QUANTITATIVE TRAIT LOCUS (QTL) MAPPING OF SEED WEIGHT, PERICARP COLOR, BRISTLING AND SEED SHATTERING IN *SETARIA*

by

SANDRA ESI ODONKOR

(Under the Direction of Katrien M. Devos)

ABSTRACT

Setaria P. Beauv is a genus of grasses which belong to the *Poaceae* (grass) family and subfamily Panicoideae. Two members of the *Setaria* genus, *S. italica*, the second most widely cultivated species of millet, and *S. viridis*, a ubiquitous problematic weed species on the planet and wild ancestor of *S. italica*, were crossed to generate a recombinant inbred line (RIL) population comprising 188 lines. This population was used to genetically map quantitative trait loci (QTL) for seed weight, pericarp color, bristling and seed shattering in *Setaria*. Four significant QTL were identified for pericarp color, bristling and seed shattering. No QTL were identified for seed weight. *Setaria italica shattering 1* (*SiSh1*), was identified as a candidate gene for seed shattering. A miniature inverted-repeat transposable element (MITE) insertion caused an inactivation of *SiSh1* thereby reducing seed shattering in *S. italica*.

INDEX WORDS: *Setaria*, QTL, Recombinant inbred lines, RIL population, Seed weight, Pericarp color, Bristling, Seed shattering, Miniature inverted-repeat transposable element, MITE, Candidate genes.

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SANDRA ESI ODONKOR

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SANDRA ESI ODONKOR

Major Professor: Katrien M. Devos

Committee: Scott A. Jackson
C. J. Tsai

Electronic Version Approved:

Julie Coffield
Interim Dean of the Graduate School
The University of Georgia
May 2015

DEDICATION

To the Almighty God

To my parents: George M. Odonkor and Gifty Narh-Odonkor

To my husband Fadel E. K. Adoe

To my son Fadel E. K. Adoe Jr.

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CHAPTER 1

INTRODUCTION

Setaria P. Beauv is a genus of grasses which belongs to the *Poaceae* (grass) family and subfamily Panicoideae. Other important members of the *Poaceae* family include maize (*Zea mays*), rice (*Oryza sativa*), and wheat (*Triticum* spp.). This diverse genus includes about 115 to 160 species of grasses distributed throughout the tropical and subtropical areas of the world (Webster, 1993). Several species have been found to be present in certain cold regions (Rominger, 1959). Several species such as *S. viridis*, *S. verticillata*, *S. geniculata*, *S. pumila* and *S. faberii* are problematic agricultural weeds which invade and adapt rapidly to a wide range of habitats around the world causing considerable economic and environmental costs (Dekker, 2003) while *S. italica* (foxtail millet), an economically important crop, is cultivated for food and pasture.

The probable origin of the genus *Setaria* is believed to be Africa due to the vast number of species (74) present there. This information is also supported by genomic evidence of a tropical origin (Lakshmi and Ranjekar, 1984; Prasada Rao et al., 1987; Rominger, 1959; Simpson, 1990; Stapf and Hubbard, 1934). *S. italica*, one of the oldest domesticated crops in the world, is known to have been domesticated from *S. viridis*, its weedy ancestor, in Northern China around 6000 BC (Bettinger et al., 2010). It continues to be a major food crop in this region (Bennetzen et al., 2012).

A short life cycle (depending on accession and photoperiod conditions), prolific seed production, simple growth requirements, short statures (15-20 cm) and efficient transformation using *Agrobacterium*-mediated methods are characteristic of *S. viridis* (Bennetzen et al., 2012; Brutnell et al., 2010; Li and Brutnell, 2011). *S. italica* is also a hardy crop with exceptional drought

tolerance and a wide-ranging germplasm collection. This provides prospects for research into the domestication process and finding new allele variants (Li and Brutnell, 2011). Much interest has developed more recently in direct crosses between *S. italica* and *S. viridis* for genetic mapping (Wang et al., 1998) and introduction of herbicide resistance from *S. viridis* into *S. italica* germplasm (Darmency and Pernes, 1985; Naciri et al., 1992) has been made possible with the *S. italica x S. viridis* cross. *S. italica* has a small diploid genome (1C=≈515 Mb), it is inbreeding in nature, and a genome sequence is available (Bennetzen et al., 2012). It is closely related and compares to the bioenergy grasses pearl millet, napiergrass and switchgrass which have large genomes and are outcrossing in nature, making it an experimental model for those grasses (Lata et al., 2013). Because of its phylogenetic position and C4 photosynthetic pathway, *Setaria* is also a promising model for C4 physiology studies and genetics (Brutnell et al., 2010; Lata et al., 2013).

Domestication of cereal crops resulted in changes in several traits which differentiate many of the wild progenitors of these crops from what we have today. Variation in seed and panicle characteristics occur in *Setaria* due to the direct interspecific cross between *S. italica* and *S. viridis*. The objective of this research is to genetically map and identify candidate genes for seed weight, pericarp color, bristling and seed shattering in a recombinant inbred line (RIL) population of *Setaria*. The RIL population comprising 188 lines was developed from a cross between *S. italica* and *S. viridis*.

CHAPTER 2

LITERATURE REVIEW

The genus *Setaria*

The genus *Setaria* includes some of the worst weedy species hampering world agriculture and land management, especially in North America. *Setaria* belongs to the subfamily Panicoideae and the tribe Paniceae, and is made up of diverse species with different traits and ploidy levels (Lata et al., 2013). It is believed that there were major waves of *Setaria* species invasions across the globe which occurred in the past, with Africa as their probable origin. This is suggested by the large number of species found in Africa (74 to 125) and evidence of tropical origins of the genus *Setaria* (Lakshmi and Ranjekar, 1984; Rominger, 1959; Simpson, 1990; Stapf and Hubbard, 1934). The genus dispersed to Eurasia invading many locations and adapting to subtropical and temperate regions. The wild progenitor that invaded Eurasia is believed to be a diploid most likely *S. viridis*, subsp. *viridis* (Kilhara and Kishimoto, 1942; Koernicke and Werner, 1885a; Li et al., 1942; Li et al., 1945; Li, 1934; Prasada Rao et al., 1987; Rominger, 1959; Simpson, 1990; Werth, 1937; Willweber-Kishimoto, 1962). Subsequently, *S. italica* (foxtail millet) was domesticated from its weedy wild antecedent *S. viridis* (around 6000 BC) in China and both continued to spread as a crop and weed, respectively (Bettinger et al., 2010). *S. pumila*, previously known as *S. glauca* (korali) has been domesticated and is currently being cultivated in India (de Wet, 1992; de Wet et al., 1979; Wang et al., 1995). Other diploid and polyploid species such as *S. verticillata* and *S. faberii* are also believed to have arisen from *S. viridis*-like ancestors (Khosla and Sharma, 1973).

S. geniculata, a weedy species and the oldest grown in the Americas, is believed to have moved from Eurasia in an ancient migration about 9000 years ago (Callen, 1965; de Wet, 1992; Smith, 1968). *S. italica* moved to the Americas principally from Asia. *Setaria* spp. adapted rapidly after their introduction to North America over the last 500 years through human emigrations from Eurasia (Dekker, 2003). More recently, the advent of herbicides to control dicotyledonous weeds, such as 2, 4-D, created an opportunity for advancement of monocotyledonous weeds such as *Setaria* (Alex et al., 1972; Blackshaw et al., 1981; Dexter, 1981; Manthey and Nalewaja, 1982; Oliver and Schreiber, 1971; Schreiber, 1977; Vanden-Born, 1971; Warwick, 1990). Grasses such as *S. faberi* have spread rapidly and northward towards Canada. New herbicide resistant *Setaria* biotypes have emerged alongside a rapid spread of some weedy *Setaria* species in the northern prairies of North America (Dekker, 2003; Ritter et al., 1989; Stoltenberg and Wiederholt, 1995; Thornhill and Dekker, 1993).

Setaria spp. are primarily self-pollinated species with slight occurrences of outcrossing mostly caused by wind in the weedy species. Natural intraspecific hybridization has been observed at rates of up to 7.6% among *S. viridis* plants in the field. Interspecific hybridization between weedy *Setaria* species occurs rarely with most of the progeny being sterile. On the other hand, interspecific hybridization between *S. italica* (foxtail millet) and *S. viridis*, its wild progenitor, generates fertile progeny. For example, *S. viridis* var. *major* (Gaudin) Posphical (giant green foxtail) is believed to have been generated from crosses between *S. italica* and *S. viridis*. More recently, direct crosses between *S. italica* and *S. viridis* have been used for genetic studies such as genetic mapping and introgression of desired traits from *S. viridis* (Darmency and Pernes, 1985; Naciri et al., 1992). Both *S. italica* and *S. viridis* have desirable traits making them good models

for C4 photosynthesis for the Panicoid grasses such as switchgrass and guinea grass (*Panicum maximum*) (Brutnell et al., 2010; Li and Brutnell, 2011).

Based on genome composition, *Setaria* spp. have been categorized into three gene pools. The primary gene pool consists of *S. italica* and *S. viridis* which are diploids (2n = 2x = 18) with AA designations (Benabdelmouna et al., 2001a). The secondary gene pool consists of the weedy tetraploid species, *S. faberi* and *S. verticillata*, which have AABB genome designations. These may have originated from a cross between the diploid species *S. viridis* and *S. adhaerans* (Benabdelmouna et al., 2001a; 2001b). Their AABB genome composition has been confirmed by genomic *in situ* hybridization and fluorescent *in situ* hybridization using 5S and 18S-5.8S-25S ribosomal DNA as probes (Benabdelmouna et al., 2001a; 2001b). The tertiary gene pool consists of *S. pumila*, *S. grisebachii*, *S. queenslandica* and *S. pallide-fusca*. *S. pumila* and *S. pallide-fusca* are polyploid species without an AA genome while *S. queenslandica* is an autotetraploid, genome composition AAAA (Benabdelmouna et al., 2001a; Benabdelmouna and Darmency, 2003; 2001b). It has recently been discovered that *S. grisebachii* has a CC genome (Wang et al., 2009)

Domestication traits

Cereal crops provide most of the calories consumed by humans and livestock. Domestication of cereals occurred thousands of years ago through convergent selection for agronomic traits. This complex process of selection resulted in profound morphological and genetic differences between domesticated lines and their wild antecedents making the wild lines more pliable to human cultivation and consumption (Fuller et al., 2010; Fuller, 2007; Kovach et al., 2007). This defines the domestication syndrome (Hammer, 1984). Domestication of all major cereal crops involved the conversion of small, coated wild seeds with natural seed dispersal to larger grains, devoid of dormancy, with solely dependent on humans for propagation (Harlan,

1992; Purugganan and Fuller, 2009; Zohary et al., 2012); although, few details of how the domestication process proceeded are known (Sang and Ge, 2007; Sweeney and McCouch, 2007). The main domestication traits in cereals are grain size, grain number, panicle size, grain quality, plant architecture, flowering time and seed shattering (Shomura et al., 2008). Over the past decade, genes involved in domestication for several traits have been characterized from several cereal crops such as rice (Konishi et al., 2006; Li et al., 2006) , maize (Doebley et al., 1997; Wang et al., 2005), sorghum (Lin et al., 2012), wheat (Simons et al., 2006) and barley (Komatsuda et al., 2007).

Studies have shown that in maize, only a few loci are responsible for the dramatic variation existing between teosinte (*Zea mays* ssp *parviglumis*), the wild progenitor, and the cultivated species (Doebley, 1990; Doebley, 2004; Matsuoka et al., 2002). Teosinte plants have a bushy appearance due to the presence of many basal and axillary tillers and bear few seeds, each covered with a stony casing, which disjoin at maturity and disperse. Teosinte kernels also have the ability to survive digestive tracts of grazing mammals and birds, aiding in their dispersal (Wilkes, 1967). Maize, on the other hand, has a single main stem with many naked seeds attached to the center of the cob. They are easily digestible by animals and birds and depend solely on humans for propagation. In crosses made between maize and teosinte, a major gene underlying morphological variation observed between teosinte and maize has been identified and characterized. *Tb1* (*Teosinte-branched1*), originally identified as a major quantitative trait locus (QTL) is mainly involved in branching architecture by controlling axillary branch formation (Doebley and Stec, 1991; Doebley et al., 1995). It also controls sex expression and inflorescence architecture (Doebley and Stec, 1991; Doebley and Stec, 1993; Hubbard et al., 2002). It encodes a transcription factor which represses organ growth in areas where it accumulates (Cubas et al., 1999; Doebley et al., 1997; Hubbard et al., 2002). The presence of a transposable element 63kb upstream of *Tb1* (in cis-

regulatory regions) increases the gene's expression in domesticated maize lines, hence decreasing branching (Clark et al., 2006; Studer et al., 2011; Wang et al., 1999).

A *Tb1* ortholog (*PgTb1*) has been identified in pearl millet (*Cenchrus americanus*). It was identified as a minor QTL which explains 10-18% of the variation observed between wild type and domesticated forms (Poncet et al., 2000; Remigereau et al., 2011). A 315 base pair (bp) miniature inverted-repeat transposable element (MITE) belonging to the *Tuareg* family was found to be present 66 bp downstream of the stop codon, in the 3' UTR of *PgTb1* (Remigereau et al., 2011). MITEs are short transposable elements derived from Class II DNA transposons (Feschotte et al., 2002a). They are non-autonomous but can be activated by the transposase of an associate autonomous Class II DNA transposable element (Feschotte et al., 2002b; Jiang et al., 2003; Kikuchi et al., 2003; Nakazaki et al., 2003; Zhang et al., 2001). MITEs are abundant in plants even though they lack coding potential. They are mostly found in low copy number and genic or regulatory regions and as such can affect the regulation of genes (Lisch and Bennetzen, 2011; Wessler et al., 1995).

In *Setaria italica*, genetic loci underlying vegetative branching reduction including the orthologue of *Tb1* have been identified. Unlike the major QTL *Tb1* in maize, *Tb1* in *Setaria* has a minor and variable effect (Doust et al., 2004).

The non-seed shattering trait can also be achieved by alterations in a few major genetic loci with large effect (Li et al., 2006; Matsui et al., 2004; Nalam et al., 2006). This finding is consistent with the identification of 2 shattering genes in rice, *qSH1* (Konishi et al., 2006) and *sh4* (Li et al., 2006). Both genes encode transcription factors involved in the formation of the abscission layer between the rachis and the inflorescence. The abscission layer is made up of cells which have very thin walls, causing the panicle to be fragile at maturity in the wild type form hence seed shattering

occurs (Panaud, 2009). A >4kb insertion in *qSh1* in intron 3 led to the loss of seed shattering in cultivated forms of rice (Lin et al., 2012). Recent whole genome sequencing of rice lines has shown that *qSh1* was under strong artificial selection during domestication (He et al., 2011; Xu et al., 2011).

Analysis of a *qSh1* (*Sh1*) orthologue in different accessions of sorghum showed variation at regulatory sites in the promoter (2.2 kb deletion) and introns (GT-to-GG splice site variant) leading to a low level of expression of *Sh1 (Lin et al., 2012)*. Maize disarticulation orthologues of *qSh1* are present on chromosome 1 and chromosome 5 (Doebley and Stec, 1991; Paterson et al., 1995). The *Sh1* ortholog on chromosome 1 (*ZmSh1-1*) harbors a large 19.3 kb intron 1 in the reference genome of B73 (Lin et al., 2012; Schnable et al., 2009). This intron is present in almost all maize inbreds and a few teosinte lines, including 3 inbreds with incomplete shattering (Lin et al., 2012). An 83 bp insertion was found to be present in exon 3 of *ZmSh1-1* of 2 maize inbreds that did not have the large intron, causing a frameshift (Lin et al., 2012).In maize chromosome 5 of the B73 reference genome, two copies of the *Sh1* ortholog (*ZmSh1-5.1* and *ZmSh1-5.2*) are present within a syntenic block and separated by a 22.8 kb insertion. This insertion is present in all maize inbreds but absent in all teosinte inbreds (Lin et al., 2012). A QTL for seed shattering has also been mapped to the syntenic block corresponding to *Sh1* in *Setaria* (Devos and Gale, 2000).

A few domestication genes underlying grain size have also been identified and characterized in rice (Fan et al., 2006; Hua et al., 2002; Jiang et al., 2005; Li et al., 2000; Roy et al., 2013; Shomura et al., 2008; Wan et al., 2008; Weng et al., 2008; Yu et al., 1997). One such gene is *qSW5,* which underlies a QTL responsible for seed width on Chromosome 5. A 1212-bp

deletion in *qSW5* in the cultivated species resulted in a significant decrease in sink size due to an increase in cell number in the flower's outer glume (Shomura et al., 2008).

Comparative genomics in grasses

The *Poaceae* (grass) family is the most important plant family in agriculture comprising more than 10,000 species and about 800 genera organized into 13 subfamilies. Grass genomes are diverse in terms of size, ploidy level and chromosome number. For example, the genomes of rice (430 Mbp) and bread wheat (17 Gbp) differ by a factor of 40 with rice being a diploid and bread wheat a hexaploid (Arumuganathan and Earle, 1991). However, early comparative genetic mapping based on restriction fragment length polymorphism (RFLP) markers demonstrated that colinearity of genes and markers is well conserved between different grass genomes which diverged from a common ancestor 50-70 million years ago (mya) (Crepet and Feldman, 1991; Gale and Devos, 1998a; Gaut, 2002; Kellogg 2001; Paterson et al., 2004; Prasad et al., 2005). It therefore seems that although the function of genes may vary in terms of expression patterns and copy numbers, most genes are shared among grass species (Bennetzen, 2007). Interestingly, gene content has also been shown not to be much different between the grasses and distant diploid relatives such as *Arabidopsis thaliana* (Bennetzen et al., 2004; Jabbari et al., 2004).

Comparative genetic maps were first developed around the late 1980s in the *Solanaceae* and *Poaceae* families (Bonierbale et al., 1988; Chao et al., 1989). As awareness of the usefulness of comparative genetic maps and knowledge on the relationship between genomes of related species increased, efficient methods were devised to lay out comparisons of multiple species. Moore et al. (1995) developed the first concentric 'crop circle' diagram showing a convenient representation of synteny of chromosomes in 5 grasses namely rice, sorghum, maize and Triticeae (wheat and barley). These grasses were illustrated as a single genetic structure, developed from 30

rice linkage blocks, thus reflecting the chromosome structure of the common ancestor (Bolot et al., 2009; Devos and Gale, 2000; Gale and Devos, 1998; Moore et al., 1995; Salse et al., 2008). Subsequently, the crop circle was expanded 8 species namely rice, foxtail millet, sorghum, pearl millet, maize, sugarcane, oat, and Triticeae (Gale and Devos, 1998a; Gale and Devos, 1998b). Other comparative maps were later developed for wild rice (*Zizania palustris*) (Kennard et al., 2000), perennial rye grass (*Lolium perenne*) (Jones et al., 2002), meadow fescue (*Festuca pratensis*) (Alm et al., 2003), finger millet (*Eleusine coracana*) (Srinivasachary, 2005), Brachypodium (Gu et al., 2009), and Miscanthus (Kim et al., 2014). The two reference genome sequences of foxtail millet provide a valuable resource for comparative and functional genomics studies of the Poaceae family by accelerating the identification of genome-wide patterns of genetic variation among species and genetic improvement of foxtail millet (Bennetzen et al., 2012; Morrell et al., 2012; Zhang et al., 2012). Comparative genomics of several traits such as flowering time (Mauro-Herrera et al., 2013), frost tolerance, drought tolerance (Alm et al., 2011), disease resistance (Silvar et al., 2012), defense response (Cantu et al., 2013), self incompability (Shinozuka et al., 2010) and yield (Faville et al., 2012; Swamy et al., 2011) has been carried out in grasses. The crop circle, developed with the aid of large scale sequencing of ESTs, includes the species rice, sorghum, foxtail millet, pearl millet, maize, fescue, Triticeae (Devos, 2005) and has since been adopted for legumes (Choi et al., 2004).

Genetic mapping and resources in *Setaria*

Most of the important traits in agriculture such as yield and plant height are quantitative indicating that they are controlled by multiple genes (Stuber et al., 1999). In *Setaria*, high variability exists in morphological characteristics such as seed size and panicle morphology across different lines (Fukunaga et al., 1997; Li et al., 1996; Sakamoto, 1978). Earlier work in foxtail millet focused on

discovering the relationship between *S. italica* and *S. viridis* (de Wet et al., 1979; Kawase and Sakamoto, 1984; Li et al., 1945). Expressed sequence tags (ESTs) and genomic simple sequence repeat (SSR) markers have been good resources for genetic markers in foxtail millet (Lata et al., 2013). A number of molecular markers and genetic linkage maps have been developed (Bennetzen et al., 2012; Devos et al., 1998; Gupta et al., 2011; Gupta et al., 2012; Heng-Sheng et al., 2011; Jia et al., 2007; Jia et al., 2009; Kajal et al., 2013; Lata et al., 2011; Sato et al., 2013; Wang et al., 1998). Similarly, a high density genetic map has been developed using about 1000 SNP markers (Bennetzen et al., 2012) as well as a set of 98 intron length polymorphic markers (Gupta et al., 2011, 2012). Presently, a number of QTL have been identified by linkage mapping including tillering and axillary branching (Doust et al., 2004), inflorescence branching (Doust et al., 2005), early seedling drought tolerance (Qie et al., 2014), flowering QTL (Mauro-Herrera et al., 2013). However, for most of the QTL found, little is known about candidate genes or the genes they encode. This may be due to the fact that many of the QTL identified have small effects. Association mapping has recently emerged as a great tool to complement information on QTL identified through linkage analysis. In *Setaria*, it has been used to identify genomic regions underlying agronomic traits contributing to yield (Gupta et al., 2014). Genome sequences of *Setaria* are now available which will help to efficiently carry out genetic studies such as comparative genomics with other grass species and gene mapping (Bennetzen et al., 2012; Zhang et al., 2012). Resequencing information of 466 *Setaria* accessions are available as well as transcriptomes or gene expression data for 8 *S. italica* accessions (genome.jgi.doe.gov). Data of short reads of *S. italica* and *S. viridis* accessions generated from Illumina Hiseq sequencing are available in the short read archive (SRA) of the National Center for Biotechnology Information (NCBI) database

(ncbi.nlm.nih.gov). A haplotype map of genomic variations and genome wide association studies of agronomic traits in *S. italica* has also been developed (Jia et al., 2013).

Due to the genetic resources available for *Setaria* and the possibility of interspecific crosses between *S. italica,* a domesticated accession, and *S. viridis*, a wild ancestor, a range of traits that are segregating in the population, including domestication traits, can be studied efficiently and results from such studies can be applied to studies in polyploid bioenergy crops such as switchgrass and napier grass.

