16	MARS4 DH2-21-7	19	10.12
17	MARS4 DH2-21-8	19	19.11
18	MARS4 DH2-22-1	19	17.59
19	MARS4 DH2-22-2	19	12.59
20	MARS4 DH2-22-6	19	13.99
21	MARS4 DH2-22-7	19	16.09
22	MARS4 DH2-24-1	19	25.61
23	MARS4 DH2-24-2	19	39.31
24	MARS4 DH2-28-1	18	25.28
25	MARS4 DH2-28-2	18	12.44
26	MARS4 DH-128-11	10	22.26
27	MARS4 DH-130-4	10	14.86
28	MARS4 DH-130-5	10	15.23
29	MARS4 DH-139-1	10	47.92
30	MARS4 DH-139-2	10	49.45
31	MARS4 DH-139-3	10	31.94
32	MARS4 DH-139-6	10	22.59
33	MARS4 DH-139-9	10	22.35
34	MARS4 DH-141-2	10	39.68
35	MARS4 DH-141-3	10	12.86
36	MARS4 DH-141-4	10	25.31
37	MARS4 DH-141-7	10	19.47
38	MARS4 DH-141-8	10	42.03
39	MARS4 DH-141-10	10	21.39
40	MARS4 DH-147-2	10	24.75
41	MARS4 DH-147-5	10	31.58

42	MARS4 DH-147-6	10	25.59
43	MARS4 DH-147-7	10	30.62
44	MARS4 DH-148-1	10	36.22
45	MARS4 DH-148-7	10	53.22
46	MARS4 DH-148-11	10	26.21
47	MARS4 DH-541-2	10	20.31
48	MARS4 DH-541-3	10	22.41
49	MARS4 DH-541-4	10	35.1
50	MARS4 DH-541-7	10	42.88
51	MARS4 DH-541-10	10	34
52	MARS4 DH-558-1	11	29.45
53	MARS4 DH-558-2	11	30.91
54	MARS4 DH-564-1	10	21.37
55	MARS4 DH-564-5	10	26.32
56	MARS4 DH-564-7	10	29.37
57	MARS4 DH-575-1	10	36.24
58	MARS4 DH-582-1	10	15.48
59	MARS4 DH-582-2	10	33.8
60	MARS4 DH-582-3	10	15.69
61	MARS4 DH-582-4	10	22.33
62	MARS4 DH-582-7	10	23.34
63	MARS4 DH-582-10	10	27.88
64	MARS4 DH-586-2	10	13.27
65	MARS4 DH-586-3	10	32.78
66	MARS4 DH-586-4	10	41.9
67	MARS4 DH-586-6	10	17.71
68	MARS4 DH-589-3	10	35.39
69	MARS4 DH-589-4	10	47.52
70	MARS4 DH-589-6	10	36.21
71	MARS4 DH-589-9	10	29.9
72	MARS4 DH-589-10	10	33.36
73	MARS4 DH-590-2	10	29.29
74	MARS4 DH-590-3	10	18.02
75	MARS4 DH-590-5	10	33.58
76	MARS4 DH-590-6	10	15.7
77	MARS4 DH-611-6	10	27.18
78	MARS4 DH-611-8	10	24.76
79	MARS4 DH-611-10	10	21.88
80	MARS4 DH-629-3	10	17.96
81	MARS4 DH-659-6	10	20.06
82	MARS4 DH-667-3	10	16.71
83	MARS4 DH-693-11	10	9.66
84	MARS4 DH-699-1	10	12.59
85	MARS4 DH-699-3	10	14.2
86	MARS4 DH-706-4	10	17.53
87	MARS4 DH-707-3	10	7.64

88	MARS4 DH-707-6	10	28.56
89	MARS4 DH-711-1	10	12.26
90	MARS4 DH-711-4	10	20.4
91	MARS4 DH-717-2	10	8.59
92	MARS4 DH-720-1	11	11.6
93	MARS4 DH-720-4	11	10.64
94	MARS4 DH-720-7	11	25.57
95	MARS4 DH-722-4	10	20.29
96	MARS4 DH-722-9	10	13.98
97	MARS4 DH-730-7	11	23.65
98	MARS4 DH-730-10	11	28.62
99	MARS4 DH-732-3	10	9.34
100	MARS4 DH-735-3	10	22.28
101	MARS4 DH-736-2	11	18.92
102	MARS4 DH-736-4	11	34.1
103	MARS4 DH-746-7	10	12.45
104	MARS4 DH-747-3	10	12.39
105	MARS4 DH-747-4	10	20.39
106	MARS4 DH-747-8	10	20.77
107	MARS4 DH-747-10	10	12.61
108	MARS4 DH-753-1	11	21.72
109	MARS4 DH-755-2	10	11.08
110	MARS4 DH-755-12	10	21.99
111	MARS4 DH-757-1	10	10.57
112	MARS4 DH-757-2	10	10.47
113	MARS4 DH-757-4	10	17.65
114	MARS4 DH-757-6	10	27.23
115	MARS4 DH-757-7	10	11.01
116	MARS4 DH-757-9	10	12.02
117	MARS4 DH-757-10	10	14.65
118	MARS4 DH-762-1	10	36.79
119	MARS4 DH-762-3	10	15.08
120	MARS4 DH-762-4	10	18.79
121	MARS4 DH-762-8	10	13.03
122	MARS4 DH-762-9	10	25.95
123	MARS4 DH-762-10	10	27.22
124	PBICR-08-004TC-3	Base population	29.07
125	PBICR-08-004TC-68	Base population	34.62
126	PBICR-08-004TC-125	Base population	21.22
127	PBICR-08-004TC-131	Base population	10.66
128	PBICR-08-004TC-149	Base population	35.14
129	PBICR-08-004TC-157	Base population	11.6
130	PBICR-08-004TC-168	Base population	38.56
131	PBICR-08-004TC-206	Base population	19.81
132	AUS29529	Parent	44.89
133	2-49/CUNNINGHAM//KENNEDY	Parent	60.08

134	SUNCO	Parent	26.36
135	Suntop	Check	35.3
136	Sunguard	Check	50.94
137	Mace	Check	71.46
138	Spitfire	Check	45.1
139	EGA Gregory	Check	35.33
140	2_49	Check	23.49
	Predicted mean		**24.22**
	Standard error of differences		**4.852**
	Standard error of mean		**0.999**
	LSD (5%)		**9.52**

Table 2: Mean of stem browning (mm) in MARS population 2.

		Stem browning	
Entry	**Line name**	**Marker combined**	**Stem browning (mm)**
1	MARS5 DH2-36-1	18	24.82
2	MARS5 DH2-36-2	18	43.55
3	MARS5 DH2-45-1	21	15.65
4	MARS5 DH2-45-2	21	35.28
5	MARS5 DH2-45-3	21	21.1
6	MARS5 DH2-45-4	21	39.42
7	MARS5 DH2-47-1	19	31.64
8	MARS5 DH2-47-2	19	24.78
9	MARS5 DH2-47-3	19	38.12
10	MARS5 DH2-47-4	19	37.08
11	MARS5 DH2-48-1	19	12.78
12	MARS5 DH2-48-2	19	15.4
13	MARS5 DH2-48-3	19	18.83
14	MARS5 DH2-48-4	19	20.95
15	MARS5 DH2-48-5	19	29.41
16	MARS5 DH2-48-6	19	35.89
17	MARS5 DH2-48-7	19	23.74
18	MARS5 DH2-48-8	19	33.29
19	MARS5 DH2-48-9	19	20.58
20	MARS5 DH2-48-10	19	30.34
21	MARS5 DH2-50-1	20	28.48
22	MARS5 DH2-50-2	20	13.39
23	MARS5 DH2-50-3	20	43.54
24	MARS5 DH2-50-4	20	25.49
25	MARS5 DH2-50-5	20	16.09
26	MARS5 DH2-50-6	20	24.25
27	MARS5 DH2-55-1	21	34.69
28	MARS5 DH2-63-1	22	29.43
29	MARS5 DH2-63-2	22	19.72
30	MARS5 DH2-63-3	22	27.82

