ABSTRACT

Title of Document: MAPPING QUANTITATIVE TRAIT LOCI FOR GRAIN YIELD AND YIELD RELATED TRAITS IN A HEXAPLOID WINTER WHEAT DOUBLED HAPLOID POPULATION

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Improving wheat grain yield potential is imperative to match the increasing food demand associated with a fast growing population. Genetic and modeling approaches were employed to investigate the genetic basis and phenotype network regarding grain yield and yield related traits in a soft red winter wheat doubled haploid population. The population and two parents were evaluated in five year-location trials in the USA and genotyped by high throughput DNA markers including simple sequence repeat (SSR) and single nucleotide polymorphism (SNP). Bi-parental linkage mapping identified a number of QTLs for grain yield and yield related traits among which sixty were for grain yield components (GYLD, grain yield; SPSM, spikes per square meter; TGW, thousand grain weight; GPS, grains per spike; GWPS, grain weight per spike), seventy four were for plant architecture (PHT, plant height; FLL, flag leaf length; FLW, flag leaf width; FLA, flag leaf area; FLS, flag leaf shape

or length/width ratio), and one hundred and nine were for spike morphology (SL, spike length; TSN, total spikelet number per spike; FSN, fertile spikelet number per spike; SSN, sterile spikelet number per spike; SC, spike compactness; GSP, grains per spikelet). In addition, structural equation modeling is described to construct a phenotype network. It revealed that GSP and FSN may mediate yield component compensation. Furthermore, doubled haploid lines DH96 and DH84 may have potential as new high-yielding cultivars for the Mid-Atlantic region.

MAPPING QUANTITATIVE TRAIT LOCI FOR GRAIN YIELD AND YIELD RELATED TRAITS IN A HEXAPLOID WINTER WHEAT DOUBLED HAPLOID POPULATION

By

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Dedication

I would like to dedicate this dissertation to my parents, Xueyi Zhou and Yuyun Hu, for their unconditional and endless love through my whole life and to my brother, Yaodi Zhou, for inspiring and supporting me along the way.

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Participants contribution

The project was initiated and guided by Dr. Jose Costa. The doubled haploid population was produced by Dr. Paul Murphy from North Carolina State University. 9K SNP array was conducted by Dr. Shiaoman Chao from USDA-ARS Small Grains Genotyping Lab at Fargo, ND. Dr. Gina Brown-Guedira from USDA-ARS Eastern Regional Small Grain Genotyping Lab at Raleigh, NC prepared the DNA library and sent it to USDA-ARS Central Small Grain Genotyping Lab at Manhattan, KS for genotyping-for-sequencing. All genotype calls were made by Dr. Gina Brown-Guedira. I performed maker quality assessment, constructed the linkage map, proposed and finished phenotype network modeling. I also performed the QTL mapping/analyses, phenotypic data analyses and wrote the manuscript. The manuscript consists of five independent prepublication chapters.

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List of Abbreviations

FLA	Flag leaf area, cm^2
FLL	Flag leaf length, cm
FLS	Flag leaf shape
FLW	Flag leaf width, cm
FSN	Fertile spikelet number per spike
GPS	Grains per spike
GSP	Grain number per spikelet
GWPS	Grain weight per spike, g
GYLD	Grain yield, g m^{-2}
HD	Heading date, days
PHT	Plant height, cm
QTL	Quantitative trait locus
SC	Spike compactness
SL	Spike length, cm
SPSM	Spikes per square meter
SSN	Sterile spikelet number per spike
TGW	Thousand-grain weight, g
LOD	Logarithm of the odds
PVE	Phenotypic variation explained, percentage
SSR	Simple sequence repeat
SNP	Single nucleotide polymorphism
SEM	Structural equation modeling

Chapter 1: Literature review

Introduction

Improving grain production is the key to ensuring food supply and social stability across the globe. In the last century, the great success of Green Revolution featuring high-yielding dwarf rice and wheat plants under heavy nitrogen fertilizers helped to feed an increasing population. However, it has come to a point where continuous yield increases driven by successful breeding management might be approaching a ceiling. This review aims to provide the most current developments in wheat grain yield improvement by examining the yield and yield contributing traits from a physiological and genetic perspective and by describing state-of-art technologies in current breeding practice.

Increasing population and food supply

According to the official estimates and projections from United Nations, the world population will reach 8.1 billion in 2025, and further increase to 9.6 billion in 2050 and 10.9 billion by 2100 (UN DESA, 2013). Meanwhile, global crop production needs to double by 2050 to meet the demands from the rising population, changing diets, and increasing biofuel consumption (FAO, 2012; Tilman et al., 2011). Yields of major crops like maize, rice, wheat, and soybean, however, are increasing at only 1.6%, 1.0% 0.9% and 1.3% per year, which is far slower than the 2.4% per year rate required to double global production by 2050 (Ray et al., 2013). Yield potential improvement is critical to meet this challenge.

Wheat evolution

The allohexaploid bread wheat (*Triticum aestivum* L.; 2n = 6x = 42 chromosomes; genomic code AABBDD) is the product of two hybridization events involving three diploid (2x; 2n = 14) grass species within the tribe Triticeae: *Triticum urartu* (AA), an unknown close relative of *Aegilops speltoides* (BB), and *Aegilops tauschii* (DD) (Marcussen et al., 2014). The first hybridization is hypothesized to happen between the A and B genome donors 300,000–500,000 years ago, resulting in the wild tetraploid emmer wheat (*Triticum turgidum*; AABB) (Marcussen et al., 2014; Peng et al., 2011). About 10,000 years ago, emmer wheat cultivation began and expanded eastwards from the Fertile Crescent to the natural habitat of wild grass *Aegilops tauschii* during which cultivated emmer wheat hybridized with this D genome donor to form modern hexaploid bread wheat (AABBDD) (Peng et al., 2011; Shewry, 2009).

Brief overview of quantitative genetics

Phenotype classification

Phenotype or the expression of a trait is an observable characteristic of an individual and varies between individuals. Phenotypes of organisms are classified into three different forms: qualitative, quantitative and threshold traits (Birnbaum, 1972). A qualitative trait is expressed discretely and individual phenotypes fall into discrete categories, as opposed to a quantitative trait, where phenotypes show a continuous range of values such as weight and height (Abiola et al., 2003). Threshold traits are dimorphic traits with polygenic bases but show a limited number of phenotypes such as molting in insects which is controlled by the levels of juvenile hormones (Moorad and Linksvayer, 2008;

Roff, 2008). In agricultural production, most agronomic traits of economic importance are quantitative traits.

Genetic and environment values

Quantitative traits have been extensively studied since the 1920s, after the establishment of quantitative genetics, which, in conjunction with statistics and Mendelian genetics, provided the scientific framework for modern plant breeding (Lamkey and Lee, 1993). Usually, quantitative traits show phenotypic variation among individuals and have a complicated genetic architecture, involving many genes throughout the genome with variable contributions to the overall phenotype (Holland, 2007). The genes controlling quantitative traits are affected by gene-by-gene and gene-by-environment interactions (Xu and Zhu, 2012). The environment, defined as the integrated influence of all nongenetic variables affecting phenotype, adds more complexity to quantitative traits (Xu and Zhu, 2012).

One of the fundamental principles of quantitative genetics is that the phenotypic value P of an individual for a given trait can be considered as the sum of that individual's genotypic value G plus the environmental value E, thus, in linear format: $P=G+E$, where G can be divided into additive (A), dominant (D) and epistatic (I) values (Walsh, 2001). To better account for quantitative traits, especially in breeding, the additive model needs to be extended to include $G\times E$, which is known as genotype-by-environment interaction (Eeuwijk, 2008). In natural populations, the variation of a quantitative trait often approximates a statistical normal distribution as it is the sum of small effects caused by genes and the environment (Xu, 2010). Most important agronomic traits that constitute

the primary focus of plant breeding such as grain yield are quantitative in nature, usually referred to as complex traits, with variation believed to be attributable to dozens if not hundreds of underlying genes (Crosbie et al., 2008). A region of the genome containing one or more genes that affect variation in a quantitative trait is known as quantitative trait locus (QTL). QTL identification and diagnostic marker development for desired traits are crucial so that modern breeders can deliver superior new cultivars with efficiency and accuracy.

Yield-related quantitative traits in wheat

Grain yield

Improving the grain yield potential of wheat has been the principal aim of wheat breeding programs worldwide and has helped to maintain the viability of agricultural systems in both developed and developing countries (Kuchel et al., 2007b). Although, genetic improvement in yield potential, resistance to diseases, and adaptation to abiotic stresses have contributed to the increases of grain production in the last three decades, it is widely accepted that the rates of progress and genetic gains from wheat breeding have slowed down and even decreased (Reynolds et al., 2012; Reynolds et al., 2009). Part of the reason is due to the lack of sufficient knowledge about the mechanisms, complex biological pathways, and their corresponding genetic basis underlying the responses of wheat in specific environments (Henry and Prasanta, 2004). In recent years, the rapid advances in biotechnology and molecular biology, as well as research on model organisms, have provided powerful tools and references for crop genetic improvement.

Our current understanding of grain yield and its genetic constraints can be expressed by the following three perspectives:

1) The classical view: *Grain yield= Spikes/m^2 × Grains/spike × Grain Weight*;
2) The carbon-economy-based view: *Grain yield= Light intercepted (LI) × Radiation use efficiency (RUE) × Harvest index (HI)*;
3) The water-use-based view: *Grain yield= W × Water use efficiency (WUE) × Harvest Index (HI)*;

where RUE is the overall photosynthetic efficiency of the crop; W is the water transpired by the crop plus direct evaporation from the soil; WUE is the ability of the crop to produce biomass per unit of water evapotranspired (Matthew et al., 2004).

A new strategy to boost wheat productivity through genetic intervention has been proposed, combining these three views. It features higher photosynthetic capacity, improved partitioning of assimilates and genetic tools to improve breeding efficiency (Reynolds et al., 2012).

Grain yield is the end product of the interaction of a large number of physiological and biochemical processes, genetically complex, and determined concurrently by multiple plant characteristics (Marza et al., 2006; Sharma et al., 2003). The conventional method to explore complex traits is to deconstruct them into simpler components for further exploration and characterization. In the case of wheat grain yield, these include grains per spike, spikes per unit area and grain weight (1000-grain-weight) (Mengistu et al., 2012). Breeding efforts focused on partitioning more assimilates to reproductive development

and less to vegetative dry matter production have resulted in modern wheat cultivars with more grains per spike and more grains per square meter (Frederick and Bauer, 1999). Wheat genetics studies have located QTLs for grain yield and yield components on all 21 chromosomes of bread wheat (Bennett et al., 2012a; Heidari et al., 2011; Wu et al., 2012). However, the quantitative nature of QTLs and their strong interaction with the environment make constant and stable QTL detection difficult and their applicability limited to a very specific environment even though a number of them are major QTLs accounting for more than 10% of the phenotypic variation, as was verified by Heidari et al. (2011). Furthermore, the unstable correlation between grain yield and yield components reported from separate studies indicates its underlying complexity (Bennett et al., 2012a; Heidari et al., 2011; Mengistu et al., 2012). Availability of large sets of phenotypic data, genomic data from SNP arrays and new QTL mapping methods will help to detect more QTLs and elucidate the relationships between grain yield and its related traits with more precision.

Plant architecture

Canopy architecture of higher plants is defined by the degree of branching, internodal elongation, and shoot determinacy or, simply, as the spatial configuration of the aboveground plant organs (Fageria et al., 2006; Wang and Li, 2008). Some of the detailed characteristics of plant architecture involve plant height, tillering, branching patterns, leaf size and shape, configuration of leaf relative to the sun and spatial arrangement of leaves (Fageria et al., 2006). Plant architecture has been a focus of research because of its close association with photosynthesis and grain yield (Hedden, 2003).

Plant height, mainly determined by stem elongation, is an important agronomic trait in cereal crops influencing plant architecture and contributing to grain yield (Wang and Li, 2008; Wang et al., 2010). In high soil fertility conditions, the stems of tall cultivars are unable to support the resultant weight of plump grains. High-yielding cultivars fall over in the field before maturity, a process known as lodging, with consequent large yield losses (Hedden, 2003). Introduction of dwarfing genes into cereal crops, such as *Rht-B1b* and *Rht-D1b* in wheat and *sd1* in rice, produced semi-dwarf plants with short strong stalks as well as more assimilate partitioned into the grain leading to the great increases of wheat and rice yield, known as the Green Revolution (Hedden, 2003). Since then, the semi-dwarf phenotype has been extensively selected as the ideal trait for high-yielding cultivars in modern crop breeding programs. However, extremely short plants are disadvantageous because leaves are very closely spaced on a short stem causing increased shading within the canopy, as well as poor ventilation and light transmission in the lower canopy, which affects seed-filling and ultimately decreases yield (Yoshida, 1972; Zhang et al., 2011). Thus, breeding a cultivar with optimum plant height for a target environment is necessary. As with grain yield, QTLs for plant height have been mapped on all 21 chromosomes of wheat (Wu et al., 2010).

Leaves are responsible for photosynthesis that provides photosynthetic products in plants. The flag leaf is the last leaf to emerge before the spike and plays a dominant role in determining grain yield (Yoshida, 1972). Translocation of carbohydrates from the flag leaf is almost entirely directed towards the grain while that from the second and third leaves is only partly directed towards the grain which underscores the important influence

of shape and size of flag leaves on yield performance (Monyo and Whittington, 1973). Both Dere and YIildirim (2006) and Monyo and Whittington (1973) found a positive correlation between the flag leaf length and width with grain yield in bread wheat. Among the few QTL studies on leaf morphology in wheat, Jia et al. (2013a) reported a major QTL explaining 28.7-35.6% of the phenotypic variation of flag leaf width and that the Wangshuibai allele reduced flag leaf width up to 3 mm. This QTL was inherited as a semi-dominant gene, designated as *TaFLW1*, and was fine-mapped to a 0.2 cM interval on chromosome 5A (Xue et al., 2013).

Spike morphology

The morphology of wheat spike is characterized by its spike length, fertile spikelet number per spike, sterile spikelet number per spike, and spikelet compactness. The wheat spike harbors spikelets where florets develop and produce grains. Spike morphology is relevant to grain yield because it determines the number of grains. Since the 1960s, genetic gains in grain yield of wheat have generally been achieved by improvements in grain number per spike and spikes per square meter, with little change in individual grain weight (Gaju et al., 2009). Thus, increasing grain number *per se* by modifying the spike morphology may open new opportunities for higher grain yield potential.

In bread wheat, *Q*, *C*, and *S1* are the three major domestication genes affect the gross morphology of the spike. The *Q* gene is located on chromosome arm 5AL and pleiotropically influences not only spike length and shape, but also other domestication related traits including seed threshability, glume keeledness, rachis fragility, plant height, and spike emergence time (Faris et al., 2014). The *C* gene is located on chromosome 2D

and defines a subspecies of hexaploid wheat known as *T. aestivum* ssp. *compactum* (Host) MacKey, or club wheat, which has a characteristic compact spike due to a dominant *C* allele (Faris et al., 2014). The *S1* gene on chromosome 3D defines another subspecies known as *T. aestivum* ssp. *sphaerococcum* (Percival) MacKey, or shot wheat, which is characterized by having round seed, round glumes, and a short dense spike (Faris et al., 2014; McIntosh et al., 2013). Therefore, common wheat (ssp. *aestivum*) has the genotype *QcS1*, club wheat (ssp. *compactum*) is *QCS1*, and shot wheat (ssp. *sphaerococcum*) is *Qcs1* (McIntosh et al., 2013). In addition to these loci, all twenty one wheat chromosomes have been associated with spike related traits (Borner et al., 2002; Cui et al., 2012; Deng et al., 2011; Kumar et al., 2007; Ma et al., 2007b; Marza et al., 2006; Wang et al., 2011). Furthermore, mapping QTL as Mendelian factors was first reported by Deng et al. (2011) who investigated wheat spike traits in a F_2 population. This population showed a clear 3:1 segregation ratio for spike number per plant, spike length, and grain number per spike. The underlying QTL was mapped to the chromosome 4B and explained 30.1 to 67.6% of the phenotypic variation across environments. Further fine mapping and molecular characterization of this region has not been reported yet.

Cloned QTL/genes related to grain yield in cereal crops

Grain related traits

Grain morphology and grain filling rate determine grain weight and thus, grain yield. The first cloned major QTL related to grain morphology was *GS3* which explained 80-90% of the variation for grain weight and length in a rice BC_3F_2 population derived from a cross between Minghui 63 (large grain) and Chuan 7 (small grain) (Fan et al., 2006). Initial QTL analysis mapped *GS3* on chromosome 3. Fine mapping narrowed down the

candidate region to a DNA fragment of 7.9 kb in length where a full-length cDNA was identified. *GS3* encodes a transmembrane protein consisting of a putative PEBP-like domain, a putative TNFR/NGFR family cysteine-rich domain and a VWFC module. A C to A mutation in its second exon changed a cysteine codon (TGC) in Chuan 7 to a termination codon (TGA) in Minghui 63 which yields a premature termination and a 178-aa truncation in the C-terminus. Overexpression of *GS3* not only produces short grains but also results in reduced plant size, including shortened height, leaves, and panicles, suggesting its role as a negative regulator with pleiotropic effects (Mao et al., 2010).

GW2 was the second cloned major QTL for grain size in rice (Song et al., 2007). This QTL was identified and molecularly characterized from a F2 population derived from a *japonica* × *indica* cross (WY3 × Fengaizhan-1). *GW2* encodes a RING protein with E3 ubiquitin ligase activity. Compared with the Fengaizhan-1 allele at locus *GW2*, the WY3 allele has a 1-bp deletion in exon 4, resulting in a premature stop codon which leads to truncation of 310 amino acid residues. This loss-of-function mutation produces substantially more and longer cells in outer parenchyma cell layer of the spikelet as well as larger endosperm cells and accelerated grain filling. Additionally, the WY3 allele increases grain size and yield with little influence on eating or cooking quality making it a useful QTL in breeding.

GS5, the first cloned positive regulator, controls grain size by regulating grain width, filling and weight in rice (Li et al., 2011). Primary QTL mapping detected this QTL on the short arm of chromosome 5 in a doubled haploid (DH) population derived from the

cross between Zhenshan 97 (large grain size) and H94 (small grain size). Fine mapping resolved *GS5* to a candidate region of 11.6-kb in length where there was only one predicted open reading frame (ORF). This ORF has ten exons and encodes a putative serine carboxypeptidase. *GS5* positively regulates grain size by increasing cell number in the inner parenchyma cell layer and the cell size of palea and *GS5* is further shown to be a positive modulator upstream of cell cycle genes whose expression is significantly elevated when *GS5* is overexpressed. The observed grain size and yield difference between Zhengshan 97 (large grain size) and H94 (small grain size) was due to the polymorphisms in the GS5 promoter region where strong/weak promoters were associated with high/low yield. The Zhengshan 97 allele was expressed with more abundance in the palea/lemma at 2, 4 and 5 day before heading and in the endosperm at 10 days after fertilization which corresponded well with critical stages for grain width and grain filling.