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CHAPTER 3

MATERIALS AND METHODS

Plant materials

S. viridis, the wild antecedent, and *S. italica*, the domesticated species show contrasting phenotypes for various traits. A total of 247 progeny resulting from a cross between A10 (a Canadian *S. viridis* line) and B100 (a *S. italica* line), first crossed in 1997, were inbred through eight generations of single-seed descent (Bennetzen et al., 2012). Two subsequent rounds of selfing were later done in the greenhouses at the University of Georgia. The resulting 188 F10 RIL lines segregate for various seed characteristics including seed weight, pericarp color and seed shattering.

Two *S. italica* lines B100 and Yugu1 as well as 2 *S. viridis* lines A10 and B100, together with 8 *S. italica* accessions from India, were used in analyses confirming candidate genes.

Genetic materials

A linkage map was developed for the RIL population using 247 F8 progeny. The map was comprised of 992 single nucleotide polymorphism (SNP) markers and spanned 9 chromosomes with a total genetic length of 1415.52 cM ranging from 124 cM to 201 cM per chromosome (Bennetzen et al., 2012). The reference genome for *Setaria* developed by Bennetzen et al. (2012) was used in this study to aid in mapping of the traits. RNA sequence (RNA-Seq) data of *S. italica* strain Zhang-gu (acc. SRX128223 (root), SRX128224 (leaf), SRX128224 (stem), SRX128224 (spica/tassel)) and *S. viridis* strain A10 (acc. SRX875194-SRX87199 and ERX358107-ERX358112 (leaves)) (ncbi.nlm.nih.gov) were used in alignments against the Yugu1 *S. italica*

reference genome. Short reads of *S. viridis* strain A10 whole genome sequence generated by the Joint Genome Institute (JGI) on an Illumina Hiseq platform were also used in alignments against the Yugu1 reference genome. Genomic data of *Oryza sativa*, *Brachypodium distachyon*, *Triticum aestivum*, and *S. italica* were employed in alignments of orthologous genes to find sequence variation (genome.jgi.doe.gov).

The crop circle was used to find corresponding chromosomes on which orthologs of putative genes for each trait might be located.

Phenotypic evaluation for traits

To phenotype the RIL population for seed weight, 139 lines out of 188 were evaluated for seed weight in the Devos lab at the University of Georgia, Athens, Georgia. The subset was comprised of lines for which more than 90 seeds were available. Hundred seed weights were extrapolated for lines with 90 or more seeds but less than 100 seeds. The weight in grams of 100 randomly selected seeds per line was determined with a Mettle Toledo weighing balance. Three weights recorded for 3 counts of 100 seeds for each line were averaged and the experiment was repeated 3 times. Data from hundred-seed weights were used for statistical analysis.

Phenotyping for pericarp color involved dehusking and scanning of six seeds from each of 169 RILs using the Microtek Scanmaker 9800XL flat-bed scanner. Data was collected for 169 RILs due to the absence of seeds for 19 lines. Scans were viewed using Adobe Photoshop elements 2.0 software (www.adobe.com/products/photoshop-elements.html). The red, green and blue (RGB) values for the entire area of each photographed seed were recorded using ImageJ 1.48v software (imagej.nih.gov/ij). The area of a seed was captured using the rectangular area selector tool in ImageJ 1.48. The 6 seeds for each RIL served as replicates, hence, six replicates were analyzed for pericarp color. The value for each sample was used for statistical analysis.

To phenotype for seed shattering, three panicles from different plants of each line from a subset of 122 RILs were clasped in a clenched fist and counts of detached seeds were recorded. The average of the 3 seed counts was used as 1 replication for QTL detection with a total of 3 replications.

Phenotyping for bristling involved measuring the length of middle bristles of the main panicle from a subset of 150 RILs. Panicles did not form for 38 lines from the population. Three replicates for the mean bristle length for 3 plants per RIL were used as data for statistical analysis. Analysis of variance (ANOVA) was carried out on the phenotypic data for all traits, RILs and replications to test for significance.

QTL detection

QTL regulating seed weight, pericarp color, seed shattering and bristling were analyzed using the phenotypic measurements from the RIL F_{10} generation as traits. Composite interval mapping (CIM) in Windows QTL cartographer 2.5 was used for QTL detection (Wang et al., 2012). In CIM, Model number 6 with forward and backward regression, a 10 cM window size and a mapping step size of 1 cM were used. The logarithm of odds (LOD) threshold, used to determine a significant QTL, was determined based on 1000 permutations and a significance level of $P = 0.05$. The LOD threshold ranged from 2.9 to 3.3 for all traits. QTL were further analyzed when present in 2 or more replicates. QTL that were present above the threshold in only one replicate, but were present at a LOD score ≥ 2.4 in a second replicate were also considered. In a situation where double peaks were present, both peaks were declared as significant QTL when the peaks were separated by >1 LOD interval. Additive effects were defined with respect to the alleles of A10. Thus, positive genetic effects indicated the alleles of A10 increased the phenotypic value, and negative values indicated that the alleles of A10 decreased the phenotypic value.

Identification of candidate genes underlying QTL

To identify candidates for QTL underlying each trait, two approaches were used. One approach was to find genes underlying similar traits on syntenic chromosomes in rice, wheat, sorghum, and maize. With the aid of the "crop circle", syntenic chromosomes of *Setaria* in other grasses were identified. Genes underlying seed weight, pericarp color, seed shattering and bristling were identified in rice and other grasses and sequences of the genes were retrieved from GENBANK (http://www.ncbi.nlm.nih.gov/genbank/). The sequences of the genes were used as queries in a nucleotide basic alignment search tool (BLASTn) search (Altschul et al., 1990) against the Setaria whole genome sequence (Bennetzen et al. 2012; www.phytozome.net) to find orthologs in *Setaria.* The physical location of orthologs was compared with that of markers flanking each QTL in *Setaria*. Orthologs located in a QTL region were considered to be gene candidates underlying the QTL and were subjected to further structural and/or functional analyses.

Quantitative trait loci with no candidate genes identified using genes underlying similar traits in other grass species were advanced to the next approach. Genes present between flanking markers were retrieved using Biomart v0.9 in Phytozome v10.1. Gene ontology (GO) terms and gene descriptions for all genes within a QTL interval were retrieved to determine their functional role. Based on GO descriptions, genes involved in pathways for each trait were identified.

Confirmation of candidates for QTL underlying traits

To confirm candidates for QTL underlying traits, short reads of A10 genome sequence generated from an Illumina Hiseq run were aligned to the Yugu1 reference genome sequence. All alignments were carried out using Bowtie 2 v2.2.3, an ultrafast, memory efficient aligner of short DNA sequences (reads) to large genomes (Langmead et al., 2009). Alignments were carried out on the Georgia Advanced Computing Resource Center's (GACRC) Linux cluster. A Bowtie 2

index was built from the DNA reference gene sequence using a bowtie2-build indexer (Langmead et al., 2009). Bowtie 2 alignment was subsequently carried out using 2 parallel search threads and a maximum fragment length for paired-end alignments of 800. Discordant alignments for paired-end reads were suppressed (Langmead et al., 2009). The alignment was viewed using Integrative Genomics Viewer (IGV) v 2.3 (Robinson et al., 2011). This was carried out to find single nucleotide polymorphisms (SNPs) and presence/absence variations (PAVs) for genes of interest underlying each QTL.

A gene underlying a QTL for shattering was confirmed by identifying a *Setaria* ortholog for the sorghum shattering gene from the *S. italica* Yugu1 reference genome. The Yugu1 shattering ortholog was used as a reference and aligned to short read Illumina sequence of the *S. viridis* A10 parent. Confirmation of the presence of a repeat region in the shattering gene was carried out by PCR amplification in 2 *S. italica* lines (B100 and Yugu1) and 2 *S. viridis* lines (A10 and Ames21516). The PCR reaction consisted of 4 µl 5x *Taq* buffer, 1.2 µl (25 µM) $MgCl_2$, 0.16 µl (25 mM) dNTPs, 2.5 µl (4 µM) forward and reverse primers of SiSh1-91, SiSh1-92 and SiSh1-93 primers, 0.16 µl of *Taq* polymerase, 2 µl (25 ng/µl) template DNA and 7.48 µl of H_2O. The PCR conditions included initial denaturation at 95 ºC for 180 s; 35 cycles of denaturation at 95 ºC for 40 s, annealing at 58 ºC for 40 s, and extension at 72 ºC for 90 s; and a final extension at 72 ºC for 300 s. The resulting PCR products were run on a 1% agarose gel, purified using the Zymo Research DNA clean and concentrator -5 and sequenced using Sanger sequencing. A BigDye reaction using forward and reverse primers of SiSh1-91, SiSh1-92, SiSh1-93 primers (Table 3.1) was ran as follows: 2 µl of (25 ng/µl) purified PCR product was added to 1 µl (10 µM) forward/reverse primer, 2 µl of 5x BigDye buffer, 0.5 µl BigDye and 4.5 µl H_2O in a total of 10 µl reaction. The BigDye reaction conditions consisted of an initial denaturation at 95 ºC for 120 s;

40 cycles of denaturation at 95 ºC for 30 s, annealing at 50 ºC for 10 s and extension at 60 ºC for 240 s; and final extension at 60 ºC for 300 s. The BigDye product was subsequently cleaned up with Sephadex G50 and run on an ABI 3730xl.

To study variation in gene orthologs across species, DNA sequences of shattering orthologs in rice (*Oryza sativa*), *Brachypodium distachyon*, wheat (*Triticum aestivum*), and foxtail millet (*S. italica*) together with mRNA sequence of rice were aligned using MuscleWS (Edgar, 2004).

RNA-Seq data of *S. italica* (Zhang-gu) and *S. viridis* (A10) were aligned to the *SiSh1* Yugu1 reference DNA sequence of the shattering gene using Tophat v2.0.14. Similar to Bowtie 2, Tophat alignments were carried out on the GACRC Linux cluster and a Bowtie 2 index was built from the Yugu1 DNA reference sequence using a bowtie2-build indexer (Langmead et al., 2009). Using 4 parallel search threads, the Tophat alignments were carried out. The alignments were viewed using Integrative Genomics Viewer (IGV) v 2.3 (Robinson et al., 2011).

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Table 3.1: Primers sequences used to amplify repeat regions of a seed shattering candidate gene on *Setaria* chromosome 9.

Primer name	Forward Sequence	Reverse sequence
SiSh1-91	GGATCATGCCTTGCACTCCT	CATGCATGCACATTTCGGCT
SiSh1-92	ATCATGCCTTGCACTCCTCG	CCATGCATGCACATTTCGGC
SiSh1-93	ATTGGAAAAGGGTGCCCCAG	TGAGCTTGCAGTCAAGACAGT

CHAPTER 4

RESULTS AND DISCUSSION

Phenotypic evaluation of traits

An F_{10} RIL population generated from an A10 (*S. viridis*) x B100 (*S. italica*) cross was phenotyped for seed and panicle characteristics namely seed weight, pericarp color, bristling and seed shattering. Hundred-seed weight, RGB values, bristle length and percentage shed seed were measured for each trait, respectively. Phenotypic distributions for each trait showed continuous variance indicating each trait was governed by more than 1 gene (Fig 4.1). Transgressive segregation was observed for all traits (Table 4.1; Fig 4.1). For each trait, phenotypic values among the RILs were significantly different from each other at a 5% significance level while values were not significantly different across replications. For pericarp color, RILs which had RGB values that differed by 25 or more across replicates were removed from the analysis, thereby reducing the population from 169 to 112. The data for these RILs were discarded to avoid wide variation across replicates which would result in inconsistent and false positive QTL.

QTL detection

Across the 4 traits, 4 significant QTL with LOD values above the threshold were detected on 3 out of the 9 linkage groups (LGs); no QTL were identified for seed weight, 1 QTL was found for pericarp color, 2 QTL for bristling, and 1 QTL for seed shattering (Table 4.2; Fig 4.2, 4.3). The 9 LGs correspond to the 9 chromosomes of *Setaria*. R^2 values for individual traits ranged from 10.17% for bristling to 19.29% for seed shattering.

The QTL for pericarp color on LG 2, identified as a significant QTL in 4 out of 6 replications, had a LOD score of 4.67 and explained 17.37% of the variation. This QTL has the expected negative additive effect corresponding to the darker pericarp color of *S. viridis* seeds relative to *S. italica*.

The 2 QTL identified on LGs 6 and 9 for bristling, were significant in 2 out of 3 replications explaining 10.17% and 14.73% of the variation observed, respectively. The QTL on LG 6 has a negative additive effect on bristling while the QTL on LG 9 has a positive effect (Table 4.2). Due to the low variation observed between the 2 parents, the contribution of both positive and negative alleles by the A10 parent was expected.

The QTL for seed shattering on chromosome 9 had a LOD score of 8.43 and explained 19.29% of the variation. This QTL was significant in 2 out of 3 replications and had the expected positive additive effect, corresponding to the larger number of shed seeds in *S. viridis* relative to *S. italica*.

Seed weight and size are major determinants of yield in cereals. Genetic variation in crops was reduced by selection of favorable alleles during domestication (Tanksley and McCouch, 1997). During domestication, large seeds were selected due to enhanced seedling vigor and ease of harvesting (Harlan et al., 1973). However, due to frequent association of small seed size with more seeds per plant, wide geographic distribution and early maturity, small seeds are favored by natural selection (Harlan, 1992). A number of seed weight/size QTL have been identified across grass species. For example Peleg et al. (2011) identified 12 thousand-kernel weight QTL in an interspecific cross between a durum wheat cultivar and a wild emmer accession. Similarly, Tan et al. (2008) identified 7 QTL for thousand-grain weight in a cross between *Oryza sativa* and *Oryza rufipogon*. Earlier work in mapping QTL for seed weight in an F_2 population generated from a

cross between A10 and B100 showed the presence of QTL with low LOD scores and R^2 values. This indicates a gradual selection for seed weight during domestication rather than selection for a single large seed weight mutant (K. M. Devos, upublished data).

Bristling, also known as awning, is an important trait in wild plants as bristles aid in seed dispersal and increase yields. In wild wheat species, as a seed falls, two distinct awns balance and drive the seed into the ground to ensure efficient germination (Elbaum et al. 2007). Yields are increased especially under drought conditions due to the ideal placement of awns and large surface area for light interception and carbon dioxide uptake (Evans et al., 1972). Photosynthetic rates near wheat ears can also be doubled and, moreover, awns are less likely to senesce relative to flag leaves as awns develop later (Evans and Rawson, 1970). In wheat, all wild species and most accessions of domesticated species have awns. New awnless cultivars have been developed over time by wheat breeding programs to suit the needs of regional breeding programs (Sood, 2008). In bread wheat, three genes are known to be responsible for inhibiting awn development, *Hd* (*Hooded*), *B1* (*Tipped 1*) and *B2* (*Tipped 2*) (McIntosh et al., 1998).

QTL for domestication traits such as plant height, awns, tiller number and shattering have been found to be concentrated in particular regions in rice (Cai and Morishima, 2002; Koinange et al., 1996; Thomson et al., 2003). Domestication QTL can be conserved across the grass species such as the shattering QTL which have been identified and characterized in rice, maize and sorghum (Doebley and Stec, 1991; Gu et al., 2005; Lin et al., 2012; Onishi et al., 2007a; Onishi et al., 2007b; Paterson et al., 1995) and major flowering time QTL which have been identified in *Setaria*, maize and sorghum (Mauro-Herrera et al., 2013).

Identification of candidate genes underlying QTL

QTL underlying pericarp color have been identified in other grass species such as rice (*Oryza sativa*). A gene underlying pericarp color has been identified on rice chromosome 7 (S.Takahashi, 1947). The *Red coleoptile color* (*Rc*) gene is a transcription factor responsible for regulating proanthocyanidin synthesis and accumulation of pigments in the pericarp of brown-colored rice grains. The *Setaria* ortholog for *Rc*, Si029106m was not present in the mapped QTL interval (region between markers flanking each QTL) and therefore Si026106 was not considered a candidate. The alternative approach to identifying putative candidate genes underlying pericarp color QTL was used in which all genes present within the flanking markers of the QTL were identified from the *Setaria* (Yugu1) genome sequence. A total of 203 genes were identified in a 1.9 Mbp interval of which a subset of 99 genes had GO IDs. The GO terms of each gene were analyzed and a number of genes had similar descriptions (e.g. 27 genes were associated with DNA binding). No genes with descriptions associated with the flavonoid biosynthesis pathway (pericarp color pathway) were identified. Further work needs to be carried out to narrow this set to fewer candidates.

No cloned genes on corresponding chromosomes in other grass species were identified for bristling (Table 4.3). The QTL for bristling on chromosome 9 recorded the largest QTL support interval of about 3.9 Mbp with fewer annotated genes (159) relative to the bristling QTL on chromosome 6 (182) and QTL for pericarp color (203) (Table 4.4). No genetic pathway has been identified for bristling among the grasses.

Shattering1 (Sh1), a gene controlling seed shattering, has been identified in sorghum (Lin et al., 2012). Other QTL have been mapped to syntenic blocks corresponding to *Sh1* in rice (Gu et al., 2005; Onishi et al., 2007a; Onishi et al., 2007b), maize (Doebley and Stec, 1991; Paterson et

al., 1995) and foxtail millet (Devos and Gale, 2000). Results from a blastn search using the *Sh1* sequence as query indicates that the ortholog for *Sh1* in *Setaria* (Si037789m or *SiSh1*) is found within the QTL support interval on chromosome 9 (Table 4.4, Fig 4.2D), suggesting that Si037789m may be a candidate gene for this QTL.

Confirmation of candidate genes underlying QTL

The *Setaria* ortholog of *Shattering1*, *Setaria italica shattering 1* (*SiSh1*), spans 7.514 kb and has 6 exons and 5 introns. *SiSh1* encodes a transcription factor belonging to the YABBY family. The YABBY family of genes, a family of transcription factors named after the Australian fresh water crustacean, have 2 highly conserved domains which aid in DNA binding of the transcription factors, a Cys-containing zinc finger domain towards the amino terminus and a helix-loop-helix (YABBY) domain towards the carboxyl end. YABBY genes are known to specify abaxial cell fate in lateral organs produced by apical and flower meristems. Exon regions corresponding to *Sh1* are conserved in foxtail millet (*SiSh1*), rice (*OsSh1*), sorghum (*Sh1*) and maize (*ZmSh1*) and wheat with variation of the gene structure present in the *Sh1* ortholog on maize chromosome 1 (19.3 kb intron and 83-bp insertion) and 5 (gene fusion) (Lin et al., 2012). Alignment of *SiSh1* to the *Sh1* orthologs in wheat, *Brachypodium*, rice and sorghum using MuscleWS confirmed the conservation of the exon regions across these different grasses together with the presence of long introns. Alignment of Illumina DNA sequence reads from *S. viridis* acc. A10 against *SiSh1* from the Yugu1 (*S. italica*) reference sequence using Bowtie 2 showed 2 nucleotide changes in introns (a 1 bp deletion and a SNP in intron 1) and the insertion of an 854 bp GC-rich repeat region 5 base pairs from the end of the exon 2 The insertion of the repeat had led to the misannotation of *SiSh1* in the Yugu1 reference sequence. Further analysis of the repeat region indicated that it is a miniature inverted terminal repeat element (MITE) belonging to the *P*-

Instability Factor (*PIF)/Harbinger* family of transposons (Figure 4.4), a group of non-autonomous DNA transposons which produce a 3 bp target site duplication upon insertion, bear terminal inverted repeats and insert mostly into low copy number sequences and gene rich regions (Jiang et al., 2003; Kapitonov and Jurka, 1999; Walker et al., 1997; Wessler et al., 1995; Zhang et al., 2001). *PIF/Harbinger*-like elements are categorized into autonomous and non-autonomous elements based on the presence of an open reading frame coding for a DDD/DDE transposase which is required for transposition (Grzebelus et al., 2007). Analysis of the MITE in *SiSh1* showed that it bears the inverted repeat sequences TGTGTTT on the amino end and AAACGCA on the carboxyl terminus. It produces the target site duplication AGCAGC.

Domestication of cereal crops resulted in a change in several traits which differentiate them from many of the wild progenitors of these crops. One of the many traits is seed shattering. To ensure plant propagation, many wild progenitors shed and dispersed their seeds which caused a reduction in yield, thus, early humans who survived on these crops applied a strong selection for plants with little to no shattering. The non-seed shattering trait can be achieved by alterations in a few major genetic loci with large effect (Li et al., 2006; Matsui et al., 2004; Nalam et al., 2006). An insertion of a transposable element into a shattering gene in *S. viridis* is likely to have inactivated the gene resulting in a non-shattering trait. In rice, an insertion of a >4 kb fragment in intron 3 of *OsSh1* leads to reduced transcription levels and a non-shattering phenotype in domesticated species. Similarly in sorghum, a 2.2 kb deletion resulting in a truncated transcript which lacks exons 2 and 3 and a GT-to-GG splice-site variant in intron 4 results in the removal of exon 4, therefore leading to reduced transcript levels in domesticated species. In maize, a 23 kb insertion present between 2 copies of *ZmSh1* genes (*ZmSh1-5.1* and *ZmSh1-5.2*) on maize chromosome 5 is absent in teosinte, leading to reduced transcription levels in maize line B73.

To validate that *S. italica* and *S. viridis* indeed vary by the presence of the MITE, primers were designed flanking the MITE at 362 bp upstream and 369 bp downstream. Polymerase chain reaction was carried out in two *S. italica* lines (the B100 parent and Yugu1) and two *S. viridis* lines (the A10 parent and Ames21519). DNA from these lines was extracted using the Cetyltrimethyl ammonium bromide (CTAB) protocol. Results from the PCR run on a 1% agarose gel showed the presence of ≈700 bp bands for the *S. viridis* lines and no bands for the *S. italica* lines (Figure 4.5). These fragments were sequenced using Sanger sequencing. The results indicated the absence of the MITE in the *S. viridis* lines hence the ≈700 bp sized fragment. The absence of a band for *S. italica* could likely be attributed to the difficulty in amplifying across the high GC rich repeat region (66.36% GC) using PCR due to its requirement of high melting temperatures (McDowell et al., 1998). Further analysis confirming the presence of the MITE in *S. italica* was carried out by designing primers in the MITE which, together with primers in the flanking regions, generated fragments spanning the gene-repeat boundaries. *S. italica* lines were expected to have a band present due to the presence of the repeat while no fragment should be amplified from *S. viridis* lines. As expected, results from the PCR run on a 1% gel showed the presence of a band for *S. italica* lines while bands were absent in *S. viridis* lines (Fig 4.6).

MITEs have been shown to be abundant in plants, especially in the grasses (Feschotte et al., 2002). A 315 base pair (bp) miniature inverted-repeat transposable element (MITE) belonging to the *Tuareg* family was found to be present 66 bp downstream of the stop codon, in the 3' UTR of *PgTb1,* a domestication gene in pearl millet (Remigereau et al., 2011). Interestingly, the *Tuareg* family of MITEs in pearl millet have been found to be related to the *PIF/Harbinger* superfamily (Remigereau et al., 2006).