31	MARS5 DH2-63-4	22	25.71
32	MARS5 DH2-63-5	22	18.23
33	MARS5 DH2-63-6	22	7.85
34	MARS5 DH2-63-7	22	34.83
35	MARS5 DH2-63-8	22	10.15
36	MARS5 DH2-66-1	22	18.33
37	MARS5 DH2-66-2	22	25.25
38	MARS5 DH2-66-3	22	32.5
39	MARS5 DH2-66-4	22	31.96
40	MARS5 DH2-66-5	22	10.45
41	MARS5 DH2-66-6	22	9.05
42	MARS5 DH2-66-7	22	29.11
43	MARS5 DH2-66-8	22	18.84
44	MARS5 DH2-66-9	22	12.84
45	MARS5 DH2-66-10	22	5.85
46	MARS5 DH2-67-1	22	10.53
47	MARS5 DH2-67-2	22	32.93
48	MARS5 DH2-67-3	22	23.34
49	MARS5 DH2-67-4	22	12.01
50	MARS5 DH2-67-5	22	23.06
51	MARS5 DH2-67-6	22	24.16
52	MARS5 DH2-69-1	22	31.01
53	MARS5 DH2-69-2	22	21.61
54	MARS5 DH2-69-3	22	20.07
55	MARS5 DH2-69-4	22	12.3
56	MARS5 DH2-69-5	22	21.66
57	MARS5 DH2-69-6	22	17.58
58	MARS5 DH2-71-1	21	23.87
59	MARS5 DH2-71-2	21	22.4
60	MARS5 DH2-71-3	21	5.74
61	MARS5 DH2-72-1	21	15.68
62	MARS5 DH2-72-2	21	19.15
63	MARS5 DH2-72-3	21	18.42
64	MARS5 DH2-72-4	21	20.54
65	MARS5 DH2-72-5	21	28.04
66	MARS5 DH2-74-1	21	23.76
67	MARS5 DH2-74-2	21	14.21
68	MARS5 DH2-74-3	21	16.55
69	MARS5 DH2-73-1	21	18.39
70	MARS5 DH2-73-2	21	11.67
71	MARS5 DH2-73-3	21	13.08
72	MARS5 DH2-73-4	21	27.39
73	MARS5 DH2-73-5	21	10.71
74	MARS5 DH2-73-6	21	16.81
75	MARS5 DH-254-1	9	44.13
76	MARS5 DH-256-1	9	29.39

77	MARS5 DH-258-1	9	22.09
78	MARS5 DH-269-1	9	34.84
79	MARS5 DH-270-1	9	44.1
80	MARS5 DH-277-1	12	25.84
81	MARS5 DH-278-1	9	35.12
82	MARS5 DH-287-1	9	24.78
83	MARS5 DH-254-2	9	12.93
84	MARS5 DH-255-2	10	29.14
85	MARS5 DH-258-2	9	12.09
86	MARS5 DH-269-2	9	24.75
87	MARS5 DH-278-2	9	30.54
88	MARS5 DH-285-2	9	33.2
89	MARS5 DH-522-2	9	37.61
90	MARS5 DH-536-2	10	12.76
91	MARS5 DH-86-3	10	32.11
92	MARS5 DH-253-3	9	23.92
93	MARS5 DH-254-3	9	20.08
94	MARS5 DH-255-3	10	30.03
95	MARS5 DH-256-3	9	30.69
96	MARS5 DH-258-3	9	17.05
97	MARS5 DH-278-3	9	20.12
98	MARS5 DH-285-3	9	27.93
99	MARS5 DH-287-3	9	19.66
100	MARS5 DH-288-3	10	32.13
101	MARS5 DH-522-3	9	33.02
102	MARS5 DH-253-4	9	27.34
103	MARS5 DH-254-4	9	36.81
104	MARS5 DH-256-4	9	40.16
105	MARS5 DH-258-4	9	27.58
106	MARS5 DH-275-4	9	26.84
107	MARS5 DH-277-4	12	31.14
108	MARS5 DH-285-4	9	34.78
109	MARS5 DH-288-4	10	22.5
110	MARS5 DH-517-4	9	25.38
111	MARS5 DH-253-5	9	17.53
112	MARS5 DH-255-5	10	35.33
113	MARS5 DH-258-5	9	22.37
114	MARS5 DH-270-5	9	24.4
115	MARS5 DH-277-5	12	24.09
116	MARS5 DH-278-5	9	10.39
117	MARS5 DH-287-5	9	36.47
118	MARS5 DH-534-5	9	26.42
119	MARS5 DH-86-6	10	30.17
120	MARS5 DH-253-6	9	22.7
121	MARS5 DH-254-6	9	25.41
122	MARS5 DH-255-6	10	33.15

123	MARS5 DH-256-6	9	16.34
124	MARS5 DH-258-6	9	32.01
125	MARS5 DH-270-6	9	44.46
126	MARS5 DH-275-6	9	17.45
127	MARS5 DH-277-6	12	19.73
128	MARS5 DH-278-6	9	22.65
129	MARS5 DH-285-6	9	20.91
130	MARS5 DH-517-6	9	14.81
131	MARS5 DH-540-6	9	27.23
132	MARS5 DH-90-7	12	37.42
133	MARS5 DH-253-7	9	24.29
134	MARS5 DH-254-7	9	26.85
135	MARS5 DH-255-7	10	22.87
136	MARS5 DH-256-7	9	28.27
137	MARS5 DH-258-7	9	35.69
138	MARS5 DH-269-7	9	11.45
139	MARS5 DH-270-7	9	21.54
140	MARS5 DH-273-7	9	17.84
141	MARS5 DH-285-7	9	26.49
142	MARS5 DH-287-7	9	46.76
143	MARS5 DH-288-7	10	36.12
144	MARS5 DH-534-7	9	15.32
145	MARS5 DH-536-7	10	13.9
146	MARS5 DH-540-7	9	22.9
147	MARS5 DH-86-8	10	42.51
148	MARS5 DH-253-8	9	29.73
149	MARS5 DH-255-8	10	17.88
150	MARS5 DH-256-8	9	29.24
151	MARS5 DH-273-8	9	26.56
152	MARS5 DH-275-8	9	24.49
153	MARS5 DH-277-8	12	37.89
154	MARS5 DH-285-8	9	32.73
155	MARS5 DH-532-8	9	27.53
156	MARS5 DH-253-9	9	15.11
157	MARS5 DH-254-9	9	26.65
158	MARS5 DH-258-9	9	34.47
159	MARS5 DH-273-9	9	18.36
160	MARS5 DH-277-9	12	24.08
161	MARS5 DH-285-9	9	26.09
162	MARS5 DH-287-9	9	27.75
163	MARS5 DH-86-10	10	20.33
164	MARS5 DH-253-10	9	38.32
165	MARS5 DH-255-10	10	20.05
166	MARS5 DH-258-10	9	26.49
167	MARS5 DH-270-10	9	11.14
168	MARS5 DH-275-10	9	33.95

169	MARS5 DH-527-10	10	25.8
170	MARS5 DH-532-10	9	24.91
171	MARS5 DH-258-11	9	31.64
172	MARS5 DH-270-12	9	30.61
173	MARS5 DH-529-13	10	29.82
174	PBICR-08-005TC-5	Base population	37.14
175	PBICR-08-005TC-16	Base population	40.24
176	PBICR-08-005TC-33	Base population	34.09
177	PBICR-08-005TC-36	Base population	29.96
178	PBICR-08-005TC-50	Base population	30.31
179	PBICR-08-005TC-100	Base population	22.81
180	CSCR16	Parent	32.2
181	2-49/CUNNINGHAM//KENNEDY	Parent	13.45
182	SUNCO/2*PASTOR	Parent	25.88
183	Suntop	Check	39.5
184	Sunguard	Check	29
185	Mace	Check	39.03
186	Sunco	Check	24.23
187	Spitfire	Check	33.24
188	EGA Gregory	Check	73.4
189	Lancer	Check	37.84
190	EGA Wylie	Check	32.37
191	2_49	Check	13.9
192	EGA Bellaroi	Check	92.99
	Predicted means for Inoculum		**26.06**
	Standard error of differences		**4.375**
	Standard error of mean		**0.772**
	LSD (5%)		**8.58**