GRAIN INCOMPLETE FILLING 1 (GIF1) was the first cloned and functionally analyzed QTL for grain-filling (Wang et al., 2008). *GIF1* is located on chromosome 4 and encodes a cell-wall invertase required for carbon partitioning during early grain-filling. Specifically, GIF1 unloads sucrose in the ovular and stylar vascular tissues for starch synthesis in the endosperm during grain-filling. The *gif1* mutant has a 1-nt deletion in the coding region which results in a premature stop and reduced grain weight. During grain filling, the wild-type *GIF1* allele is expressed in the ovular vascular trace, pericarp and endosperm tissues. In contrast, the cultivated *GIF1* allele is mainly confined to the ovular trace which leads to a higher accumulation level of glucose, fructose and sucrose and,

hence, increased grain weight. This restricted expression pattern of cultivated *GIF1* gene is caused by accumulated mutations in its promoter region during rice domestication both in *japonica* and *indica*.

Plant architecture

The generalization of dwarfing genes in wheat and rice cultivars was crucial to the success of the Green Revolution. *Reduced height-B1b (Rht-B1b)* and *Reduced height-D1b (Rht-D1b)* are known as the green revolution genes in wheat (Peng et al., 1999). Their wild-type alleles *Rht-B1a* and *Rht-D1a* encode DELLA proteins which are transcriptional regulators that repress gibberellin (GA)-responsive growth. *Rht-B1b* and *Rht-D1b* both contain single nucleotide substitutions causing premature stop codons in the N-terminal coding region leading to truncated proteins with increased repression of GA signal transduction. *semidwarf-1 (sd-1)* is known as the green revolution gene in rice and encodes gibberellin 20-oxidase ($GA20_{ox}$) which is an enzyme catalyzing three intermediate steps of reactions converting GA precursors to GA (GA_{53} → GA_{44}→ GA_{19}→ GA_{20}) (Monna et al., 2002; Sasaki et al., 2002). Its widely-used allele is from the Chinese cultivar, Dee-geo-woo-gen that contains a 383-bp deletion in the GA20ox gene (known as *OsGA20ox2*) resulting in a premature stop codon and a highly truncated inactive enzyme (Hedden, 2003).

MONOCULM 1 (MOC1) is the first cloned key regulator of rice tiller number (Li et al., 2003). A screen of mutants with altered tiller numbers identified a rice plant with only one main culm, named *monoculm 1 (moc1)*. *moc1* is caused by a recessive mutation at a single locus and was mapped to the chromosome 6 of rice. *MOC1* encodes a plant-

specific GRAS family nuclear protein and is mainly expressed in the axillary buds to initiate axillary buds and to promote their outgrowth. Rice plants with enhanced expression of *MOC1* produced more tillers as expected. In contrast, *moc1* is not able to initiate axillary meristem and therefore, has only one main culm.

Rice *Narrow leaf 1(Nal1)* encodes a plant specific protein preferentially expressed in vascular tissues with rich abundance (Qi et al., 2008). A 30-bp deletion in its coding region is significantly associated with reduced polar auxin transport capacity and affects the distribution pattern of vascular bundles leading to narrower leaves with fewer longitudinal veins. *NARROW AND ROLLED LEAF 1 (NRL1)* was mapped to chromosome 12 in rice. It encodes the cellulose synthase-like protein D4 (OsCsID4) which plays a crucial role in leaf expansion in rice (Hu et al., 2010). Its three mutants (single base substitutions at three different loci) *nrl1-1, nrl1-2, and nrl1-2* are smaller and show erect, narrow and semi-rolled leaves compared to the *NRL1* genotype.

Spike morphology

Grain number per panicle is one of the most important yield components in cereals. The first cloned QTL for grain number per panicle was *Gn1a* in rice (Ashikari et al., 2005). This QTL was mapped by using 96 backcross inbred lines derived from the cross between Habtaki (higher grain number) and Koshihikari (lower grain number). A major QTL contributed by Habataki explained 44% of the grain number variation and was identified on chromosome 1. This QTL was further fine-mapped to a region of 6.3 kb, where there was only one predicted open reading frame. Molecular characterization of *Gn1a* showed that it encodes a cytokinin oxidase/dehydrogenase (OsCKX2) whose

reduced expression causes cytokinin accumulation in the inflorescence meristem and increases the number of reproductive organs which leads to higher grain number per panicle enhancing grain yield. Based on comparative genomics, *TaCKX6-D1* a wheat ortholog of the rice *OsCKX*, was cloned and located on the wheat chromosome 3D (Zhang et al., 2012). This gene was mapped by using a set of 199 RILs derived from a cross between two Chinese Spring cultivars Yanzhan1 and Neixiang188. The Yanzhan1 allele, named *TaCKX6-D1a,* has an 18-bp indel in its second intron where the Neixiang188 allele, named *TaCKX6-D1b,* has an insertion in this region. *TaCKX6-D1a* is associated with higher 1000-grain weight and its additive effect is 1.3~1.4 g per 1000 grains. Four more alleles of *TaCKX6-D1* were found and named *TaCKX6-D1c*─*TaCKX6-D1e*. Evolutionary analysis showed that alleles *c*, *e* and *d* are ancient haplotypes occurring only in the wild species, whereas alleles *a* and *b* are newly derived, present most commonly in both modern cultivars and landraces.

Quantitative trait loci *WFP (WEALTHY FARMER'S PANICLE)* and *IPA1 (IDEAL PLANT ARCHITECTURE)* were cloned in the same year by two research groups independently and were found to share the same underlying gene *OsSPL14* (Jiao et al., 2010; Miura et al., 2010). *OsSPL14* is located on the chromosome 8 of rice and encodes a plant-specific transcription factor SQUAMOSA PROMOTER BINDING PROTEIN-LIKE (OsSPL14) which is conserved in sorghum, wheat, maize and *Arabidopsis thalinana* (Miura et al., 2010). Higher expression of *OsSPL14* promotes panicle branching in the reproductive stage. Sequence analysis showed that *OsSPL14* contains a microRNA-targeted sequence in the third exon (targeted by OsmiR156). OsmiR156 is

highly expressed in the vegetative stage and cleaves the *OsSPL14* mRNA suppressing the expression of *OsSPL14*. In the reproductive stage, OsmiR156 disappears leading to a higher expression level of *OsSPL14* and the subsequent enhanced primary branching on the panicle.

DEP1 is the first cloned QTL that acts through the determination of panicle architecture (Huang et al., 2009). *DEP1* is located on chromosome 9 of rice and encodes a phosphatidylethanolamine-binding protein-like domain protein. Its dominant loss-of-function allele *dep1* from cultivars such as Nanjing 11 and Nipponbare produces erect panicles with a shorter inflorescence internode, increased number of both primary and secondary panicle branches and increased number of grains. Although the 1000-grain weight of NIL-*dep1* was slightly lower than that of NIL-*DEP1* plants, the overall grain yield of NIL-*dep1* was 40.9% higher. Moreover, the downregulation of *TaDEP1*, a homolog of *DEP1* in wheat, showed a longer panicle with fewer spikelets suggesting that this locus and its homologs in other small grain cereals may provide an option for increasing grain yield.

Ghd7 is the first cloned quantitative trait locus that controls grain numbers per panicle, plant height and heading date simultaneously (Xue et al., 2008b). *Ghd7* was mapped on chromosome 7 of rice using both $F_{2:3}$ and RIL populations derived from a cross between Zhenshan 97 (lower grain number and days to heading) and Minghui 63 (higher grain number and days to heading). *Ghd7* encodes a CCT (CO, CO-LIKE and TOC1) domain protein. However, comparison with other CCT domain-containing proteins showed that t

GHD7 is distinct from all other members of the CCT domain protein family and is considered to be an evolutionary new gene in the lineage. *Ghd7* is a key upstream transcription factor in the photoperiod flowering pathway and its Minghui 63 allele allow rice plants to fully utilize light and temperature by delaying flowering under long-day conditions. As a result, larger panicles with more grain numbers occur. Furthermore, the Minghui 63 allele is mainly expressed in young tissues and also has a positive effect on stem growth by producing more nodes, a longer upper-most internode and thicker stems with improved lodging resistance. All these pleiotropic effects contribute to a high grain yield. *Ghd8* is a major QTL on chromosome 8 with similar pleiotropic effects as *Ghd7* (Yan et al., 2011). *Ghd8* encodes the OsHAP3 subunit of the HAP complex and acts upstream of rice florigen genes *Fhd1, Hd3a, and RFT1*. In addition, *Ghd8* has a positive effect on rice tiller number, primary and secondary branches, by up-regulating *MOC1* which is a key gene controlling tillering and branching.

QTL mapping and cloning in breeding programs

Basics of QTL Mapping

Historically, genetics relied entirely on phenotypic information to determine the relative importance of genetic versus environmental factors through techniques such as analysis of variance and heredity analysis (Walsh, 2001). However, merely based on phenotypic evaluation, it is generally not possible to identify relevant loci influencing a trait. The development and combination of genetic marker technologies, molecular biology and biometric methods has made QTL mapping possible in complex traits studies.

QTL mapping is a set of statistical methods attempting to explore the relationship between DNA sequence variation and natural phenotypic variation for quantitative or complex traits and is widely utilized in modern genetics (Haley, 2002; Kearsey and Farquhar, 1998 ; Majumder and Ghosh, 2005; Myles et al., 2009). By combining phenotypic data (trait measurements) and genotypic data (usually molecular markers), QTL mapping allows researchers to link certain complex phenotypes to specific regions of chromosomes (Miles and Wayne, 2008). Although the principles of QTL mapping have been known since the early twentieth century, genetic dissection of complex traits was limited to a few model organisms due to the lack of polymorphic markers (Mackay et al., 2009). Since the discovery of abundant molecular markers in late 1980s, advances in rapid and cost-effective genotyping methods and the employment of statistical methods have revolutionized the field of QTL mapping (Mackay et al., 2009). Statistical methods developed for QTL mapping are based on homologous recombination at meiosis, during which the genetic material is exchanged by crossing over (Myles et al., 2009; Nordborg and Weigel, 2008).

To perform QTL mapping for a measurable quantitative trait, a mapping population and linkage map are needed. Coupling this map with phenotypic data for the trait (e.g. yield) allows the region of the genome associated with the phenotype to be identified. Therefore, the three requirements for QTL mapping are: 1) a mapping population where individuals differ genetically with regard to traits of interest; 2) genetic markers that distinguish these lines; and 3) quantitative data for the traits to be explored; (Miles and Wayne 2008).

Mapping population

In plant breeding, the most common mapping populations include F_2, recombinant inbred lines (RILs), and doubled haploids (DH). The simplest form of a mapping population is a collection of F_2 plants derived directly by selfing a F_1 plant. In this case, the expected segregation ratio for each codominant marker is 1:2:1 (homozygous like P1:heterozygous:homozygous like P2) (Schneider, 2005). However, an F_2 populations can only be used once since they are not immortal and generally cannot be clonally propagated (Schneider, 2005). This makes phenotypic evaluation in multi-location/year difficult to perform.

Recombinant inbred lines (RILs) are generated by repeated selfing of F_2 individuals for at least six generations using the single seed descent method (Snape and Riggs, 1975). Once established, RILs can be propagated eternally and shared by other groups in the research community (Broman, 2005). A second advantage of RILs is that after several rounds of meiosis before homozygosity is reached, the degree of recombination and the resolution of the linkage map are both higher compared to that of F2 populations and the map positions of even tightly linked markers can be determined (Schneider, 2005). Despite the fact that RILs are among the most effective population designs, it is time consuming to construct homozygous RIL populations, typically requiring at least six generations of self-fertilization starting from a heterozygous F_1 (Seymour et al., 2012).

Another option for mapping is to develop a doubled haploid (DH) population. Haploid gametes produced from F_1 meiosis contain all recombination information but only half

the number of chromosomes. To make a DH population in plants, F_1 flowers are pollinated with incompatible pollen, leaving a haploid embryo. After embryo rescue and tissue culture, haploid seedlings are treated with colchicine, preventing cytokinesis after mitosis and leading to doubled haploids (Schneider, 2005). Each DH contains two identical sets of chromosomes in each cell and is completely homozygous at every locus. This time-efficient process can be finished in only two steps and has been widely used in QTL mapping in a variety of species, especially in grasses (Seymour et al., 2012).

Genetic markers

Genetic markers are heritable biological features that are determined by allelic forms of genes or genetic loci and can be measured in one or more populations (Davey et al., 2011; Xu, 2010). Thus, they can be used as experimental probes or tags to keep track of an individual, a tissue, a cell, a nucleus, a chromosome or a gene and are the cornerstone of modern genetics (Davey et al., 2011; Xu, 2010). As Xu (2010) summarized, genetic markers fall into two categories: 1) classical markers and 2) DNA markers. Classical markers include morphological markers, cytological markers and biochemical markers. DNA markers include randomly amplified polymorphic DNA (RAPD), simple sequence repeats (SSR) or microsatellites, amplified fragment length polymorphisms (AFLP), single nucleotide polymorphisms (SNP), and diversity arrays technology markers (DarT).

After the first identification and use of DNA-based molecular markers in 1980s, such as restriction fragment length polymorphism (RFLP), the development and use of molecular markers has increased explosively in human genetics, plant breeding and genetics, animal breeding and genetics, and germplasm characterization and management (Botstein et al.,

1980; Jiang, 2013). This technological revolution began with low-throughput RFLP and culminated with SNPs in recent years (Gupta et al., 2008). First identified in the human genome, SNPs make up about 90% of all human genetic variation, happen every 100–300 bases, and have been proven to be universal in plant and animal systems as well (Wang, 1998; Xu, 2010). SNP identification is usually achieved by aligning genomic or expressed sequence tag (EST) sequences available in databases, or via next-generation sequencing (NGS)-based sequencing or resequencing of candidate genes/ PCR products and even whole genomes in more than one genotype (Gupta et al., 2008). Once discovered, many platforms are available to carry out SNP genotyping, such as Genechip, Infinium II and Goldengate (Kumar et al., 2012).

In crop plants, abundant and high-density SNPs can accelerate high-density genetic mapping and identification of genes/QTLs for traits of economic and agronomic importance as well as the application of marker-assisted breeding and genomic selection (Trebbi et al., 2011). Recently, SNP discovery has been reported in many crop plants such as rice, maize, barley, wheat, and sunflower (Bachlava et al., 2012; Cavanagh et al., 2013; Close et al., 2009; Ganal et al., 2011; Hu et al., 2013; McCouch et al., 2010). For example, Trebbi et al. (2011) discovered and validated a set of 275 SNPs in durum wheat using 12 durum cultivars through complexity reduction of polymorphic sequences (CroPS) technology and Illumina Golden Gate technology. Ganal et al. (2011) developed a large maize SNP array containing 57,838 markers across the genome, out of which 49,585 markers, representing 17,520 genes were storable and of good quality for further

genotyping. Additionally, using the RICE6K SNP array, Hu et al. (2013) mapped 5 novel QTLs for rice grain shape for marker-assisted selection in rice.

Genotyping by sequencing

The decreasing cost of next-generation sequencing (NGS) makes high-throughput genome-wide genetic marker discovery applicable not only to model organisms with reference genome sequences but also to non-model species without genome data (Davey et al., 2011). Recently, genotyping by sequencing (GBS), a low coverage genotyping method suitable for high diversity and large genome species, was proposed. It is reported to be "simple, quick, extremely specific, highly reproducible, and may reach important regions of the genome that are inaccessible to sequence capture approaches" (Elshire et al., 2011). Compared with restriction-site-associated DNA sequencing (RAD-seq), GBS has simpler library preparation protocols but produces equivalent results at a very low cost per sample (Davey et al., 2011). After the digestion of genomic DNA with restriction enzymes, barcode and common adapters are ligated to sticky ends of digested DNA fragments after which samples can directly go to PCR amplification followed by DNA sequencing (Elshire et al., 2011). Since no fragment size selection and few enzymatic and purification steps are involved, this protocol is time and cost efficient (Elshire et al., 2011). In maize, for example, 200,000 markers were identified and mapped in a very short time at a cost of $8,000 (Elshire et al., 2011). During this study, GBS was coupled with multiplex technology and simultaneously processed up to 2,688 samples per sequencing run (384 samples per channel ×7 channels) (Elshire et al., 2011).

Statistical models for linkage mapping

Traditionally, QTL detection is achieved by linkage mapping, where two homozygous inbred parental lines are crossed to create a mapping population/family and attempts are made to identify cosegregation of genetic markers and phenotypes within this family (Myles et al., 2009).

In the late 1980s, markers and advances in genotyping technology led to the development of statistical methods for use in QTL mapping of complex quantitative traits. A landmark method for QTL mapping is interval mapping (IM) (Lander and Botstein, 1989).This method established a statistical framework for most methods that are currently used to analyze QTLs of complex traits (Xu and Zhu, 2012). In IM, phenotypic data is used to compute a log likelihood (LOD) value at a DNA marker interval. As the marker interval slides along the chromosome (genome scanning), LOD values change accordingly. A QTL associated with a quantitative trait is assumed to be located on the genome under the peak where the LOD is higher than a specified threshold. The precision of IM was improved by including associated markers as covariant variables (Zeng, 1994). This method is known as composite interval mapping (CIM). Under the assumption of no QTL× environment interaction, CIM can produce unbiased estimations of QTL positions and effects. The IM and CIM methods have been widely applied in experimental populations, such as F_2, recombinant inbred lines (RIL), and doubled haploids (DH) (Xu and Zhu, 2012). Other well-recognized mapping models include multiple interval mapping (MIM) (Kao et al., 1999), inclusive composite interval mapping (ICIM) (Li et

al., 2007a), conditional QTL mapping (Wen and Zhu, 2005; Zhu, 1995), and QTL mapping based on mixed linear model (Wang et al., 1999; Yang et al., 2007).