To determine if the transition from shattering to non-shattering occurred multiple times during domestication, the presence of other *sh1* alleles was investigated in *S. italica* germplasm. PCR using the primers designed earlier was carried out on 8 *S. italica* lines from India that were available in the Devos lab. All 8 lines from India showed the presence of a band when the primers spanning the gene-repeat boundaries were used, consistent with the presence of the MITE as had previously been observed for *S. italica* lines B100 and Yugu1 (Fig 4.5). Additional germplasm needs to be evaluated from different parts of the world to potentially identify novel *Sh1* mutations.

To determine the role of the MITE in inactivating the gene, alignment of short RNA-Seq reads of *S. italica* strain Zhang-gu (acc. SRX128223 (root), SRX128224 (leaf), SRX128224 (stem), SRX128224 (spica/tassel) and *S. viridis* strain A10 (acc. SRX875194-SRX87199 and ERX358107-ERX358112 (leaves) was carried out using Tophat v2.0.14. The alignments indicated that RNA transcript varied in structure between *S.italica* and *S. viridis*. The *S. viridis* transcript was derived from exon regions of the gene suggesting that normal intron splicing occurred in *S. viridis*. Two alternative transcripts were observed in *S. italica*. One transcript corresponded to exon1, exon2, the MITE, intron 2, and exons 3, 4 5 and 6. The second transcript consisted of exons 1, 3, 4, 5 and 6. Interestingly, a splice site 12 bp upstream of the normal splice acceptor site for intron 2 was used in this alternative transcript. These data suggest that the insertion of the MITE affected splicing of the *SiSh1* gene. Further expression analysis needs to be carried out in *S. italica* lines to confirm the results suggested by the RNA-Seq results.

Seed shattering is caused by seed abscission, which is also caused by degradation of the middle lamellae and cell walls of cells of the abscission layer (Ji et al., 2006). The identification of the *Sh1* gene in *Setaria* and the conservation of *Sh1* orthologs and differences in gene structure across other cereals; maize, rice and sorghum, together with the transition from shattering to non-

shattering caused by inactivation of an orthologous gene across the different grasses suggest that the *Sh1* genes have undergone parallel selection during domestication in different cereals as mentioned earlier by Lin et al. (2012).

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Table 4.1**:** Phenotypic values of the parents and RIL progeny of A10 x B100. Traits were measured in 3 replications.

Trait	Parents		F2			
	A10	B100	Min	Max	Mean	SD
Seed weight (g)	0.12	0.24	0.12	0.30	0.22	0.04
Pericarp color	180.20	199.43	142.10	213.69	187.03	13.84
Bristling (mm)	3.85	3.20	0.00	10	3.25	1.90
Seed shattering	20.44	9.57	0.00	263.00	14.62	24.61

Table 4.2: Genomic regions significantly associated with QTL for phenotyped traits in the A10 x B100 population.

Trait	Linkage Group	Map QTL position	Flanking Markers	Map Position	Max LOD	R2	Additive	Dominant
Pericarp color	2	2.40	2_S10_158_V2	1.38	4.13	0.1737	-7.8306	0.0000
			2_S10_161_V2	4.66				
Bristling	6	12.10	7_S48_701_V2	11.80	3.60	0.1017	-0.5227	0.0000
			7_S48_700_V2	17.785				
	9	92.8	x_Sx11_994_V2	92.54	4.96	0.1473	0.8183	0.0000
			1_S4_92_V2	93.21				
Seed Shattering	9	57.60	1_S2_31_V2	56.62	9.14	0.1929	10.09	0.0000
			1_S2_32_V2	59.057				

Table 4.3: Location of *Setaria* orthologs of genes underlying similar traits in other grass species and to determine candidate genes for QTL of phenotyped traits in the A10 x B100 population.

Trait	Linkage Group	QTL interval (Start)	QTL interval (End)	Similar trait gene on corresponding chromosome	Ortholog in *Setaria*	Physical location (Start)	Physical location (End)	Candidate gene?
Pericarp color	2	535,281	2,416,066	*Rc* (rice)	Si029106m	7,108,302	7,113,595	No
Bristling	6	1,520,446	3,040,456	-	-	-	-	-
	9	30,514,400	34,357,118	-	-	-	-	-
Seed shattering	9	10,071,774	10,678,158	*Sh-1* (sorghum)	Si037789m	10,073,005	10,080,518	Yes

Table 4.4: Genetic and physical location of genomic regions significantly associated with QTL for phenotyped traits in the A10 x B100 population.

Trait	Linkage Group	Flanking Markers	Physical location (Start)	Physical location (End)	Physical interval distance (bp)	Number of genes between flanking markers
Pericarp color	2	2_S10_158_V2	433,075	433,207	1,880,785	203
		2_S10_161_V2	1,474,334	1,474,466		
Bristling	6	7_S48_702_V2	3,040,324	3,040,456	1,520,010	182
		7_S48_698_V2	1,520,446	1,520,578		
	9	x_sx11_994_V2	30,514,400	30,514,532	3,842,718	159
		1_S4_92_V2	34,356,986	34,357,118		
Seed Shattering	9	1_S2_31_V2	10,071,774	10,071,906	606,384	79
		1_S2_32_V2	10,678,026	10,678,158		

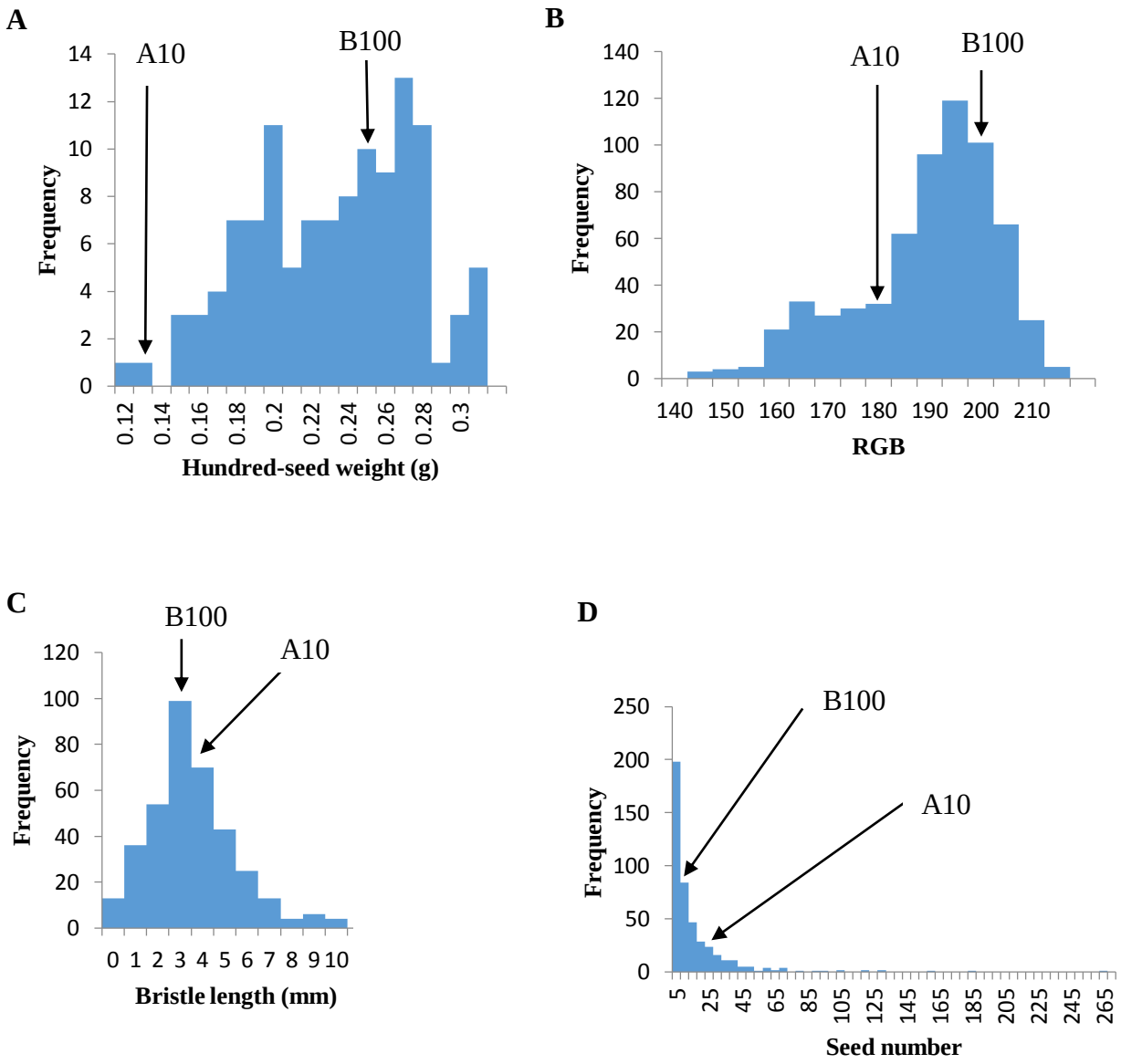


Figure 4.1: Phenotype distributions for the RIL mapping population A) Hundred-seed weight (g), B) Pericarp color (Red, Green, Blue values in the ratio, 0.299R+0.587G+0.114B) C) Seed shattering (seed number) D) Bristle length (mm).

A

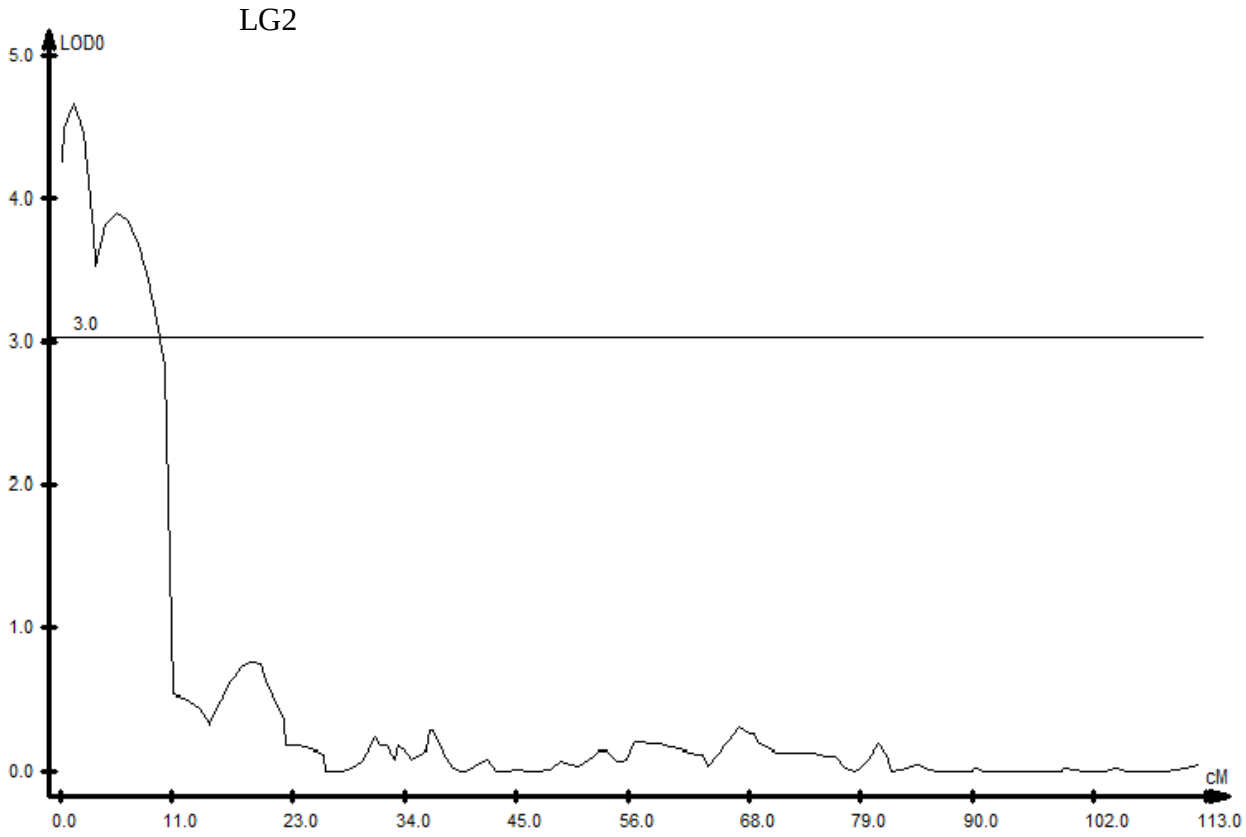
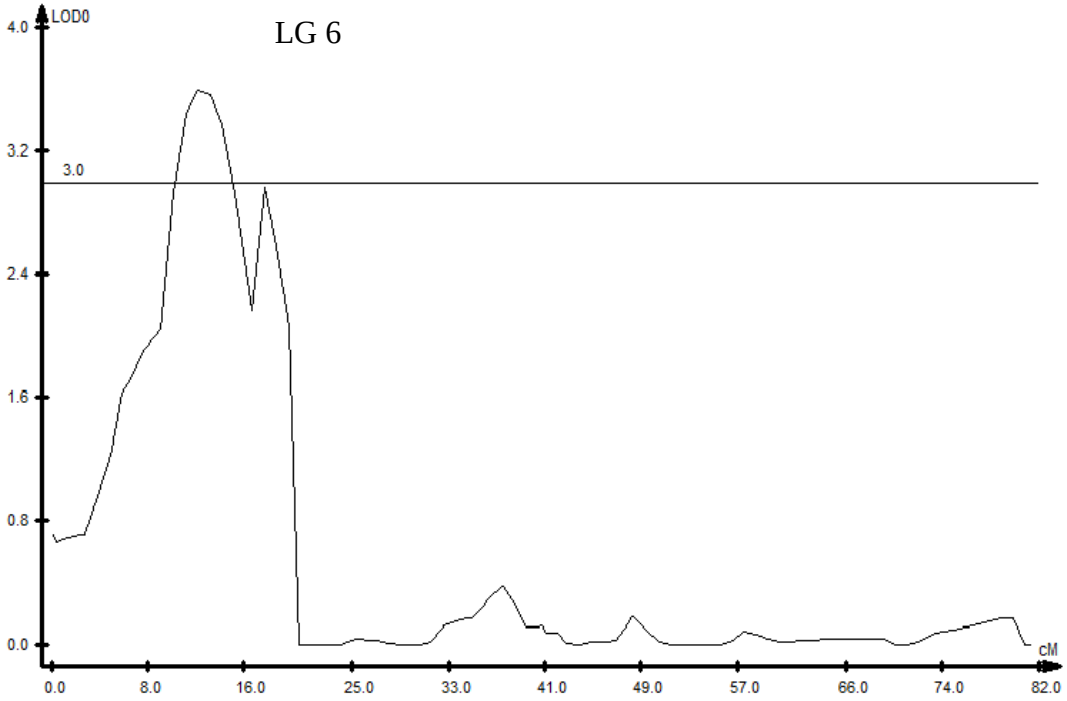
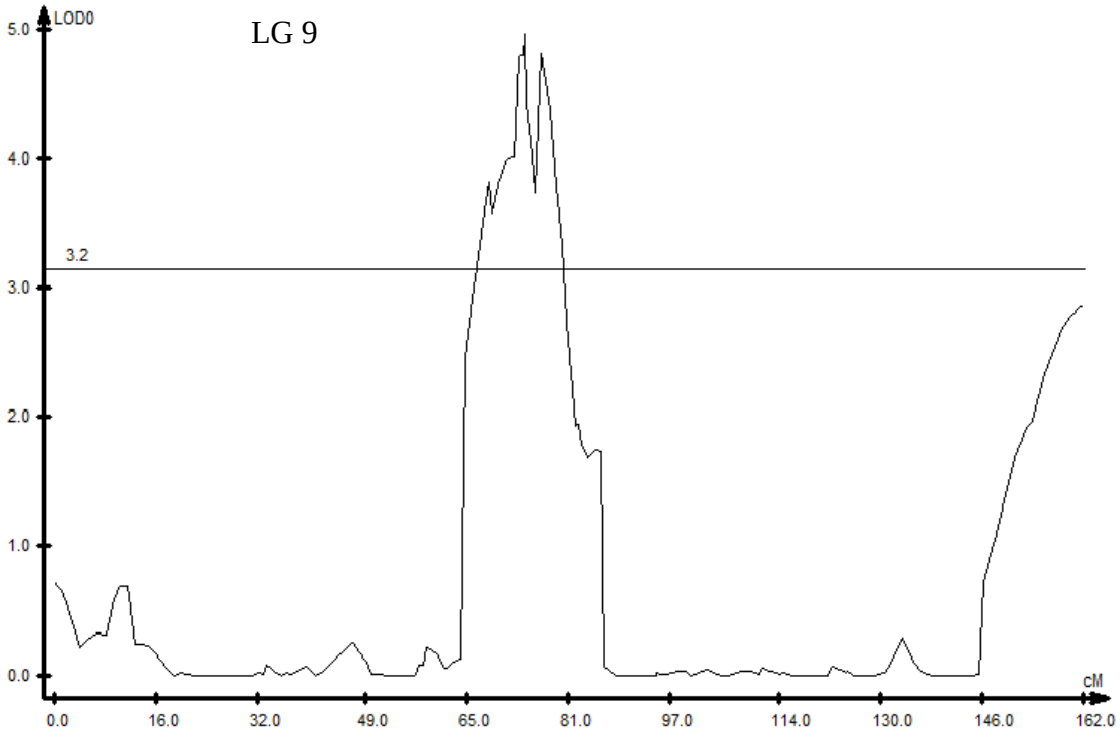


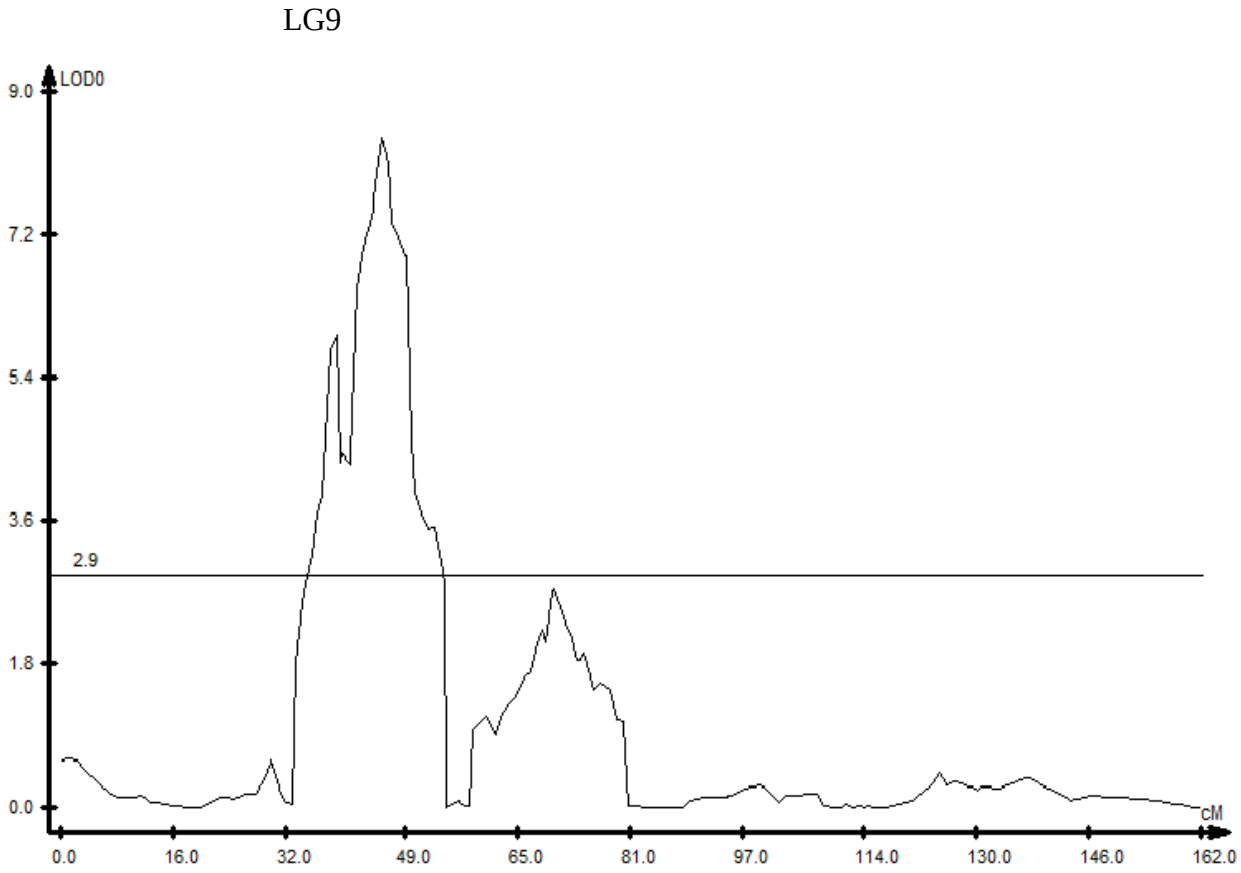
Figure 4.2: Significant QTL detected in the *Setaria* RIL population by composite interval mapping for the different traits A) Pericarp color; B) Bristling; C) Seed shattering. (The Y axis represents the LOD values and the X axis represents the position in cM).