Table 3: Wald statistics from the tests of fixed effects for traits evaluated under inoculated (Plus) and un-inoculated (Nil) environment in the MARS population 1

	Wald statistics				
Source of variation	Yield	TKW	Screenings	White head	Stem browning
Classes (Par_BP_Rec_Che)	2.25ns	3.83ns	17.1**	4.32ns	254.44**
Inoculum	178.9**	5.79ns	145.45**	165.82**	-
Classes x Inoculum	1.45ns	0.35ns	1ns	4.94ns	-
	Treatment mean				
Nil	3197	34.79	1.983	0.381	-
Plus	2467	34.2	3.609	7.04	-
SED	125.5	0.68	0.32	1.51	-
LSD	294.92	1.94	1.32	2.88	-

Note: TKW, thousand kernel weight; Par, parents; BP, base population; Rec, recombination; Che, checks

Table 4: Wald statistics from the tests of fixed effects for traits evaluated under inoculated (Plus) and un-inoculated (Nil) environment in the MARS population 2

	Wald statistics			
Source of variation	Yield	TKW	Screenings	Stem browning
Classes (Par_BP_Che_Rec)	5.98^{ns}	30.95**	7.92^{ns}	61.76**
Inoculum	173.84**	41.31**	173.32**	
Classes x Inoculum	1.73^{ns}	0.95^{ns}	0.63^{ns}	
	Treatment mean			
Nil	3203	37.66	1.53	
Plus	2437	36.23	3.042	
SED	124.3	0.49	0.22	
LSD	243.68	0.96	0.44	

Note: TKW, thousand kernel weight; Par, parents; BP, base population; Rec, recombination; Che, checks

Table 5: Mean for genotype x inoculum of grain yield (kg ha^{-1}) and TKW (g) in MARS population 1.

			Grain yield (kg ha^{-1}) and TKW (g)			
			Yield		**TKW**	
Entry	**Line Name**	**Marker combined**	**Nil**	**Plus**	**Nil**	**Plus**
1	MARS4 DH-128-11	10	3170	2055	33.2	32.06
2	MARS4 DH-130-4	10	3003	2482	40.66	38.57
3	MARS4 DH-130-5	10	3482	2515	36.03	35.13
4	MARS4 DH-139-1	10	3756	2523	38.4	35.03
5	MARS4 DH-139-2	10	3488	2394	34.31	32.14
6	MARS4 DH-139-3	10	2363	1881	34.26	34.19
7	MARS4 DH-139-6	10	3180	2078	34.85	34.54
8	MARS4 DH-139-9	10	3246	2272	34.02	35.12
9	MARS4 DH-141-2	10	3458	2375	36.75	34.07
10	MARS4 DH-141-3	10	3496	2545	31.96	32.01
11	MARS4 DH-141-4	10	2885	2258	36.43	35.44
12	MARS4 DH-141-7	10	3141	2407	34.32	34.2
13	MARS4 DH-141-8	10	3330	2954	34.07	32.68
14	MARS4 DH-141-10	10	3589	2832	35.15	31.3
15	MARS4 DH-147-2	10	3102	2077	36.04	34.31
17	MARS4 DH-147-6	10	3610	2295	35.97	34.07
18	MARS4 DH-147-7	10	2832	2043	39.54	35.41
19	MARS4 DH-148-1	10	2948	1911	32.89	31.38
20	MARS4 DH-148-7	10	3799	2683	34.3	31.55
21	MARS4 DH-148-11	10	3087	1867	40.27	37.06
22	MARS4 DH-541-2	10	1650	2232	39.49	37.37
23	MARS4 DH-541-3	10	2879	2147	38.02	36.22
24	MARS4 DH-541-4	10	3426	1905	35.98	34.71
25	MARS4 DH-541-7	10	4016	2825	36.32	34.06
26	MARS4 DH-541-10	10	2860	2080	38.96	36.85

27	MARS4 DH-558-1	11	3447	2153	40.3	39.52
28	MARS4 DH-558-2	11	3888	2721	35.34	36.46
29	MARS4 DH-564-1	10	3647	2841	36.68	38.2
30	MARS4 DH-564-5	10	2610	1875	36.47	33.94
31	MARS4 DH-564-7	10	2499	2179	36.81	32.97
32	MARS4 DH-575-1	10	2860	2021	34.36	33.28
34	MARS4 DH-582-2	10	3375	2329	34.38	35.44
35	MARS4 DH-582-3	10	2879	1805	34.81	32.49
36	MARS4 DH-582-4	10	2476	1900	32.9	32.7
37	MARS4 DH-582-7	10	3347	2254	35.09	34.54
38	MARS4 DH-582-10	10	3773	2608	33.5	30.7
39	MARS4 DH-586-2	10	3236	1875	43.6	42.12
40	MARS4 DH-586-3	10	3079	1993	41.72	39.51
41	MARS4 DH-586-4	10	2953	1867	40.23	38.64
42	MARS4 DH-586-6	10	3480	1835	39.08	36.5
43	MARS4 DH-589-3	10	3170	2242	34.85	34.62
44	MARS4 DH-589-4	10	3573	2642	35.66	38.86
45	MARS4 DH-589-6	10	3613	2400	37.67	31.97
46	MARS4 DH-589-9	10	3196	1900	40.54	39
47	MARS4 DH-589-10	10	3450	2192	38.94	37.11
48	MARS4 DH-590-2	10	3014	2210	37.02	37.78
49	MARS4 DH-590-3	10	2821	1979	36.89	36.9
50	MARS4 DH-590-5	10	3277	2040	36.54	39.12
51	MARS4 DH-590-6	10	3274	2098	42.77	42.89
52	MARS4 DH-611-6	10	3483	2167	34.72	32.69
53	MARS4 DH-611-8	10	3162	2616	36.51	33.99
54	MARS4 DH-611-10	10	2534	1738	30.27	32.46
55	MARS4 DH-629-3	10	3601	2439	35.26	33.95
56	MARS4 DH-659-6	10	3247	2442	30.44	32.09
57	MARS4 DH-667-3	10	3275	2845	34.36	32.97
58	MARS4 DH-693-11	10	3453	2505	30.32	29.22
59	MARS4 DH-699-1	10	2628	2353	30.76	30.14
60	MARS4 DH-699-3	10	3545	2917	30.11	29.61
61	MARS4 DH-706-4	10	3363	2855	30.71	30.02
62	MARS4 DH-707-3	10	3792	2632	31.56	30.96
63	MARS4 DH-707-6	10	3062	2761	30.41	29.3
64	MARS4 DH-711-1	10	2956	2066	32.08	34.04
65	MARS4 DH-711-4	10	3127	1955	42.34	41.32
66	MARS4 DH-717-2	10	3039	2442	30.57	28.84
67	MARS4 DH-720-1	11	3186	2844	30.67	30.35
68	MARS4 DH-720-4	11	3268	2679	32.06	29.72
69	MARS4 DH-720-7	11	3067	2158	31	29.76
71	MARS4 DH-722-9	10	2594	2319	32.87	31.96
72	MARS4 DH-730-7	10	2966	2187	32.49	32.49
73	MARS4 DH-730-10	10	3677	2393	32.02	33.85
74	MARS4 DH-732-3	10	3333	2700	31.57	30.97