Linkage mapping, however, has its own drawbacks. It is based on a highly controlled population structure that goes through relatively few meiosis events. Therefore, recombination has not had sufficient time to shuffle and rearrange the genome and QTLs may end up in large chromosomal regions making it difficult to capture the precise location of promising QTLs and to distinguish pleiotropic effects of a single QTL from multiple independent linked QTLs (Xu, 2010). The resulting low precision can be partially improved by using a larger mapping population with more recombination events and a high-density marker coverage across the genome. Lastly, due to this rigid population structure, QTLs identified in linkage mapping populations are usually limited to specific crosses and may not be generalized to other populations.

Association mapping

In association mapping, genotype data and phenotype data are collected from a natural population (assuming random mating) where the experimenter has no control over the structure of the mapping population (Myles et al., 2009). This advantage leads to its enormous success in human disease research, for which obtaining a controlled population is almost impossible (Collins, 2007). Association mapping employs historical recombination events that have happened between QTLs and marker alleles providing higher mapping resolution and thus requires a smaller number of individuals compared with linkage mapping (Mackay et al., 2009). The application of association mapping expanded enormously with the advent of next generation sequencing technology which

has the capacity of discovering, sequencing and genotyping large numbers of molecular markers, mostly SNP, across almost any genome of interest in a short time and in a cost-effective manner (Davey et al., 2011). Having the whole genome covered with molecular markers enables researchers to conduct genome-wide association studies with revolutionary resolution.

A randomly mating population, however, almost does not exist in practice and this nonrandom mating population structure can generate complex patterns of population structure and relatedness in plants which is a strong confounding factor, especially for the traits that are to be introgressed into local cultivars (Myles et al., 2009; Nordborg and Weigel, 2008). Despite the fact that statistical methods have been developed to correct for various types of relatedness, one should recognize that these methods are still subject to further improvement (Myles et al., 2009). In addition, association mapping cannot detect alleles with low frequency in the population, even if they have a large effect on the phenotype (Davey et al., 2011). However, population genetics suggests that, in the majority of species, most alleles are rare, which makes it difficult to explain phenotypic variation via association mapping. (Myles et al., 2009). Thus, biparental mapping is still an important tool.

The power of association mapping highly depends on the strength of the association between molecular markers and the corresponding functional variants/QTLs, which is known as linkage disequilibrium (LD). LD happens, considering two separate loci located on the same chromosome, when the presence of the genotype at one locus is not

independent of the other. In other words, they are linked and tend to occur together. Since it is described through DNA recombination, the strength of LD is a function of the distance between two loci: the closer they are, the stronger the LD (Mackay and Powell, 2007). In association analysis, the final mapping resolution relies on the decay of LD over distance, which differs both between and within species (Collins, 2007). Therefore, association mapping may have less power when performed on a bi-parental mapping population where LD is higher.

Cloning QTLs in wheat

To breeders, QTL cloning is not a routine option and is economical only for those loci with clear added value (Salvi and Tuberosa, 2007). Only a very few QTLs in bread wheat have been cloned through map-based cloning and the underlying gene characterized (Liu et al., 2013; Uauy et al., 2006). QTL cloning in wheat is challenging partly because of its large and complex genome and the lack of a high quality reference sequence. This issue could be addressed by synteny.

Cereal genomes show substantial conservation in gene order, known as synteny or colinearity (Akhunov et al., 2013; Dubcovsky et al., 2001; Qi et al., 2013; Sorrells et al., 2003). This has great important applications. For example, Akhunov et al. (2013) used the syntenic relationships between wheat and *Brachypodium distachyon*, rice, and sorghum to order contigs and scaffolds of wheat chromosome 3A. Salse et al. (2008) studied the evolution of grasses through comprehensive analysis of intragenomic duplications and comprehensive synteny. However, macro-collinearity does not always predict micro-colinearity (Sorrells et al., 2003). An abundance of rearrangements,

insertions, deletions, and duplications exist when grass genomes are compared (La Rota and Sorrells, 2004). Therefore, for QTL cloning, synteny is mostly reliable when a relatively small genomic region is examined.

In general, four steps are generally involved in cloning a QTL in wheat. First, a bi-parental population is used to locate a QTL and its flanking markers on a certain chromosome. Second, a fine-mapping population derived from a cross between two parents differing only in the flanking marker-defined region is used to construct a precise genetic map indicating the position of the QTL of interest. In this step, the QTL is physically mapped to one of wheat's deletion bins based on the physical position of its flanking markers (Abeysekara et al., 2010; Hua et al., 2009). Wheat geneticists have developed a collection of deletion stocks that physically dissect wheat chromosomes into bins (Endo and Gill, 1996). A number of simple sequence repeats (SSRs) and expressed sequence tag (ETSs) are also physically mapped to these deletion bins through Southern hybridization experiments (Qi et al., 2004; Sourdille et al., 2004). Thirdly, the sequences of the ESTs that mapped to the same deletion bin with the QTL of interest are used as query sequences to search the rice and *Brachypodium distachyon* genome sequences to identify a collinear region. Namely, saturation mapping via synteny (Zhang et al., 2013). Rice and *Brachypodium distachyon* genes residing within a colinear region are used to search the wheat ESTs database to identify previously unmapped ESTs to saturate the flanking marker-defined region. The fourth step involves sequencing BAC clones (Liu et al., 2013). After saturation mapping, the QTL region is narrowed down. The two closest flanking markers are used to screen BAC libraries and chromosome walking as well as

sequencing of the target interval leads to the identification of candidate genes (Krattinger et al., 2009).

Trends in wheat breeding

High-throughput phenotyping

Linking genotypic variation to observed traits/phenotypes is essential for marker assisted selection and breeding by design in breeding practice (Peleman and van der Voort, 2003; Tester and Langridge, 2010). The rapid development of genomics-based genotyping technologies in the past decade, especially sequencing capability, has offered breeders powerful tools and resources to access a wealth of genomic information on a breeding population at a relatively low cost (Davey et al., 2011). In contrast, phenotyping a large breeding population for multiple traits at multiple environments is still technically challenging and laborious (Furbank and Tester, 2011). The lack of access to high-throughput and high-dimensional phenotypic data on organism-wide scale has become a new bottleneck that limits our ability to dissect the genetics of quantitative traits in both crop improvement and basic research (Houle et al., 2010).

Interest in developing high-throughput phenotyping platforms (HTPPs) has arisen from both private and public sectors to address the issue (Araus and Cairns, 2014). Collaborative networks have formed to build HTPPs. Some of the most advanced and fully automated public facilities for indoor experimentation include the Australian Plant Phenomics Facility and the European Plant Phenotyping Network. These platforms are equipped with robotics, conveyor systems, imaging stations, watering stations, and computing infrastructure and are able to operate automatically to collect data for 3D plant

canopy architecture, canopy temperature, leaf color and morphology, and photosynthesis at different developmental stages (http://www.plantphenomics.org.au; http://www.plant-phenotyping-network.eu). Under field conditions, HTPPs employs, mostly, remote sensing and imaging and near-infrared reflectance spectroscopy analysis to finish rapid assessment of traits such as vegetation indices at more or less frequent intervals during the crop cycle (Araus and Cairns, 2014). Field HTPPs carry multiple sets of sensors and often use high-clearance tractors, cable robots, helicopters, aerostats, and drones as sensor carriers (White et al., 2012). Accurate and rapid phenotypic data produced on HTTPs (indoor and outdoor) helps breeders and crop scientists to exploit genomic information and gain new insights that are hard or unable to access before. For example, rice researchers built a high-throughput rice phenotyping facility and demonstrated that, when combined with genome wide association studies, high-throughput phenotyping better dissected the genetic architecture of rice complex traits such as shoot weight and green leaf area than traditional manual measurements (Yang et al., 2014). In addition, an image-based high-throughput field phenotyping system for crop roots was developed and identified 13 new plant root traits that differentiated nine maize genotypes 8 weeks after planting (Bucksch et al., 2014). High-throughput genotyping is emerging as a new crop breeding frontier and is revolutionizing many areas of plant science (Araus and Cairns, 2014; Kloth et al., 2015; Klukas et al., 2014).

Genomic selection

Prediction of crop performance as a function of genetic architecture is a major challenge for crop research (White et al., 2012). Marker-assisted selection (MAS) has been successfully and efficiently used to select elite cultivars with desired qualitative

characters such as enhanced disease resistance. However, since MAS has traditionally relied on markers linked to large-effect quantitative trait loci (QTL), it has been less effective for quantitative traits that are complex and controlled by many genes with small effects (Jannink et al., 2010). Genomic selection has been proposed and implemented as a new breeding approach to address the deficiency of MAS and to accelerate genetic gains in plant and animal breeding (Crossa et al., 2014; Meuwissen et al., 2001). In contrast to MAS, genomic selection simultaneously estimates the allelic effects of all available markers spread across the genome to predict phenotypic performance and does not test the significance of a link between a marker and a QTL (Massman et al., 2013).

Genomic selection first uses a 'training population' of individuals that have been both genotyped and phenotyped to produce genomic estimated breeding values (GEBVs) for each marker which are further used by a prediction model to predict the performance of a 'candidate population' from which individuals are only genotyped and, then, selected based on their GEBVs for advancement in the breeding cycle (Jannink et al., 2010). Genomic selection has been evaluated with simulation data and real data in dairy cattle (Hayes et al., 2009), mice (Legarra et al., 2008), rye (Wang et al., 2014), sugar beet (Wurschum et al., 2013), rice (Xu et al., 2014), wheat (Poland et al., 2012), and maize (Crossa et al., 2013). The correlation between true breeding value and the estimated breeding value has reached levels of 0.85 even for polygenic low heritability traits (Heffner et al., 2009). With its continuously improved prediction accuracy, genomic selection could dramatically change the role of phenotyping from selecting lines to updating prediction models and substantially accelerate the breeding cycle (Heffner et al.,

2009; Morrell et al., 2012). It is expected that genomic selection will revolutionize plant and animal breeding in the next decade (Henryon et al., 2014; Morrell et al., 2012).

Synthetic wheat

Hexaploid wheat evolved from the hybridization between *T. turgidum* (AABB) and *Ae. tauschii* (DD). It is believed that only a limited number of these two donor species were involved in the speciation process and, thus, the genetic diversity of hexaploid wheat was largely reduced (Yang et al., 2009). To address this evolutionary bottleneck and introduce favorable alleles into hexaploid wheat from its wild relatives, synthetic wheats have been made via artificial synthesis of hexaploid wheat (*T.turgidum* × *Ae. tauschii*) in a manner analogous to the natural evolution of hexaploid wheat (Trethowan and van Ginkel, 2009). Many of these wild species, especially *Ae. tauschii*, possess novel and elite genes for biotic and abiotic stresses which can provide synthetic wheat with exceptional disease resistance and stress tolerance (Dreisigacker et al., 2008; Jia et al., 2013b). In addition, synthetic wheat is also a valuable source of alleles to improve grain yield and yield components (del Blanco et al., 2001). Since the early 1990s, the International Maize and Wheat Improvement Center (CIMMYT) has started making synthetic wheat and transferring favorable traits to CIMMYT elite breeding lines (Dreisigacker et al., 2008). To date, more than 1000 syntheitc wheats have been produced by CIMMYT and are being used by breeding programs worldwide (Dreisigacker et al., 2008; Yang et al., 2009). Synthetic wheat and synthetic wheat-derived cultivars have great potential for enhancing grain yield and adaptation of modern hexaploid wheat (Li et al., 2014; Trethowan and van Ginkel, 2009). Thus, a new generation of wheat varieties produced from synthetic wheats is on the horizon (van Ginkel and Ogbonnaya, 2007).

Chapter 2: Quantitative trait loci mapping of grain yield in a doubled haploid population of soft red winter wheat

Abstract

Understanding the genetic basis of grain yield and yield components is the key to improving grain yield potential in common wheat (*Triticum aestivum* L.). My objective was to identify quantitative trait loci (QTL) associated with grain yield (GYLD), spikes m^{-2} (SPSM), grain weight per spike (GWPS), grains per spike (GPS) and thousand-grain-weight (TGW) using a doubled haploid (DH) population. The DH population was evaluated in five environments and was genotyped with single nucleotide polymorphism (SNPs), simple sequence repeats (SSRs), and a morphological marker. The linkage map spanned 1977.6 cM with an average interval length of 2.3 cM. Sixty four putative QTLs for GYLD, SPSM, GWPS, and GPS were detected on eighteen wheat chromosomes. The phenotypic variance explained by these QTLs ranged from 3.7% for GWPS to 71.2% for TGW. The major GYLD QTL (*QYld.cz-3B.2*) and TGW QTL (*QTgw.cz-7A.5*) identified in the present study explained 21.2% and 71.2% of the phenotypic variation, respectively. GYLD QTLs closely linked to *Fhb1* and *Ppd-D1* genes were identified. Eleven QTLs exhibited pleiotropic effects. A genomic region with significant pleiotropic effects for GYLD, SPSM, GWPS, and GPS was located on 1A. In addition, QTL × environment interaction, epistasis and epistasis × environment interactions were detected. Major QTLs identified in this study could be used in marker-assisted breeding to increase grain yield or QTL fine mapping.

Introduction

Wheat (*Triticum aestivum* L.) is the staple food for more than 40% of the world's population. Increasing wheat production is essential to meet the demand of wheat consumption from an increasing population worldwide. As one of the key economic drivers behind the wheat cropping enterprise, improving grain yield potential is a major goal in both public and private breeding programs (Kuchel et al., 2007b). Grain yield is a resultant complex trait influenced by many processes that involve vegetative and reproductive growth and developmental stages (Yoshida, 1972). Grain yield is determined by yield component traits, such as grains per spike (GPS), spikes m^{-2} (SPSM), grain weigh per spike (GWPS), thousand-grain-weight (TGW) and affected by other yield related traits, e.g. plant architecture. Yield and yield component traits are genetically controlled by multiple quantitative trait loci (QTL) with major and minor effects that are highly influenced by environmental conditions (Deng et al., 2011; Kumar et al., 2007).

Identification of QTLs on specific chromosomes for yield and yield components can facilitate incorporating these traits into regionally adapted cultivars in an effective manner through marker assisted selection (MAS) (Carter et al., 2011). This allows breeders to test for the presence and to track down the proven QTL by targeting its closely linked markers for a more efficient and accurate selection of superior cultivars (Kuchel et al., 2007b). A large number of QTL studies have been reported in wheat (Heidari et al., 2011; Kuchel et al., 2007b; Kumar et al., 2007; Wu et al., 2012) and QTLs for grain yield and yield components have been identified in all wheat chromosomes

mostly with minor genetic effects (Wu et al., 2012; Zhang et al., 2010). For example, using two wheat mapping populations, Kumar et al. (2007) detected eighty-six QTLs out of which six were pleiotropic/coincident involving more than one yield related trait. Kuchel et al. (2007b) found in a DH population that although the higher yielding parent contributed most of the favorable alleles, the lower yielding parent also possessed higher yielding QTLs based on the data from eighteen environments. Li et al. (2007b) identified five environment-specific QTLs for GYLD on chromosome 1D, 2D, and 3B explaining 10.4-23.0% of the phenotypic variation. Groos et al. (2003) reported a stable QTL for TGW on chromosome 2B which explained up to 20% of the phenotypic variation in seven trials. Interestingly, the favorable allele was from Récital, the parental line with lower TGW. Heidari et al. (2011) identified a genomic region on chromosome 1A for GPS explaining up to 22.4% of the phenotypic variation in two environments and three QTLs for SPSM on chromosome 1A, 7A, and 2D explaining up to 21.4% of the phenotypic variation. Several large-effect loci affecting grain yield per se such as *Rht1* and *Ppd-D1* have been cloned and molecularly characterized (Boden et al., 2015; Pearce et al., 2011). One locus, *TaCKX6-D1,* significantly associated with TGW in wheat was isolated and shown to be orthologus to rice gene *OsCK2*. Moreover, yield component traits are less environmentally sensitive and generally exhibit higher heritability than grain yield, as a result of which, indirect selection on yield component traits tends to result in higher stable genetic gain than direct selection for grain yield (Kumar et al., 2007; Wu et al., 2012). Therefore, examining yield components when evaluating grain yield per se is necessary for sustained yield potential improvement (Wu et al., 2012).

Additionally, additive main effects, digenic epistasis, QTL × environment interactions (additive × environment interaction and epistasis × environment interactions) also are crucial factors determining the expression of quantitative traits (Mackay, 2001). In classical Mendelian genetics, the masking of genotypic effects at one locus by genotypes of another is called epistasis which is also broadly used to indicate any statistical interaction between genotypes at two (or more) loci in quantitative genetics (Mackay et al., 2009). Epistasis can be synergistic or antagonistic depending on whether the effect of one locus is enhanced or suppressed by the second locus (Mackay, 2001). As a result, the phenotype of a certain genotype would not be a simple sum of the additive effects of all loci involved. When plants are challenged by fluctuations in environmental conditions, both additive and epistatic effects of the same loci are modified to some extent so that plants can adapt to new situations by changing its phenotypic expression, known as phenotypic plasticity (El-Soda et al., 2014). A thorough understanding of the interactions mentioned above in breeding populations would help breeders predict the performance of genotypes across years and locations with more confidence. However, due to the lack of appropriate methodology and easy-to-use statistical software, QTL detection was typically conducted under the assumption of additive main effects only until the mixed-model based composite interval mapping (MCIM) was developed (Wang et al., 1999). MCIM showed high accuracy and power in mapping QTLs with epistatic effects and QTL × environment interactions by using the-best-linear-unbiased prediction (BLUP) method (Wang et al., 1999) and has been well accepted ever since (Li et al., 2007b; Xing et al., 2002; Zhang et al., 2009). Another big constraint in accurate QTL mapping and subsequent application of MAS was the lack of fast and large-scale genotyping platform

as the cost of initial genotyping approaches were high. A recent development in DNA marker technology is single nucleotide polymorphisms (SNPs). In contrast to traditional simple sequence repeats (SSRs) and amplified fragment length polymorphisms (AFLPs), SNPs are more abundant across genomes of many species and constitute ~90% of the genetic variation in virtually all organisms (Gupta et al., 2008). Recently, SNP discovery and QTL mapping using SNPs have been reported in many crop plants such as rice, maize, barley, wheat, and sunflower (Bachlava et al., 2012; Cavanagh et al., 2013; Close et al., 2009; Ganal et al., 2011; Hu et al., 2013; McCouch et al., 2010). Trebbi et al. (2011) discovered and validated a set of 275 SNPs in durum wheat using 12 durum cultivars through complexity reduction of polymorphic sequences (CroPS) technology and Illumina Golden Gate technology. Ganal et al. (2011) developed a large maize SNP array containing 57,838 markers across the genome, out of which 49,585 markers, representing 17,520 genes were storable and of good quality for further genotyping. This SNP array was then used to genotype two recombinant inbred line populations and two high density linkage maps were also established with 20,913 and 14,524 markers respectively. Moreover, using the RICE6K SNP array, Hu et al. (2013) mapped five novel QTLs for rice grain shape. Furthermore, genotyping by sequencing (GBS) is a new SNP genotyping method suitable for high diversity and large genomes and has shown to be "simple, quick, extremely specific, highly reproducible, and may reach important regions of the genome that are inaccessible to sequence capture approaches" (Elshire et al., 2011). Compared with other sequencing-based genotyping method such as restriction-site-associated DNA sequencing (RAD-seq), GBS has simpler library preparation protocols but produces equivalent results at very low cost per sample (Davey et al.,

2011). Coupling GBS with multiplex technology, up to 2,688 samples/breeding lines can be processed simultaneously per sequencing run (Elshire et al., 2011). In maize, for example, 200,000 markers were identified and mapped in a very short time at a cost of $8,000 (Elshire et al., 2011).