B


LG 6
LOD0
4.0
3.2
3.0
2.4
1.6
0.8
0.0
cM
0.0
8.0
16.0
25.0
33.0
41.0
49.0
57.0
66.0
74.0
82.0


LG 9
LOD0
5.0
4.0
3.2
3.0
2.0
1.0
0.0
cM
0.0
16.0
32.0
49.0
65.0
81.0
97.0
114.0
130.0
146.0
162.0

C


LG9
LOD0
9.0
7.2
5.4
3.6
2.9
1.8
0.0
cM
0.0
16.0
32.0
49.0
65.0
81.0
97.0
114.0
130.0
146.0
162.0

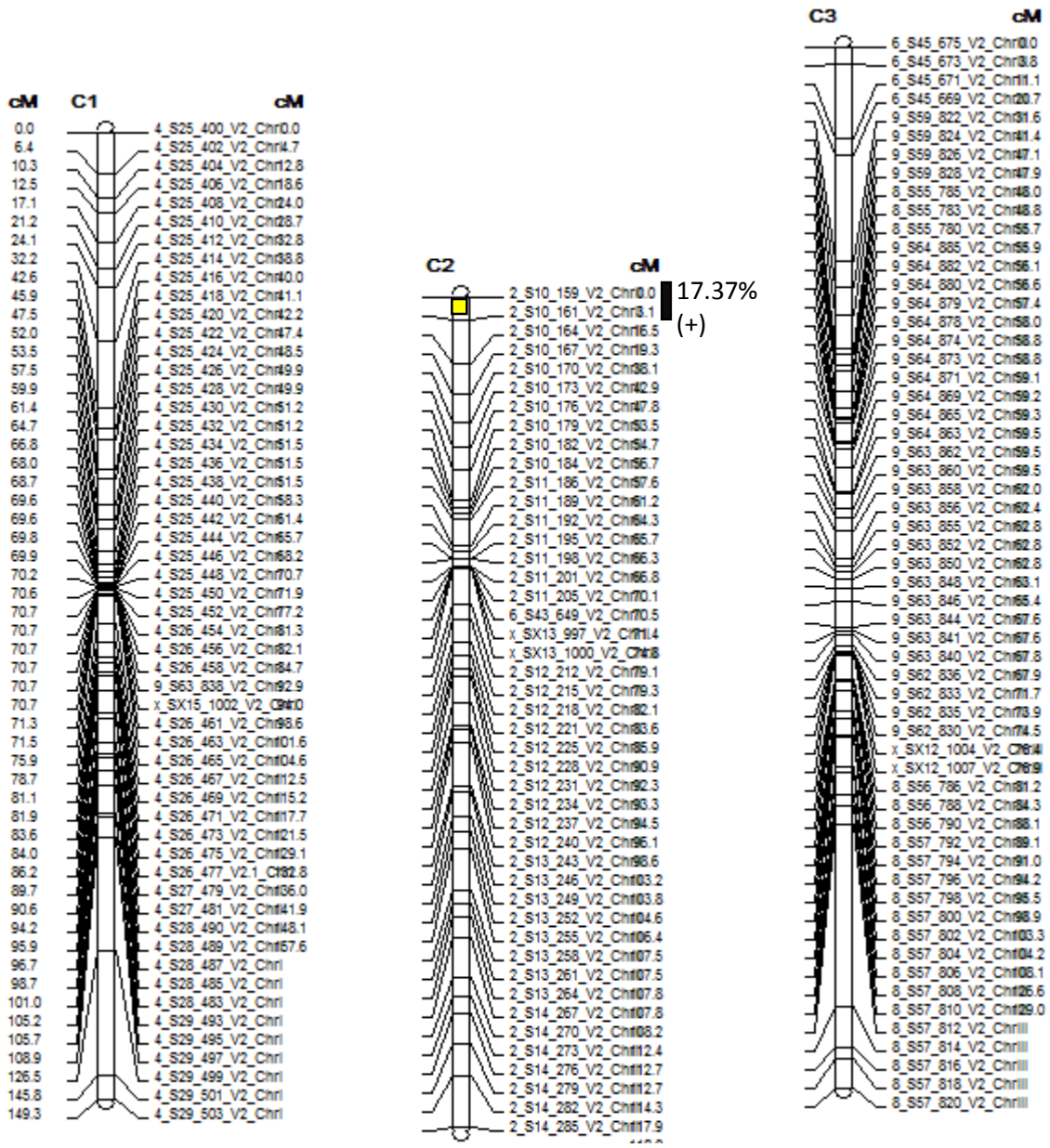
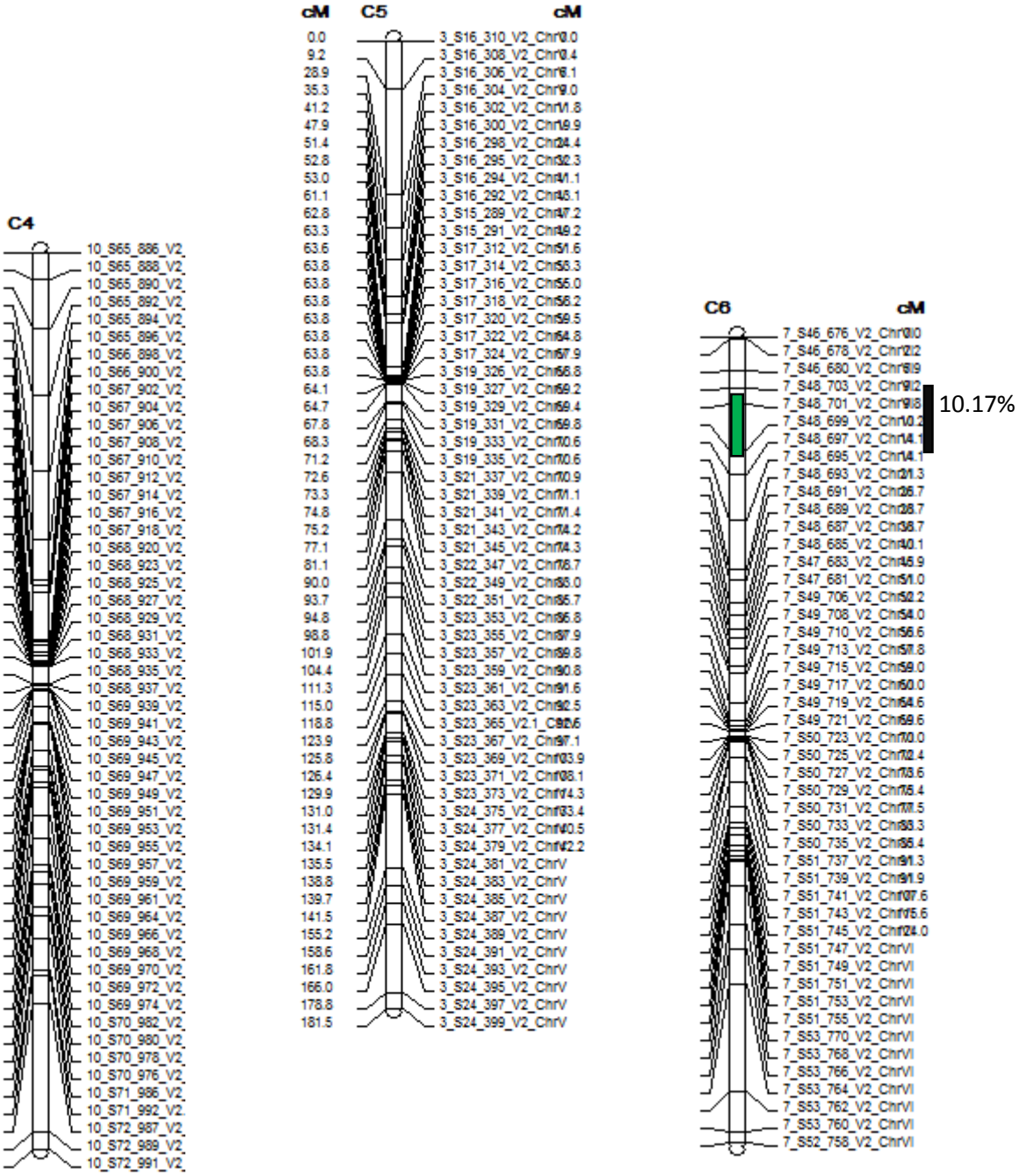
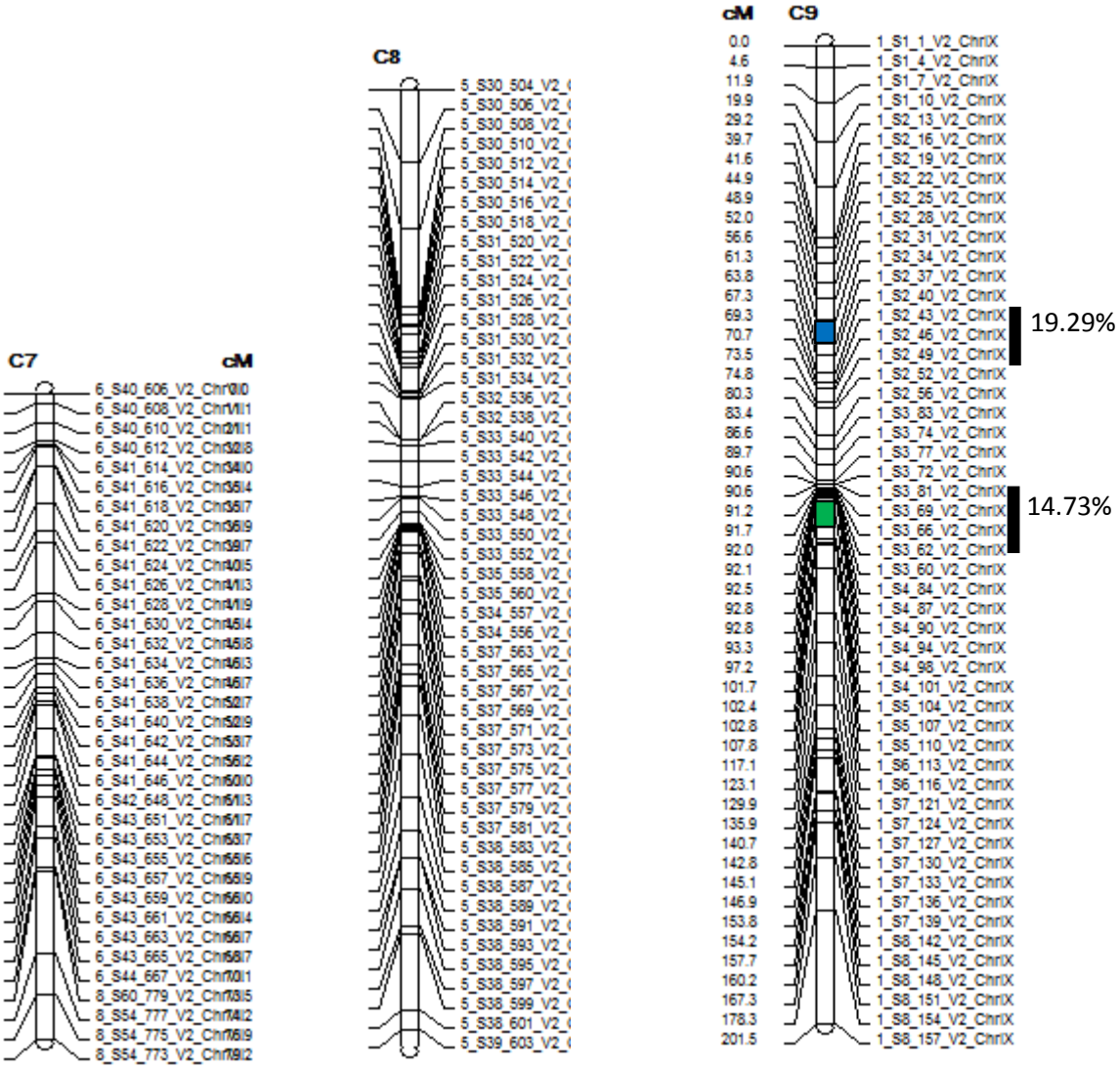


Figure 4.3: Map positions of significant QTL on each linkage group. Yellow bars represent pericarp color, green bars represent bristling and blue bars represent seed shattering. Percentage of variation explained by QTL and additive effect of QTL are indicated by side bars.


C4
C5
C6
cM
10.17%


C7
cM
C8
C9
cM
19.29%
14.73%

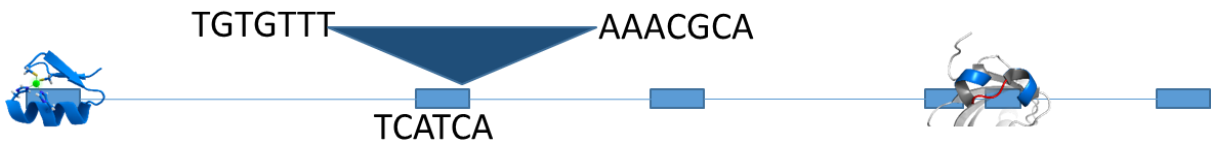


Figure 4.4: Presence of a miniature inverted-repeat element (MITE) in *SiSh1*. *SiSh1* bears a zinc finger domain on the amino terminus and a YABBY (helix-loop-helix) domain on the carboxyl terminus. Gray rectangles represent exons. Blue triangle represents the 854 bp MITE. The MITE bears a terminal inverted repeat of TGTGTTT on the amino terminus and AAACGCA on the carboxyl terminus.

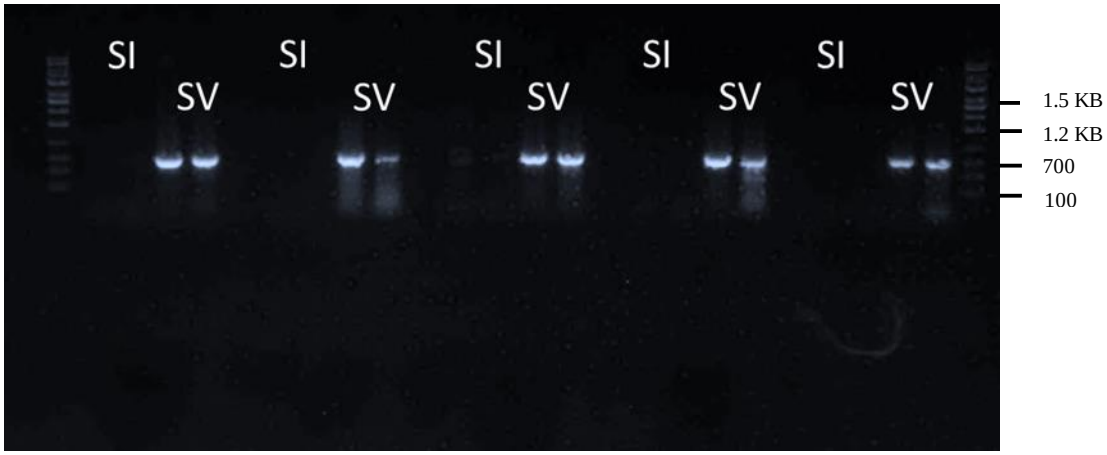


Figure 4.5: PCR amplification using primers designed ~350 bp upstream and downstream of the MITE insertion site. A seven hundred bp fragment is present in *Setaria viridis* (SV) lines indicating absence of the MITE. A 1.5 kb fragment was expected in *Setaria italica* (SI) lines. PCR reaction in these lines may have failed due to presence of a GC-rich region in the MITE. PCR products were run on a 1% agarose gel.

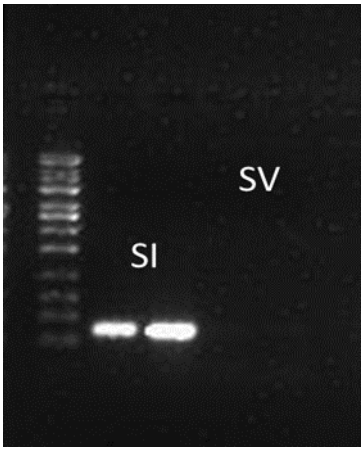


Figure 4.6: PCR amplification of ~400 bp fragment spanning 146 bp of the MITE sequence and 225 bp flanking sequence. The fragment is present in *Setaria italica* (SI) lines due to presence of the MITE and absent in *S. viridis* lines due to absence of the MITE. PCR product was run on 1% agarose gel.

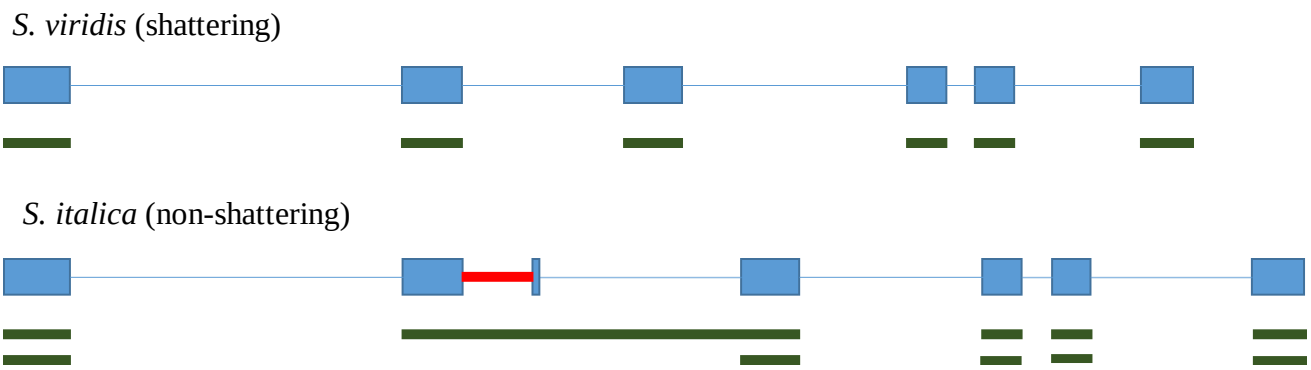


Figure 4.7: MITE insertion affects intron splicing in *S. italica*. Blue rectangles represent exons and blue lines represent introns. Green rectangles represent RNA transcripts and red rectangle represents MITE. Normal intron splicing occurs in *S. viridis* while intron splicing in *S. italica* is affected by MITE insertion which leads to transcription of the MITE and 2nd intron.

CHAPTER 5

CONCLUSION

The genus *Setaria* is a very diverse genus which includes some of the worst agricultural weeds. The species, *S. italica* and *S. viridis* are 2 of the most important species found in this genus. Due to their small genome size and close relation to several biofuel grasses with complex genomes, they are tractable models for crops such as switchgrass and napier grass. Interspecific crosses between S. italica and S. viridis have been used for genetic mapping and to introduce desired traits from *S. viridis* to *S. italica.*

With domestication, many crops available today show significant variation from their wild forms. Interspecific crosses between wild forms and domesticated forms create opportunities to study the genetic basis of domestication. In this study, mapping QTL for seed weight, pericarp color, bristling and seed shattering in a RIL population of 188 lines generated from a cross between B100, a *S. italica* strain (domesticated form), and A10, a *S. viridis* strain (wild ancestor) resulted in the identification of QTL for pericarp color (1 QTL), bristling (2 QTL) and seed shattering (1 QTL). Precise phenotyping greatly increases the chances of identifying QTL. Interestingly, despite the fact that we used a rudimentary approach to phenotyping seed shattering, that is clasping the panicle in a clenched fist and counting shed seeds, a QTL with a LOD score of 9.14 and explaining 19.29% of the variation was identified. Because this method was prone to error due to variation in clasping power, the QTL likely explains a larger part of the variation for shattering than indicated by our study.

Using comparative information, a candidate gene underlying the QTL for seed shattering was identified. Many domestication traits have come about due to mutations in a few loci with major effects. In this study, the insertion of a MITE into exon 2 of a YABBY transcription factor in *S. italica* leads to non-shattering. The MITE was present in the *S. italica* accessions studied and absent in all *S. viridis* lines analyzed. The insertion of the MITE affects intron splicing leading to two alternative transcripts in *S. italica*. Future work will focus on identifying alleles for *SiSh1* in a larger collection of *S. italica* germplasm. Furthermore, analysis of transcription levels of *SiSh1* in different tissues and validation of the alternative splice forms will broaden our understanding of the role of the MITE in inactivating the gene.

APPENDICES

A: Data of 100-seed weights (g) of each RIL. Three sets of 100 seeds were randomly selected and weighed for each RIL. The three sets were used as replicates.

RIL	Replication 1	Replication 2	Replication 3
1	0.193233333	0.192533333	0.186566667
2	*	*	*
3	*	*	*
4	*	*	*
5	*	*	*
6	*	*	*
7	0.2225	0.218166667	0.211766667
8	*	*	*
9	*	*	*
10	0.247566667	0.2519	0.216033333
11	0.251866667	0.2497	0.233433333
12	*	*	*
13	0.221366667	0.2183	0.2208
14	*	*	*
15	0.226766667	0.2249	0.220966667
16	*	*	*
17	*	*	*
18	*	*	*
19	*	*	*
20	*	*	*
21	*	*	*
22	0.1915	0.1902	0.1934
23	0.173766667	0.189	0.1432
24	0.166233333	0.176966667	0.145833333
25	0.169533333	0.1808	0.167433333

RIL	Replication 1	Replication 2	Replication 3
26	0.169133333	0.176833333	0.160466667
27	0.2712	0.272	0.2592
28	0.2176	0.2163	0.1975
29	*	*	*
30	0.227666667	0.224133333	0.2154
31	0.2225	0.2236	0.2302
32	*	*	0.2183
33	*	*	*
34	0.2654	0.264466667	0.258666667
35	0.2596	0.2594	0.263866667
36	*	*	*
37	*	*	*
38	0.2752	0.2729	0.2658
39	0.3075	0.301	0.2685
40	*	*	*
41	0.280133333	0.3025	0.300433333
42	0.262066667	0.2596	0.2528
43	0.267366667	0.2637	0.259866667
44	0.277966667	0.277066667	0.273433333
45	0.304233333	0.3027	0.2984
46	0.280033333	0.2732	0.276833333
47	0.249033333	0.2487	0.244833333
48	0.275933333	0.272933333	0.275766667
49	0.2511	0.244633333	0.246333333
50	*	*	*
51	0.298	0.2981	0.2938
52	*	*	*
53	0.254866667	0.2554	0.2553
54	0.266733333	0.262233333	0.266966667
55	*	*	*
56	*	*	*
57	0.276033333	0.2734	0.274966667
58	0.269633333	0.267	0.259966667
59	*	*	*
60	0.273866667	0.271433333	0.2662
61	0.2988	0.2972	0.2788
62	*	*	*
63	0.2568	0.262866667	0.2571
64	0.274666667	0.275766667	0.272666667

RIL	Replication 1	Replication 2	Replication 3
65	0.30743333	0.30233333	0.303633333
66	0.261733333	0.26025	0.263166667
67	0.2778	0.271466667	0.2754
68	0.2567	0.256733333	0.256866667
69	*	*	*
70	0.261633333	0.262266667	0.258866667
71	0.303533333	0.3009	0.3037
72	*	*	*
73	0.257366667	0.2624	0.257433333
74	0.2451	0.2525	0.239
75	0.2394	0.2378	0.242
76	*	*	*
77	*	*	*
78	0.2963	0.2899	0.288673
79	0.261566667	0.2596	0.2621
80	0.272533333	0.272933333	0.264266667
81	0.2606	0.2531	0.260667
82	0.295133333	0.298033333	0.296166667
83	0.1942	0.197833333	0.1899
84	*	*	*
85	*	*	*
86	*	*	*
87	0.266566667	0.266366667	0.269533333
88	*	*	*
89	*	*	*
90	0.194766667	0.191433333	0.189966667
91	0.258933333	0.2637	0.2561
92	*	*	*
93	*	*	*
94	*	*	*
95	*	*	*
96	*	*	*
97	*	*	*
98	*	*	*
99	0.2414	0.239433333	0.2442
100	*	*	*
101	0.2444	0.244466667	0.241833333
102	*	*	*
103	*	*	*

RIL	Replication 1	Replication 2	Replication 3
104	*	*	*
105	0.268933333	0.269733333	0.264166667
106	0.267433333	0.2676	0.2705
107	0.197766667	0.1991	0.1927
108	0.2097	0.207666667	0.204466667
109	0.2398	0.2414	0.2414
110	0.2445	0.242633333	0.2458
111	0.227733333	0.242633333	0.215566667
112	0.210066667	0.231566667	0.202133333
113	0.226066667	0.207433333	0.218366667
114	0.245333333	0.232033333	0.240433333
115	0.232633333	0.239633333	0.228133333
116	0.242933333	0.233733333	0.2415
117	0.2337	0.242433333	0.221933333
118	0.246	0.223833333	0.239366667
119	0.228233333	0.233766667	0.208333333
120	*	*	*
121	0.2197	0.2175	0.216
122	0.2328	0.2259	0.218866667
123	0.242733333	0.2451	0.245966667
124	0.2443	0.2441	0.245766667
125	*	*	*
126	*	*	*
127	0.201766667	0.196533333	0.2011
128	0.232633333	0.2376	0.232966667
129	*	*	*
130	*	*	*
131	0.2114	0.2099	0.215
132	*	*	*
133	*	*	*
134	*	*	*
135	0.2261	0.2275	0.219333
136	0.2268	0.2227	0.218266667
137	0.2047	0.2026	0.205978
138	0.2182	0.2118	0.218433333
139	0.1224	0.12	0.1175
140	0.1172	0.1205	0.1185
141	0.2047	0.2039	0.2056
142	0.2168	0.214333333	0.210166667

RIL	Replication 1	Replication 2	Replication 3
143	0.2744	0.273333333	0.267066667
144	0.2658	0.2508	0.254444
145	0.2016	0.1961	0.195157
146	*	*	*
147	0.217133333	0.214633333	0.207666667
148	0.1701	0.1652	0.165533333
149	*	*	*
150	0.2019	0.1982	0.198444
151	*	*	*
152	0.198466667	0.192666667	0.194766667
153	*	*	*
154	*	*	*
155	*	*	*
156	*	*	*
157	*	*	*
158	0.268033333	0.263333333	0.264733333
159	*	*	*
160	0.178366667	0.183366667	0.170366667
161	0.190133333	0.186766667	0.175933333
162	0.192066667	0.183466667	0.175266667
163	*	*	*
164	0.1722	0.1669	0.169565
165	*	*	*
166	0.1835	0.190133333	0.175833333
167	*	*	*
168	0.175066667	*	0.1729
169	0.1773	0.172933333	0.1826
170	*	*	*
171	0.175133333	0.179466667	0.179033333
172	*	*	*
173	0.1488	0.1478	0.1444
174	0.183533333	0.182333333	0.180466667
175	0.179433333	0.1803	0.176133333
176	0.166766667	0.1736	0.1675
177	0.182	0.1956	0.177433333
178	0.149733333	0.152133333	0.1433
179	*	*	*
180	0.1722	0.1701	0.168211
181	0.1622	0.166666667	0.156866667

RIL	Replication 1	Replication 2	Replication 3
182	0.1681	0.168766667	0.165533333
183	0.149466667	0.1497	0.148
184	0.169733333	0.1711	0.166433333
185	0.145133333	0.143866667	0.1379
186	*	*	*
187	0.1689	0.1594	0.164
188	0.163966667	0.1584	0.148066667

B: Data of Red, Blue and Green (RGB) values used to analyze pericarp color. Values for 6 seeds per RIL were used as replicates.