75	MARS4 DH-735-3	10	2811	2409	33.54	32.8
76	MARS4 DH-736-2	11	3218	2494	27.7	28.93
77	MARS4 DH-736-4	11	3099	2339	31.95	30.73
78	MARS4 DH-746-7	10	3479	2320	34.43	34.15
79	MARS4 DH-747-3	10	3469	2840	31.04	29.53
80	MARS4 DH-747-4	10	3637	3114	29.41	29.37
81	MARS4 DH-747-8	10	3575	2993	30.06	29.5
82	MARS4 DH-747-10	10	3747	3060	30.11	30.45
83	MARS4 DH-753-1	11	2849	2212	31.76	30.73
84	MARS4 DH-755-2	10	2347	1798	34.31	32.6
85	MARS4 DH-755-12	10	3012	2219	33.09	32.93
86	MARS4 DH-757-1	10	3312	2667	30.69	29.75
87	MARS4 DH-757-2	10	3484	2992	31.39	30.06
88	MARS4 DH-757-4	10	3224	2580	30.01	36.54
89	MARS4 DH-757-6	10	3545	3041	30.65	29.7
90	MARS4 DH-757-7	10	2861	2801	36.99	29.99
91	MARS4 DH-757-9	10	3089	2466	30.53	28.86
92	MARS4 DH-757-10	10	3091	2655	30.47	28.65
93	MARS4 DH-762-1	10	3665	2250	35.31	34.09
94	MARS4 DH-762-3	10	3200	2377	31.03	30.49
95	MARS4 DH-762-4	10	2689	1601	25.87	25.1
96	MARS4 DH-762-8	10	5462	2478	30.91	30.18
97	MARS4 DH-762-9	10	2696	2293	31.43	31.82
98	MARS4 DH-762-10	10	3029	2508	32	33.22
99	PBICR-08-004TC-3	Base population	2562	1833	37.71	37.96
100	PBICR-08-004TC-68	Base population	2618	1914	38.3	37.18
101	PBICR-08-004TC-125	Base population	3749	3228	33.76	32.7
102	PBICR-08-004TC-131	Base population	3440	2226	32.54	31.5
103	PBICR-08-004TC-149	Base population	3230	2352	35.79	35.04
104	PBICR-08-004TC-157	Base population	3215	2720	31.62	32.02
105	PBICR-08-004TC-168	Base population	1631	2329	30.58	29.27
106	PBICR-08-004TC-206	Base population	2704	2206	41.34	41.42
107	AUS29529	Parent	2320	2280	41.64	40.56
108	2-49/CUNNINGHAM//KENNEDY	Parent	2959	2109	38.9	37.09
109	SUNCO	Parent	3764	2922	31.94	32.07
110	Suntop	Check	3593	2591	39.12	38.05
111	Sunguard	Check	3639	3073	32.35	32.17
112	Mace	Check	3366	2624	37.63	35.62
113	Sunco	Check	3391	2794	32.02	33.51
114	Spitfire	Check	3497	2376	33.71	30.3
115	EGA Gregory	Check	3700	2306	33.05	36.6
116	Lancer	Check	4202	2981	33.22	32.86
117	EGA Wylie	Check	1843	2136	35.36	34.53
118	2_49	Check	2129	1859	29.42	29.08
119	EGA Bellaroi	Check	3114	2223	36.47	34.96
	Predicted mean		**3193**	**2372**	**34.51**	**33.62**

SED	**543.1**		**1.801**	
Standard error of mean	**46.86**	**33.49**	**0.332**	**0.316**
LSD (5%) (Genotype x Inoculum)	**1068.42**		**3.54**	
LSD (5%) (Genotype)	**668.37**		**2.75**	

Table 6: Mean for genotype x inoculum of % screenings loss and % white head in MARS population 1.

			Percent screenings and percent white heads			
			% screenings		**% White heads**	
Entry	**Line Name**	**Marker combined**	**Nil**	**Plus**	**Nil**	**Plus**
1	MARS4 DH-128-11	10	2.862	6.352	0	16.32
2	MARS4 DH-130-4	10	1.726	3.01	1.2	10.25
3	MARS4 DH-130-5	10	2.877	4.986	0.476	10.447
4	MARS4 DH-139-1	10	0.894	4.946	0.21	14.977
5	MARS4 DH-139-2	10	2.384	6.381	0	24.754
6	MARS4 DH-139-3	10	2.698	3.766	0	1.546
7	MARS4 DH-139-6	10	2.163	3.282	1.84	21.095
8	MARS4 DH-139-9	10	2.266	5.535	1.4	22.754
9	MARS4 DH-141-2	10	0.835	4.538	0.279	20.01
10	MARS4 DH-141-3	10	1.594	3.937	0.752	10.255
11	MARS4 DH-141-4	10	2.566	3.879	1.181	8.324
12	MARS4 DH-141-7	10	1.047	4.771	1.749	16.435
13	MARS4 DH-141-8	10	1.999	6.305	1.736	9.592
14	MARS4 DH-141-10	10	3.065	8.427	1.438	13.309
15	MARS4 DH-147-2	10	3.964	6.105	0	12.225
17	MARS4 DH-147-6	10	1.851	4.599	0.309	30.001
18	MARS4 DH-147-7	10	1.047	3.14	0	5.03
19	MARS4 DH-148-1	10	2.22	4.945	1.642	7.77
20	MARS4 DH-148-7	10	2.07	6.136	0.073	35.355
21	MARS4 DH-148-11	10	0.139	5.164	0.92	34.673
22	MARS4 DH-541-2	10	1.257	3.596	0	7.484
23	MARS4 DH-541-3	10	1.737	4.601	0.755	7.47
24	MARS4 DH-541-4	10	3.761	6.195	1.605	16.563
25	MARS4 DH-541-7	10	3.302	5.469	0.244	7.873
26	MARS4 DH-541-10	10	1.555	3.823	0.161	8.111
27	MARS4 DH-558-1	11	0.613	4.03	0	20.321
28	MARS4 DH-558-2	11	4.497	7.731	0	18.904
29	MARS4 DH-564-1	10	2.742	3.162	1.436	4.151
30	MARS4 DH-564-5	10	1.993	5.849	0.819	20.096
31	MARS4 DH-564-7	10	0.634	3.301	0.142	13.157
32	MARS4 DH-575-1	10	4.729	7.111	0.395	12.6
34	MARS4 DH-582-2	10	3.555	5.22	0.604	12.699
35	MARS4 DH-582-3	10	3.75	6.746	0.56	25.562
36	MARS4 DH-582-4	10	3.24	6.143	1.766	24.438
37	MARS4 DH-582-7	10	4.736	6.059	0.942	8.17