High grain yield of any crop can be achieved only when a proper combination of cultivar, environment, and agronomic practices is obtained (Yoshida, 1972). Understanding the genetic effects of QTLs, how QTLs interact with each other, and how these QTLs and their interactions are affected in different environments is important for breeders. In the present study, quantitative trait loci mapping in a DH population of soft red winter wheat was attempted (1) to identify QTLs affecting grain yield and yield components mostly with SNP makers, (2) to determine the additive genetic effects, digenic epistasis effects and their interactions with environments.

Materials and Methods

Genetic resources

A doubled haploid (DH) population was established from the cross of the soft red winter wheat germplasm line MD01W233-06-1 (MDW233) (Costa et al., 2010) and soft red winter wheat cultivar Southern States 8641 (SS8641) (Johnson et al., 2007b). The population consists of 124 DH lines and shows a wide range of phenotypic variation for yield and yield components. MDW233 was produced by crossing the soft red winter wheat cultivar 'McCormick' (VA92–51–39 (IN71761A4–31–5-48//VA71–54–147/'McNair 1813')/AL870365 ('Coker 747*2/'Amigo')) (PI632691) (Griffey et al., 2005) with 'Choptank' ('Coker 9803'/'Freedom') (PI 639724) (Costa et al., 2006) and

was released by the Maryland Agricultural Experiment Station in 2009 with enhanced *Fusarium* Head Blight (FHB) resistance. MDW233 carries the *Rht-D1b* dwarfing gene and the *Ppd-D1b* photoperiod sensitive allele. SS8641 was photoperiod insensitive and was released by the University of Georgia Experiment Station in 2007, with high yield and multiple disease resistance (Johnson et al., 2007b). It is a medium-maturing, white-chaffed, medium-tall line derived from the cross 'GA 881130 / 2* GA 881582'. The pedigree of GA 881130 is 'KSH8998 / FR81-10 // Gore'. KSH8998 was developed from the cross of a hard wheat with *Ae. tauschii* to transfer Hessian fly resistance gene *H13*. FR81-10 was selected because of its resistance to leaf rust (*Lr37* and *Yr17*) from the cross 'Novisad 138 /4/*Ae.ventricosa*/*T.persicum*/2/ Marve*3/3/Moisson'.

Field experiments

The DH mapping population and parents were grown in five environments: Clarksville, MD and Queenstown, MD in 2013 and 2014 and at Kinston, NC in 2014. The entries were evaluated in field trials with two replications in a randomized complete block design. Yield plots at Maryland consisted of seven rows 15.2 cm apart. Seed density was 22 seeds per 0.305 m in each row. The length of rows harvested was 4.17 m, making the harvest area 3.8 m^2. Yield plots at North Carolina had seven rows 19.1 cm apart with a seed density of 24 seeds per 0.305 m in each row. The length of rows harvested was 3.35m, making the harvest area 3.8 m^2. Growing season rainfall and temperature data were obtained from respective research farms for Clarksville, MD and Queenstown, MD and the National Oceanic and Atmospheric Administration (NOAA) measurements for Kinston, NC (National Climatic Data Center 2014) (Table 2.1). Soil fertility management followed recommended management practices for each location. All trials were sprayed

with the metconazole fungicide (Caramba®, BASF) at anthesis to reduce potential infection by *Fusarium graminearum*.

Phenotypic data collection

At maturity, plots were mechanically harvested using a small plot combine (Wintersteiger Nurserymaster Elite, Ried, Austria). Plot weight and moisture-content data of the wheat trials were obtained with a HarvestMaster HM1000b (Juniper Systems, Logan, UT) attached to the plot combine. Gain yield was measured from seed collected from the combine as pounds per plot and reported as grams per square meter. Grains per spike was recorded as the mean of the number of grains of ten random spikes from each plot. Grain weight per spike was measured using ten random spikes harvested from each plot. Spikes per square meter was calculated by dividing grain yield by grain weight per spike. Thousand-grain-weight was computed from the weight of 200 random grains from a sample harvested from each plot.

Statistical analysis of traits

Analysis of variance (ANOVA) for GYLD, GPS, GWPS, SPSM, and TGW was performed separately for each environment and for the five environments combined using the PROC GLM procedure of SAS version 9.3 (SAS Institute, Raleigh, NC 2013). The ANOVA model for single environment analysis was Y= replication + genotype + error, where replication and genotype were fixed and error was random. Combined ANOVA was performed to examine the effects of environments and the model was Y = environment + replication within environment + genotype + genotype × environment + error, where error was considered random and all others were fixed. Pearson's correlation

coefficients were calculated using the PROC CORR procedure of SAS. Broad-sense heritability (h^2) (defined as $h^2 = \sigma_G^2/(\sigma_G^2+(\sigma_{GE}^2/e)+(\sigma_E^2/re))$, where σ_G^2 is the variance of genotypic effect, σ_{GE}^2 is the genotype × environment variance, and e and r are the number of environments and replicates, respectively) was calculated on a family mean basis using the PROC MIXED procedure of SAS, as described by Holland et al. (2003). The descriptive statistics of all traits were calculated using the PROC MEANS procedure of SAS (Table 2.2).

Genotyping

SSR genotyping was performed at the USDA-ARS Eastern Regional Small Grain Genotyping Lab at Raleigh, NC, USA. Approximately 25 mg of leaf tissue of the parents and 124 doubled haploid lines were collected from 2-3 week-old seedlings for genomic DNA extraction which was performed according to the protocol of Pallotta et al. (2003). For all SSR markers, the polymerase chain reaction (PCR) master mix consisted of 2 µL of 20 ng μL^{-1} genomic DNA template, 0.40 µL of a 10 µM mixture of forward and reverse primers, 0.18 µL (0.9 U) of *Taq* polymerase, 1.20 µL of 10x buffer (10 mM Tris-HCL, 50 mM KCl, and 1.5 mM MgCl2, pH 8.3), 0.96 µL of a 100 µM mixture of deoxyribonucleotide triphosphates (dNTPs), and 7.26 µL of water, bringing the total reaction volume to 12 µL. A touchdown profile was used that consisted of an initial denaturation at 95°C followed by 15 cycles of 95°C for 45s, 65°C for 45s decreasing by 1°C each cycle, and 72°C for 60s, followed by 25 cycles of 50°C annealing temperature. The forward primers were 5'-modified to include one of the following fluorescent dyes: 6-FAM, VIC, NED, or PET. Amplifications were performed using an Eppendorf Mastercycler (Eppendorf AG, Hamburg, Germany). Sizing of PCR products was

performed by capillary electrophoresis using an ABI3130xl Genetic Analyzer (Applied BioSystems, Foster City, CA). Analysis of PCR fragments was performed using GeneMarker 1.60 software (SoftGenetics, LLC, State College, PA)

SNP genotyping was performed on the 9K iSelect SNP genotyping array containing 9,000 wheat SNP markers developed by Illumina Inc. (San Diego, CA, USA). This assay was designed under the protocols of the International Wheat SNP Consortium (Cavanagh et al., 2013). Additionally, genotyping-by-sequencing (GBS) was also employed for SNP genotyping as was described by Elshire et al. (2011). The SNP array was conducted at the USDA-ARS Small Grains Genotyping Lab at Fargo, ND, USA and GBS assay at the USDA-ARS Central Small Grain Genotyping Lab at Manhattan, KS, USA.

Map construction and QTL analysis

Markers with more than 20% missing rate and those that were monomorphic and distorted (differing significantly from the expected 1:1 segregation ratio) were eliminated from the analyses. The remaining polymorphic markers were used to construct linkage groups using the MAP function in software IciMapping version 4.0 with a LOD value of 10 (Li et al., 2008). Recombination frequencies were converted to centimorgans (cM) using the Kosambi mapping function. Assignment of linkage groups to chromosomes was based on the SNP consensus map (Cavanagh et al., 2013) and on the SSR consensus map (Somers et al., 2004), and as well as with wheat POPSEQ data (http://wheat-urgi.versailles.inra.fr/), after which, genetic distance of markers on the same chromosome was recalculated with RECORD and COUNT algorithm in IciMapping version 4.0.

Detecting QTL with additive effects was performed by IciMapping version 4.0 using the additive module (ICIM-ADD). The walking speed for all traits was 1 cM. Reference LOD values were determined by 1,000 permutations (Doerge, 2002). Type I error to determine the LOD from the permutation test was 0.05. The LOD threshold to declare the presence of a significant QTL was 3.0. The position at which the LOD score curve reaches its maximum was used as the estimate of the QTL location. Further QTL analysis for digenetic QTL epistasis (A×A or Q×Q), additive × environment (A×E or Q×E) and epistasis × environment (QQ×E) interactions was performed with QTLNetwork version 2.1 using mixed-model based composite interval mapping (MCIM) (Wang et al., 1999; Yang et al., 2007). All effects mentioned above were estimated by Monte Carlo Markov Chain method with a scanning speed of 1 cM step with a 0.05 experiment-wise type I error.

Results

Environment conditions

Phenotypic data for QTL analysis was collected from five environments (Table 2.1, Appendix C). The conditions at five environments varied for rainfall and average monthly temperature during each growing season. In 2013 and 2014, Queenstown had more precipitation and higher average temperature than that of Clarksville. However, both of these two locations had less precipitation and lower average monthly temperature than that at Kinston 2014. In 2013, the precipitation at Clarksville was lower than that of 2014 but the average temperature was higher implying that 2013 was a relatively warmer and drier growing season. At Queenstown, the 2013 season had more precipitation and higher average monthly temperature than that of 2014.

Table 2.1 Growing season precipitation (cm) and average monthly temperature (°C) at five environments during 2013 and 2014.

Environments	Precipitation (cm)						Temperature (°C)					
	Feb.	Mar.	Apr.	May	Jun.	Total	Feb.	Mar.	Apr.	May	Jun.	Average
Queenstown 2013	6.1	9.3	11.8	4.9	24.9	57.1	2.0	5.1	12.7	17.7	23.0	12.1
Queenstown 2014	11.3	11.9	13.2	9.3	7.0	52.7	0.9	3.8	11.7	18.2	22.2	11.4
Clarksville 2013	5.0	6.5	4.7	9.0	12.7	37.9	0.6	3.8	11.8	16.5	21.9	10.9
Clarksville 2014	6.1	9.9	17.1	10.4	8.4	51.9	-1.2	2.4	10.7	17.2	22.2	10.3
Kinston 2014	6.5	14.2	11.0	8.9	26.3	67.0	8.4	9.8	17.9	22.9	25.4	16.9

Phenotypic performance

Analysis of variance (ANOVA) performed separately for each environment indicated significant differences ($P<0.001$) among all traits (data not shown). Combined ANOVA showed that genotype × environment interaction was significant ($P<0.001$) for GYLD, GWPS, SPSM, TGW, and GPS (Table 2.2). MDW233 had more SPSM while SS8641 had higher GPS, GWPS, and TGW across all five environments except for Clarksville 2014 where MDW233 produced slightly higher TGW than SS8641 (Table 2.2). For grain yield, MDW233 performed better in all four Maryland environments but not as well as SS8641 in Kinston 2014. Furthermore, SPSM had the most variation (measured by coefficient of variation) among all traits across five environments (Table 2.2). The DH lines showed transgressive segregation for all traits (Figure 2.1, Table 2.2). The heritability estimates were highest for thousand-grain-weight (0.92) and grain weight spike^{-1} (0.90) followed by spikes m-^{2} (0.84) and grains spike-1 (0.81), but was lowest for grain yield (0.74) (Table 2.4).

Correlation analysis (Table 2.3) showed consistently that grain yield was positively correlated with SPSM and TGW ($P<0.001$). The correlation between GYLD and GPS was positive at Queenstown 2014 but was negative at Clarksville 2013 and Clarksville

2014. In general, GYLD showed the strongest positive correlation with SPSM followed by TGW. SPSM was negatively correlated with GPS and GWPS in all five environments. TGW was positively correlated with GWPS and was negatively correlated with GPS in all five environments.

Table 2.2 Phenotypic summary of grain yield (GYLD, g m^{-2}), grains per spike (GPS), grain weight per spike (GWPS, g), spikes per square meter (SPSM), and thousand-grain-weight (TGW, g) evaluated in five environments during 2013 and 2014.

Environments	Traits	Parents		DHs				
		MDW233	SS8641	Mean	SD†	Minimum	Maximum	CV‡
Clarksville 2013	GYLD	671.4	598.6	566.7	110.9	268.7	1091.6	19.6%
	GPS	38.4	45.8	39.9	5.2	27.2	54.8	12.9%
	GWPS	1.2	1.5	1.2	0.2	0.9	1.7	15.0%
	SPSM	565.8	393.9	473.6	110.9	182.9	863.0	23.4%
	TGW	33.4	34.8	31.5	2.3	25.7	37.4	7.3%
Queenstown 2013	GYLD	712.0	664.8	736.6	144.4	363.4	1071.2	19.6%
	GPS	45.7	52.4	43.5	5.5	30.9	58.2	12.7%
	GWPS	1.5	1.8	1.4	0.2	1.0	2.0	12.9%
	SPSM	474.2	372.5	529.3	124.2	222.9	951.3	23.5%
	TGW	33.1	33.9	32.2	2.1	25.5	38.6	6.6%
Clarksville 2014	GYLD	830.2	740.0	787.3	106.1	473.2	1098.1	13.5%
	GPS	34.7	41.4	35.7	4.0	25.0	48.0	11.1%
	GWPS	1.0	1.3	1.0	0.1	0.6	1.4	14.3%
	SPSM	794.3	572.9	806.0	160.4	490.3	1257.7	19.9%
	TGW	30.7	30.3	29.4	2.5	15.8	36.6	8.4%
Queenstown 2014	GYLD	614.9	594.5	614.2	73.9	379.3	769.0	12.0%
	GPS	34.8	39.2	39.6	4.8	26.8	55.8	12.0%
	GWPS	1.0	1.2	1.1	0.1	0.8	1.5	13.0%
	SPSM	622.8	487.6	553.1	83.5	351.9	774.5	15.1%
	TGW	29.7	31.8	29.2	2.1	23.5	35.2	7.1%
Kinston 2014	GYLD	615.0	679.4	555.1	92.8	228.7	837.8	16.7%
	GPS	35.2	46.0	42.4	5.2	32.0	59.3	12.2%
	GWPS	1.1	1.5	1.2	0.1	0.7	1.6	12.5%
	SPSM	534.8	449.3	474.6	82.7	274.9	737.9	17.4%
	TGW	30.3	31.5	27.5	2.9	18.3	35.5	10.7%

† Standard deviation
‡ Coefficient of variation

Table 2.3 Pearson correlation coefficients among grain yield (GYLD), grains per spike (GPS), grain weight per spike (GWPS), spikes per square meter (SPSM), and thousand-grain-weight (TGW) in five environments during 2013 and 2014.

Environments	Traits	GPS	GWPS	SPSM	TGW
Clarksville 2013	GYLD	-0.20***	0.05	0.79***	0.33***
	GPS		0.75***	-0.62***	-0.15*
	GWPS			-0.54***	0.36***
	SPSM				0.06
Queenstown 2013	GYLD	-0.06	0.06	0.83***	0.21***
	GPS		0.82***	-0.50***	-0.22***
	GWPS			-0.48***	0.22***
	SPSM				0.09
Clarksville 2014	GYLD	-0.16***	-0.03	0.69***	0.29***
	GPS		0.64***	-0.57***	-0.24***
	GWPS			-0.70***	0.34***
	SPSM				-0.07
Queenstown 2014	GYLD	0.13*	0.22***	0.60***	0.21***
	GPS		0.77***	-0.52***	-0.30***
	GWPS			-0.62***	0.22***
	SPSM				-0.03
Kinston 2014	GYLD	-0.07	0.33***	0.74***	0.44***
	GPS		0.61***	-0.49***	-0.39***
	GWPS			-0.36***	0.36***
	SPSM				0.17**

* Significant at the 0.05 probability level.
** Significant at the 0.01 probability level.
*** Significant at the 0.001 probability level.

Table 2.4 Pooled analyses of variance over five environments and heritability estimates for grain yield (GYLD), grains per spike (GPS), grain weight per spike (GWPS), spikes per square meter (SPSM), and thousand-grain-weight (TGW) in five environments during 2013 and 2014.

		Mean squares				
Source of Variation	df	GYLD	GPS	GWPS	SPSM	TGW
Environment	4	2697855.85*	2260.17*	5.64*	4679695.46*	841.21*
Rep (environment)	5	100996.06*	179.67*	0.45*	429149.39*	8.00*
Genotype	123	40596.54*	136.50*	0.11*	47696.44*	38.96*
Genotype × environment	492	10475.85*	13.18*	0.02*	8954.60*	3.29*
R^2		0.85	0.85	0.86	0.88	0.95
Heritability (h^2) †		0.74 (0.04)	0.81 (0.03)	0.90 (0.01)	0.84 (0.02)	0.92 (0.01)

* Significant at the 0.001 probability level.
† Values in parenthesis are standard errors for h^2

Linkage map construction

The DH population was analyzed with 4981 markers that were polymorphic between the two parents (4956 SNPs, 24 SSRs and 1 morphological marker). A total of 4972 markers (99.8%) were assigned to 39 linkage groups representing all 21 wheat chromosomes (Table 2.5). After excluding co-segregating markers, the final genetic linkage map was constructed with 859 unique makers that spanned 1977.62 cM in length (Appendix A). The average interval length was 2.3 cM. Since the recommended map distance for QTL analysis is ten re-combinations per 100 meiotic events, or an interval length less than 10 cM (Doerge, 2002), the map is suitable for QTL analysis in this study.

Table 2.5 Distribution of markers and length of linkage maps for twenty one wheat chromosomes.