RIL	Replication 1	Replication 2	Replication 3	Replication 4	Replication 5	Replication 6
1	201.057	197.286	201.3	199.2	194.567	208.52
2	*	*	*	*	*	*
3	204.762	196.738	202.444	202.829	200.067	198.24
4	*	*	*	*	*	*
5	*	*	*	*	*	*
6	192.354	200.778	210.952	192.943	194	205.84
7	201.771	202.524	207.943	197.029	202.967	213.056
8	201.971	208.167	198.85	205.057	204.5	201.333
9	*	*	*	*	*	*
10	*	*	*	*	*	*
11	*	*	*	*	*	*
12	*	*	*	*	*	*
13	*	*	*	*	*	*
14	188	190.271	200.371	197.81	197.786	198.268
15	188.095	194.667	193.629	195.543	182.548	188.929
16	*	*	*	*	*	*
17	*	*	*	*	*	*
18	187.881	186.354	184.556	204.452	183.083	190.449
19	*	*	187.733	196.45	*	*
20	194.524	190.714	*	*	*	*
21	*	*	192.694	199.171	*	*
22	188.857	188.02	200.225	187.686	188.4	185.571
23	198.095	207.653	200.75	211.743	205.967	199.31
24	205.306	191.653	199.533	195.76	195.325	197.857
25	206.333	204.184	203.343	192.979	205.92	211.3

RIL	Replication 1	Replication 2	Replication 3	Replication 4	Replication 5	Replication 6
26	194.5	206.095	213.69	203.6	193.68	192.933
27	*	*	*	*	*	*
28	206.595	205.024	188.048	196.083	187.381	188.184
29	184.469	196.286	187.762	183.238	190.167	195.476
30	*	*	*	*	*	*
31	196.292	199.905	202.056	205.167	184.167	201.694
32	197.143	193.224	208.333	202.958	205.9	204.556
33	195.458	191.312	205.083	200.278	204.694	202.472
34	191.959	195.444	196.929	192.905	192.952	199.208
35	176.119	189.776	193.429	191.214	188.19	190.357
36	175.314	*	169.5	170.194	172.714	168.31
37	188.952	192.286	187.571	189.312	197.167	187.867
38	*	*	*	*	*	*
39	*	*	*	*	*	*
40	*	*	*	*	*	*
41	207.286	196.104	186.214	201.479	201.143	195.633
42	196.548	199.367	196.9	200.4	202.861	196.833
43	200.048	190.417	190.5	192.943	195.528	188.405
44	183.119	191.905	195.333	184.952	192.111	187.548
45	182.786	202.327	193.833	195.812	207.778	196.533
46	171.767	184.833	180.825	190.6	188.51	180.755
47	*	*	*	*	*	*
48	194.667	192.786	184.571	178.914	194.389	193.111
49	166.5	160.188	173.457	155.743	165.367	164.4
50	*	*	199.583	*	*	*
51	*	*	*	*	*	*
52	181.143	187.306	189.314	189.625	195.75	185.119
53	199.143	198.524	194.917	187.5	198.056	192.381
54	181.98	164.619	187.767	174.929	180.1	164.024
55	*	*	*	*	*	*
56	154.433	175.056	174.486	165.08	172.119	167.4
57	185.524	192.796	189.45	195.075	186.833	196.639
58	172.224	180.548	168.5	186.314	180.306	190.6
59	*	*	*	*	*	*
60	178.095	166.146	182.708	177.914	177.19	183.686
61	*	*	*	*	*	*
62	160.071	162.429	145.367	169.629	147.722	164.143
63	198.262	197.898	203.232	*	186.214	191.643
64	181.98	193.875	194.6	195.65	189.31	179.917

RIL	Replication 1	Replication 2	Replication 3	Replication 4	Replication 5	Replication 6
65	*	*	*	*	*	*
66	192.905	198.643	204.971	188.583	208.278	202.417
67	*	*	*	*	*	*
68	188.905	195.551	195.881	191.625	194.143	194.959
69	*	*	*	*	*	*
70	*	*	*	*	*	*
71	188	204.857	198.976	198.095	208.762	193.5
72	197.51	195.312	186.143	193.333	195.224	193.381
73	198.095	188.083	206.114	*	192.657	203.543
74	188.786	196.554	204.188	194.214	195.833	201.571
75	187.184	192.708	196.4	195.306	178.776	192.976
76	195.898	201.829	178.25	189.768	184.889	1:.048
77	*	*	*	*	*	*
78	*	*	*	*	*	*
79	195	190.776	189.667	*	196.125	173.457
80	170.612	161.762	171.143	164.405	180.467	157.917
81	194.196	194.271	192.071	189.738	193.667	194.528
82	*	*	*	*	*	*
83	*	*	*	*	*	*
84	*	*	*	*	*	*
85	172	178.222	187.675	194.229	191.528	181.071
86	193.886	191.143	194.229	188.286	187.444	202.306
87	193.667	199.625	197.786	193.286	198.417	197.457
88	*	*	*	*	*	*
89	*	*	*	*	*	*
90	*	*	*	*	*	*
91	*	*	*	*	*	*
92	*	*	182.9	187.057	*	*
93	*	*	*	*	*	*
94	187.143	176.933	183.4	199.733	183.861	183.657
95	180.262	*	204.8	186.521	*	*
96	195.979	*	185.156	176.881	178.143	199.722
97	*	*	*	*	*	*
98	*	*	*	*	*	*
99	189.143	179.238	188.619	193.333	185.449	189.257
100	*	*	*	*	*	*
101	190.833	186.583	181.143	178.262	194.889	178.408
102	*	*	*	*	*	*
103	*	*	183.833	*	*	*

RIL	Replication 1	Replication 2	Replication 3	Replication 4	Replication 5	Replication 6
104	*	*	180.306	*	*	*
105	167.457	181.857	191.095	*	177.861	179.306
106	185.167	182.2	178.286	161.775	182.967	183.917
107	*	*	*	*	*	*
108	193.381	190.408	192.69	198.426	182.639	188.688
109	194.959	194.411	195.381	198.6	199.881	192.184
110	193	188.02	200.233	193.214	193.056	197.357
111	163.381	169.905	173.343	166.095	171.861	161.467
112	*	*	*	*	*	*
113	*	*	*	*	*	*
114	185.686	181.929	183.771	186.357	193.143	199.556
115	158.35	156	173.639	174.3	165	160.139
116	192.095	186.286	196.88	193.056	196.75	191.583
117	156.881	163.19	167.333	175.222	159.306	163.1
118	*	*	*	*	*	*
119	*	*	*	*	*	*
120	*	*	*	*	*	*
121	178.417	181.667	193.139	187.889	196.467	189.629
122	160.19	167.133	173.033	167.417	155.944	158.556
123	194.521	194.188	190.833	190.619	202.733	200.643
124	190.762	186.796	191.524	199.5	191.467	195.472
125	*	*	*	*	*	*
126	*	*	171.444	*	*	*
127	*	*	*	*	*	*
128	156.056	156.833	167.167	161.971	157.514	164.5
129	188	*	200.286	*	199.639	187.8
130	*	*	203.583	*	188.222	*
131	*	*	*	*	*	*
132	*	*	*	*	*	*
133	183.286	188	199.524	194	195.8	193.514
134	*	*	166.952	162.806	*	*
135	158.02	144.9	168.972	163.738	163	168.314
136	*	*	*	*	*	*
137	203.786	197.571	197.262	197.735	198.357	203.694
138	*	*	*	*	*	*
139	*	*	*	*	*	*
140	*	*	*	*	*	*
141	171.472	156.31	157.886	153.778	160.4	152.886
142	192.69	185.592	192.111	189.755	177.684	183.143

RIL	Replication 1	Replication 2	Replication 3	Replication 4	Replication 5	Replication 6
143	*	*	*	*	*	*
144	165.486	183.786	166.7	174.833	179.222	183.571
145	*	*	*	*	*	*
146	156.9	159.3	158.314	162.371	158.886	168.143
147	178.229	179.514	190.029	200.633	188.333	187.444
148	201.125	195.812	202.6	201.6	201.917	206.5
149	*	*	*	*	*	*
150	*	*	*	*	*	*
151	*	*	*	*	*	*
152	*	*	*	*	*	*
153	*	*	*	*	*	*
154	*	*	*	*	*	*
155	*	*	183.343	*	*	*
156	160.433	144.306	154.429	149.139	152.4	161.36
157	*	*	197.567	*	*	*
158	178.262	184.548	188.714	186.067	179.867	184.333
159	186.889	183.325	168.229	179.686	181.067	*
160	187.686	191.812	189.967	192.381	195.133	187.833
161	*	*	*	*	*	*
162	*	*	*	*	*	*
163	*	*	*	*	*	*
164	*	*	*	*	*	*
165	185.457	203.171	187.306	190.2	186.429	193.786
166	201.028	185.595	188.833	184.194	193.944	190.714
167	196.262	196.556	196.967	190.19	183.472	187.548
168	194.405	191.571	192.405	187.429	186.467	184.806
169	*	*	*	*	*	*
170	183.889	194.25	177.257	181.444	196.143	175.071
171	187.694	170.262	167.829	172.067	185	170.167
172	190.896	190.357	181.786	174.275	192.25	180.267
173	*	*	*	*	*	*
174	182.444	202.357	186.371	191.611	195.133	193.44
175	199.083	183.25	184.257	181.829	200.24	193.6
176	195.5	203.389	202.88	204.25	196.917	194.4
177	*	*	*	*	*	*
178	172.143	163.171	158.767	172.72	170.062	159.875
179	*	*	*	*	*	*
180	*	*	*	*	*	*
181	142.1	161.357	161	149.629	155.28	166.32

RIL	Replication 1	Replication 2	Replication 3	Replication 4	Replication 5	Replication 6
182	*	*	*	*	*	*
183	161.886	160.429	166.033	168.143	163.733	163.84
184	188.25	188.722	209.7	203.429	197.64	202.2
185	174.533	174.667	177.6	*	181.8	170.75
186	*	*	*	*	*	*
187	203.367	192.095	191.686	209.375	204.95	187.5
188	*	*	*	*	*	*

C: Data of bristle lengths (mm) of 3 panicles of 3 plants for each RIL. Bristle lengths were taken at the middle of panicles.

RIL	Replication 1	Replication 2	Replication 3
1	*	*	1.75
2	3	*	*
3	3	*	0.25
4	*	0	*
5	*	7	*
6	*	3.75	*
7	2.333333333	*	3.5
8	4.333333333	4	3.75
9	3.5	*	*
10	*	*	3
11	5.333333333	3.75	5
12	*	4.5	1
13	2	4	4.75
14	*	*	*
15	*	*	5
16	3.25	4.666666667	4.5
17	3	*	*
18	5	10	10
19	*	*	*
20	3.25	*	*
21	3	5.5	6
22	0.333333333	*	*
23	2.75	4.333333333	*
24	3	*	6.5
25	*	2	1

RIL	Replication 1	Replication 2	Replication 3
26	*	*	1.5
27	*	*	*
28	4.666666667	3	*
29	2.333333333	*	2.333333333
30	2.75	3.25	3.25
31	*	*	*
32	*	4	5.5
33	3	1.5	2.5
34	3.333333333	*	4
35	*	1.666666667	0
36	3	*	*
37	*	4.666666667	4.5
38	3.75	3.666666667	*
39	6	*	5
40	2.75	0.333333333	1
41	3	3.25	4.25
42	3.333333333	2	*
43	*	*	5.5
44	*	*	1
45	*	*	*
46	2	1	0.5
47	3.5	2.5	3.25
48	2	*	0
49	*	*	5
50	*	*	3
51	0	0	*
52	*	6.333333333	*
53	1.666666667	0.75	*
54	4.666666667	3	2.666666667
55	2.666666667	3	2.333333333
56	0.5	2	*
57	0.666666667	*	1.333333333
58	0	1	0.25
59	2.666666667	4.75	3.5
60	4.333333333	2.5	2
61	3	5	5.5
62	*	9.333333333	*
63	1	2	*
64	2.5	1.25	1.25
65	3.333333333	3.5	*

RIL	Replication 1	Replication 2	Replication 3
66	3	5.666666667	*
67	*	2.666666667	3.75
68	3.666666667	2	*
69	1.666666667	2.25	*
70	*	*	*
71	*	2	1.25
72	2.333333333	1.75	*
73	4	*	2.25
74	4.333333333	*	3
75	0	*	3
76	4.333333333	7	6.75
77	3.5	*	*
78	2	*	2
79	*	*	*
80	3.25	3	2
81	*	*	*
82	7.666666667	5.25	4
83	2.5	2.666666667	3.333333333
84	3.666666667	4	5.25
85	2.666666667	0	*
86	6	6.75	8.25
87	5.25	5.75	*
88	5.5	*	*
89	*	*	1.5
90	2.75	1	*
91	3	2	*
92	6	4.75	4.75
93	*	1	*
94	4.666666667	*	*
95	*	*	*
96	2	3	*
97	1.333333333	1.75	0.5
98	2.5	*	*
99	1.666666667	*	4.25
100	*	1	0
101	3	1	*
102	4.25	3	*
103	8.333333333	0	0.25
104	3	*	*

RIL	Replication 1	Replication 2	Replication 3
105	*	*	*
106	1.666666667	2.25	2.5
107	*	*	*
108	3.25	6.5	*
109	2.5	3	2.75
110	*	*	*
111	7.333333333	9	2
112	2	2.5	*
113	3	3	3
114	4.25	*	4.75
115	2.75	3.75	*
116	*	7.333333333	*
117	2	3.5	2.333333333
118	1	1.5	4.5
119	3.75	3	1.5
120	*	*	3.5
121	1.666666667	2	0
122	2.666666667	3	0
123	1.5	1.5	*
124	3.25	3	*
125	6.5	8.5	*
126	3.5	3.333333333	4
127	3.333333333	3.666666667	2.5
128	*	3.25	1
129	2.75	3.5	2.5
130	*	*	*
131	4	3	*
132	*	3.5	*
133	3	1	2.5
134	3.5	1.666666667	2.5
135	5.5	6.333333333	4
136	4.666666667	3.666666667	*
137	1	*	2.25
138	3.25	*	2
139	1	*	3.333333333
140	*	4	2
141	2.333333333	2	5
142	*	4.5	3.5
143	3	2.75	*

RIL number	Replication 1	Replication 2	Replication 3
144	*	*	2
145	3.75	3.25	*
146	*	0.5	3
147	1	0.5	2.5
148	3.333333333	3	5
149	2.25	4.25	*
150	3	*	1.5
151	3	*	*
152	*	2.5	4
153	*	0.333333333	*
154	2	9.5	*
155	4.75	4	3
156	1.75	4.25	*
157	4.666666667	2.25	*
158	1.75	4	3
159	*	*	*
160	1	1	2
161	2.5	2.333333333	6.333333333
162	3.25	2.666666667	1
163	*	*	3.25
164	4	3	5
165	4	3	*
166	3	3	3.333333333
167	7	8	5.25
168	*	*	1.5
169	2.25	*	3.5
170	5	6	4.75
171	4.5	5.25	3
172	3	*	*
173	1.5	2.666666667	5.75
174	1.333333333	*	1
175	*	5.5	*
176	*	*	*
177	*	5.75	6
178	5.333333333	6	0.666666667
179	2.666666667	*	*
180	3.5	*	9
181	2.75	*	*
182	3	3.666666667	*

RIL number	Replication 1	Replication 2	Replication 3
183	4.75	9	*
184	3.666666667	*	*
185	5	6.5	*
186	*	2.5	1
187	3	6.333333333	2.5
188	3.25	2	0

D: Data for seed shattering of seed counts detached from 3 panicles from 3 different plants of each RIL.

RIL	Replication 1	Replication 2	Replication 3
1	*	*	3.75
2	8.75	*	8
3	16.25	*	14.25
4	10	2	13.5
5	0	25	0.5
6	24	7.5	1.666666667
7	6	14	3.5
8	1.5	8.666666667	2
9	3.5	*	7.666666667
10	*	*	2.666666667
11	0.75	0.5	0
12	2.25	5	3.666666667
13	1.25	4	4.25
14	*	*	4.5
15	*	*	0
16	26	40	19.25
17	9	*	43.75
18	5.666666667	1.333333333	1.333333333
19	*	*	*
20	27.25	*	*
21	0.5	21	1.5
22	1.5	*	10.66666667
23	7	11.5	16
24	1.25	*	66
25	9.25	9.5	*

RIL	Replication 1	Replication 2	Replication 3
26	4.75	*	0.25
27	*	*	9.75
28	14.75	55.75	12.5
29	11.5	*	*
30	0.5	10.75	4.75
31	0.25	*	7.333333333
32	*	49.66666667	1
33	2	1.5	3
34	14.5	*	5.75
35	1.5	5.333333333	2.333333333
36	1	*	*
37	7.5	5.75	4
38	8.5	6.75	0.5
39	0.25	*	0
40	8.75	8	1.75
41	3	16	13.75
42	7	46.25	1
43	*	*	0.666666667
44	2.5	4.5	0.333333333
45	*	*	50
46	6	25	3
47	14.75	13	6
48	70	*	*
49	*	*	1.5
50	17.66666667	*	*
51	9	0.5	3.5
52	7.25	47.66666667	39.5
53	3.75	36	25
54	0.333333333	1.666666667	0.666666667
55	2.333333333	*	0.333333333
56	35	*	7.666666667
57	4.333333333	*	5.333333333
58	0	10	2.333333333
59	1.75	5.5	11.66666667
60	1	7	7
61	3.5	8.25	1.5
62	7.25	11.25	17.75
63	19.5	28	1.25
64	1.75	12	0.25
65	1.75	4	1

RIL	Replication 1	Replication 2	Replication 3
66	16	16.66666667	27.5
67	129.5	101.6666667	20
68	18.66666667	6	31.66666667
69	5.666666667	3	4.5
70	*	*	*
71	1	3	1.5
72	3.75	2	27.5
73	8.5	*	13.5
74	5.25	*	24
75	1.75	*	1
76	21.5	2	1.5
77	0.666666667	*	0
78	2.25	*	1
79	*	*	*
80	17	2	28
81	*	*	3
82	0.25	2.25	0.25
83	0.75	0	5
84	9.75	15.66666667	6
85	19.33333333	120	66.33333333
86	5.25	5.75	1
87	0	4.25	1
88	7.25	7.666666667	0.5
89	*	*	2.25
90	2.75	1.5	*
91	7.333333333	10.66666667	8.5
92	27.5	20.5	16
93	*	*	*
94	18.5	1.75	6.5
95	*	*	*
96	88	4	15
97	9	13.5	8.75
98	3.25	0.666666667	13.5
99	14.66666667	*	10.25
100	0	0.25	0.5
101	1.75	7.666666667	9.5
102	0.25	13	0
103	6	2	18.5
104	1.25	0	2
105	*	*	*

RIL	Replication 1	Replication 2	Replication 3
106	8.333333333	22.25	11.5
107	*	*	*
108	22.5	*	*
109	37	2.333333333	0
110	*	*	*
111	4	27.33333333	8.75
112	4.25	1	1
113	1.75	0.5	15
114	0.5	2	10
115	12.75	47.5	23.66666667
116	6.666666667	8	0.75
117	2.666666667	25	8.333333333
118	1	1	0.5
119	12.66666667	8	0.5
120	13	*	14
121	76.25	63.33333333	*
122	15.25	30	11
123	14	9.333333333	*
124	156.25	38.33333333	*
125	0.5	2.5	6.5
126	6.5	13.25	*
127	3	19.33333333	17.5
128	3	22.5	5
129	1.5	2.5	3.5
130	*	*	1
131	13	14.5	33
132	*	2.25	1
133	1.25	6	1
134	1.75	6	30.5
135	5	6.75	1.666666667
136	23.66666667	60	42.5
137	1.75	*	185
138	3.5	*	*
139	22.75	*	9
140	*	91.66666667	10
141	38.5	2.333333333	42
142	20.5	100.5	4
143	2.5	2.25	19.75
144	*	*	6.75

RIL	Replication 1	Replication 2	Replication 3
145	6.5	22.75	22.5
146	*	17.5	40
147	3.5	19	16.5
148	3	30	4
149	3.25	9	1.5
150	13.5	19	40.75
151	7.25	*	13.5
152	*	263	1.666666667
153	34.75	34.33333333	32.66666667
154	3	3.333333333	33.66666667
155	21	40	28
156	3.5	5.75	35
157	29.66666667	27.66666667	127.5
158	0.5	2.666666667	0
159	*	*	*
160	1.25	4	0
161	4	0.333333333	1
162	12	10	18.33333333
163	*	*	*
164	7.5	21	13.25
165	13	29.5	3.333333333
166	2.5	4.5	7
167	19.33333333	3.5	1.5
168	*	*	37.66666667
169	11	*	2.333333333
170	57	35.5	55
171	7	29.5	2
172	5	12.33333333	25
173	5	3.333333333	4.5
174	1.666666667	*	1.5
175	4.333333333	7.5	8
176	*	*	*
177	12.25	6.75	56.5
178	14	60.66666667	3
179	27.33333333	*	20
180	21	5.5	33
181	21.25	*	38.25
182	13.33333333	116.6666667	30.25
183	3.666666667	2	2.75
184	12.25	67.5	10.5

RIL 1	Replication 1	Replication 2	Replication 3
185	0.666666667	7.5	4
186	4	24.5	4
187	16.33333333	41	9.333333333
188	2	8.333333333	2

E: Genes (203) located within QTL support interval for pericarp color on *Setaria* chromosome 2 and their gene ontology descriptions.