38	MARS4 DH-582-10	10	4.529	7.755	0	14.245
39	MARS4 DH-586-2	10	0.97	3.36	0	16.863
40	MARS4 DH-586-3	10	1.819	4.239	0.918	35.042
41	MARS4 DH-586-4	10	2.027	4.525	2.646	18.881
42	MARS4 DH-586-6	10	2.031	7.432	1.163	39.214
43	MARS4 DH-589-3	10	4.214	5.621	0	8.385
44	MARS4 DH-589-4	10	5.227	3.625	2.361	8.343
45	MARS4 DH-589-6	10	4.061	6.078	1.637	20.733
46	MARS4 DH-589-9	10	1.901	5.45	0.462	31.786
47	MARS4 DH-589-10	10	2.877	7.119	0.822	25.457
48	MARS4 DH-590-2	10	2.851	3.284	0.875	2.556
49	MARS4 DH-590-3	10	1.441	2.95	1.433	21.389
50	MARS4 DH-590-5	10	1.984	2.086	0.165	8.267
51	MARS4 DH-590-6	10	0.9	2.485	0.061	5.392
52	MARS4 DH-611-6	10	3.406	6.821	0.487	35.901
53	MARS4 DH-611-8	10	3.28	6.43	1.198	9.318
54	MARS4 DH-611-10	10	3.41	2.808	0.925	13.277
55	MARS4 DH-629-3	10	3.046	2.939	0.802	2.065
56	MARS4 DH-659-6	10	2.627	2.097	1.385	11.756
57	MARS4 DH-667-3	10	1.208	4.136	1.303	7.923
58	MARS4 DH-693-11	10	1.543	4.195	0.887	8.182
59	MARS4 DH-699-1	10	1.395	2.513	0.99	2.179
60	MARS4 DH-699-3	10	2.226	3.726	2.625	3.781
61	MARS4 DH-706-4	10	1.477	2.91	0	1.321
62	MARS4 DH-707-3	10	1.493	3.565	0	2.456
63	MARS4 DH-707-6	10	1.608	2.664	0.024	0.015
64	MARS4 DH-711-1	10	1.726	3.233	0.615	15.498
65	MARS4 DH-711-4	10	1.668	3.494	1.677	23.219
66	MARS4 DH-717-2	10	1.726	4.758	0	1.134
67	MARS4 DH-720-1	11	1.388	2.629	0.723	1.416
68	MARS4 DH-720-4	11	1.023	3.495	0.606	3.044
69	MARS4 DH-720-7	11	1.131	3.102	0	1.244
71	MARS4 DH-722-9	10	1.35	1.726	1.077	2.493
72	MARS4 DH-730-7	10	1.378	2.355	1.015	6.239
73	MARS4 DH-730-10	10	3.938	3.41	0	13.836
74	MARS4 DH-732-3	10	1.841	2.718	0.851	0.88
75	MARS4 DH-735-3	10	1.153	1.399	0.531	0.408
76	MARS4 DH-736-2	11	2.039	2.736	0.279	0.145
77	MARS4 DH-736-4	11	1.162	1.893	0	0.261
78	MARS4 DH-746-7	10	1.688	3.197	0.217	12.846
79	MARS4 DH-747-3	10	1.572	4.018	1.498	4.299
80	MARS4 DH-747-4	10	2.078	2.87	0.096	0.876
81	MARS4 DH-747-8	10	2.391	3.76	0	0.289
82	MARS4 DH-747-10	10	1.331	2.789	0	1.169
83	MARS4 DH-753-1	11	1.502	3.658	1.296	5.051
84	MARS4 DH-755-2	10	1.463	3.237	0.072	7.732

85	MARS4 DH-755-12	10	1.947	2.834	1.848	4.556
86	MARS4 DH-757-1	10	2.479	3.162	1.152	1.504
87	MARS4 DH-757-2	10	1.478	2.83	0	0.119
88	MARS4 DH-757-4	10	1.855	4.358	0.842	2.357
89	MARS4 DH-757-6	10	2.154	3.445	0.276	1.433
90	MARS4 DH-757-7	10	1.702	2.52	0.167	0.753
91	MARS4 DH-757-9	10	2.108	3.738	0	0.9
92	MARS4 DH-757-10	10	1.763	3.642	0	0.46
93	MARS4 DH-762-1	10	1.543	2.84	0	9.617
94	MARS4 DH-762-3	10	0.938	2.438	0	7.486
95	MARS4 DH-762-4	10	2.119	5.411	0	1.887
96	MARS4 DH-762-8	10	0.742	2.087	0	1.333
97	MARS4 DH-762-9	10	0.833	2.114	0.273	2.217
98	MARS4 DH-762-10	10	1.592	2.285	1.141	2.19
99	PBICR-08-004TC-3	Base population	1.125	3.04	2.298	5.972
100	PBICR-08-004TC-68	Base population	1.162	3.546	1.906	5.681
101	PBICR-08-004TC-125	Base population	1.922	2.225	1.269	3.449
102	PBICR-08-004TC-131	Base population	1.208	3.564	0	4.597
103	PBICR-08-004TC-149	Base population	2.01	3.177	3.102	4.705
104	PBICR-08-004TC-157	Base population	3.63	5.018	0.355	4.118
105	PBICR-08-004TC-168	Base population	7.691	10.719	2.521	27.102
106	PBICR-08-004TC-206	Base population	1.005	2.006	0.115	2.129
107	AUS29529	Parent	0.134	-0.038	1.24	2.854
108	2-49/CUNNINGHAM//KENNEDY	Parent	0.864	2.652	1.075	2.816
109	SUNCO	Parent	1.426	2.62	0.117	1.332
110	Suntop	Check	1.722	2.408	0.078	2.22
111	Sunguard	Check	1.062	2.397	0.399	2.511
112	Mace	Check	2.22	3.352	0.859	5.606
113	Sunco	Check	1.148	2.108	0.529	3.71
114	Spitfire	Check	2.409	7.249	0	8.123
115	EGA Gregory	Check	1.035	4.374	0.314	36.842
116	Lancer	Check	1.581	5.065	0.614	4.749
117	EGA Wylie	Check	1.547	3.88	0	7.732
118	2_49	Check	2.307	2.823	0	0
119	EGA Bellaroi	Check	2.149	3.173	1.509	15.878
	Predicted mean		**2.087**	**4.048**	**0.536**	**10.154**
	SED		**1.101**		**5.818**	
	Standard error of mean		**0.107**	**0.159**	**0.0679**	**0.908**
	LSD (5%) (Genotype x Inoculum)		**2.16**		**11.44**	
	LSD (5%) (Genotype)		**1.74**		**8.38**	

Table 7: Mean of % yield loss and stem browning (mm) in MARS population 1.

		Yield loss and stem browning		
Entry	**Line Name**	**Marker combined**	**% Yield Loss**	**WSB in Plus**
1	MARS4 DH-128-11	10	27.09	15.68

2	MARS4 DH-130-4	10	19.31	19.27
3	MARS4 DH-130-5	10	28.79	38.81
4	MARS4 DH-139-1	10	34.66	26.69
5	MARS4 DH-139-2	10	28.29	42.64
6	MARS4 DH-139-3	10	26.54	6.85
7	MARS4 DH-139-6	10	33.12	7.64
8	MARS4 DH-139-9	10	32.49	33.78
9	MARS4 DH-141-2	10	34.54	12.53
10	MARS4 DH-141-3	10	28.91	4.87
11	MARS4 DH-141-4	10	23.46	13.11
12	MARS4 DH-141-7	10	21.06	11.77
13	MARS4 DH-141-8	10	13.3	11.53
14	MARS4 DH-141-10	10	20.13	28.65
15	MARS4 DH-147-2	10	35.42	7.75
17	MARS4 DH-147-6	10	38.61	22.22
18	MARS4 DH-147-7	10	27.85	26.41
19	MARS4 DH-148-1	10	38.37	36.65
20	MARS4 DH-148-7	10	28.18	11.35
21	MARS4 DH-148-11	10	35.04	19.19
22	MARS4 DH-541-2	10	25.5	18.53
23	MARS4 DH-541-3	10	20.33	10.87
24	MARS4 DH-541-4	10	43.63	12.35
25	MARS4 DH-541-7	10	31.55	14.16
26	MARS4 DH-541-10	10	30.17	8.54
27	MARS4 DH-558-1	11	34.1	29.22
28	MARS4 DH-558-2	11	30.03	26.42
29	MARS4 DH-564-1	10	19.98	8.97
30	MARS4 DH-564-5	10	23.23	29.82
31	MARS4 DH-564-7	10	19.96	21.14
32	MARS4 DH-575-1	10	34.48	12.66
34	MARS4 DH-582-2	10	34.51	28.3
35	MARS4 DH-582-3	10	30.83	13.54
36	MARS4 DH-582-4	10	22.42	21.35
37	MARS4 DH-582-7	10	32.99	26.57
38	MARS4 DH-582-10	10	28.33	24.81
39	MARS4 DH-586-2	10	45.08	16.61
40	MARS4 DH-586-3	10	41.76	26.94
41	MARS4 DH-586-4	10	34.23	23.59
42	MARS4 DH-586-6	10	42.22	35.55
43	MARS4 DH-589-3	10	24.82	24.08
44	MARS4 DH-589-4	10	24.44	22.83
45	MARS4 DH-589-6	10	33.52	19
46	MARS4 DH-589-9	10	43.8	23.86
47	MARS4 DH-589-10	10	36.15	21.57
48	MARS4 DH-590-2	10	26.55	17.08
49	MARS4 DH-590-3	10	35.97	8.03