Chromosome	Number of markers	Length (cM)
1A	521	67.71
2A	298	112.3
3A	333	216.84
4A	272	158.28
5A	218	190.04
6A	242	95.05
7A	365	171.5
1B	257	144.13
2B	516	139.83
3B	488	134
4B	121	134.51
5B	430	123.21
6B	286	112.39
7B	245	177.83
1D	55	85.55
2D	116	125.93
3D	29	72.74
4D	8	76.77
5D	36	179.45
6D	81	144.64
7D	55	259.8

Table 2.6 Quantitative trait loci (QTLs), LOD score, percentage of variation explained (PVE), and additive effects of each QTL for grain yield (GYLD, g m^{-2}), grains per spike (GPS), grain weight per spike (GWPS, g), spikes per square meter (SPSM), and thousand-grain-weight (TGW, g) in five environments during 2013 and 2014.

QTL	Trait	Environment	Position (cM)	Marker interval	LOD score	PVE (%)	Additive effect
Qyld.cz-1A	GYLD	Clarksville 2013	0	*Xwmc496-Xsnp1970*	3.4128	7.4686	-25.6006
Qyld.cz-2A	GYLD	Kinston 2014	0	*Xsnp2477-Xsnp2432*	4.2968	9.9008	25.211
Qyld.cz-3A	GYLD	Clarksville 2014	0	*Xsnp3027-Xsnp3744*	3.0403	8.6136	-24.2575
Qyld.cz-6A	GYLD	Queenstown2014	75	*Xsnp4211-Xsnp4186*	3.455	9.7424	19.1153
Qyld.cz-1B	GYLD	Clarksville 2013	74	*Xsnp4928-Xsnp2107*	5.6376	13.2401	-35.0708
Qyld.cz-3B.1	GYLD	Kinston 2014	7	*Xbarc147-Xsnp3328*	4.5878	10.9125	-26.2832
Qyld.cz-3B.2	GYLD	Clarksville 2014	60	*Xsnp3382-Xsnp3372*	6.7965	21.2499	-38.2413
Qyld.cz-5B.1	GYLD	Clarksville 2013	66	*Xsnp4059-Xsnp4061*	5.5119	12.7278	-33.4221
Qyld.cz-5B.2	GYLD	Kinston 2014	115	*Xsnp4011-Xsnp4073*	4.4601	10.2934	25.6696
Qyld.cz-6B	GYLD	Kinston 2014	6	*Xsnp4444-Xsnp4453*	4.6423	10.9935	26.3474
Qyld.cz-2D	GYLD	Queenstown2013	54	*Xsnp2862-XPpdD1*	4.5148	17.7026	52.6542
Qyld.cz-6D	GYLD	Clarksville 2013	137	*Xsnp4465-Xsnp4487*	6.677	15.5547	-37.1149
QGps.cz-1A.1	GPS	Kinston 2014	1	*Xsnp1970-Xbarc28*	14.2219	26.511	2.439
QGps.cz-1A.2	GPS	Clarksville 2013	2	*Xbarc28-Xsnp2005*	21.1713	44.118	2.9461
QGps.cz-1A.2	GPS	Clarksville 2014	2	*Xbarc28-Xsnp2005*	11.0378	22.5923	1.6195
QGps.cz-1A.2	GPS	Queenstown2013	2	*Xbarc28-Xsnp2005*	12.5949	29.3932	2.681
QGps.cz-1A.2	GPS	Queenstown2014	2	*Xbarc28-Xsnp2005*	8.5734	18.1522	1.7105
QGps.cz-2A	GPS	Queenstown2014	40	*Xsnp2448-Xsnp2475*	4.6006	8.99	-1.2111
QGps.cz-3A.1	GPS	Kinston 2014	2	*Xsnp3048-Xsnp1466*	4.4227	6.9464	1.2484
QGps.cz-3A.2	GPS	Clarksville 2013	5	*Xsnp3049-Xsnp3021*	24.1227	51.9916	-3.1986
QGps.cz-3A.3	GPS	Clarksville 2013	124	*Xsnp3037-Xsnp3023*	5.1633	8.0188	1.264
QGps.cz-3A.4	GPS	Clarksville 2014	126	*Xsnp3023-Xsnp3383*	3.4903	6.0965	0.8454
QGps.cz-3A.4	GPS	Kinston 2014	126	*Xsnp3023-Xsnp3383*	5.269	8.2402	1.3662
QGps.cz-4A	GPS	Queenstown2014	138	*Xsnp3464-Xsnp3547*	3.2552	6.2726	1.0236
QGps.cz-2B	GPS	Queenstown2013	62	*Xsnp2752-Xsnp2786*	3.9483	7.8456	-1.3878
QGps.cz-3B.1	GPS	Kinston 2014	34	*Xsnp3344-Xsnp3253*	6.3159	10.277	1.5188
QGps.cz-3B.2	GPS	Queenstown2013	36	*Xsnp3253-Xsnp3349*	4.5431	9.3033	1.5085
QGps.cz-3B.3	GPS	Clarksville 2014	47	*Xsnp3119-Xsnp3395*	7.0831	13.3475	1.2462
QGps.cz-5B.1	GPS	Clarksville 2013	45	*Xsnp3973-Xsnp4062*	4.5948	6.7766	-1.1547
QGps.cz-5B.2	GPS	Queenstown2014	48	*Xsnp4083-Xsnp3988*	7.6516	15.9459	-1.6031
QGps.cz-5B.3	GPS	Clarksville 2014	58	*Xsnp3988-Xsnp1006*	5.6091	10.3121	-1.0956
QGps.cz-5B.4	GPS	Kinston 2014	68	*Xsnp4061-Xsnp4027*	6.9909	11.3158	-1.5936
QGps.cz-3D	GPS	Queenstown2014	72	*Xsnp3422-Xsnp3187*	3.8018	7.4961	-1.1211
QGws.cz-1A.1	GWPS	Clarksville 2013	0	*Xwmc496-Xsnp1970*	12.1722	28.5671	0.079
QGws.cz-1A.2	GWPS	Clarksville 2014	1	*Xsnp1970-Xbarc28*	11.5142	33.1833	0.0641
QGws.cz-1A.2	GWPS	Kinston 2014	1	*Xsnp1970-Xbarc28*	7.284	20.32	0.0599
QGws.cz-1A.2	GWPS	Queenstown2013	1	*Xsnp1970-Xbarc28*	11.28	32.2485	0.0937
QGws.cz-1A.3	GWPS	Queenstown2014	2	*Xbarc28-Xsnp2005*	5.0104	15.4379	0.0446
QGws.cz-3A	GWPS	Clarksville 2014	188	*Xsnp2984-Xsnp2934*	3.1047	7.4815	-0.0306
QGws.cz-5A	GWPS	Clarksville 2013	87	*Xsnp3843-Xsnp3820*	4.6284	9.4469	0.046
QGws.cz-5B	GWPS	Clarksville 2013	20	*Xsnp4130-Xsnp3884*	3.602	7.2761	-0.0398
QGws.cz-6B	GWPS	Kinston 2014	63	*Xsnp4421-Xsnp4451*	4.8634	13.2328	0.0483
QGws.cz-7B	GWPS	Clarksville 2014	58	*Xsnp4927-Xsnp489*	3.1066	7.472	0.0305

Table 2.6 Continued

QTL	Trait	Environment	Position (cM)	Marker interval	LOD score	PVE (%)	Additive effect
QSsm.cz-1A.1	SPSM	Clarksville 2013	0	Xwmc496-Xsnp1970	13.8851	30.1443	-50.8488
QSsm.cz-1A.1	SPSM	Clarksville 2014	0	Xwmc496-Xsnp1970	4.434	10.2247	-35.3148
QSsm.cz-1A.2	SPSM	Kinston 2014	1	Xsnp1970-Xbarc28	15.5894	22.0811	-34.0394
QSsm.cz-1A.3	SPSM	Queenstown2013	3	Xbarc28-Xsnp2005	8.2625	22.9784	-51.5593
QSsm.cz-1A.3	SPSM	Queenstown2014	2	Xbarc28-Xsnp2005	6.9139	15.2758	-25.0824
QSsm.cz-2A.1	SPSM	Kinston 2014	0	Xsnp2477-Xsnp2432	3.3285	3.7029	14.0568
QSsm.cz-2A.2	SPSM	Queenstown2014	75	Xsnp2382-Xsnp2401	4.8376	10.2491	20.7007
QSsm.cz-3A	SPSM	Kinston 2014	1	Xsnp3744-Xsnp3048	3.5396	3.9658	-14.4323
QSsm.cz-6A	SPSM	Clarksville 2014	81	Xsnp4197-Xsnp473	3.6434	8.2722	31.9406
QSsm.cz-1B.1	SPSM	Kinston 2014	8	Xsnp2205-Xsnp4503	3.241	3.6256	-13.836
QSsm.cz-1B.2	SPSM	Clarksville 2013	72	Xsnp4928-Xsnp2107	3.362	6.142	-23.355
QSsm.cz-3B.1	SPSM	Queenstown2014	24	Xsnp3405-Xsnp3389	5.7956	12.7812	-23.0253
QSsm.cz-3B.2	SPSM	Kinston 2014	31	Xsnp3389-Xsnp3344	5.9097	6.9082	-19.0795
QSsm.cz-3B.3	SPSM	Clarksville 2014	46	Xsnp3335-Xsnp3119	3.8828	8.9779	-33.1306
QSsm.cz-3B.4	SPSM	Kinston 2014	129	Xsnp3401-Xsnp3358	3.3933	3.8222	-14.2074
QSsm.cz-5B.1	SPSM	Clarksville 2013	75	Xsnp4072-Xsnp4085	3.1264	5.6471	-22.0261
QSsm.cz-5B.2	SPSM	Kinston 2014	116	Xsnp4011-Xsnp4073	5.1611	6.03	17.9303
QSsm.cz-6B	SPSM	Kinston 2014	3	Xsnp4456-Xsnp107	10.2874	13.4102	26.5311
QSsm.cz-2D	SPSM	Queenstown2013	57	Xsnp2862-XPpdD1	4.7473	12.6431	38.5899
QSsm.cz-3D	SPSM	Queenstown2014	57	Xsnp3422-Xsnp3187	4.858	10.5722	21.1958
QSsm.cz-6D	SPSM	Clarksville 2013	137	Xsnp4465-Xsnp4487	3.2886	5.8034	-22.4133
QTgw.cz-3A.1	TGW	Clarksville 2013	126	Xsnp3023-Xsnp3383	5.3262	8.2592	-0.6336
QTgw.cz-3A.2	TGW	Queenstown2013	136	Xsnp1758-Xsnp1485	6.4554	11.2965	-0.6975
QTgw.cz-3A.3	TGW	Queenstown2014	137	Xsnp1485-Xsnp2964	4.5797	9.3414	-0.6078
QTgw.cz-3A.4	TGW	Clarksville 2014	143	Xsnp2885-Xsnp2987	3.0018	4.914	-0.514
QTgw.cz-3A.5	TGW	Kinston 2014	147	Xsnp2937-Xsnp4728	4.9325	12.6304	-1.0067
QTgw.cz-3A.6	TGW	Clarksville 2013	208	Xsnp2951-Xsnp2971	4.2346	6.7403	-0.5712
QTgw.cz-5A.1	TGW	Kinston 2014	53	Xsnp218-Xsnp49	3.5745	8.8337	0.8469
QTgw.cz-5A.2	TGW	Clarksville 2013	58	Xsnp3838-Xbarc100	7.3695	11.6843	0.7601
QTgw.cz-5A.3	TGW	Clarksville 2014	60	Xbarc100-Xsnp4843	5.4004	9.237	0.7158
QTgw.cz-5A.3	TGW	Queenstown2013	61	Xbarc100-Xsnp4843	5.7471	10.1805	0.6715
QTgw.cz-7A.1	TGW	Queenstown2013	18	Xsnp4718-Xsnp4759	4.8786	8.2581	-0.5963
QTgw.cz-7A.2	TGW	Clarksville 2013	105	Xsnp4637-Xsnp4567	5.1786	8.0243	0.6267
QTgw.cz-7A.3	TGW	Queenstown2014	107	Xsnp4946-Xsnp4546	6.7631	14.7144	0.7671
QTgw.cz-7A.4	TGW	Clarksville 2014	115	Xsnp4935-Xsnp4622	5.7396	9.8599	0.7303
QTgw.cz-7A.5	TGW	Queenstown2013	123	Xsnp4588-Xsnp4620	26.7529	71.1913	-1.7692
QTgw.cz-1B.1	TGW	Clarksville 2013	85	Xsnp2084-Xsnp2113	6.3088	9.8591	-0.6978
QTgw.cz-1B.1	TGW	Clarksville 2014	86	Xsnp2084-Xsnp2113	3.6645	6.0751	-0.5787
QTgw.cz-1B.2	TGW	Queenstown2014	87	Xsnp2113-Xsnp2091	3.6309	7.2769	-0.5424
QTgw.cz-2B	TGW	Clarksville 2014	58	Xbarc10-Xsnp2744	6.1855	10.8214	0.7626
QTgw.cz-2B	TGW	Kinston 2014	58	Xbarc10-Xsnp2744	4.7936	12.1618	0.9873
QTgw.cz-4B	TGW	Queenstown2013	75	Xsnp3721-Xsnp1656	4.2407	7.1261	0.5646
QTgw.cz-7B.1	TGW	Clarksville 2014	58	Xsnp4927-Xsnp489	5.7036	10.3833	0.747
QTgw.cz-7B.1	TGW	Queenstown2013	58	Xsnp4927-Xsnp489	3.0727	5.3189	0.4786
QTgw.cz-7B.2	TGW	Clarksville 2013	63	Xsnp838-Xsnp4852	7.3537	11.8238	0.7572
QTgw.cz-7B.3	TGW	Queenstown2014	65	Xsnp4852-Xsnp4943	4.2808	9.5333	0.6163
QTgw.cz-5D	TGW	Clarksville 2013	95	Xsnp4170-Xsnp4157	3.6356	5.4776	0.5138

QTL with additive and additive × environment interaction effects

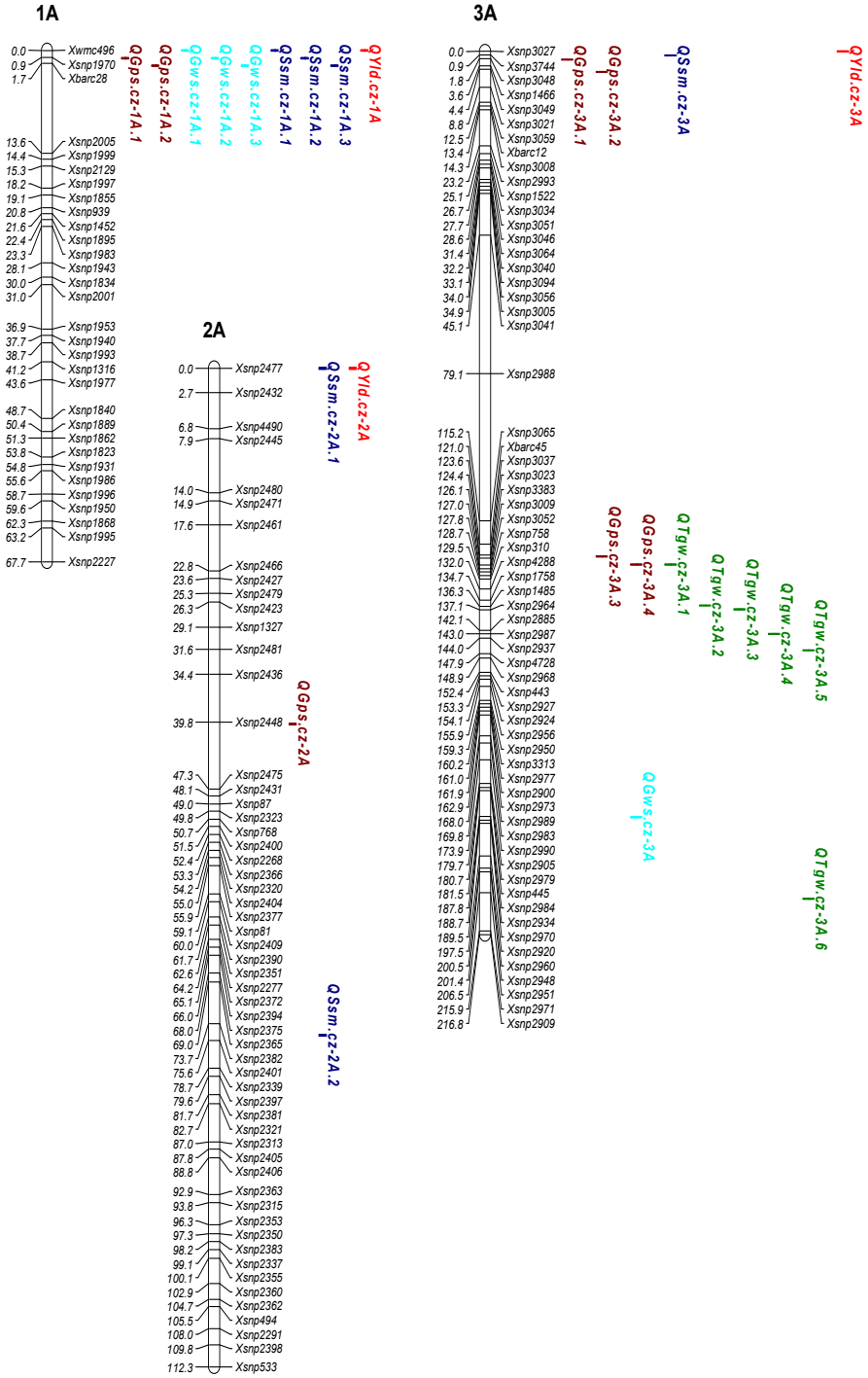
ICIM-ADD mapping detected a total of 64 putative QTLs for grain yield and yield components at five environments (Table 2.6). Significant QTLs were detected on all chromosomes except 1D, 4D, and 7D. QTLs were unevenly distributed across the three homoeologous groups and twenty one chromosomes of wheat. Thirty QTLs (46.9%) were in the A genome, also 30 QTLs (46.9%) were in the B genome, and only 4 (6.3%) were in the D genome. Distribution of QTLs was also unbalanced on chromosomes among homologous chromosome groups as follows: 7 on chromosomes 1 (11.1%), 6 on chromosomes 2 (9.4%), 22 on chromosomes 3 (34.4%), 2 on chromosomes 4 (3.1%), 13 on chromosomes 5 (20.3%), 6 on chromosomes 6 (9.4%), and 8 on chromosomes 7 (12.5%).