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si029757m.g	1191104	1194313	protein binding
Si033316m.g	666900	668258	transferase activity, transferring acyl groups other than amino-acyl groups
Si033203m.g	1902506	1903630	
Si033042m.g	844538	847241	binding
Si032450m.g	616101	616408	integral to membrane
Si032450m.g	616101	616408	transport
Si031309m.g	1972614	1973357	extracellular region
Si032404m.g	1060279	1060717	
Si031702m.g	2153265	2153563	
Si033263m.g	1187935	1189056	
Si033068m.g	1857307	1859428	aspartate-tRNA ligase activity
Si033068m.g	1857307	1859428	nucleic acid binding
Si033068m.g	1857307	1859428	cytoplasm
Si033068m.g	1857307	1859428	aminoacyl-tRNA ligase activity
Si033068m.g	1857307	1859428	tRNA aminoacylation for protein translation
Si033068m.g	1857307	1859428	ATP binding
Si033068m.g	1857307	1859428	nucleotide binding
Si033068m.g	1857307	1859428	aspartyl-tRNA aminoacylation
Si033378m.g	1281133	1282466	
Si029354m.g	570457	575171	protein binding
Si033471m.g	1758731	1759264	
Si030192m.g	1161955	1164606	protein binding
Si032180m.g	1345882	1347444	
Si030402m.g	1921233	1923697	
Si033252m.g	1546883	1548202	
Si033029m.g	1062169	1063287	protein binding
Si032823m.g	2331657	2332427	

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si033364m.g	900172	902697	
Si029256m.g	1195746	1198073	
Si032343m.g	866356	867199	copper ion binding
Si032343m.g	866356	867199	oxidoreductase activity
Si032343m.g	866356	867199	oxidation-reduction process
Si032541m.g	1512780	1516075	1,3-beta-D-glucan synthase complex
Si032541m.g	1512780	1516075	1,3-beta-D-glucan synthase activity
Si032541m.g	1512780	1516075	(1->3)-beta-D-glucan biosynthetic process
Si032541m.g	1512780	1516075	membrane
Si032183m.g	1579094	1580178	protein binding
Si032356m.g	631362	633611	
Si032957m.g	605238	606329	protein binding
Si031328m.g	2384943	2385834	
Si028919m.g	2350421	2357355	DNA binding
Si028919m.g	2350421	2357355	chromatin binding
Si031256m.g	1864961	1865831	extracellular region
Si031256m.g	1864961	1865831	growth factor activity
Si031256m.g	1864961	1865831	cell proliferation
Si029570m.g	582603	584117	ADP binding
Si029425m.g	1786102	1788203	
Si031454m.g	2032667	2033652	sequence-specific DNA binding transcription factor activity
Si031454m.g	2032667	2033652	regulation of transcription, DNA-dependent
Si031454m.g	2032667	2033652	nucleus
Si031454m.g	2032667	2033652	sequence-specific DNA binding
Si031454m.g	2032667	2033652	DNA binding
Si032501m.g	1451945	1453458	
Si029185m.g	1945680	1950031	DNA binding
Si029185m.g	1945680	1950031	regulation of transcription, DNA-dependent
Si029185m.g	1945680	1950031	sequence-specific DNA binding transcription factor activity
Si033377m.g	1861079	1861720	

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si030576m.g	1780297	1783735	protein binding
Si033644m.g	2151218	2151642	
Si032413m.g	1589685	1590749	protein binding
Si032385m.g	1172209	1173339	protein binding
Si032538m.g	2189373	2190049	
Si033677m.g	560908	561513	
Si032429m.g	1879467	1880494	sequence-specific DNA binding
Si032429m.g	1879467	1880494	sequence-specific DNA binding transcription factor activity
Si032429m.g	1879467	1880494	regulation of transcription, DNA-dependent
Si032231m.g	1117165	1118656	ADP binding
Si032691m.g	835458	837573	
Si032670m.g	1831545	1833035	ADP binding
Si030226m.g	2300624	2305086	
Si029029m.g	903382	909243	protein kinase activity
Si029029m.g	903382	909243	protein tyrosine kinase activity
Si029029m.g	903382	909243	protein phosphorylation
Si029029m.g	903382	909243	ATP binding
Si029029m.g	903382	909243	transferase activity, transferring phosphorus-containing groups
Si029029m.g	903382	909243	protein serine/threonine kinase activity
Si033200m.g	2200730	2202035	protein binding
Si033018m.g	1468655	1470200	
Si031750m.g	1461069	1461552	
Si033167m.g	1585987	1587209	
Si032679m.g	1390202	1390597	
Si033287m.g	653756	655463	oxidation-reduction process
Si033287m.g	653756	655463	iron ion binding
Si033287m.g	653756	655463	heme binding
Si033287m.g	653756	655463	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
Si032196m.g	2195417	2199338	protein kinase activity
Si032196m.g	2195417	2199338	protein tyrosine kinase activity

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si032196m.g	2195417	2199338	protein binding
Si032196m.g	2195417	2199338	protein phosphorylation
Si032196m.g	2195417	2199338	ATP binding
Si032196m.g	2195417	2199338	transferase activity, transferring phosphorus-containing groups
Si029501m.g	1397449	1399325	
Si033338m.g	1009592	1009867	
Si029134m.g	2052608	2054641	protein kinase activity
Si029134m.g	2052608	2054641	protein tyrosine kinase activity
Si029134m.g	2052608	2054641	carbohydrate binding
Si029134m.g	2052608	2054641	protein serine/threonine kinase activity
Si029134m.g	2052608	2054641	transferase activity, transferring phosphorus-containing groups
Si029134m.g	2052608	2054641	ATP binding
Si029134m.g	2052608	2054641	protein phosphorylation
Si032933m.g	2349927	2350298	
Si032868m.g	966385	968264	
Si032275m.g	1383627	1386202	
Si033490m.g	2204066	2207513	
Si031893m.g	894219	894642	
Si029675m.g	2127350	2131421	
Si032867m.g	1812229	1813833	protein binding
Si028668m.g	2287176	2295192	protein binding
Si029092m.g	991942	994528	
Si033087m.g	1898337	1899477	
Si032047m.g	895440	898185	binding
Si032697m.g	745074	747283	ADP binding
Si030226m.g	2301816	2305086	
Si031240m.g	2358180	2361238	
Si030087m.g	1728484	1730467	biosynthetic process
Si030087m.g	1728484	1730467	catalytic activity
Si030087m.g	1728484	1730467	metabolic process

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si030087m.g	1728484	1730467	transferase activity, transferring acyl groups
Si030071m.g	1822241	1825989	transferase activity, transferring phosphorus-containing groups
Si030071m.g	1822241	1825989	ATP binding
Si029893m.g	851392	854775	protein binding
Si032135m.g	1714735	1716078	hydrolase activity
Si032135m.g	1714735	1716078	metabolic process
Si032555m.g	1908770	1909672	metal ion binding
Si032893m.g	2282850	2284976	protein tyrosine kinase activity
Si032893m.g	2282850	2284976	protein kinase activity
Si032893m.g	2282850	2284976	protein phosphorylation
Si032893m.g	2282850	2284976	transferase activity, transferring phosphorus-containing groups
Si032893m.g	2282850	2284976	protein serine/threonine kinase activity
Si032893m.g	2282850	2284976	ATP binding
Si032864m.g	945114	945335	
Si033803m.g	1026643	1026782	
Si033208m.g	938104	940281	
Si029592m.g	1109678	1111177	ADP binding
Si031302m.g	2387982	2388854	
Si033347m.g	1836935	1838455	ADP binding
Si030145m.g	1024159	1026512	
Si033044m.g	727817	731644	
Si032652m.g	1549305	1550562	
Si031739m.g	1027045	1027582	
Si033490m.g	2203169	2207513	
Si032941m.g	1567885	1568973	protein binding
Si031962m.g	1839105	1840853	protein phosphorylation
Si031962m.g	1839105	1840853	protein serine/threonine kinase activity
Si031962m.g	1839105	1840853	transferase activity, transferring phosphorus-containing groups
Si031962m.g	1839105	1840853	ATP binding
Si031962m.g	1839105	1840853	protein kinase activity

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si031962m.g	1839105	1840853	protein tyrosine kinase activity
Si032804m.g	1951845	1955090	
Si031172m.g	1749551	1750691	
Si032268m.g	548828	549976	protein binding
Si029609m.g	564588	566081	ADP binding
Si032410m.g	1482423	1483958	
Si029216m.g	1766992	1770723	
Si029593m.g	2325374	2329477	oxidoreductase activity
Si029593m.g	2325374	2329477	oxidation-reduction process
Si029593m.g	2325374	2329477	purine nucleotide biosynthetic process
Si029593m.g	2325374	2329477	catalytic activity
Si029593m.g	2325374	2329477	IMP dehydrogenase activity
Si030043m.g	1891905	1895804	
Si029441m.g	927868	930382	copper ion binding
Si029441m.g	927868	930382	oxidoreductase activity
Si029441m.g	927868	930382	oxidation-reduction process
Si029447m.g	589555	594286	ATP binding
Si029447m.g	589555	594286	protein folding
Si029447m.g	589555	594286	cellular protein metabolic process
Si029447m.g	589555	594286	unfolded protein binding
Si032862m.g	2121305	2122429	DNA binding
Si032862m.g	2121305	2122429	protein dimerization activity
Si033004m.g	1349319	1350812	
Si030158m.g	1925576	1929267	nucleotide binding
Si030158m.g	1925576	1929267	nucleic acid binding
Si029701m.g	1723994	1726391	glycerolipid biosynthetic process
Si029701m.g	1723994	1726391	diacylglycerol O-acyltransferase activity
Si032294m.g	1131974	1136347	protein serine/threonine kinase activity
Si032294m.g	1131974	1136347	transferase activity, transferring phosphorus-containing groups
Si032294m.g	1131974	1136347	ATP binding

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si032294m.g	1131974	1136347	protein phosphorylation
Si032294m.g	1131974	1136347	protein kinase activity
Si032294m.g	1131974	1136347	protein tyrosine kinase activity
Si033498m.g	1692018	1692527	
Si030775m.g	2374854	2376688	
Si032474m.g	1210859	1211767	protein binding
Si032155m.g	543914	545074	
Si030099m.g	1904777	1907652	
Si032438m.g	2065364	2067352	protein phosphorylation
Si032438m.g	2065364	2067352	ATP binding
Si032438m.g	2065364	2067352	transferase activity, transferring phosphorus-containing groups
Si032438m.g	2065364	2067352	protein serine/threonine kinase activity
Si032438m.g	2065364	2067352	protein kinase activity
Si032438m.g	2065364	2067352	protein tyrosine kinase activity
Si032438m.g	2065364	2067352	carbohydrate binding
Si029153m.g	2036907	2039082	protein kinase activity
Si029153m.g	2036907	2039082	carbohydrate binding
Si029153m.g	2036907	2039082	protein tyrosine kinase activity
Si029153m.g	2036907	2039082	protein phosphorylation
Si029153m.g	2036907	2039082	transferase activity, transferring phosphorus-containing groups
Si029153m.g	2036907	2039082	protein serine/threonine kinase activity
Si029153m.g	2036907	2039082	ATP binding
Si031492m.g	567356	570681	
Si032783m.g	809477	811068	
Si031242m.g	1964557	1965439	extracellular region
Si029022m.g	748206	758588	nucleus
Si029383m.g	1530901	1537216	protein binding
Si029023m.g	1791906	1800637	protein binding
Si030775m.g	2374854	2376697	
Si032486m.g	987810	988385	

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si032244m.g	776124	777807	
Si028794m.g	2157495	2161200	protein binding
Si028794m.g	2157495	2161200	protein kinase activity
Si028794m.g	2157495	2161200	protein tyrosine kinase activity
Si028794m.g	2157495	2161200	transferase activity, transferring phosphorus-containing groups
Si028794m.g	2157495	2161200	protein serine/threonine kinase activity
Si028794m.g	2157495	2161200	ATP binding
Si028794m.g	2157495	2161200	protein phosphorylation
Si030286m.g	920360	922357	DNA binding
Si033226m.g	613708	615081	transferase activity, transferring acyl groups other than amino-acyl groups
Si032190m.g	1561365	1563045	
Si033124m.g	1374209	1375138	
Si033210m.g	1732475	1734803	transposition, DNA-mediated
Si033210m.g	1732475	1734803	transposase activity
Si033210m.g	1732475	1734803	zinc ion binding
Si033210m.g	1732475	1734803	DNA binding
Si031883m.g	1322130	1323694	
Si031722m.g	2365588	2366102	
Si030975m.g	1959524	1962558	
Si031603m.g	2063142	2064331	
Si031499m.g	1806091	1806797	
Si032952m.g	1566205	1567707	
Si030775m.g	2374854	2376697	
Si030158m.g	1925576	1929267	nucleotide binding
Si030158m.g	1925576	1929267	nucleic acid binding
Si032586m.g	1290355	1292602	
Si029867m.g	1643605	1645156	
Si032187m.g	1429060	1430622	
Si032654m.g	848771	849781	
Si029806m.g	2409969	2414119	protein binding

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si029348m.g	2181638	2185770	transferase activity, transferring phosphorus-containing groups
Si029348m.g	2181638	2185770	ATP binding
Si029348m.g	2181638	2185770	protein phosphorylation
Si029348m.g	2181638	2185770	protein kinase activity
Si029348m.g	2181638	2185770	protein tyrosine kinase activity
Si032120m.g	2370535	2372049	
Si031944m.g	1165915	1167459	protein binding
Si032080m.g	1809686	1811779	nucleoside-triphosphatase activity
Si032080m.g	1809686	1811779	nucleotide binding
Si032080m.g	1809686	1811779	ATP binding
Si032080m.g	1809686	1811779	ATPase activity
Si032293m.g	1801433	1801903	
Si032757m.g	2041451	2043475	protein phosphorylation
Si032757m.g	2041451	2043475	ATP binding
Si032757m.g	2041451	2043475	protein serine/threonine kinase activity
Si032757m.g	2041451	2043475	transferase activity, transferring phosphorus-containing groups
Si032757m.g	2041451	2043475	protein tyrosine kinase activity
Si032757m.g	2041451	2043475	carbohydrate binding
Si032757m.g	2041451	2043475	protein kinase activity
Si031965m.g	1085854	1087493	
Si030202m.g	2395798	2398949	oxidoreductase activity
Si030202m.g	2395798	2398949	oxidation-reduction process
Si029566m.g	1216166	1217683	protein binding
Si031925m.g	1527427	1528575	
Si030217m.g	1914128	1915736	
Si033219m.g	674768	675975	protein binding
Si028960m.g	1871788	1876801	nucleic acid binding
Si028960m.g	1871788	1876801	DNA binding
Si028960m.g	1871788	1876801	helicase activity
Si028960m.g	1871788	1876801	ATP binding

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si029731m.g	2105045	2106995	
Si030188m.g	1153615	1155548	protein binding
Si029946m.g	2346599	2349346	coenzyme binding
Si029946m.g	2346599	2349346	catalytic activity
Si029946m.g	2346599	2349346	galactose metabolic process
Si029946m.g	2346599	2349346	UDP-glucose 4-epimerase activity
Si029946m.g	2346599	2349346	cellular metabolic process
Si032755m.g	1181540	1182784	regulation of transcription, DNA-dependent
Si032755m.g	1181540	1182784	DNA binding
Si033344m.g	1067343	1068641	protein binding
Si031775m.g	1224464	1225136	
Si032775m.g	1600766	1603057	
Si032781m.g	1540537	1541601	protein binding
Si030013m.g	577608	579706	protein binding
Si029293m.g	1143962	1146260	galactoside 2-alpha-L-fucosyltransferase activity
Si029293m.g	1143962	1146260	cell wall biogenesis
Si029293m.g	1143962	1146260	membrane
Si032334m.g	2072518	2074581	protein phosphorylation
Si032334m.g	2072518	2074581	protein serine/threonine kinase activity
Si032334m.g	2072518	2074581	transferase activity, transferring phosphorus-containing groups
Si032334m.g	2072518	2074581	ATP binding
Si032334m.g	2072518	2074581	protein kinase activity
Si032334m.g	2072518	2074581	carbohydrate binding
Si032334m.g	2072518	2074581	protein tyrosine kinase activity
Si029498m.g	732878	736059	
Si032366m.g	1519757	1520854	
Si030477m.g	2317476	2319091	regulation of transcription, DNA-dependent
Si030477m.g	2317476	2319091	DNA binding
Si031297m.g	1977136	1977915	extracellular region
Si032612m.g	1104337	1105818	ADP binding

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si031540m.g	1438756	1439393	
Si033480m.g	2043586	2044986	
Si031433m.g	2085119	2086377	
Si032604m.g	740531	743295	ADP binding
Si032604m.g	740531	743295	defense response
Si032415m.g	2089968	2092349	
Si032554m.g	2186814	2187462	
Si029988m.g	2368300	2369722	protein kinase activity
Si029988m.g	2368300	2369722	protein tyrosine kinase activity
Si029988m.g	2368300	2369722	protein serine/threonine kinase activity
Si029988m.g	2368300	2369722	transferase activity, transferring phosphorus-containing groups
Si029988m.g	2368300	2369722	ATP binding
Si029988m.g	2368300	2369722	protein phosphorylation
Si032344m.g	1011336	1011569	
Si033108m.g	2077512	2079530	protein phosphorylation
Si033108m.g	2077512	2079530	protein serine/threonine kinase activity
Si033108m.g	2077512	2079530	transferase activity, transferring phosphorus-containing groups
Si033108m.g	2077512	2079530	ATP binding
Si033108m.g	2077512	2079530	carbohydrate binding
Si033108m.g	2077512	2079530	protein tyrosine kinase activity
Si033108m.g	2077512	2079530	protein kinase activity
Si032506m.g	1200389	1201834	ADP binding
Si033278m.g	1817513	1818688	
Si031907m.g	1544289	1546114	
Si031996m.g	585924	588893	protein binding
Si030168m.g	1574912	1576735	
Si033480m.g	2043586	2044986	
Si031950m.g	1986224	1988453	
Si031113m.g	723141	727369	
Si032517m.g	1095137	1098623	protein kinase activity

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si032517m.g	1095137	1098623	protein tyrosine kinase activity
Si032517m.g	1095137	1098623	ATP binding
Si032517m.g	1095137	1098623	calcium ion binding
Si032517m.g	1095137	1098623	protein serine/threonine kinase activity
Si032517m.g	1095137	1098623	transferase activity, transferring phosphorus-containing groups
Si032517m.g	1095137	1098623	protein phosphorylation
Si029651m.g	562000	563587	
Si029647m.g	1487660	1489441	
Si033296m.g	819139	820726	
Si032465m.g	2389781	2390973	
Si032630m.g	1393629	1395676	
Si032437m.g	1494200	1497607	protein binding
Si033021m.g	598412	599468	
Si033305m.g	1759308	1760567	DNA binding
Si033305m.g	1759308	1760567	regulation of transcription, DNA-dependent
Si031930m.g	676133	678678	protein binding
Si032109m.g	567865	569363	ADP binding
Si030685m.g	1763485	1766055	
Si031981m.g	766772	767590	protein binding
Si032316m.g	1228272	1229968	protein binding
Si033142m.g	2056473	2058512	protein phosphorylation
Si033142m.g	2056473	2058512	protein serine/threonine kinase activity
Si033142m.g	2056473	2058512	transferase activity, transferring phosphorus-containing groups
Si033142m.g	2056473	2058512	ATP binding
Si033142m.g	2056473	2058512	carbohydrate binding
Si033142m.g	2056473	2058512	protein tyrosine kinase activity
Si033142m.g	2056473	2058512	protein kinase activity
Si032608m.g	621739	622776	
Si029111m.g	2049630	2051864	protein phosphorylation
Si029111m.g	2049630	2051864	ATP binding

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si029111m.g	2049630	2051864	protein serine/threonine kinase activity
Si029111m.g	2049630	2051864	transferase activity, transferring phosphorus-containing groups
Si029111m.g	2049630	2051864	protein tyrosine kinase activity
Si029111m.g	2049630	2051864	carbohydrate binding
Si029111m.g	2049630	2051864	protein kinase activity
Si030028m.g	2403171	2405889	protein dimerization activity
Si032041m.g	1471332	1471535	
Si030146m.g	557656	559951	
Si032053m.g	773927	775396	
Si032039m.g	706027	708696	protein binding
Si032426m.g	1078388	1079473	

F: Genes (182) located within QTL support interval for bristling on *Setaria* chromosome 6 and their gene ontology descriptions

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si013178m.g	2184372	2190867	protein tyrosine kinase activity
Si013178m.g	2184372	2190867	protein kinase activity
Si013178m.g	2184372	2190867	protein binding
Si013178m.g	2184372	2190867	protein phosphorylation
Si013178m.g	2184372	2190867	ATP binding
Si013178m.g	2184372	2190867	transferase activity, transferring phosphorus-containing groups
Si013178m.g	2184372	2190867	protein serine/threonine kinase activity
Si014469m.g	1708799	1709726	DNA binding
Si014469m.g	1708799	1709726	regulation of transcription, DNA-dependent
Si014469m.g	1708799	1709726	sequence-specific DNA binding transcription factor activity
Si015381m.g	2597274	2598693	
Si013889m.g	2386084	2390523	GTP binding
Si015177m.g	2984495	2984986	protein dimerization activity
Si015177m.g	2984495	2984986	DNA binding
Si014474m.g	1704568	1705485	DNA binding
Si014474m.g	1704568	1705485	sequence-specific DNA binding transcription factor activity
Si014474m.g	1704568	1705485	regulation of transcription, DNA-dependent
Si015183m.g	2232315	2232681	
Si015561m.g	2471819	2473683	
Si014420m.g	2852267	2853430	manganese ion binding
Si014420m.g	2852267	2853430	nutrient reservoir activity
Si013267m.g	1967704	1971859	nucleus
Si013267m.g	1967704	1971859	DNA binding
Si013409m.g	2405635	2409926	RNA binding
Si014185m.g	2718297	2722029	lactoylglutathione lyase activity
Si014185m.g	2718297	2722029	metal ion binding
Si014601m.g	2393536	2397273	oxygen evolving complex