50	MARS4 DH-590-5	10	32.15	11.34
51	MARS4 DH-590-6	10	31.42	11.27
52	MARS4 DH-611-6	10	36.55	18.72
53	MARS4 DH-611-8	10	11.62	16.79
54	MARS4 DH-611-10	10	28.55	6.92
55	MARS4 DH-629-3	10	33.64	13.12
56	MARS4 DH-659-6	10	25.43	3.07
57	MARS4 DH-667-3	10	10.33	14.3
58	MARS4 DH-693-11	10	31.78	8.67
59	MARS4 DH-699-1	10	7.73	5.58
60	MARS4 DH-699-3	10	18.39	4.75
61	MARS4 DH-706-4	10	18.25	3.05
62	MARS4 DH-707-3	10	28.99	11.9
63	MARS4 DH-707-6	10	10.09	10.32
64	MARS4 DH-711-1	10	27.86	2.69
65	MARS4 DH-711-4	10	40.37	16.96
66	MARS4 DH-717-2	10	23.03	8.6
67	MARS4 DH-720-1	11	12.37	4.42
68	MARS4 DH-720-4	11	21.36	14.3
69	MARS4 DH-720-7	11	25.17	6.83
71	MARS4 DH-722-9	10	10.64	3.4
72	MARS4 DH-730-7	10	23.03	2.19
73	MARS4 DH-730-10	10	36.28	12.58
74	MARS4 DH-732-3	10	27.08	5.64
75	MARS4 DH-735-3	10	14.18	5.05
76	MARS4 DH-736-2	11	25.43	10.22
77	MARS4 DH-736-4	11	25.95	8.56
78	MARS4 DH-746-7	10	32.6	4.26
79	MARS4 DH-747-3	10	16.44	4.03
80	MARS4 DH-747-4	10	15.87	10.52
81	MARS4 DH-747-8	10	17.46	5.85
82	MARS4 DH-747-10	10	16.24	6.06
83	MARS4 DH-753-1	11	23.12	8.02
84	MARS4 DH-755-2	10	23.2	8.96
85	MARS4 DH-755-12	10	27.44	13.59
86	MARS4 DH-757-1	10	15.78	9.84
87	MARS4 DH-757-2	10	13.2	14.52
88	MARS4 DH-757-4	10	16.58	7.64
89	MARS4 DH-757-6	10	15.62	4.59
90	MARS4 DH-757-7	10	13.51	5.91
91	MARS4 DH-757-9	10	23.38	4.11
92	MARS4 DH-757-10	10	11.85	8.81
93	MARS4 DH-762-1	10	37.02	15.03
94	MARS4 DH-762-3	10	26.54	9.54
95	MARS4 DH-762-4	10	40.58	7.7
96	MARS4 DH-762-8	10	43.96	9.88

97	MARS4 DH-762-9	10	20.99	5.07
98	MARS4 DH-762-10	10	12.66	2.35
99	PBICR-08-004TC-3	Base population	29.28	37.87
100	PBICR-08-004TC-68	Base population	22.36	17.64
101	PBICR-08-004TC-125	Base population	13.6	16.29
102	PBICR-08-004TC-131	Base population	33.77	16.87
103	PBICR-08-004TC-149	Base population	25.22	15
104	PBICR-08-004TC-157	Base population	13.91	16.74
105	PBICR-08-004TC-168	Base population	22.93	11.68
106	PBICR-08-004TC-206	Base population	22.05	17.56
107	AUS29529	Parent	0	4.49
108	2-49/CUNNINGHAM//KENNEDY	Parent	28.75	27.77
109	SUNCO	Parent	24.52	16.87
110	Suntop	Check	29.14	37.7
111	Sunguard	Check	16.82	13.15
112	Mace	Check	22.32	31.68
113	Sunco	Check	14.94	23.68
114	Spitfire	Check	34.06	25.66
115	EGA Gregory	Check	34.06	44.86
116	Lancer	Check	29.27	19.08
117	EGA Wylie	Check	27.23	28.05
118	2_49	Check	12.72	10.5
119	EGA Bellaroi	Check	27.27	14.66
	SED		**11.27**	**3.295**
	Standard error of mean		**0.842**	**0.905**
	LSD (5%) (genotype)		**22.18**	**6.4**

Table 8: Mean for genotype x inoculum of grain yield (kg ha^{-1}) and TKW (g) in MARS population 2.

Grain yield (kg ha^{-1}) and TKW (g)						
			Yield		**TKW**	
Entry	**Line**	**Marker combined**	**Nil**	**Plus**	**Nil**	**Plus**
1	MARS5 DH-254-1	10	3848	3071	39.57	38.89
2	MARS5 DH-256-1	9	2690	1811	39.08	38.68
3	MARS5 DH-258-1	9	3856	3558	40.31	39.74
4	MARS5 DH-269-1	9	3141	2220	38.62	36.05
5	MARS5 DH-270-1	9	4032	3253	38.39	36.99
6	MARS5 DH-277-1	12	4363	3284	36.6	35.83
7	MARS5 DH-278-1	9	3687	2892	38.55	37.17
8	MARS5 DH-287-1	9	4108	3399	38.08	37.48
9	MARS5 DH-254-2	10	4204	3598	37.61	37.4
10	MARS5 DH-255-2	10	2894	2535	35.62	34.74
11	MARS5 DH-258-2	9	3204	2065	35.03	34.88
12	MARS5 DH-269-2	9	3919	3235	37.33	34.56
13	MARS5 DH-278-2	9	3368	711	39.24	37.67

14	MARS5 DH-285-2	9	3853	3099	39.14	37.42
15	MARS5 DH-522-2	9	3753	3010	32.94	32.66
16	MARS5 DH-536-2	10	3221	2348	36.04	36.09
17	MARS5 DH-86-3	10	3342	2871	39.47	38.22
18	MARS5 DH-253-3	10	3181	2426	38.63	35.38
19	MARS5 DH-254-3	10	4100	3596	38.27	34.37
20	MARS5 DH-255-3	10	3574	3221	40.61	37.51
21	MARS5 DH-256-3	9	2876	1180	37.11	37.65
22	MARS5 DH-258-3	9	3375	2890	39.44	38.87
23	MARS5 DH-278-3	9	3736	2880	38.26	38.06
24	MARS5 DH-285-3	9	3776	2867	38.03	38.98
25	MARS5 DH-287-3	9	3662	3282	36.61	34.78
26	MARS5 DH-288-3	10	3847	3327	37.94	37.13
27	MARS5 DH-522-3	9	3737	2432	33.33	32.25
28	MARS5 DH-253-4	10	3650	3259	42.03	39.55
29	MARS5 DH-254-4	10	3962	3096	36.73	36.54
30	MARS5 DH-256-4	9	3637	2962	41.2	38.96
31	MARS5 DH-258-4	9	2591	1651	35.57	34.97
33	MARS5 DH-277-4	12	3771	3116	37	35.47
34	MARS5 DH-285-4	9	4260	3662	37.92	38.31
35	MARS5 DH-288-4	10	3811	3285	37.12	35.15
36	MARS5 DH-517-4	9	3493	3507	38.27	36.78
37	MARS5 DH-253-5	10	3686	2793	40.84	37.97
38	MARS5 DH-255-5	10	3381	2884	38.25	36.21
39	MARS5 DH-258-5	9	3351	2290	38.11	36.14
40	MARS5 DH-270-5	9	3467	2473	37.34	35
41	MARS5 DH-277-5	12	3958	3137	36.92	33.64
42	MARS5 DH-278-5	9	3653	3177	40.36	38.99
43	MARS5 DH-287-5	9	3989	2715	36.8	34.45
44	MARS5 DH-534-5	9	3328	1818	42.62	39.41
45	MARS5 DH-86-6	10	2808	2021	44.51	42.24
46	MARS5 DH-253-6	10	3523	3031	41.9	39.11
47	MARS5 DH-254-6	10	4029	3099	38.69	37.18
48	MARS5 DH-255-6	10	3362	3307	37.4	36.6
49	MARS5 DH-256-6	9	2931	2228	38.05	36.49
50	MARS5 DH-258-6	9	3346	2845	35.99	33.92
51	MARS5 DH-270-6	9	4203	3694	38.96	36.12
52	MARS5 DH-275-6	9	2779	2344	38.61	37.52
53	MARS5 DH-277-6	12	3341	2870	37.92	36.07
54	MARS5 DH-278-6	9	3421	2712	36.53	37.46
55	MARS5 DH-285-6	9	3785	2965	39.35	38.21
56	MARS5 DH-517-6	9	3027	1836	39.45	37.88
57	MARS5 DH-540-6	9	4010	2712	36.11	34.13
58	MARS5 DH-90-7	12	2608	1403	41.65	38.97
59	MARS5 DH-253-7	10	4000	3257	37.69	36.37
60	MARS5 DH-254-7	10	4134	4075	40.25	37.04