The number of QTL for individual traits ranged from 8 to 22. Specifically, 12 QTL were identified for grain yield and each of them explained 7.5% to 21.3% of the phenotypic variation; 17 QTL were identified for grains spike^{-1} explaining 6.1 % to 44.1% of the phenotypic variation; 19 QTL were detected for spikes m^{-2} and 8 QTL were for grain weight spike^{-1} accounting for 3.7% to 15.6% and 7.3% to 33.2% of the phenotypic variation respectively; 22 significant QTL were found to explain 5.5% to 71.2% of the phenotypic variation of thousand grain weight. In addition, 11 marker intervals where QTL co-location existed were estimated to have pleiotropic effects. Among all QTL identified, 6 QTL were repeatedly detected in more than one environment.

Additive × environment interaction effects were detected for all traits evaluated except for TGW. Of the five significant QTLs, three were detected with additive main effects in previous single environment mapping and the other two were insignificant (LOD<3) for additive main effects, hence, were environment-specific QTLss (Table 2.7). The heritability of additive × environment interactions ranged from 0.2% to 27.4%. Clarksville 2013 had the most additive × environment interactions, followed by Queenstown 2014. One additive × environment interaction was detected for Clarksville 2014 and Kinston 2014 and none were detected for Clarksville 2013.

QTL with epistatic and epistasis × environment interaction effects

A total of 7 pairs of significant epistatic interactions (*P<0.001*) were identified across five environments for yield and yield components except for SPSM (Table 2.8). The epistatic interactions were observed within and across chromosomes (mostly in the A and B genome) with heritability ranging from 0.2% to 6% and 0.1% to 2.7% for epistatic and epistatic × environment interaction effects, respectively. The only significant epistatic × environment interaction identified in this study was in Queenstown 2013. Furthermore, two marker intervals *Xbarc28-Xsnp2005* and *Xsnp3253-Xsnp3349*, had already been detected for significant additive effects (Table 2.6) while the rest were detected only for epistatic interactions.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62.3 Xsnp1868
63.2 Xsnp1995
67.7 Xsnp2227
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QGws.cz-1A.2
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QSsm.cz-1A.1
QSsm.cz-1A.2
QSsm.cz-1A.3
QYld.cz-1A
2A
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6.8 Xsnp4490
7.9 Xsnp2445
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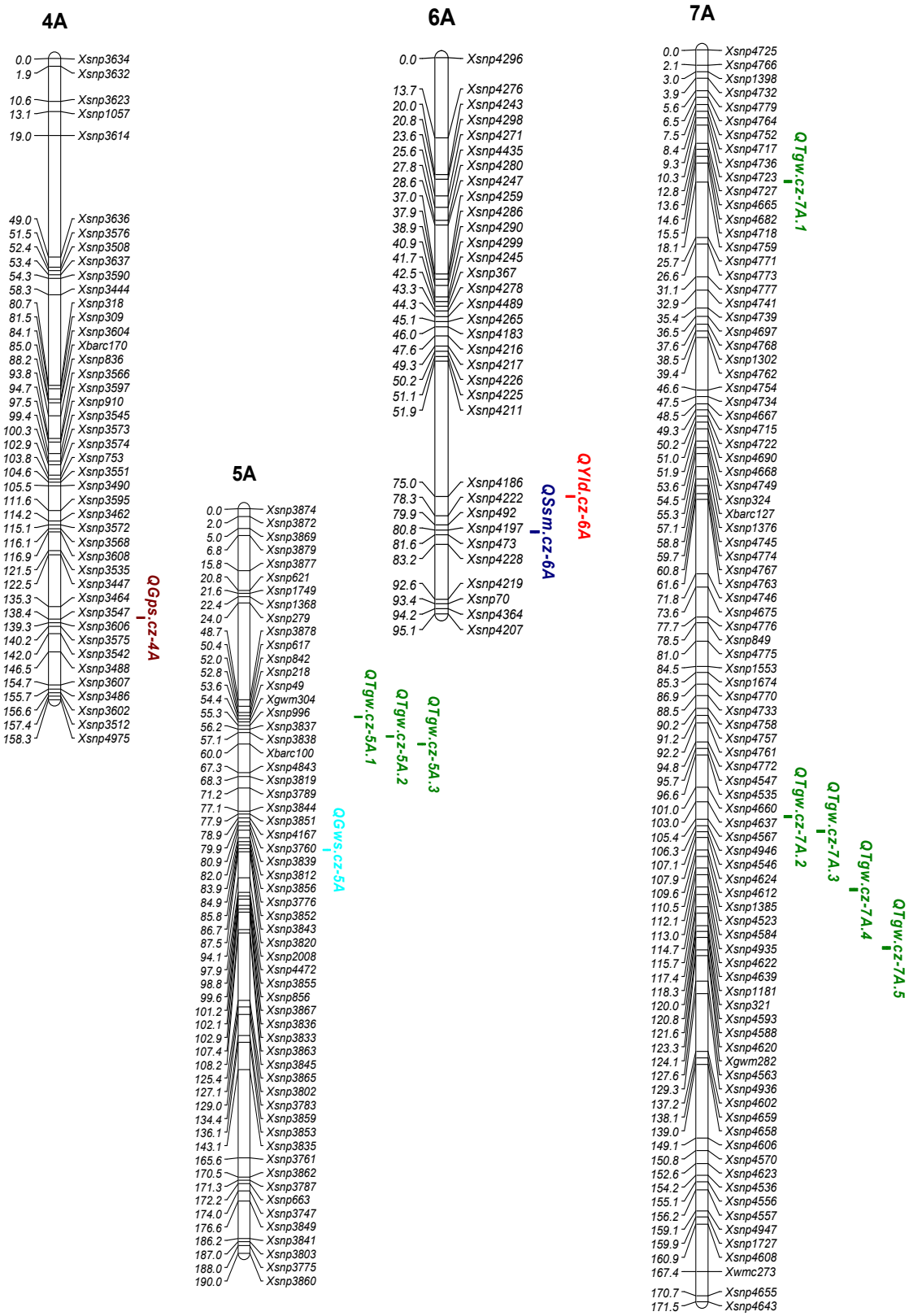
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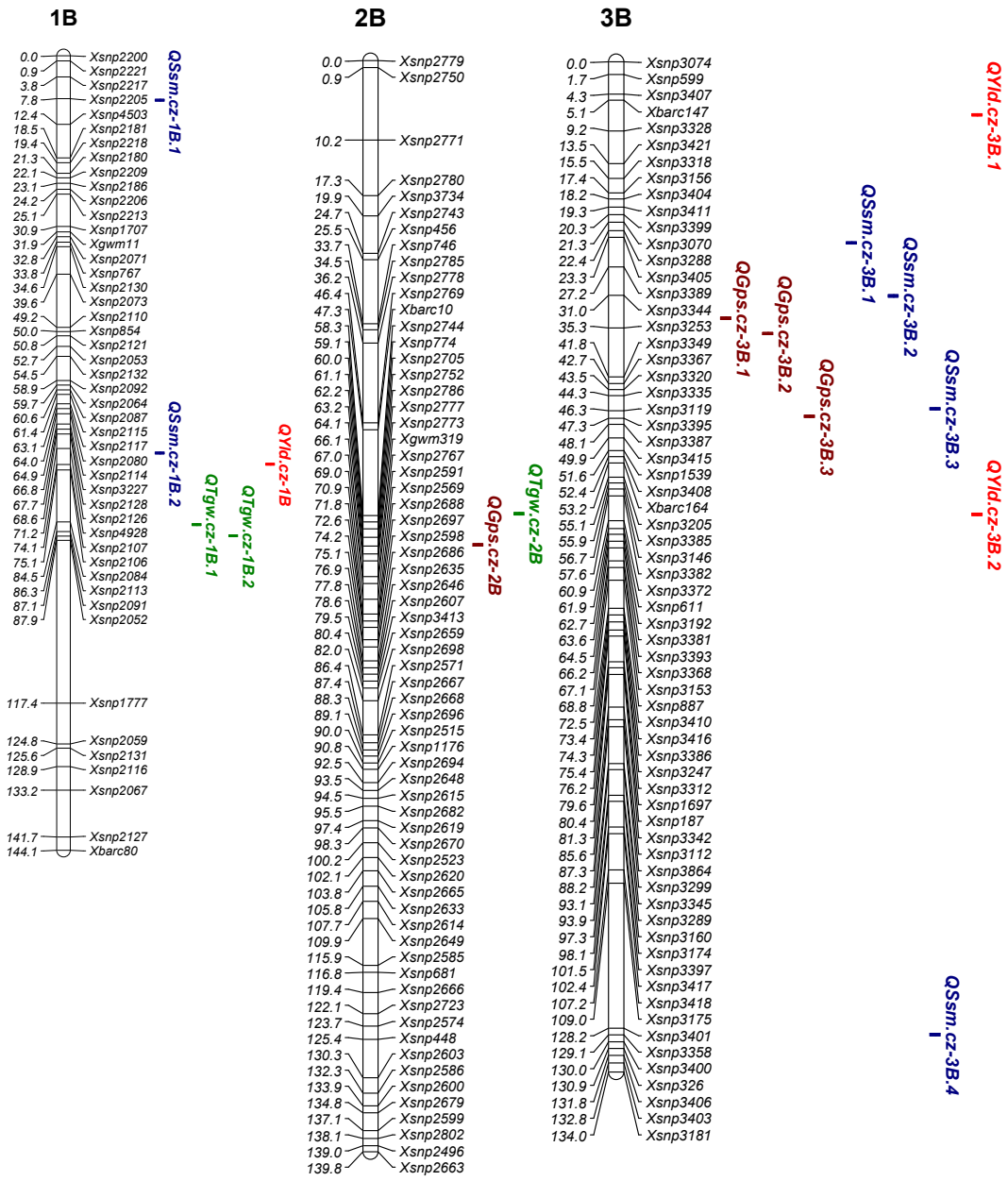
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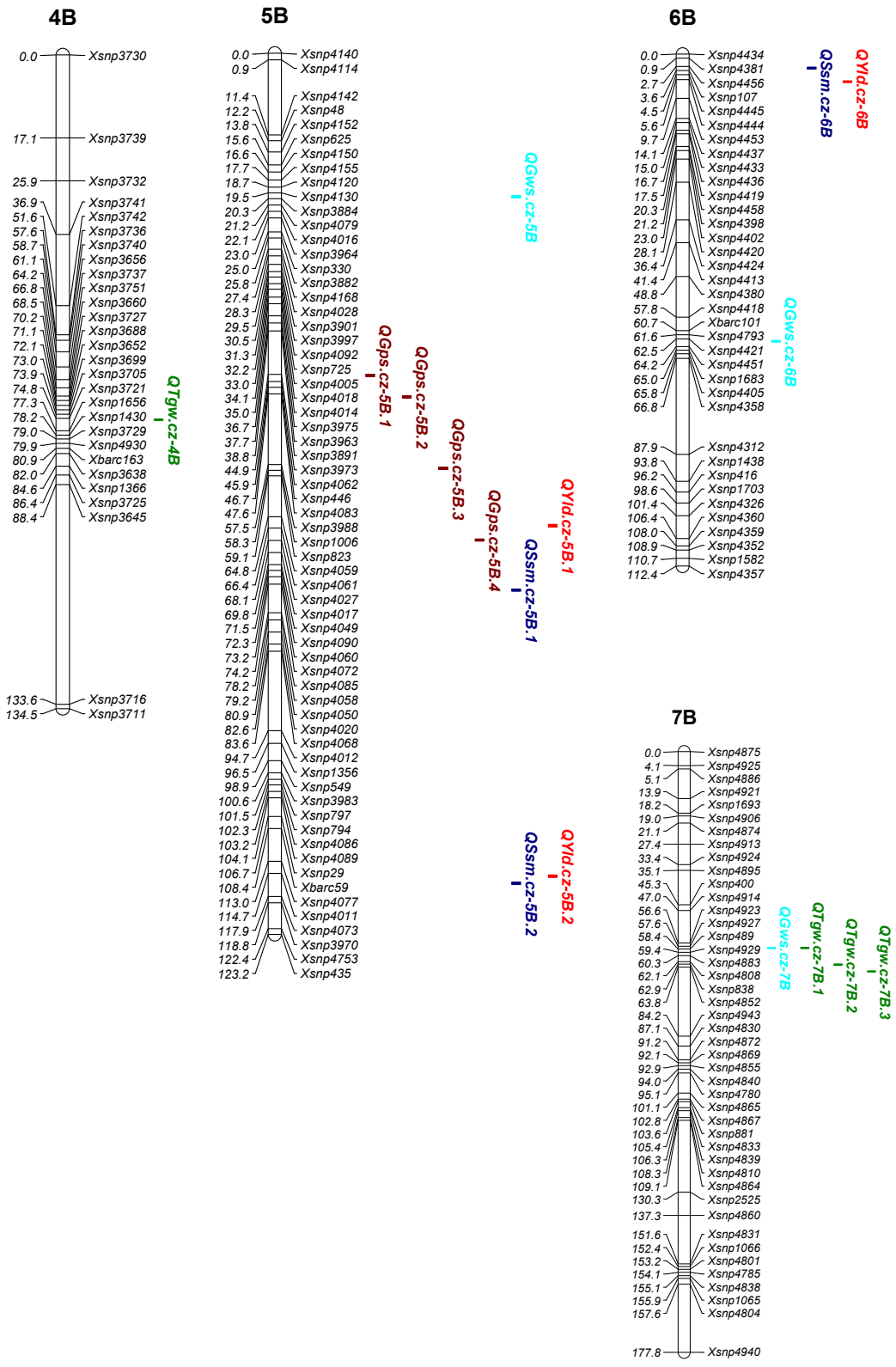
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61.1 Xsnp3656
64.2 Xsnp3737
66.8 Xsnp3751
68.5 Xsnp3660
70.2 Xsnp3727
71.1 Xsnp3688
72.1 Xsnp3652
73.0 Xsnp3699
73.9 Xsnp3705
74.8 Xsnp3721
77.3 Xsnp1656
78.2 Xsnp1430
79.0 Xsnp3729
79.9 Xsnp4930
80.9 Xbarc163
82.0 Xsnp3638
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86.4 Xsnp3725
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133.6 Xsnp3716
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5B
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12.2 Xsnp48
13.8 Xsnp4152
15.6 Xsnp625
16.6 Xsnp4150
17.7 Xsnp4155
18.7 Xsnp4120
19.5 Xsnp4130
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22.1 Xsnp4016
23.0 Xsnp3964
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30.5 Xsnp3997
31.3 Xsnp4092
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34.1 Xsnp4018
35.0 Xsnp4014
36.7 Xsnp3975
37.7 Xsnp3963
38.8 Xsnp3891
44.9 Xsnp3973
45.9 Xsnp4062
46.7 Xsnp446
47.6 Xsnp4083
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78.2 Xsnp4085
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82.6 Xsnp4020
83.6 Xsnp4068
94.7 Xsnp4012
96.5 Xsnp1356
98.9 Xsnp549
100.6 Xsnp3983
101.5 Xsnp797
102.3 Xsnp794
103.2 Xsnp4086
104.1 Xsnp4089
106.7 Xsnp29
108.4 Xbarc59
113.0 Xsnp4077
114.7 Xsnp4011
117.9 Xsnp4073
118.8 Xsnp3970
122.4 Xsnp4753
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QGps.cz-5B.1
QGps.cz-5B.2
QGps.cz-5B.3
QGps.cz-5B.4
QGws.cz-5B
QYld.cz-5B.1
QSsm.cz-5B.1
QYld.cz-5B.2
QSsm.cz-5B.2
6B
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2.7 Xsnp4456
3.6 Xsnp107
4.5 Xsnp4445
5.6 Xsnp4444
9.7 Xsnp4453
14.1 Xsnp4437
15.0 Xsnp4433
16.7 Xsnp4436
17.5 Xsnp4419
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41.4 Xsnp4413
48.8 Xsnp4380
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QSsm.cz-6B
QYld.cz-6B
QGws.cz-6B
7B
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137.3 Xsnp4860
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155.9 Xsnp1065
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QTgw.cz-7B.1
QTgw.cz-7B.2
QTgw.cz-7B.3

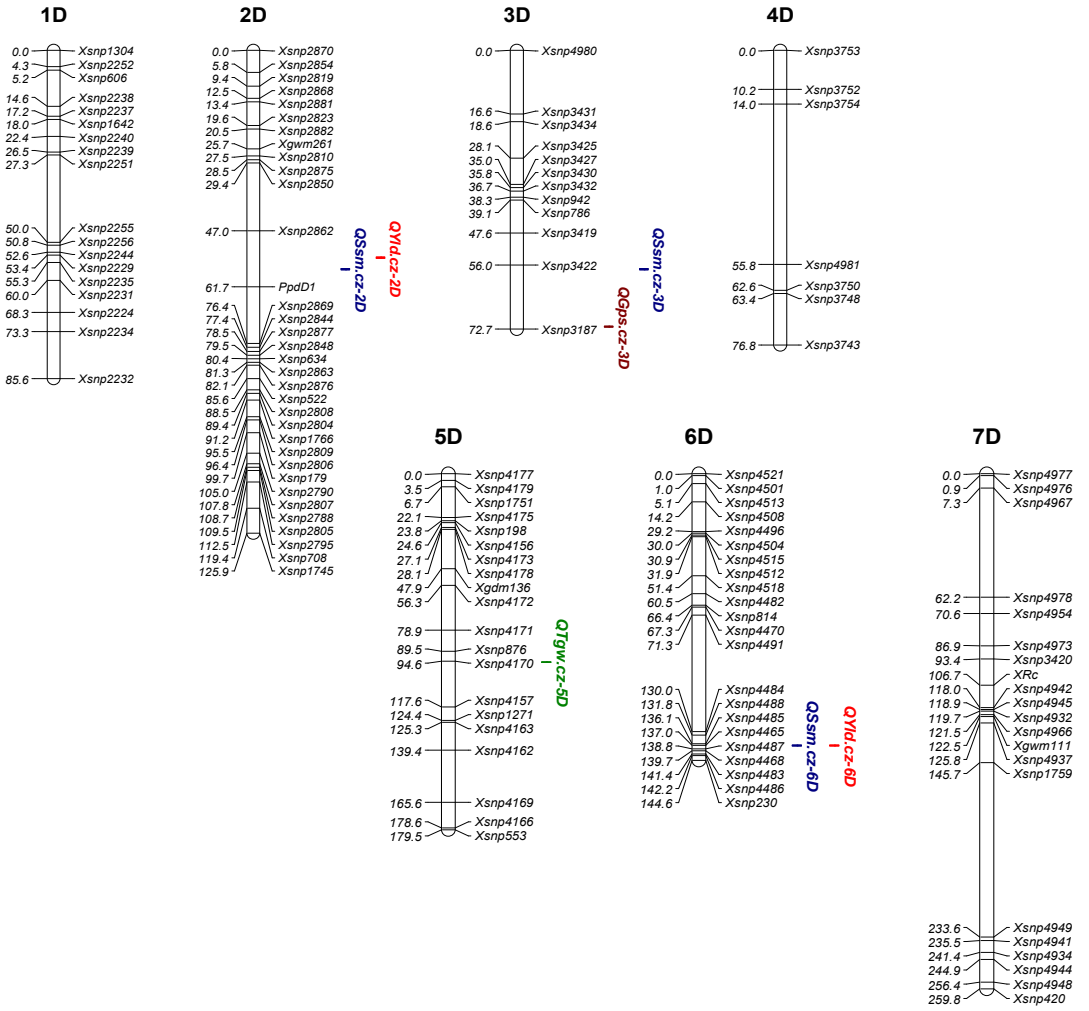


Figure 2.1 Genetic linkage map and position of quantitative trait loci (QTLs) detected in a doubled haploid mapping population derived from MD01W233-06-1 × SS8641. Locus marker names are shown on the right side of the chromosomes and values to the left of chromosomes show the genetic distance (cM) for each marker. QTLs are labeled with trait abbreviations and the QTL number for each trait. QTLs for the same trait are in the same color.