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si014601m.g	2393536	2397273	photosynthesis
Si014601m.g	2393536	2397273	photosystem II
Si014601m.g	2393536	2397273	thylakoid membrane
Si015116m.g	2082286	2082744	
Si013804m.g	1569032	1573423	biosynthetic process
Si013804m.g	1569032	1573423	catalytic activity
Si015415m.g	1746267	1749216	
Si015225m.g	1977936	1978313	defense response
Si015631m.g	1737086	1737779	negative regulation of translation
Si015631m.g	1737086	1737779	rRNA N-glycosylase activity
Si013372m.g	2289889	2292848	
Si014259m.g	2931840	2933091	manganese ion binding
Si014259m.g	2931840	2933091	nutrient reservoir activity
Si013411m.g	1820704	1823801	protein binding
Si014072m.g	1666205	1670160	catalytic activity
Si015241m.g	2881744	2882337	
Si013444m.g	2757245	2759429	metabolic process
Si013444m.g	2757245	2759429	oxidation-reduction process
Si013444m.g	2757245	2759429	oxidoreductase activity
Si013444m.g	2757245	2759429	catechol oxidase activity
Si015205m.g	2974099	2974936	manganese ion binding
Si015205m.g	2974099	2974936	nutrient reservoir activity
Si014984m.g	2892594	2893432	nutrient reservoir activity
Si014984m.g	2892594	2893432	manganese ion binding
Si013813m.g	1582380	1586777	integral to membrane
Si014020m.g	1762508	1765000	porphyrin-containing compound biosynthetic process
Si014020m.g	1762508	1765000	coproporphyrinogen oxidase activity
Si014020m.g	1762508	1765000	oxidation-reduction process
Si013178m.g	2184372	2190867	protein binding
Si013178m.g	2184372	2190867	protein kinase activity

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si013178m.g	2184372	2190867	protein tyrosine kinase activity
Si013178m.g	2184372	2190867	ATP binding
Si013178m.g	2184372	2190867	transferase activity, transferring phosphorus-containing groups
Si013178m.g	2184372	2190867	protein serine/threonine kinase activity
Si013178m.g	2184372	2190867	protein phosphorylation
Si013723m.g	1722282	1729028	core TFIIH complex
Si013723m.g	1722282	1729028	nucleotide-excision repair
Si013723m.g	1722282	1729028	nucleus
Si013723m.g	1722282	1729028	ATP-dependent DNA helicase activity
Si016010m.g	2800258	2800458	
Si013813m.g	1582380	1586777	integral to membrane
Si014867m.g	2270896	2272422	
Si013786m.g	2177977	2179410	protein binding
Si015604m.g	1906062	1908792	
Si015745m.g	2876135	2878573	cysteine-type peptidase activity
Si015745m.g	2876135	2878573	proteolysis
Si015621m.g	2625525	2630940	isoprenoid biosynthetic process
Si013964m.g	2989741	2992513	RNA binding
Si014162m.g	1753219	1755886	metalloexopeptidase activity
Si014162m.g	1753219	1755886	proteolysis
Si014162m.g	1753219	1755886	aminopeptidase activity
Si013468m.g	2346200	2348934	protein binding
Si013631m.g	1950114	1954400	nucleotidyltransferase activity
Si013631m.g	1950114	1954400	metabolic process
Si014815m.g	2124620	2125283	
Si015376m.g	2592622	2594512	protein binding
Si014601m.g	2395864	2397273	thylakoid membrane
Si014601m.g	2395864	2397273	photosystem II
Si014601m.g	2395864	2397273	photosynthesis
Si014601m.g	2395864	2397273	oxygen evolving complex

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si014908m.g	2021171	2021840	iron ion binding
Si014908m.g	2021171	2021840	oxidoreductase activity
Si014908m.g	2021171	2021840	oxidation-reduction process
Si014908m.g	2021171	2021840	fatty acid biosynthetic process
Si013190m.g	1576471	1581589	binding
Si015634m.g	1603276	1605613	
Si015045m.g	1806870	1811913	RNA-directed RNA polymerase activity
Si014417m.g	2959911	2960686	nutrient reservoir activity
Si014417m.g	2959911	2960686	manganese ion binding
Si015140m.g	2467272	2467707	
Si013367m.g	2506772	2511871	protein phosphorylation
Si013367m.g	2506772	2511871	ATP binding
Si013367m.g	2506772	2511871	transferase activity, transferring phosphorus-containing groups
Si013367m.g	2506772	2511871	protein serine/threonine kinase activity
Si013367m.g	2506772	2511871	protein tyrosine kinase activity
Si013367m.g	2506772	2511871	carbohydrate binding
Si013367m.g	2506772	2511871	protein kinase activity
Si014671m.g	2737096	2740223	
Si014857m.g	2098652	2099678	
Si013795m.g	2276879	2282674	
Si014937m.g	2294677	2298093	
Si015073m.g	1689298	1692796	ADP binding
Si015073m.g	1689298	1692796	defense response
Si016037m.g	1529140	1529534	
Si014779m.g	2121529	2122357	
Si014666m.g	1721344	1721823	
Si015798m.g	2963789	2964653	nutrient reservoir activity
Si015798m.g	2963789	2964653	manganese ion binding
Si015210m.g	2474498	2476331	
Si013889m.g	2386084	2392411	GTP binding

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si014805m.g	1620981	1621366	
Si015231m.g	1624566	1625492	ATP binding
Si015231m.g	1624566	1625492	transferase activity, transferring phosphorus-containing groups
Si015231m.g	1624566	1625492	protein serine/threonine kinase activity
Si015231m.g	1624566	1625492	protein phosphorylation
Si015231m.g	1624566	1625492	protein kinase activity
Si015231m.g	1624566	1625492	protein tyrosine kinase activity
Si014565m.g	2818906	2821894	
Si013439m.g	1979231	1984175	phosphoribosylaminoimidazolecarboxamide formyltransferase activity
Si013439m.g	1979231	1984175	catalytic activity
Si013439m.g	1979231	1984175	purine nucleotide biosynthetic process
Si013439m.g	1979231	1984175	IMP cyclohydrolase activity
Si015043m.g	1738831	1739742	
Si013336m.g	1712791	1717937	protein phosphorylation
Si013336m.g	1712791	1717937	transferase activity, transferring phosphorus-containing groups
Si013336m.g	1712791	1717937	protein serine/threonine kinase activity
Si013336m.g	1712791	1717937	ATP binding
Si013336m.g	1712791	1717937	protein kinase activity
Si013336m.g	1712791	1717937	protein tyrosine kinase activity
Si014601m.g	2396677	2397273	thylakoid membrane
Si014601m.g	2396677	2397273	photosynthesis
Si014601m.g	2396677	2397273	oxygen evolving complex
Si014601m.g	2396677	2397273	photosystem II
Si013207m.g	2661885	2665253	protein kinase activity
Si013207m.g	2661885	2665253	protein tyrosine kinase activity
Si013207m.g	2661885	2665253	protein binding
Si013207m.g	2661885	2665253	protein phosphorylation
Si013207m.g	2661885	2665253	transferase activity, transferring phosphorus-containing groups
Si013207m.g	2661885	2665253	protein serine/threonine kinase activity
Si013207m.g	2661885	2665253	ATP binding

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si014025m.g	2057643	2060016	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxo
Si014025m.g	2057643	2060016	oxidation-reduction process
Si014025m.g	2057643	2060016	oxidoreductase activity
Si014185m.g	2718297	2722029	metal ion binding
Si014185m.g	2718297	2722029	lactoylglutathione lyase activity
Si013971m.g	2665521	2670012	isoprenoid biosynthetic process
Si013583m.g	2127335	2132720	transaminase activity
Si013583m.g	2127335	2132720	catalytic activity
Si013583m.g	2127335	2132720	pyridoxal phosphate binding
Si014901m.g	1735605	1736792	
Si013565m.g	2638539	2640298	
Si014601m.g	2395864	2397273	oxygen evolving complex
Si014601m.g	2395864	2397273	photosynthesis
Si014601m.g	2395864	2397273	photosystem II
Si014601m.g	2395864	2397273	thylakoid membrane
Si015929m.g	1917565	1918120	
Si015123m.g	1948448	1950003	pectinesterase activity
Si015123m.g	1948448	1950003	cell wall
Si015123m.g	1948448	1950003	cell wall modification
Si013370m.g	2822030	2825509	
Si014424m.g	2926690	2927898	manganese ion binding
Si014424m.g	2926690	2927898	nutrient reservoir activity
Si013441m.g	2709681	2714433	protein binding
Si014404m.g	1758471	1761185	DNA binding
Si014414m.g	2865311	2866534	manganese ion binding
Si014414m.g	2865311	2866534	nutrient reservoir activity
Si014416m.g	2913662	2914870	nutrient reservoir activity
Si014416m.g	2913662	2914870	manganese ion binding
Si014254m.g	1558667	1562709	
Si013192m.g	2806717	2814321	metabolic process

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si013192m.g	2806717	2814321	4 iron, 4 sulfur cluster binding
Si015989m.g	1857377	1857803	
Si014185m.g	2718297	2722029	lactoylglutathione lyase activity
Si014185m.g	2718297	2722029	metal ion binding
Si013121m.g	2790448	2799808	biosynthetic process
Si013121m.g	2790448	2799808	starch binding
Si013121m.g	2790448	2799808	starch synthase activity
Si013121m.g	2790448	2799808	glucan biosynthetic process
Si015779m.g	2558196	2558997	
Si013326m.g	2354633	2359056	sequence-specific DNA binding transcription factor activity
Si013326m.g	2354633	2359056	regulation of transcription, DNA-dependent
Si013326m.g	2354633	2359056	nucleic acid binding
Si013326m.g	2354633	2359056	sequence-specific DNA binding
Si013326m.g	2354633	2359056	DNA binding
Si014184m.g	2722604	2726474	metal ion binding
Si014184m.g	2722604	2726474	lactoylglutathione lyase activity
Si015877m.g	2368253	2368853	
Si013178m.g	2184372	2190867	ATP binding
Si013178m.g	2184372	2190867	protein serine/threonine kinase activity
Si013178m.g	2184372	2190867	transferase activity, transferring phosphorus-containing groups
Si013178m.g	2184372	2190867	protein phosphorylation
Si013178m.g	2184372	2190867	protein binding
Si013178m.g	2184372	2190867	protein tyrosine kinase activity
Si013178m.g	2184372	2190867	protein kinase activity
Si015540m.g	2965328	2966165	nutrient reservoir activity
Si015540m.g	2965328	2966165	manganese ion binding
Si015377m.g	2645983	2649887	protein tyrosine kinase activity
Si015377m.g	2645983	2649887	protein kinase activity
Si015377m.g	2645983	2649887	protein binding
Si015377m.g	2645983	2649887	protein phosphorylation

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si015377m.g	2645983	2649887	ATP binding
Si015377m.g	2645983	2649887	protein serine/threonine kinase activity
Si015377m.g	2645983	2649887	transferase activity, transferring phosphorus-containing groups
Si013354m.g	2686302	2691007	nucleotide binding
Si013354m.g	2686302	2691007	nucleic acid binding
Si013963m.g	2416210	2418131	ATP binding
Si013963m.g	2416210	2418131	protein serine/threonine kinase activity
Si013963m.g	2416210	2418131	transferase activity, transferring phosphorus-containing groups
Si013963m.g	2416210	2418131	protein phosphorylation
Si013963m.g	2416210	2418131	protein tyrosine kinase activity
Si013963m.g	2416210	2418131	protein kinase activity
Si014418m.g	2948131	2949269	nutrient reservoir activity
Si014418m.g	2948131	2949269	manganese ion binding
Si013411m.g	1820704	1823801	protein binding
Si013463m.g	1613142	1617352	
Si015775m.g	1988052	1988633	intracellular
Si015775m.g	1988052	1988633	sequence-specific DNA binding
Si015775m.g	1988052	1988633	protein heterodimerization activity
Si013226m.g	2023753	2036635	protein binding
Si013152m.g	2621250	2625355	protein phosphorylation
Si013152m.g	2621250	2625355	protein serine/threonine kinase activity
Si013152m.g	2621250	2625355	transferase activity, transferring phosphorus-containing groups
Si013152m.g	2621250	2625355	ATP binding
Si013152m.g	2621250	2625355	protein kinase activity
Si013152m.g	2621250	2625355	protein tyrosine kinase activity
Si013152m.g	2621250	2625355	protein binding
Si013601m.g	1651088	1652901	heme binding
Si013601m.g	1651088	1652901	oxidation-reduction process
Si013601m.g	1651088	1652901	iron ion binding
Si013601m.g	1651088	1652901	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si013372m.g	2289889	2292848	
Si014415m.g	2972406	2973424	nutrient reservoir activity
Si014415m.g	2972406	2973424	manganese ion binding
Si013241m.g	2304979	2311899	lipid biosynthetic process
Si013241m.g	2304979	2311899	oxidation-reduction process
Si013241m.g	2304979	2311899	oxidoreductase activity
Si014267m.g	1815605	1818460	proteasome regulatory particle
Si014267m.g	1815605	1818460	proteolysis
Si015963m.g	2593495	2594003	
Si014648m.g	2049768	2050729	
Si014180m.g	2442469	2444921	regulation of transcription, DNA-dependent
Si014180m.g	2442469	2444921	DNA binding
Si015305m.g	2084276	2084871	
Si013285m.g	3018231	3023315	regulation of transcription, DNA-dependent
Si013285m.g	3018231	3023315	lipid binding
Si013285m.g	3018231	3023315	sequence-specific DNA binding transcription factor activity
Si013285m.g	3018231	3023315	sequence-specific DNA binding
Si013285m.g	3018231	3023315	nucleus
Si013285m.g	3018231	3023315	DNA binding
Si016048m.g	2993050	2993363	
Si013320m.g	2198999	2201511	regulation of transcription, DNA-dependent
Si013320m.g	2198999	2201511	sequence-specific DNA binding transcription factor activity
Si013320m.g	2198999	2201511	sequence-specific DNA binding
Si014033m.g	2253118	2254458	
Si015452m.g	2680636	2681908	
Si014355m.g	2977979	2978919	
Si014162m.g	1753219	1755886	aminopeptidase activity
Si014162m.g	1753219	1755886	metalloexopeptidase activity
Si014162m.g	1753219	1755886	proteolysis
Si015356m.g	2164816	2164938	

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si015393m.g	2776414	2785871	starch binding
Si015393m.g	2776414	2785871	biosynthetic process
Si015393m.g	2776414	2785871	starch synthase activity
Si015393m.g	2776414	2785871	glucan biosynthetic process
Si015595m.g	2317078	2319268	
Si015735m.g	1996101	2000112	potassium ion transmembrane transport
Si015735m.g	1996101	2000112	potassium ion transmembrane transporter activity
Si015735m.g	1996101	2000112	membrane
Si015639m.g	2537590	2540434	protein binding
Si013907m.g	2995219	2999285	integral to membrane
Si013907m.g	2995219	2999285	transport
Si013907m.g	2995219	2999285	membrane
Si013907m.g	2995219	2999285	transporter activity
Si013657m.g	2692068	2694056	protein binding
Si015739m.g	2331680	2333716	hydrolase activity, acting on ester bonds
Si015739m.g	2331680	2333716	lipid metabolic process
Si015714m.g	2080207	2080665	
Si013409m.g	2406539	2409926	RNA binding
Si015277m.g	2089540	2093463	proteolysis
Si015277m.g	2089540	2093463	serine-type carboxypeptidase activity
Si016023m.g	1665510	1666000	
Si015164m.g	2571014	2572482	protein binding
Si014185m.g	2718297	2722029	lactoylglutathione lyase activity
Si014185m.g	2718297	2722029	metal ion binding
Si015503m.g	3028194	3029939	
Si013265m.g	2399796	2402691	protein binding
Si014763m.g	2541334	2541848	
Si014162m.g	1753774	1755886	metalloexopeptidase activity
Si014162m.g	1753774	1755886	proteolysis
Si014162m.g	1753774	1755886	aminopeptidase activity

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si015249m.g	2338277	2341188	protein binding
Si014024m.g	1912515	1917125	ubiquitin-dependent protein catabolic process
Si013583m.g	2127335	2132720	transaminase activity
Si013583m.g	2127335	2132720	pyridoxal phosphate binding
Si013583m.g	2127335	2132720	catalytic activity
Si014743m.g	2705248	2706014	
Si013192m.g	2806717	2814321	4 iron, 4 sulfur cluster binding
Si013192m.g	2806717	2814321	metabolic process
Si016024m.g	2452922	2453138	
Si013804m.g	1569032	1573423	catalytic activity
Si013804m.g	1569032	1573423	biosynthetic process
Si013285m.g	3018231	3023684	DNA binding
Si013285m.g	3018231	3023684	sequence-specific DNA binding
Si013285m.g	3018231	3023684	nucleus
Si013285m.g	3018231	3023684	lipid binding
Si013285m.g	3018231	3023684	regulation of transcription, DNA-dependent
Si013285m.g	3018231	3023684	sequence-specific DNA binding transcription factor activity
Si014983m.g	2104237	2104832	
Si013727m.g	1838930	1841963	transferase activity, transferring acyl groups other than amino-acyl groups
Si013723m.g	1724490	1728712	nucleus
Si013723m.g	1724490	1728712	nucleotide-excision repair
Si013723m.g	1724490	1728712	core TFIIH complex
Si013723m.g	1724490	1728712	ATP-dependent DNA helicase activity
Si013873m.g	1934401	1937608	transmembrane transport
Si013873m.g	1934401	1937608	membrane
Si013873m.g	1934401	1937608	integral to membrane
Si013873m.g	1934401	1937608	metal ion transmembrane transporter activity
Si013873m.g	1934401	1937608	zinc ion transmembrane transporter activity
Si013873m.g	1934401	1937608	metal ion transport
Si013873m.g	1934401	1937608	zinc ion transmembrane transport

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si014601m.g	2395864	2397273	photosynthesis
Si014601m.g	2395864	2397273	oxygen evolving complex
Si014601m.g	2395864	2397273	photosystem II
Si014601m.g	2395864	2397273	thylakoid membrane
Si013219m.g	1698343	1702026	defense response
Si013219m.g	1698343	1702026	ADP binding
Si013767m.g	1919706	1923379	GTP binding
Si013767m.g	1919706	1923379	intracellular
Si013767m.g	1919706	1923379	RNA binding
Si015847m.g	2545538	2547419	protein binding
Si013213m.g	2228462	2232014	defense response
Si013213m.g	2228462	2232014	ADP binding
Si015643m.g	1566692	1566790	
Si014697m.g	1659663	1662420	mitochondrial pyruvate transport
Si014697m.g	1659663	1662420	mitochondrial inner membrane
Si013202m.g	3008738	3017518	metal ion binding
Si015421m.g	1848652	1850457	
Si014697m.g	1659663	1662428	mitochondrial inner membrane
Si014697m.g	1659663	1662428	mitochondrial pyruvate transport
Si013156m.g	1530944	1535205	defense response
Si013156m.g	1530944	1535205	ADP binding
Si015878m.g	2925314	2925638	
Si015853m.g	2840851	2841153	
Si014762m.g	1837054	1838157	
Si015454m.g	2077951	2078546	
Si015822m.g	1834985	1836661	
Si015115m.g	1924647	1926123	transferase activity, transferring acyl groups other than amino-acyl groups
Si015115m.g	1924647	1926123	oxidoreductase activity
Si015115m.g	1924647	1926123	oxidation-reduction process
Si015115m.g	1924647	1926123	zinc ion binding

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si015353m.g	2675014	2676333	
Si015459m.g	2203123	2203323	serine-type endopeptidase inhibitor activity
Si015459m.g	2203123	2203323	response to wounding
Si015058m.g	2906011	2906889	manganese ion binding
Si015058m.g	2906011	2906889	nutrient reservoir activity
Si014793m.g	1567420	1568011	
Si013813m.g	1582380	1586777	integral to membrane
Si013505m.g	1877138	1879539	
Si013645m.g	1592772	1597639	hydrolase activity, hydrolyzing O-glycosyl compounds
Si013645m.g	1592772	1597639	carbohydrate metabolic process
Si013127m.g	1671078	1687088	zinc ion binding
Si013127m.g	1671078	1687088	protein binding
Si014810m.g	2800486	2800884	
Si015804m.g	2094950	2095913	
Si014468m.g	2151681	2153297	
Si013297m.g	1630333	1638165	catalytic activity
Si013297m.g	1630333	1638165	intramolecular transferase activity
Si014162m.g	1753219	1755886	aminopeptidase activity
Si014162m.g	1753219	1755886	proteolysis
Si014162m.g	1753219	1755886	metalloexopeptidase activity
Si013804m.g	1569032	1572179	catalytic activity
Si013804m.g	1569032	1572179	biosynthetic process
Si016004m.g	2108331	2109111	
Si013463m.g	1613142	1617352	
Si014409m.g	2969306	2970162	nutrient reservoir activity
Si014409m.g	2969306	2970162	manganese ion binding
Si014671m.g	2737096	2740223	
Si015075m.g	2833254	2834447	transferase activity, transferring acyl groups other than amino-acyl groups
Si013736m.g	2838838	2844045	nucleotide binding
Si013736m.g	2838838	2844045	nucleic acid binding

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si014267m.g	1815605	1818027	proteasome regulatory particle
Si014267m.g	1815605	1818027	proteolysis
Si014836m.g	2741543	2745178	DNA binding
Si014836m.g	2741543	2745178	transcription, DNA-dependent
Si014836m.g	2741543	2745178	DNA-directed RNA polymerase activity
Si015313m.g	1641711	1643798	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
Si015313m.g	1641711	1643798	iron ion binding
Si015313m.g	1641711	1643798	oxidation-reduction process
Si015313m.g	1641711	1643798	monooxygenase activity
Si015313m.g	1641711	1643798	heme binding
Si014852m.g	2153512	2154465	
Si014991m.g	2450698	2452748	
Si015810m.g	2430625	2433488	protein tyrosine kinase activity
Si015810m.g	2430625	2433488	protein kinase activity
Si015810m.g	2430625	2433488	protein phosphorylation
Si015810m.g	2430625	2433488	ATP binding
Si015810m.g	2430625	2433488	transferase activity, transferring phosphorus-containing groups
Si015810m.g	2430625	2433488	protein serine/threonine kinase activity
Si014020m.g	1762508	1764592	porphyrin-containing compound biosynthetic process
Si014020m.g	1762508	1764592	coproporphyrinogen oxidase activity
Si014020m.g	1762508	1764592	oxidation-reduction process
Si014718m.g	1618578	1619824	
Si014653m.g	1971967	1973864	
Si014961m.g	1959529	1961580	carbohydrate binding
Si014961m.g	1959529	1961580	protein tyrosine kinase activity
Si014961m.g	1959529	1961580	protein kinase activity
Si014961m.g	1959529	1961580	protein phosphorylation
Si014961m.g	1959529	1961580	transferase activity, transferring phosphorus-containing groups
Si014961m.g	1959529	1961580	ATP binding
Si015172m.g	1976899	1977289	defense response