61	MARS5 DH-255-7	10	3738	2455	38.06	36.57
62	MARS5 DH-256-7	9	3372	1292	38.9	37.2
63	MARS5 DH-258-7	9	2960	2450	34.86	33.24
64	MARS5 DH-269-7	9	3947	3719	38.77	35.66
65	MARS5 DH-270-7	9	3196	2580	38.22	36.18
66	MARS5 DH-273-7	9	3441	2379	38.26	36.48
67	MARS5 DH-285-7	9	2837	1734	39.17	38.65
68	MARS5 DH-287-7	9	3354	2978	37.32	36.12
69	MARS5 DH-288-7	10	3671	3051	39.88	37.66
70	MARS5 DH-534-7	10	3282	1937	38.3	40.05
71	MARS5 DH-536-7	9	3700	2820	39.31	38.63
72	MARS5 DH-540-7	10	2880	2205	37.23	35.3
73	MARS5 DH-86-8	10	3320	2659	41.94	37.97
74	MARS5 DH-253-8	10	4462	3483	39.77	36.78
75	MARS5 DH-255-8	9	3091	2813	39.02	38.4
76	MARS5 DH-256-8	9	3940	3249	38.56	37.2
77	MARS5 DH-273-8	9	3887	3073	38.03	38.05
78	MARS5 DH-275-8	12	2820	1431	38.78	37.9
79	MARS5 DH-277-8	9	3461	2712	37.81	36.66
80	MARS5 DH-285-8	9	2833	2461	39.56	34.83
81	MARS5 DH-532-8	10	3288	2635	38.49	34.16
82	MARS5 DH-253-9	10	4296	3353	39.21	36.96
83	MARS5 DH-254-9	9	3640	2721	36.78	35.16
84	MARS5 DH-258-9	9	3577	3215	38.98	37.45
85	MARS5 DH-273-9	12	3602	2971	39.91	37.57
86	MARS5 DH-277-9	9	4078	3427	39.61	38.6
87	MARS5 DH-285-9	9	3550	2186	41.31	37.69
88	MARS5 DH-287-9	10	3656	2862	35.93	34.09
89	MARS5 DH-86-10	10	2791	1990	39	36.57
90	MARS5 DH-253-10	10	4082	3373	55.83	37.52
91	MARS5 DH-255-10	9	4048	3453	38.57	37.49
92	MARS5 DH-258-10	9	2863	2377	38.05	35.32
93	MARS5 DH-270-10	9	3427	2952	39.77	37.62
94	MARS5 DH-275-10	10	3652	2813	37.99	36.42
95	MARS5 DH-527-10	9	3921	2908	37.41	34.47
96	MARS5 DH-532-10	9	3129	2184	39.01	37.51
97	MARS5 DH-258-11	9	3652	3084	37.33	36.67
98	MARS5 DH-270-12	10	3279	2612	37.25	36.39
99	MARS5 DH-529-13	Base population	2861	1376	42.57	43.99
100	PBICR-08-005TC-5	Base population	3031	1955	37.97	38.1
101	PBICR-08-005TC-16	Base population	3172	2844	39.36	36.97
102	PBICR-08-005TC-33	Base population	3410	2421	39.1	35.91
103	PBICR-08-005TC-36	Base population	3003	2658	39.19	38.74
104	PBICR-08-005TC-50	Base population	3646	2912	40.31	37.14
105	PBICR-08-005TC-100	parent	3275	2290	40.89	39.81
106	CSCR16	parent	2355	1621	34.15	36.09

107	2-49/CUNNINGHAM//KENNEDY	parent	2703	2162	38.73	36.5
108	SUNCO/2*PASTOR	Check	3430	3113	33.16	31.04
109	Suntop	Check	3228	2430	38.08	38.64
110	Sunguard	Check	3629	3259	32.5	33.73
111	Mace	Check	3726	1252	39.14	39.45
112	Sunco	Check	3635	2599	34.81	33.85
113	Spitfire	Check	3130	2222	36.16	33.26
114	EGA Gregory	Check	3915	2371	39.7	36.44
115	Lancer	Check	3886	3517	35.86	35.1
116	EGA Wylie	Check				
117	249	Check	2509	1999	30.86	30.11
118	EGA Bellaroi	Check	2594	1828	39.41	38.55
	Predicted Mean		**3487**	**2696**	**38.4**	**36.75**
	Standard error of mean		**42.55**	**58.98**	**0.248**	**0.19**
	SED		**559.7**		**2.068**	
	LSD (5%) (Genotype x Inoculum)		**550.51**		**2.03**	
	LSD (5%) (Genotype)		**391.41**		**1.44**	

Table 9. Mean for genotype x inoculum of % screenings loss, and mean of % yield loss and stem browning (mm) in MARS population 2.

Entry	**Line**	**Marker combined**	**% Screenings** **Nil**	 **Plus**	**% Yield loss**	**WSB in Plus**
1	MARS5 DH-254-1	10	0.925	2.333	19.41	18.34
2	MARS5 DH-256-1	9	1.218	2.9	31.5	16.41
3	MARS5 DH-258-1	9	1.094	2.841	3.43	10.98
4	MARS5 DH-269-1	9	1.592	4.353	27.87	37.77
5	MARS5 DH-270-1	9	2.478	3.788	21.68	23.89
6	MARS5 DH-277-1	12	4.039	3.497	19.76	13.53
7	MARS5 DH-278-1	9	2.273	1.709	25.96	22.89
8	MARS5 DH-287-1	9	1.646	1.256	16.23	28.92
9	MARS5 DH-254-2	10	3.009	4.146	12.61	47.49
10	MARS5 DH-255-2	10	2.079	2.415	13.66	17.98
11	MARS5 DH-258-2	9	1.88	4.206	9.82	23.7
12	MARS5 DH-269-2	9	3.673	4.977	16.93	19.28
13	MARS5 DH-278-2	9	1.769	2.858		22.21
14	MARS5 DH-285-2	9	1.477	2.547	21.66	18.19
15	MARS5 DH-522-2	9	6.641	9.847	25.41	6.74
16	MARS5 DH-536-2	10	2.377	3.699	27.13	11.82
17	MARS5 DH-86-3	10	1.046	2.069	14.39	15.28
18	MARS5 DH-253-3	10	0.996	2.923	26.45	20.01
19	MARS5 DH-254-3	10	1.777	5.223	10.88	59.09
20	MARS5 DH-255-3	10	0.788	2.822	9.9	26.61
21	MARS5 DH-256-3	9	3.744	2.181	7.6	20.78
22	MARS5 DH-258-3	9	1.812	2.812	13.13	12.75
23	MARS5 DH-278-3	9	0.885	2.689	23.6	21.8
24	MARS5 DH-285-3	9	2.108	3.035	27.26	16.41