Table 2.7 QTL × Environment interactions influencing grain yield (GYLD), grains per spike (GPS), grain weight per spike (GWPS), spikes per square meter (SPSM), and thousand-grain-weight (TGW) in five environments during 2013 and 2014.

Trait	Chr.	Position	Interval	AE1†	AE2†	AE3†	AE4†	AE5†	$h^2(ae)$‡
GYLD	2A	23.6	*Xsnp2427-Xsnp2479*			-15.27*		12.78*	0.002
GYLD	2A	88.8	*Xsnp2406-Xsnp2363*			19.00**			0.030
GPS	1A	3.7	*Xbarc28-Xsnp2005*§			0.52*	-0.66**		0.274
SPSM	1A	1.7	*Xbarc28-Xsnp2005*§				12.87*		0.217
SPSM	3B	46.2	*Xsnp3119-Xsnp3395*§		-14.30*				0.099

† AE is the additive × environment interaction effect at each environment. E1: Clarksville 2013; E2: Clarksville 2014; E3: Queenstown 2013; E4: Queenstown 2014; E5: Kinston 2014.
‡ h^2 (ae) is heritability estimate of the additive × environment interaction effect across five environments.
§ Interval with significant additive effect.
* Significantly different from zero at the 0.05 probability level.
** Significant difference from zero at the 0.01 probability level.

Table 2.8 Chromosome locations of digenetic epistatic QTLs for grain yield (GYLD), grains per spike (GPS), grain weight per spike (GWPS), spikes per square meter (SPSM), and thousand-grain-weight (TGW) in five environments in 2013 and 2014.

Trait	Interval†	Chr†	Position†	Interval‡	Chr‡	Position‡	AA§	E1¶	E2¶	E3 ¶	E4 ¶	E5¶	h^2(aa) #	h^2(aae) ††
GYLD	*Xsnp4749-Xsnp324*	7A	53.6	*Xsnp3312-Xsnp1697*	3B	76.2				23.79***			0.2%	2.7%
GYLD	*Xsnp4171-Xsnp876*	5D	83.9	*Xsnp4518-Xsnp4482*	6D	56.4	17.11***						2.5%	0.9%
GPS	*Xbarc28-Xsnp2005*‡‡	1A	3.7	*Xsnp1006-Xsnp823*	5B	58.3	-0.50***						1.5%	0.5%
GPS	*Xsnp4715-Xsnp4722*	7A	49.3	*Xsnp2780-Xsnp3734*	2B	17.3	-0.46***						1.5%	0.6%
GWPS	*Xsnp2956-Xsnp2950*	3A	155.9	*Xsnp2571-Xsnp2667*	2B	86.4	0.03***						3.5%	0.9%
TGW	*Xsnp4050-Xsnp4020*	5B	80.9	*Xsnp4451-Xsnp1683*	6B	64.2	0.29***						3.1%	0.1%
TGW	*Xsnp3253-Xsnp3349*‡‡	3B	35.3	*Xsnp3175-Xsnp3401*	3B	120	0.65***						6.0%	0.1%
TGW	*Xsnp3645-Xsnp3716*	4B	114.4	*Xsnp4948-Xsnp420*	7D	256.4	-0.58***						4.3%	0.1%

† The flanking markers, chromosome and position of the first interval involved in the epistasis.
‡ The flanking markers, chromosome and position of the second interval involved in the epistasis.
§ The additive × additive effect.
¶ The epistasis × environment effect at each environment. E1: Clarksville 2013; E2: Clarksville 2014; E3: Queenstown 2013; E4: Queenstown 2014; E5: Kinston 2015.
# The heritability estimates for additive × additive interaction effects across five environment.
†† The heritability estimates for epistasis × environment interaction effects across five environments.
‡‡ Interval with significant additive effect.
*** Significantly different from zero at the 0.001 probability level.

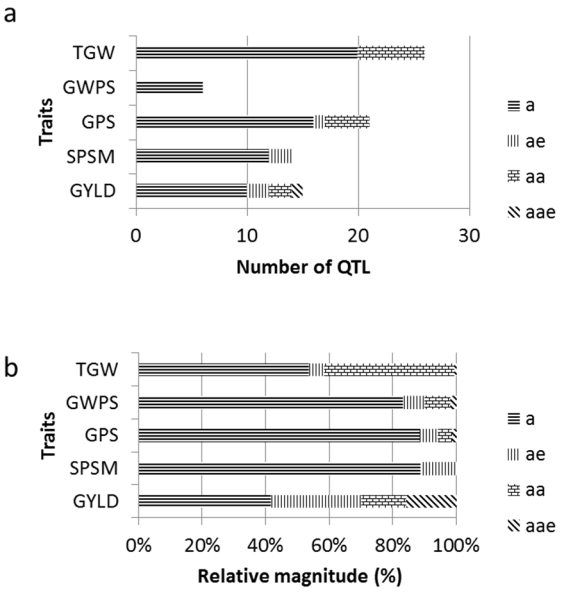


Figure 2.2 Distribution of genetic and non-genetic components for grain yield and yield related traits: grain yield (GYLD), spikes m^{-2} (SPSM), grains per spike (GPS), grain weight per spike (GWPS), thousand-grain-weight (TGW). a) total number of QTLs detected for additive (*a*), additive × environment (*ae*), epistasis (*aa*), and epistasis × environment interactions (*aae*) effects. b) relative magnitude of *a*, *ae*, *aa*, and *aae* effects.

Discussion

Grain yield and yield components are complex quantitative traits determined by genetic components, environmental factors, and the interaction between them (Cooper et al., 2009; Eeuwijk, 2008; Holland, 2007; Mackay, 2001). In this study, I used a mixed linear model to investigate the genetic basis of grain yield and yield components in a DH population of 124 lines by dividing genetic effects into additive main effect (A), additive × additive epistatic main effects (A×A or Q×Q), and their environmental interaction effects (A×E, AA×E or Q×E, QQ×E) (Wang et al., 1999; Yang et al., 2007). As single environment experiment could underestimate the number of QTL controlling a certain trait, whereas repeated experiments are useful in detecting stable QTL over environments (Paterson et al., 1991), I evaluated the DH population and parents in five environments in the US East Coast. For genotyping, I relied mostly on SNPs by using the 9K SNP array and GBS in addition to SSRs to get more coverage of the wheat genome. The map contained 4972 polymorphic markers and is highly consistent with the previously published 9K SNP consensus map (Cavanagh et al., 2013). The rank correlation coefficient between them was as high as 0.99 for most chromosomes in terms of SNP order (data not shown). Furthermore, the average interval length of the map (2.3 cM) was much smaller than that observed in previous studies (Carter et al., 2011; Heidari et al., 2011; Li et al., 2013), indicating a better resolution.

QTLs for grain yield

In this study, grain yield was defined as yield m^{-2} as reported by previous researchers (Heidari et al., 2011; Lopes et al., 2013). Twelve grain yield QTLs were detected (Table 2.6). Both parents carried favorable QTL alleles. Seven loci of MDW233 alleles increased grain yield on 1A, 3A, 3B, 5B, 6D, accounting for 7.5 to 21.3% of the phenotypic variation. The SS8641 alleles were associated greater grain yield at the other five loci on 2A, 6A, 5B, 6B, 2D, accounting for 9.7 to 17.7% of the phenotypic variation. Grain yield was the only trait that had no stable QTL detected over five environments in this study. This was expected as similar results were obtained by Kumar et al. (2007) and Li et al. (2007b), verifying that grain yield is strongly influenced by environment. Furthermore, QTL is a genomic region that may contain several functional genes or sub-QTLs that are closely linked and may have opposite genetic effects and as well as being subject to environmental influences (Mackay et al., 2009). The detection of a QTL indicates that the net effects of all sub-QTLs within it are significant whereas a non-significant QTL may still contain significant sub-QTLs (Mackay et al., 2009). Therefore, increasing marker density and population size would allow for the discovery of more QTLs as well as develop more detailed insights into the genetic basis of quantitative traits in this DH population.

Eight QTL (*QYld.cz-1B, QYld.cz-3B.1, QYld.cz-3B.2, QYld.cz-5B.1, QYld.cz-5B.2, QYld.cz-6B, QYld.cz-2D, QYld.cz-6D*) explained more than 10 % of the phenotypic variation of grain yield (Table 2.6). The QTL *QYld.cz-3B.2* was detected at

Clarksville 2014 with LOD=6.8 and the effect of MDW233 allele was very large accounting for the highest genetic variation for gain yield (PVE=21.3%). In this region, Bennett et al. (2012a) and Bennett et al. (2012b) also reported QTLs for grain yield, spike length, thousand grain weight repeatedly in heat, drought and high yield potential environments and Zhang et al. (2010) identified two meta-QTLs for grain yield and yield associated traits in a meta-QTL analysis based on 59 independent studies. Other studies also identified QTLs for plant height, harvest index, isotope discrimination, and canopy temperature in this region (Bennett et al., 2012b; Cuthbert et al., 2008; Kumar et al., 2007; Rebetzke et al., 2008). To date, the region where *QYld.cz-3B.2* resides appears to have pleiotropic effect on grain yield and should be given high priority for fine mapping and candidate gene identification, so that diagnostic gene-specific markers can be developed and utilized within breeding programs.

QYld.cz-2D (LOD=4.5148, PVE=17.7%) was flanked by *Xsnp2862* and *Ppd-D1*. *Ppd-D1* is a photoperiod-sensitivity gene that largely confers wheat dominant insensitivity to short day length. It enhances grain yield by allowing earlier heading under the short days of spring so that grain-filling can occur before heat and drought stress often associated with late summer (Nelson et al., 2006). Moreover, a recent study showed that *Ppd-D1* controlled photoperiod dependent floral induction in wheat and had a major inhibitory effect on paired spikelet formation by regulating the expression of *FLOWERING LOCUS T* (*FT*) (Boden et al., 2015). The yield-increasing effect of *QYld.cz-2D* may be due to the pleiotropic effect of *Ppd-D1*.

QYld.cz-3B.1 (LOD=4.6, PVE=10.9%) was mapped on the short arm of chromosome 3B and may be related to the one detected by Li et al. (2007b). Another well-known QTL, *Qfhs.ndsu-3BS* (also known as resistance gene *Fhb1*), is located in the same region (Schweiger et al., 2013). This suggests a possible new way to improve wheat disease resistance and grain yield by deploying this genomic region in breeding lines. Additionally, QTL *QYld.cz-1A* was in a region similar to that identified by Heidari et al. (2011) which controlled the expression of both grains per spike and grain weight per spike. Previous studies also detected QTL for grain yield in similar regions for *QYld.cz-3A* (Campbell et al., 2003; Mengistu et al., 2012), *QYld.cz-1B* (Huang et al., 2003), *QYld.cz-5B.1* (Bennett et al., 2012b), *QYld.cz-6A* (Kuchel et al., 2007b; Simmonds et al., 2014), *QYld.cz-6B* (Marza et al., 2006), and *QYld.cz-6D* (Kumar et al., 2007). Yield QTLs reported by Kumar et al. (2007) and Groos et al. (2003) were located in a region more than 10 cM away from *QYld.cz-2A* and *QYld.cz-5B.2*, respectively. This suggests that *QYld.cz-2A* and *QYld.cz-5B.2* may be new QTLs or this could be due to the difference in linkage map resolution.

QTLs for yield components

In this study, TGW had the highest heritability and number of QTLs among all traits evaluated (Table 2.4 and 2.6). Of the twenty-two QTLs identified, four were detected in more than one environment. They were located on chromosomes 5A, 1B, 2B, and 7B. However, the strongest QTL was on chromosome 7A, designated as *QTgw.cz-7A.5*, and explained up to 71.2% of the variation of TGW in Queenstown 2013. The positive allele for this QTL was from MDW233, the parental line with the lower

TGW. Similarly, Groos et al. (2003) also reported a stable QTL in this region for TGW explaining 5.2 to 10.3% of the phenotypic variation across seven trials. Thus, *QTgw-7A.5* may be the underlying QTL in both studies. Four QTL clusters were found on 3A, 1B, 5A and 7B as QTLs on those chromosomes were detected in proximity to each other and exhibited the same direction of genetic effects (Cai and Morishima, 2002). Specifically, favorable allelic clusters on 3A and 1B came from MDW233 while those alleles from SS8641 were associated with higher TGW for the allelic clusters on 5A and 7B. Extensive studies have focused on 3A, which is known to contain QTL/genes controlling grain yield and associated traits, and several loci for TGW were identified (Dilbirligi et al., 2006; Mengistu et al., 2012; Rustgi et al., 2013). However, after a close comparison of previous results, I found that *QTgw.cz-3A.6* appeared to be a new QTL for TGW since no TGW QTLs were reported in this region before. Clusters/QTL have also been reported in similar regions for the ones on 3A (Huang et al., 2004), 5A (Cuthbert et al., 2008), 7B (Hai et al., 2008; Huang et al., 2003),1B (Huang et al., 2004), *QTgw.cz-2B* (Hai et al., 2008), *QTgw.cz-5D* (Li et al., 2007b).

QTLs for GPS have been identified on all wheat chromosomes (Tang et al., 2011; Wu et al., 2012; Zhang et al., 2010). In the present study, several major GPS QTLs on 1A, 3A and 5B were detected and formed QTL clusters. The QTL cluster on 1A was detected in all five environments and explained 18.2 to 44% of the phenotypic variation. Heidari et al. (2011) found the same region significantly associated with GPS but with less PVE. The QTL cluster (*QGps.cz-3A.1* and *QGps.cz-3A.2*) at the

distal end short arm of 3A is comparable with the region identified for GPS, GYLD, and TGW by Campbell et al. (2003). *QGps.cz-3A.2* had the most influence on GPS (PVE=52%) and its SS8641 allele decreased GPS, which was opposite to the effect of *QGps.cz-3A.1*. This may be due to environmental difference and Q × E interaction where *QGps.cz-3A.1* was detected in a warmer location with more precipitation whereas *QGps.cz-3A.2* was detected in a cooler location with less precipitation. The other cluster on 3A was located next to *Xbarc45*, a marker 8 cM away from *Xwmc664* according to the high-density microsatellite consensus map (Somers et al., 2004). Mengistu et al. (2012) found *Xwmc664* to be the most significant marker for GPS QTL *QKps.neb-3A.1* in a recombinant inbred line population derived from cultivar Cheyenne and its 3A substitution line and that *QKps.neb-3A.1* was in a cluster with nearby QTL. Therefore, it is supposed that the cluster on 3A may represent the same cluster identified by Mengistu et al. (2012). Moreover, Li et al. (2007b) detected two QTLs at the distal end of 3AS. Its estimated position on the microsatellite consensus map was approximately 40 cM based on the information of *Xgwm77* (Somers et al., 2004). The cluster identified in this study (*QGps.cz-3B.1*, *QGps.cz-3B.2*, and *QGps.cz-3B.3*) was positioned in the same region, suggesting those two clusters may be the same. Another cluster of QTLs with similar influence on GPS was on 5B and the genetic effects of those QTLs were in the same direction. Marza et al. (2006) detected the same region in six environments explaining 18.5% of the phenotypic variation of GYLD. These findings suggested that this cluster improved grain yield by modifying GPS. Additionally, QTLs for GPS or other yield traits have been reported in or close to *QGps.cz-2A* (Li et al., 2007b), *QGps.cz-2B* (Marza et al.,

2006), *QGps.cz-4A (Kirigwi et al., 2007)*, *QGps.cz-4A(Huang et al., 2004)*, and *QGps.cz-3D* (Quarrie et al., 2005).

Multiple environment experiments allowed the identification of eight QTLs for GWPS in five environments (Table 2.6). Three closely linked QTLs in which SS8641 alleles increased GWPS were located on 1A and were the strongest QTL associated with GWPS explaining 15.4 to 33.2% of the phenotypic variation. Additional evidence of QTL for GWPS was reported in 3A, 5A and 6B (Zhang et al., 2010). A summary of preceding studies showed that chromosomes 5B and 7B had the fewest number of QTL for yield and yield associated traits (Zhang et al., 2010). Thus, it was not surprising to find no QTLs previously reported in the region of *QGws.cz-5B* and *QGws.cz-7B*.

Under current agricultural production systems, improving spikes m^{-2} or grains m^{-2} rather than other yield components has been generally agreed to be the key to raising grain yield potential worldwide (Gaju et al., 2009). Therefore, QTL analysis for SPSM has been the target of many studies. Heidari et al. (2011) reported QTLs for SPSM on 1A, 7A, and 2D in a DH population. The QTLs they reported on 1A are comparable to the ones identified at the distal end of 1AS in this study. Marza et al. (2006) found 1B, 4A, 7B and 7D to be associated with SPSM in a wheat population derived from Ning7840 × Clark, where the QTL on 1B was located in the similar region of *Qsm.cz-1B.1* I detected in this study. Similarly, additional SPSM QTLs were located in the region previously described by Huang et al. (2004) on

chromosome 1B, Groos et al. (2003) on chromosome 3B, Bennett et al. (2012b) on chromosomes 3B and 5B, Campbell et al. (2003) on chromosome 3A, Huang et al. (2003) on chromosomes 2A, 2D, and 6D.