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si015973m.g	1564688	1566001	
Si014072m.g	1666205	1670160	catalytic activity
Si014267m.g	1815605	1818460	proteolysis
Si014267m.g	1815605	1818460	proteasome regulatory particle
Si015845m.g	1731723	1731908	
Si013673m.g	2145771	2148546	nucleoside transmembrane transporter activity
Si013673m.g	2145771	2148546	integral to membrane
Si013673m.g	2145771	2148546	transport
Si013626m.g	1901210	1905419	oxidation-reduction process
Si013626m.g	1901210	1905419	oxidoreductase activity
Si013626m.g	1901210	1905419	transferase activity, transferring acyl groups other than amino-acyl groups
Si013626m.g	1901210	1905419	zinc ion binding
Si015290m.g	2527145	2527971	protein binding
Si014804m.g	2404926	2405384	
Si015317m.g	1769059	1774760	RNA-directed RNA polymerase activity
Si013463m.g	1613142	1617352	
Si013267m.g	1967704	1971859	
Si014024m.g	1912515	1917125	ubiquitin-dependent protein catabolic process
Si014410m.g	2900135	2901240	manganese ion binding
Si014410m.g	2900135	2901240	nutrient reservoir activity
Si014823m.g	1682875	1683197	
Si014578m.g	2320212	2321042	zinc ion binding
Si014578m.g	2320212	2321042	metal ion binding
Si014578m.g	2320212	2321042	protein binding
Si015551m.g	2534373	2536674	protein binding
Si015701m.g	1548314	1549667	

G: Genes (159) located within QTL support interval for bristling on *Setaria* chromosome 9 and their gene ontology descriptions

Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si036012m.g	31621489	31627927	zinc ion binding
Si036012m.g	31621489	31627927	oxidation-reduction process
Si036012m.g	31621489	31627927	oxidoreductase activity
Si038090m.g	32146319	32147617	
Si039859m.g	33574918	33575674	
Si038743m.g	33186625	33188091	ADP binding
Si040418m.g	32820753	32823206	
Si039401m.g	32893518	32893956	
Si039591m.g	33792543	33792770	
Si038950m.g	33758750	33760750	nucleic acid binding
Si040185m.g	32862677	32863365	extrinsic to membrane
Si040185m.g	32862677	32863365	calcium ion binding
Si040185m.g	32862677	32863365	photosynthesis
Si040185m.g	32862677	32863365	oxygen evolving complex
Si040185m.g	32862677	32863365	photosystem II
Si037750m.g	32522047	32525092	protein binding
Si037750m.g	32522047	32525092	metal ion binding
Si037750m.g	32522047	32525092	zinc ion binding
Si038804m.g	33410441	33411607	
Si040346m.g	32821139	32821510	
Si035069m.g	32201009	32206039	
Si039155m.g	32560464	32561803	protein binding
Si034010m.g	32021957	32025449	protein binding
Si034010m.g	32021957	32025449	protein kinase activity

Si034010m.g	32021957	32025449	protein tyrosine kinase activity
Si034010m.g	32021957	32025449	ATP binding
Si034010m.g	32021957	32025449	transferase activity, transferring phosphorus-containing groups
Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si034010m.g	32021957	32025449	protein serine/threonine kinase activity
Si034010m.g	32021957	32025449	protein phosphorylation
Si040407m.g	32045868	32046243	
Si036336m.g	32956168	32960301	
Si037904m.g	31801384	31803143	catalytic activity
Si037904m.g	31801384	31803143	metabolic process
Si034352m.g	32781616	32791091	1,3-beta-D-glucan synthase complex
Si034352m.g	32781616	32791091	(1->3)-beta-D-glucan biosynthetic process
Si034352m.g	32781616	32791091	1,3-beta-D-glucan synthase activity
Si034352m.g	32781616	32791091	membrane
Si034862m.g	34273582	34276219	membrane
Si034862m.g	34273582	34276219	transporter activity
Si034862m.g	34273582	34276219	transport
Si033901m.g	33659341	33670403	
Si033963m.g	32794970	32808573	1,3-beta-D-glucan synthase complex
Si033963m.g	32794970	32808573	1,3-beta-D-glucan synthase activity
Si033963m.g	32794970	32808573	(1->3)-beta-D-glucan biosynthetic process
Si033963m.g	32794970	32808573	membrane
Si038711m.g	33035089	33036355	
Si036478m.g	33124112	33128511	transcription factor binding
Si036478m.g	33124112	33128511	small GTPase mediated signal transduction
Si036478m.g	33124112	33128511	GTP binding
Si036478m.g	33124112	33128511	ATP binding
Si036478m.g	33124112	33128511	protein transport
Si036478m.g	33124112	33128511	regulation of transcription, DNA-dependent
Si037837m.g	33684091	33684765	
Si038706m.g	31888494	31889621	

Si035285m.g	31908656	31912522	carbon-nitrogen ligase activity, with glutamine as amido-N-donor
Si038673m.g	32651984	32660801	zinc ion binding
Si038673m.g	32651984	32660801	hydrolase activity, hydrolyzing O-glycosyl compounds
Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si038673m.g	32651984	32660801	alpha-mannosidase activity
Si038673m.g	32651984	32660801	mannose metabolic process
Si038673m.g	32651984	32660801	mannosidase activity
Si038673m.g	32651984	32660801	carbohydrate metabolic process
Si038673m.g	32651984	32660801	catalytic activity
Si038673m.g	32651984	32660801	carbohydrate binding
Si040162m.g	34280339	34283381	zinc ion binding
Si040162m.g	34280339	34283381	nucleic acid binding
Si038056m.g	31815604	31817322	
Si036389m.g	31837398	31838760	
Si034905m.g	33508598	33511113	drug transmembrane transport
Si034905m.g	33508598	33511113	antiporter activity
Si034905m.g	33508598	33511113	transmembrane transport
Si034905m.g	33508598	33511113	membrane
Si034905m.g	33508598	33511113	drug transmembrane transporter activity
Si034012m.g	31264944	31271247	ATP binding
Si034012m.g	31264944	31271247	microtubule-based movement
Si034012m.g	31264944	31271247	microtubule binding
Si034012m.g	31264944	31271247	microtubule motor activity
Si039575m.g	32924310	32926762	
Si038982m.g	32461884	32464010	
Si034933m.g	34160798	34164523	oligopeptide transport
Si034933m.g	34160798	34164523	transport
Si034933m.g	34160798	34164523	membrane
Si034933m.g	34160798	34164523	transporter activity
Si035356m.g	32427166	32428692	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
Si035356m.g	32427166	32428692	iron ion binding

Si035356m.g	32427166	32428692	oxidation-reduction process
Si035356m.g	32427166	32428692	heme binding
Si038368m.g	31835026	31835497	
Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si037526m.g	32964777	32966428	
Si037219m.g	33616663	33617707	
Si034925m.g	32942134	32950987	vesicle docking involved in exocytosis
Si034925m.g	32942134	32950987	vesicle-mediated transport
Si035652m.g	34212495	34216502	membrane
Si035652m.g	34212495	34216502	transporter activity
Si035652m.g	34212495	34216502	transport
Si039705m.g	31809481	31812479	
Si038578m.g	32514278	32515747	
Si039777m.g	32192369	32192623	
Si037860m.g	32197101	32197707	
Si039239m.g	32044436	32047454	
Si037130m.g	33880927	33882959	protein binding
Si036222m.g	32563352	32566346	protein binding
Si038815m.g	31013634	31017884	ubiquitin-dependent protein catabolic process
Si034995m.g	31875588	31877395	hydrolase activity, hydrolyzing O-glycosyl compounds
Si034995m.g	31875588	31877395	carbohydrate metabolic process
Si040259m.g	31703175	31704925	
Si034906m.g	34076460	34079482	transport
Si034906m.g	34076460	34079482	membrane
Si034906m.g	34076460	34079482	transporter activity
Si035381m.g	33783304	33788379	nucleotide binding
Si035381m.g	33783304	33788379	nucleic acid binding
Si039940m.g	33423202	33426004	heme binding
Si039940m.g	33423202	33426004	iron ion binding
Si039940m.g	33423202	33426004	oxidation-reduction process
Si039940m.g	33423202	33426004	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen

Si038866m.g	32381092	32383970	
Si036516m.g	31915135	31917829	hexose metabolic process
Si036516m.g	31915135	31917829	catalytic activity
Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si036516m.g	31915135	31917829	carbohydrate binding
Si036516m.g	31915135	31917829	isomerase activity
Si036516m.g	31915135	31917829	carbohydrate metabolic process
Si036201m.g	32596341	32600821	
Si039383m.g	33530765	33532440	
Si036496m.g	34319907	34322025	oxidation-reduction process
Si036496m.g	34319907	34322025	heme binding
Si036496m.g	34319907	34322025	peroxidase activity
Si036496m.g	34319907	34322025	response to oxidative stress
Si037688m.g	30719271	30721253	
Si034003m.g	31818636	31830806	
Si038480m.g	33665448	33665858	
Si034008m.g	34087197	34091481	protein binding
Si034008m.g	34087197	34091481	ADP binding
Si034008m.g	34087197	34091481	defense response
Si038675m.g	33732435	33733733	transferase activity, transferring acyl groups other than amino-acyl groups
Si040041m.g	32509991	32512025	
Si039515m.g	32174926	32175666	
Si037461m.g	32101563	32103052	
Si036449m.g	34303444	34305785	response to oxidative stress
Si036449m.g	34303444	34305785	peroxidase activity
Si036449m.g	34303444	34305785	heme binding
Si036449m.g	34303444	34305785	oxidation-reduction process
Si039485m.g	33826082	33826791	
Si040263m.g	34091889	34093778	protein binding
Si036480m.g	34299500	34302068	oxidation-reduction process
Si036480m.g	34299500	34302068	heme binding

Si036480m.g	34299500	34302068	peroxidase activity
Si036480m.g	34299500	34302068	response to oxidative stress
Si039072m.g	34098558	34100618	
Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si039251m.g	30681870	30682577	enzyme inhibitor activity
Si039251m.g	30681870	30682577	pectinesterase activity
Si036374m.g	33906200	33907591	oxidoreductase activity
Si036374m.g	33906200	33907591	oxidation-reduction process
Si037230m.g	32085051	32086299	
Si039262m.g	33394411	33394635	
Si040120m.g	33066577	33067713	
Si035412m.g	32054537	32056409	
Si035142m.g	31697504	31700211	
Si037688m.g	30719271	30721253	
Si040203m.g	33047999	33049111	
Si039069m.g	32853251	32856451	
Si035837m.g	33461838	33463112	ubiquitin ligase complex
Si035837m.g	33461838	33463112	protein ubiquitination
Si035837m.g	33461838	33463112	ubiquitin-protein ligase activity
Si035837m.g	33461838	33463112	binding
Si038724m.g	33540502	33544857	
Si037193m.g	31781001	31784253	transferase activity, transferring alkyl or aryl (other than methyl) groups
Si038680m.g	32644589	32645533	
Si039616m.g	33385921	33386949	
Si039938m.g	32922738	32923613	proteolysis
Si039938m.g	32922738	32923613	cysteine-type peptidase activity
Si035406m.g	33128914	33130516	ADP binding
Si037738m.g	32833765	32834512	extracellular region
Si039391m.g	32183513	32184248	
Si038614m.g	31834205	31834741	protein folding
Si038614m.g	31834205	31834741	peptidyl-prolyl cis-trans isomerase activity

Si039447m.g	33714568	33714810	
Si036336m.g	32956168	32960342	
Si039805m.g	32141131	32143095	protein binding
Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si039805m.g	32141131	32143095	binding
Si038667m.g	33207004	33208381	ADP binding
Si033901m.g	33659341	33670710	
Si039836m.g	33875696	33878454	zinc ion binding
Si039590m.g	32676169	32678397	
Si036108m.g	33086366	33089373	protein binding
Si035525m.g	33523407	33526123	transferase activity, transferring acyl groups other than amino-acyl groups
Si039709m.g	33766292	33767179	
Si039241m.g	32145117	32145392	
Si038899m.g	33709702	33709884	
Si036028m.g	32533500	32537243	queuine tRNA-ribosyltransferase activity
Si036028m.g	32533500	32537243	queuosine biosynthetic process
Si036028m.g	32533500	32537243	tRNA modification
Si038541m.g	32624823	32626466	DNA binding
Si038541m.g	32624823	32626466	regulation of transcription, DNA-dependent
Si034906m.g	34076440	34079482	transport
Si034906m.g	34076440	34079482	membrane
Si034906m.g	34076440	34079482	transporter activity
Si035381m.g	33784973	33788365	
Si039225m.g	31889827	31891475	
Si038819m.g	32818733	32819918	protein binding
Si037723m.g	32033572	32034607	
Si038548m.g	32725844	32727217	
Si040492m.g	31785579	31786336	
Si038407m.g	32760248	32761927	
Si035943m.g	31668724	31676713	zinc ion binding
Si035943m.g	31668724	31676713	oxidation-reduction process

Si035943m.g	31668724	31676713	oxidoreductase activity
Si039594m.g	33117718	33120911	oxidoreductase activity
Si039594m.g	33117718	33120911	oxidation-reduction process
Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si039594m.g	33117718	33120911	cofactor binding
Si039594m.g	33117718	33120911	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor
Si039594m.g	33117718	33120911	zinc ion binding
Si035434m.g	33309671	33311294	ADP binding
Si039540m.g	32306085	32306189	
Si039406m.g	32179575	32180298	
Si038953m.g	31738780	31740399	transferase activity, transferring acyl groups other than amino-acyl groups
Si038953m.g	31738780	31740399	membrane
Si038953m.g	31738780	31740399	catalytic activity
Si038953m.g	31738780	31740399	metabolic process
Si038953m.g	31738780	31740399	fatty acid biosynthetic process
Si038953m.g	31738780	31740399	transferase activity, transferring acyl groups
Si036425m.g	32879957	32882485	nucleic acid binding
Si036425m.g	32879957	32882485	nucleotide binding
Si039331m.g	33671125	33672605	integral to membrane
Si036108m.g	33086397	33089373	protein binding
Si036516m.g	31915135	31917829	isomerase activity
Si036516m.g	31915135	31917829	carbohydrate binding
Si036516m.g	31915135	31917829	catalytic activity
Si036516m.g	31915135	31917829	carbohydrate metabolic process
Si036516m.g	31915135	31917829	hexose metabolic process
Si039676m.g	32891082	32893299	membrane
Si037809m.g	33705537	33706207	
Si037005m.g	32108283	32109576	
Si039318m.g	31848239	31848595	ubiquitin-dependent protein catabolic process
Si037840m.g	33686880	33687548	
Si040193m.g	33929699	33931212	metabolic process

Si040193m.g	33929699	33931212	transferase activity, transferring hexosyl groups
Si039138m.g	32619733	32620941	
Si038896m.g	33093936	33095276	protein binding
Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si038884m.g	33611034	33614191	protein phosphorylation
Si038884m.g	33611034	33614191	transferase activity, transferring phosphorus-containing groups
Si038884m.g	33611034	33614191	ATP binding
Si038884m.g	33611034	33614191	protein tyrosine kinase activity
Si038884m.g	33611034	33614191	protein kinase activity
Si038884m.g	33611034	33614191	protein binding
Si038856m.g	33822888	33823454	
Si036397m.g	32661800	32663645	hydrolase activity, acting on ester bonds
Si036397m.g	32661800	32663645	lipid metabolic process
Si036397m.g	32661800	32663645	lipase activity
Si036397m.g	32661800	32663645	hydrolase activity
Si034121m.g	31443278	31451391	ubiquitin-specific protease activity
Si034121m.g	31443278	31451391	ubiquitin-dependent protein catabolic process
Si034905m.g	33508598	33511089	drug transmembrane transport
Si034905m.g	33508598	33511089	antiporter activity
Si034905m.g	33508598	33511089	membrane
Si034905m.g	33508598	33511089	transmembrane transport
Si034905m.g	33508598	33511089	drug transmembrane transporter activity
Si034056m.g	32629767	32641406	carbohydrate metabolic process
Si034056m.g	32629767	32641406	mannosidase activity
Si034056m.g	32629767	32641406	alpha-mannosidase activity
Si034056m.g	32629767	32641406	mannose metabolic process
Si034056m.g	32629767	32641406	carbohydrate binding
Si034056m.g	32629767	32641406	catalytic activity
Si034056m.g	32629767	32641406	zinc ion binding
Si034056m.g	32629767	32641406	hydrolase activity, hydrolyzing O-glycosyl compounds
Si038106m.g	32194045	32194980	

Si035381m.g	33783304	33788365	nucleic acid binding
Si035381m.g	33783304	33788365	nucleotide binding
Si034988m.g	34119014	34121403	membrane
Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si034988m.g	34119014	34121403	transporter activity
Si034988m.g	34119014	34121403	transport
Si034988m.g	34119014	34121403	oligopeptide transport
Si038665m.g	32863530	32863998	nucleotide binding
Si038665m.g	32863530	32863998	nucleic acid binding
Si037486m.g	31685191	31686227	
Si037837m.g	33684091	33684765	
Si035545m.g	33200461	33201945	ADP binding
Si037193m.g	31781001	31783384	transferase activity, transferring alkyl or aryl (other than methyl) groups
Si039217m.g	33602239	33604151	ATP binding
Si039217m.g	33602239	33604151	transferase activity, transferring phosphorus-containing groups
Si039217m.g	33602239	33604151	protein phosphorylation
Si039217m.g	33602239	33604151	protein kinase activity
Si039217m.g	33602239	33604151	protein tyrosine kinase activity
Si039425m.g	32865319	32865978	
Si038768m.g	32027155	32030575	protein phosphorylation
Si038768m.g	32027155	32030575	transferase activity, transferring phosphorus-containing groups
Si038768m.g	32027155	32030575	protein serine/threonine kinase activity
Si038768m.g	32027155	32030575	ATP binding
Si038768m.g	32027155	32030575	protein tyrosine kinase activity
Si038768m.g	32027155	32030575	protein kinase activity
Si038768m.g	32027155	32030575	protein binding
Si037306m.g	31682027	31683887	
Si039834m.g	33855929	33860309	protein tyrosine kinase activity
Si039834m.g	33855929	33860309	protein kinase activity
Si039834m.g	33855929	33860309	protein phosphorylation
Si039834m.g	33855929	33860309	transferase activity, transferring phosphorus-containing groups

Si039834m.g	33855929	33860309	calcium ion binding
Si039834m.g	33855929	33860309	protein serine/threonine kinase activity
Si039834m.g	33855929	33860309	ATP binding
Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si035371m.g	33202945	33204490	
Si038843m.g	34135291	34138749	
Si038305m.g	31863610	31863889	
Si037586m.g	32702389	32703494	
Si038604m.g	32258619	32260269	
Si036298m.g	33739439	33741736	guanyl nucleotide binding
Si036298m.g	33739439	33741736	signal transducer activity
Si036298m.g	33739439	33741736	G-protein beta/gamma-subunit complex binding
Si036298m.g	33739439	33741736	signal transduction
Si036298m.g	33739439	33741736	G-protein coupled receptor signaling pathway
Si036298m.g	33739439	33741736	GTPase activity
Si040460m.g	31785579	31786166	
Si036080m.g	32359625	32361766	
Si040000m.g	30616203	30616511	
Si040156m.g	32390160	32391242	protein binding
Si035381m.g	33784973	33788365	nucleotide binding
Si035381m.g	33784973	33788365	nucleic acid binding
Si039162m.g	32775163	32776746	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
Si039162m.g	32775163	32776746	heme binding
Si039162m.g	32775163	32776746	iron ion binding
Si039162m.g	32775163	32776746	oxidation-reduction process
Si040172m.g	33839482	33843366	protein kinase activity
Si040172m.g	33839482	33843366	protein tyrosine kinase activity
Si040172m.g	33839482	33843366	calcium ion binding
Si040172m.g	33839482	33843366	protein serine/threonine kinase activity
Si040172m.g	33839482	33843366	transferase activity, transferring phosphorus-containing groups
Si040172m.g	33839482	33843366	ATP binding

Si040172m.g	33839482	33843366	protein phosphorylation
Si036449m.g	34303444	34305785	oxidation-reduction process
Si036449m.g	34303444	34305785	heme binding
Gene Name	Gene Start (bp)	Gene End (bp)	GO Description
Si036449m.g	34303444	34305785	peroxidase activity
Si036449m.g	34303444	34305785	response to oxidative stress
Si038622m.g	31898415	31899820	acyl-[acyl-carrier-protein] desaturase activity
Si038622m.g	31898415	31899820	oxidoreductase activity
Si038622m.g	31898415	31899820	oxidation-reduction process
Si038622m.g	31898415	31899820	fatty acid metabolic process
Si039041m.g	32170805	32172865	
Si034812m.g	34257861	34260620	transport
Si034812m.g	34257861	34260620	transporter activity
Si034812m.g	34257861	34260620	membrane
Si034352m.g	32781616	32791091	1,3-beta-D-glucan synthase activity
Si034352m.g	32781616	32791091	(1->3)-beta-D-glucan biosynthetic process
Si034352m.g	32781616	32791091	membrane
Si034352m.g	32781616	32791091	1,3-beta-D-glucan synthase complex
Si033990m.g	33896911	33900449	protein phosphorylation
Si033990m.g	33896911	33900449	ATP binding
Si033990m.g	33896911	33900449	transferase activity, transferring phosphorus-containing groups
Si033990m.g	33896911	33900449	protein serine/threonine kinase activity
Si033990m.g	33896911	33900449	protein kinase activity
Si033990m.g	33896911	33900449	protein tyrosine kinase activity
Si033990m.g	33896911	33900449	protein binding
Si034934m.g	34172276	34174852	oligopeptide transport
Si034934m.g	34172276	34174852	transport
Si034934m.g	34172276	34174852	transporter activity
Si034934m.g	34172276	34174852	membrane
Si039100m.g	33545957	33548297	zinc ion binding
Si035943m.g	31668724	31676713	oxidoreductase activity

Si035943m.g	31668724	31676713	oxidation-reduction process
Si035943m.g	31668724	31676713	zinc ion binding