25	MARS5 DH-287-3	9	1.924	3.154	15.2	22.61
26	MARS5 DH-288-3	10	1.927	3.699	11.95	24.88
27	MARS5 DH-522-3	9	5.771	9.258	31.69	8.38
28	MARS5 DH-253-4	10	1.065	2.066	14.37	15.99
29	MARS5 DH-254-4	10	1.766	2.338	19.12	20.35
30	MARS5 DH-256-4	9	0.955	2.58	16.66	25.52
31	MARS5 DH-258-4	9	2.961	6.131	6.61	20.82
33	MARS5 DH-277-4	12	1.701	4.339	15.68	52.09
34	MARS5 DH-285-4	9	2.738	2.163	10.3	32.23
35	MARS5 DH-288-4	10	1.704	4.122	13.35	29.79
36	MARS5 DH-517-4	9	1.945	3.381	10.27	46.8
37	MARS5 DH-253-5	10	1.2	2.621	23.94	19.14
38	MARS5 DH-255-5	10	1.157	2.78	8.8	20.07
39	MARS5 DH-258-5	9	1.358	2.384	33.41	16.26
40	MARS5 DH-270-5	9	1.987	4.63	21.82	18.4
41	MARS5 DH-277-5	12	2.286	4.519	20.41	41.94
42	MARS5 DH-278-5	9	1.012	1.669	8.82	16.4
43	MARS5 DH-287-5	9	1.9	2.829	34.45	38.06
44	MARS5 DH-534-5	9	1.91	5.544	42.36	12.91
45	MARS5 DH-86-6	10	0.59	2.032	29.2	18.2
46	MARS5 DH-253-6	10	0.924	2.051	9.67	22.16
47	MARS5 DH-254-6	10	2.025	2.436	21.29	17.54
48	MARS5 DH-255-6	10	1.918	3.123	17.38	31.42
49	MARS5 DH-256-6	9	0.78	3.657	21.6	30.38
50	MARS5 DH-258-6	9	2.067	5.021	12.07	29.82
51	MARS5 DH-270-6	9	2.263	2.785	15.27	9.58
52	MARS5 DH-275-6	9	1.616	2.417	17.9	13.89
53	MARS5 DH-277-6	12	1.985	3.935	12.37	14.87
54	MARS5 DH-278-6	9	2.059	2.831	13.52	13.1
55	MARS5 DH-285-6	9	1.508	1.491	20.22	26.26
56	MARS5 DH-517-6	9	0.467	4.192	34.71	11.94
57	MARS5 DH-540-6	9	2.955	4.908	31.93	20.22
58	MARS5 DH-90-7	12	0.653	2.885	13.68	8.33
59	MARS5 DH-253-7	10	2.854	2.479	19.79	13.36
60	MARS5 DH-254-7	10	1.746	3.137	14.22	33.88
61	MARS5 DH-255-7	10	1.326	3.637	33.87	15.89
62	MARS5 DH-256-7	9	0.686	2.088	28.01	18.23
63	MARS5 DH-258-7	9	1.533	5.092	18.93	31.2
64	MARS5 DH-269-7	9	1.003	3.235	0.89	74.14
65	MARS5 DH-270-7	9	1.114	3.192	16.95	28.04
66	MARS5 DH-273-7	9	1.676	3.157	29.88	21.9
67	MARS5 DH-285-7	9	1.254	2.832	31.51	39.65
68	MARS5 DH-287-7	9	0.993	2.401	7.94	15.25
69	MARS5 DH-288-7	10	1.726	2.112	20.25	10.81
70	MARS5 DH-534-7	10	2.606	4.165	17.47	9.42
71	MARS5 DH-536-7	9	1.419	2.344	22.55	5.51

72	MARS5 DH-540-7	10	1.129	5.305	18.76	10.2
73	MARS5 DH-86-8	10	0.843	2.566	22.06	8.64
74	MARS5 DH-253-8	10	2.4	2.506	22.58	35.98
75	MARS5 DH-255-8	9	0.76	1.664	10.84	17.03
76	MARS5 DH-256-8	9	2.24	3.314	15.26	26.82
77	MARS5 DH-273-8	9	2.125	3.679	19.49	15.81
78	MARS5 DH-275-8	12	0.906	2.298	25.73	23.21
79	MARS5 DH-277-8	9	1.041	2.269	19.61	17.48
80	MARS5 DH-285-8	9	1.051	2.841	8.16	16.39
81	MARS5 DH-532-8	10	1.858	4.547	22.33	18.01
82	MARS5 DH-253-9	10	1.721	2.677	20.89	23.03
83	MARS5 DH-254-9	9	1.749	3.369	24.47	38.82
84	MARS5 DH-258-9	9	1.767	3.107	9.34	25.36
85	MARS5 DH-273-9	12	1.201	2.554	14.16	16.55
86	MARS5 DH-277-9	9	1.181	1.493	17.47	9.82
87	MARS5 DH-285-9	9	1.385	3.188	8.97	44.34
88	MARS5 DH-287-9	10	2.883	4.325	21.7	22.72
89	MARS5 DH-86-10	10	1.134	2.641	24.06	10.03
90	MARS5 DH-253-10	10	1.316	2.762	18.73	21.09
91	MARS5 DH-255-10	9	2.217	2.778	13.33	9.59
92	MARS5 DH-258-10	9	0.787	2.051	15.15	30.64
93	MARS5 DH-270-10	9	1.803	3.487	11.77	15.95
94	MARS5 DH-275-10	10	2.144	3.726	25.06	21.66
95	MARS5 DH-527-10	9	2.981	4.506	27.63	12.52
96	MARS5 DH-532-10	9	1.529	3.243	31.41	9.27
97	MARS5 DH-258-11	9	2.104	3.463	15.81	35.31
98	MARS5 DH-270-12	10	1.885	3.158	19.05	15.71
99	MARS5 DH-529-13	Base population	0.809	2.691	51.48	21.98
100	PBICR-08-005TC-5	Base population	2.053	3.348	21.91	14.29
101	PBICR-08-005TC-16	Base population	1.625	4.785	13.2	36.18
102	PBICR-08-005TC-33	Base population	2.181	3.714	27.18	18.31
103	PBICR-08-005TC-36	Base population	1.651	3.034	13.18	10.84
104	PBICR-08-005TC-50	Base population	1.501	3.194	19.04	26.09
105	PBICR-08-005TC-100	parent	1.817	3.386	33.52	10.25
106	CSCR16	parent	0.994	2.287	39.79	14.07
107	2-49/CUNNINGHAM//KENNEDY	parent	1.408	3.13	19.05	31.79
108	SUNCO/2*PASTOR	Check	0.937	2.101	8.75	15.02
109	Suntop	Check	1.516	2.193	21.95	15.99
110	Sunguard	Check	0.974	2.179	9.24	11.09
111	Mace	Check	1.637	2.778	25.07	15.34
112	Sunco	Check	0.752	1.369	27.7	11.56
113	Spitfire	Check	1.841	4.51	26.23	20.24
114	EGA Gregory	Check	1.488	3.335	32.38	24.16
115	Lancer	Check	1.063	2.544	13.89	17.96
116	EGA Wylie	Check				
117	249	Check	1.653	2.474	17.66	6.5

118	EGA Bellaroi	Check	1.974	3.32	28.52	20.22
	Predicted Mean		**1.744**	**3.232**	**19.75**	**21.05**
	Standard error of mean		**0.084**	**0.119**	**0.799**	**1.048**
	SED		**0.9313**		**9.508**	**4.034**
	LSD (5%) (Genotype x Inoculum)		**0.91**			
	LSD (5%) (Genotype)		**0.65**		**9.38**	**2.48**