Pleiotropic effects of QTLs

Correlated traits are often affected by pleiotropic effects of the same QTL/gene(s) or closely linked QTL/gene(s), which would enable the selection of a complex trait via a closely correlated single trait (Hai et al., 2008). In the present study, a significant positive correlation was observed between GYLD and SPSM in all five environments (Table 2.3) and five loci with genetic effect of same direction were detected for GYLD and SPSM (Table 2.6). Favorable alleles came from both parents. The MDW233 allele increased GYLD and SPSM at *QYld.cz-1A*/*QSsm.cz.-1A.1*, *QYld.cz-1B*/*QSsm.cz.-1B.2*, and *QYld.cz-6D*/*QSsm.cz.-6D* while the SS8641 allele improved GYLD and SPSM jointly at *QYld.cz-2A*/*QSsm.cz.-2A.1* and *QYld.cz-2D*/*QSsm.cz.-2D*. The negative correlation between SPSM and both GWPS and GPS may be due to the pleiotropic effects of loci flanked by *Xbar28-Xsnp2005* which increased SPSM but decreased GWPS and GPS or vice versa. These findings supported the existence of a QTL with pleiotropic effect and provided a genetic explanation of observed phenotypic correlation. Although a significant positive correlation was also observed between GYLD and TGW, no pleiotropic QTL was detected. This may indicate that the expression of GYLD was through TGW and conditional mapping was needed to investigate the underlying mechanism (Zhu, 1995).

Q×E and QQ×E interactions

Generally, a QTL with low or no Q × E interaction can be utilized in a broad range of environments, whereas a QTL with significant Q × E interaction can only be used in the specific environment in which it is detected (Zhao and Xu, 2012). In this study, the DH population was evaluated in five environments spanning two crop years. Two loci for SPSM, Two for GY and 1 for GPS showed significant additive × environment interaction. The majority of the significant Q × E effects were found in Queenstown 2013 and Queenstown 2014. Those two environments had relative higher precipitation and average monthly temperature during the growing season indicating that high rainfall and temperature may contribute to Q × E expression in this study. The intervals *Xsnp2427-Xsnp2479* and *Xbar28-Xsnp2005* were detected for Q × E interactions in two environments with opposite effects confirming that the QTL effects were subject to change due to environments and that the environment suitable for the expression of one QTL may not be suitable for another QTL. The SS8641 allele of the locus located in *Xbar28-Xsnp2005* was found to be pleiotropic in Queenstown 2014. It increased GPS but decreased SPSM. However, its Q × E interaction effects were opposite which decreased GPS and increased SPSM, suggesting that the additive effect alone was not enough to characterize the genetic effect of this QTL. It was also apparent that only a small portion of QTL with additive main effect was involved in Q × E interaction. This suggests that a QTL with no main effects can exercise its effect through interaction with the environment. Therefore, to develop genotypes for target environments or genotypes with broad

adaptation, the Q × E interaction should be investigated and assessed in plant breeding programs (Basford and Cooper, 1998; El-Soda et al., 2014).

Epistasis has long been recognized to describe a situation where the effect of a particular genotype depends on the genetic background or generally as an interaction between a pair of loci, in which the phenotypic effect of one locus depends on the genotype at the second locus (Bocianowski, 2013; Carlborg and Haley, 2004). Understanding epistasis has been regarded as a necessity to characterize the genetic basis of complex traits (Carlborg and Haley, 2004; Phillips, 2008). Although epistasis was not well investigated in most previous QTL-mapping studies in wheat and its effect may not be as significant (Bennett et al., 2012a; Carter et al., 2011; Heidari et al., 2011; Marza et al., 2006; Mengistu et al., 2012), ignoring epistasis could affect the efficiency and accuracy of MAS as a result of overestimating or underestimating QTL effects (Bocianowski, 2013; Carlborg and Haley, 2004). Also, a simulation study showed that the genetic advance of selection on additive effects became fixed after several cycles of selection when epistasis was present (Wang et al., 2004). In this study, 7 pairs of significant epistatic interactions influencing grain yield and yield components were detected (Table 2.8). However, only two intervals/loci were detected by ICIM-ADD. This suggested many intervals in two locus analysis may escape detection by ICIM-ADD. Kumar et al. (2007) reported similar results and pointed out that this phenomena was more conspicuous in some populations and was perhaps also due to density of map used for QTL analysis. The fact that most epistasis involved only QTL with no main effects indicated that

epistasis between non-significant loci may be an important genetic basis of grain yield and yield components in wheat. This has also been found in maize and rice (Li et al., 1997; Ma et al., 2007a; Xing et al., 2014). Besides, it should be noted that the effects of some significant locus (e.g. the one located in *Xbarc28-Xsnp2005*) was completely changed to the opposite direction through interaction with another locus (e.g. the one located in *Xsnp1006-Xsnp823*), implying the need to account for epistasis to avoid an inflated estimate of the net QTL effect. In contrast, the genetic effect of QTL located in *Xsnp3253-Xsnp3349* was enhanced by interacting with the one in *Xsnp3175-Xsnp3401* suggesting that pyramiding QTL/genes could further improve the trait of interest when the direction of epistatic effect among QTL/genes is in the same direction with the additive effects of each QTL/gene involved.

Although both additive and epistatic effects contributed to the phenotypic performance of grain yield and yield components, the contribution from significant epistasis was much smaller compared to that from additive loci for all traits investigated in this study (Figure 2.2), suggesting the essential role of additive main effects in determining yield and yield components in the current DH population and potential targets for MAS. This agreed with recent studies on rice, barley and wheat, where significant epistatic effects for yield and yield components were small in magnitude relative to the additive effects (Wu et al., 2012; Xing et al., 2002; Xu and Jia, 2007; Zhuang et al., 2002). And the low percentage of phenotypic variance explained by epistasis is largely due to a large number of QTLs with small effects (Wu et al., 2012). This might also explain why Q×E and QQ×E interactions were not

examined by researchers in some recent studies in wheat (Carter et al., 2011; Heidari et al., 2011; Kato et al., 2000; Marza et al., 2006).

Conclusion

In the current study the genetic basis of grain yield and yield components in a DH population was investigated by QTL mapping. Significant QTLs for GYLD, GWPS, GPS, SPSM, and TGW were detected almost on every wheat chromosome confirming the general involvement of loci (major QTL clusters and scattered minor QTLs) across the whole genome in the expression of yield and yield components. Although additive main effects, additive × additive epistatic main effects, and their interactions with environments all served as genetic determinants of grain yield and yield components, the additive main effects were the major contributors in this DH population and the magnitude and directions of QTL effects may change due to epistasis and QTL× environment interactions. Additionally, the observed phenotypic correlations between yield and yield components in this study were possibly caused by pleiotropy from QTLs located on 1A, 2A, 2D and 6D. Moreover, a major gene such as *Ppd-D1* was involved in the expression of grain yield per se. Finally, major QTLs identified in this study such as *QYld.cz-3B.2* for GYLD and *QTgw.cz-7A.5* for TGW could be utilized by breeders for MAS and QTL fine mapping.

Chapter 3: Quantitative trait loci mapping of plant architecture traits in a doubled haploid population of soft red winter wheat

Abstract

Higher wheat grain yields are required to feed an increasing population. An optimized plant architecture may play a crucial role in increasing grain yield. Quantitative trait loci (QTLs) analysis was conducted in a doubled haploid (DH) population to study the genetic basis of plant architecture traits (plant height, PHT; flag leaf length, FLL; flag leaf width, FLW; flag leaf area, FLA; Flag leaf shape (length/width ratio), FLS) across six year-location trials. The DHs showed normal distribution with transgressive segregation, suggesting that plant architecture traits are controlled by polygenes. Seventy four QTLs were detected on all wheat chromosomes. Twenty were for PHT, thirteen were for FLL, sixteen were for FLW, twelve were for FLA, and eleven were for FLS. Major QTLs such as *QPht.cz-2D.2* and QTL clusters on chromosome 2D, 3B, 6A etc. are first reports for plant architecture traits. These QTLs provide useful information for understanding the genetic mechanisms regulating plant architecture in wheat and for marker-assisted selection in designing desirable plant height and flag leaf morphology to increase yield.

Introduction

Plant architecture involves several traits, such as plant height, tillering, branching patterns, leaf size and shape, configuration of leaf relative to the sun and spatial arrangement of leaves (Fageria et al., 2006) and is closely associated with photosynthetic ability and grain yield in wheat (*Triticum aestivum* L.) (Hedden, 2003). Under high soil fertility conditions, the stems of tall plants are generally

unable to support the resultant weight of plump grains and fall over in the field before maturity, a process known as lodging, with consequent large yield losses (Hedden, 2003). This situation was greatly improved after the introduction of dwarfing genes into cereal crops, such as *Rht-B1b* and *Rht-D1b* in wheat and *sd1* in rice which produce semi-dwarf plants with short strong stalks as well as more assimilate partitioned into the grain, leading to large yield increases in wheat and rice known as Green Revolution (Hedden, 2003). However, extremely short plants are disadvantageous because leaves are very closely spaced on a short stem causing increased shading within the canopy, as well as poor ventilation and light transmission in the lower canopy, which affects grain filling and decreases grain yield (Yoshida, 1972; Zhang et al., 2011). Thus, appropriate plant height is a requirement for achieving the desired yield level in wheat breeding programs. The closest leaf from the spike, the flag leaf, is the primary source of assimilates for grain filling and thus grain yield and it also stays green longer than other leaves (Ali et al., 2010). Translocation of carbohydrates from the flag leaf is almost entirely directed towards the grain while that from the lower leaves is only partly directed towards the grain and the detachment of flag leaf considerably decreases grain yield (Ali et al., 2010; Monyo and Whittington, 1973)

Plant height and leaf morphology (flag leaf length, width, and area) are generally considered quantitative traits and influenced by the environment. Understanding the genetic bases of these traits is useful in wheat improvement. To date, more than twenty reduced height genes have been named and some are molecularly

characterized (McIntosh et al., 2013). Height-reducing genes fall into two groups depending on their reaction to endogenous gibberellic acid (GA). Firstly, GA-insensitive genes such as *Rht-B1b* and *Rht-D1b* encode mutant proteins that belong to the DELLA subfamily of GRAS regulatory proteins which repress GA responsive growth by decreasing the sensitivity of vegetative and reproductive tissues to endogenous GA, leading to reduced stem internode length and overall plant height (Tan et al., 2013). Secondly, plants carrying GA-responsive genes, such as *Rht4* and *Rht8*, retain GA responsiveness but show decreased levels of endogenous bioactive GA not due to defective gibberellin biosynthesis or signaling, but possibly to a reduced sensitivity to brassinosteroids (Chen et al., 2015; Gasperini et al., 2012). It should be noted that unfavorable effects such as reduced seedling vigor associated with GA-insensitive genes and delayed anthesis date associated with GA-responsive genes do occur (Chen et al., 2013). Therefore, breeders may need new alternative dwarfing genes to achieve the appropriate height reduction without introducing too much of a negative effect.

In wheat, studies on flag leaf characteristics have focused on their relationship with grain yield and plant adaptation (Blake et al., 2007; Dere and YIildirim, 2006; Monneveux et al., 2004) and few on QTL analysis. A previous report from Jia et al. (2013a) detected six QTLs for flag leaf length and width among which a major QTL named *QFlw.nau-5A.1* explained 28.7 to 35.6% of the phenotypic variation. *QFlw.nau-5A.1* was inherited like a semidominant gene, designated as *TaFLW1*, and fine mapped in a 0.2 cM interval on chromosome 5A (Xue et al., 2013). The

Wangshuibai *TaFLW1* allele reduced flag leaf width up to 3 mm and was closely linked to the type I Fusarium head blight resistance gene *Fhb5* (Wu et al., 2014; Xue et al., 2013). QTLs controlling leaf morphology have been cloned in rice. A 30-bp deletion in the coding region of rice *Narrow leaf 1(Nal1)* was significantly associated with reduced polar auxin transport capacity which affected the distribution pattern of vascular bundles leading to narrower leaves with fewer longitudinal veins. *NARROW AND ROLLED LEAF 1 (NRL1),* on rice chromosome 12, encodes the cellulose synthase-like protein D4 (OsCsID4) which plays a crucial role in leaf expansion in rice (Hu et al., 2010). Its three mutants (single base substitutions at three different loci) *nrl1-1, nrl1-2, and nrl1-2* are shorter and show erect, narrow and semi-rolled leaves compared with the *NRL1* carrying plant (Hu et al., 2010).

QTL mapping studies of plant architecture, especially of flag leaf morphology at the whole genome level, have rarely been reported in wheat. To further explore QTLs for plant architecture and provide information for QTL pyramiding, I conducted experiments to map QTLs for plant architecture in a doubled haploid (DH) population of soft red winter wheat. The objective of this study was to identify QTLs with additive effects, epistatic effects, and Q×E interactions for wheat plant height, flag leaf width, length, area, and shape to help design strategies for attaining the desired plant architecture in wheat breeding programs.

Material and Methods

Genetic resources and field experiments

A doubled-haploid population of 124 lines derived from a cross between a soft red winter wheat germplasm line MD01W233-06-1 (MDW233) (Costa et al., 2010) and a soft red winter wheat cultivar SS8641 (Johnson et al., 2007b) was used for this study. MDW233 carries the *Rht-D1b* dwarfing gene the *Ppd-D1b* photoperiod sensitive allele as well as the 1RS/1AL translocation. A genetic linkage map with single nucleotide polymorphism (SNPs), simple sequence repeats (SSRs), and a morphological marker (coleoptile color) was constructed with an average interval length of 2.3 cM (Chapter 2 of this dissertation).

The 124 DH lines, together with the parents MDW233 and SS8641, were planted in the greenhouse and research fields at the University of Maryland. The greenhouse evaluation was carried out in the 2011-2012 and 2012-2013 crop seasons. The population was germinated at room temperature and placed in a growth chamber (4°C, 16 hour light and 8 hour darkness) for eight weeks for vernalization and then transferred to to greenhouse (20°C, 16 hour light and 8 hour darkness) with each line planted in a one-gallon pot. Regular irrigation was used to keep soil moist. Fertilizers were applied directly to each pot in seedling stage. Pots were randomized with three replications in the 2011-2012 season and four replications in the 2012-2013 season. Field tests were conducted in research fields at Clarksville, MD and Queenstown, MD for the 2012-2013 and 2013-2014 crop seasons. The DH lines and two parents evaluated in field plots which were arranged in a randomized complete block design

with two replications. Each field plot consisted of seven rows separated by 15.2 cm. Seed density was 22 seeds per 0.305 m in each row. Growing season rainfall and temperature data were obtained from respective research farms for Clarksville, MD and Queenstown, MD (Figure 3.1). Soil fertility management followed recommended management practices for each location. All trials were sprayed with the metconazole fungicide (Caramba®, BASF Corporation) at anthesis to reduce potential infection by *Fusarium graminearum*.

Traits and measurements

At maturity, five plants were randomly chosen from each plot of the field study for plant architecture traits evaluation. Plants likely affected by the border effect were avoided. A total of five traits were measured including plant height (PHT, cm), flag leaf length (FLL, cm), flag leaf width (FLW, cm), and flag leaf area (FLA, cm^2). FLW was taken at the widest part of the flag leaf. Flag leaf length was measured from the auricle to the apex. Flag leaf area (FLA) was derived (FLA=FLL×FLW×0.79) as previously described (Simpson, 1968; Spagnoletti Zeuli and Qualset, 1990). In the greenhouse study, PHT, FLL, FLW, FLA values were collected from each replication from three individual plants for 2011-2012 and four individual plants for 2012-2013 and averaged for further analyses.

Data analysis

An analysis of variance (ANOVA) for PHT, FLL, FLW, FLA, and FLS was performed separately for each environment and for six environments combined using the PROC GLM procedure of SAS version 9.3 (SAS Institute, Raleigh, NC 2013).

The ANOVA model for single environment analysis was Y= replication + genotype + error, where replication and genotype were fixed and error was random. The ANOVA model for combined analysis was Y = environment + replication within environment + genotype + genotype × environment + error, where error was considered random and all others were fixed. Pearson's correlation coefficients were calculated using the PROC CORR procedure of SAS to detect the association among plant architecture traits. Broad-sense heritability (h^2) (defined as $h^2 = \sigma_G^2/(\sigma_G^2+(\sigma_{GE}^2/e)+ (\sigma_E^2/re))$, where σ_G^2 is the variance of genotypic effect, σ_{GE}^2 is the genotype × environment variance, and e and r are the number of environments and replicates, respectively) for each trait was calculated on a family mean basis using the PROC MIXED procedure of SAS, as described by Holland et al. (2003). The distributions of all evaluated traits were produced using the JMP® Pro, Version 11 (SAS Institue, Cary, NC 2014) (Figure 3.2).

QTL analysis

In this study, QTL analysis was performed using IciMapping version 4.0 (Li et al., 2008) for additive effects and QTLNetwork version 2.1 for digenetic QTL epistasis (A×A or Q×Q), additive × environment (A×E or Q×E) and epistasis × environment (QQ×E) interactions (Wang et al., 1999; Yang et al., 2007). For IciMapping version 4.0, inclusive composite interval mapping of additive module (ICIM-ADD) was used and the walking speed for all traits was 1 cM. Reference LOD values were determined by 1, 000 permutations (Doerge, 2002). Type I error to determine the LOD from the permutation test was 0.05. The LOD threshold to declare the presence of a significant QTL was 3.0. The position at which the LOD score curve reached its

maximum was used as the estimate of the QTL location. For QTLNetwork version 2.1, mixed-model based composite interval mapping (MCIM) was used and Q×E, Q×Q, and QQ×E effects were estimated by the Monte Carlo Markov Chain method with a scanning speed of 1 cM step and the experiment-wise type I error for putative QTL detection of 0.05.

Results

Phenotypic data analysis

The performance of the two parents and the DH lines is shown in Figure 3.2. In all six environments, plant architecture traits segregated continuously as typical quantitative traits. Transgressive segregation, progenies with higher or lower phenotype values than the respective parents, was observed for all traits investigated. The ANOVA revealed that the difference between DH lines for all plant architecture traits was highly significant (Table 3.1). Pairwise correlation between plant architecture traits are shown in Table 3.2. Four traits related to flag leaf morphology (FLL, FLW, FLA, and FLS) were significantly intercorrelated across all six environments. Positive correlations were found between FLL and FLW, FLA, and FLS whereas FLW was negatively correlated with FLS. An additional significant negative correlation was identified between PHT and FLW in two of the six environments. The direction of the correlation between FLL and PHT varied among environments.

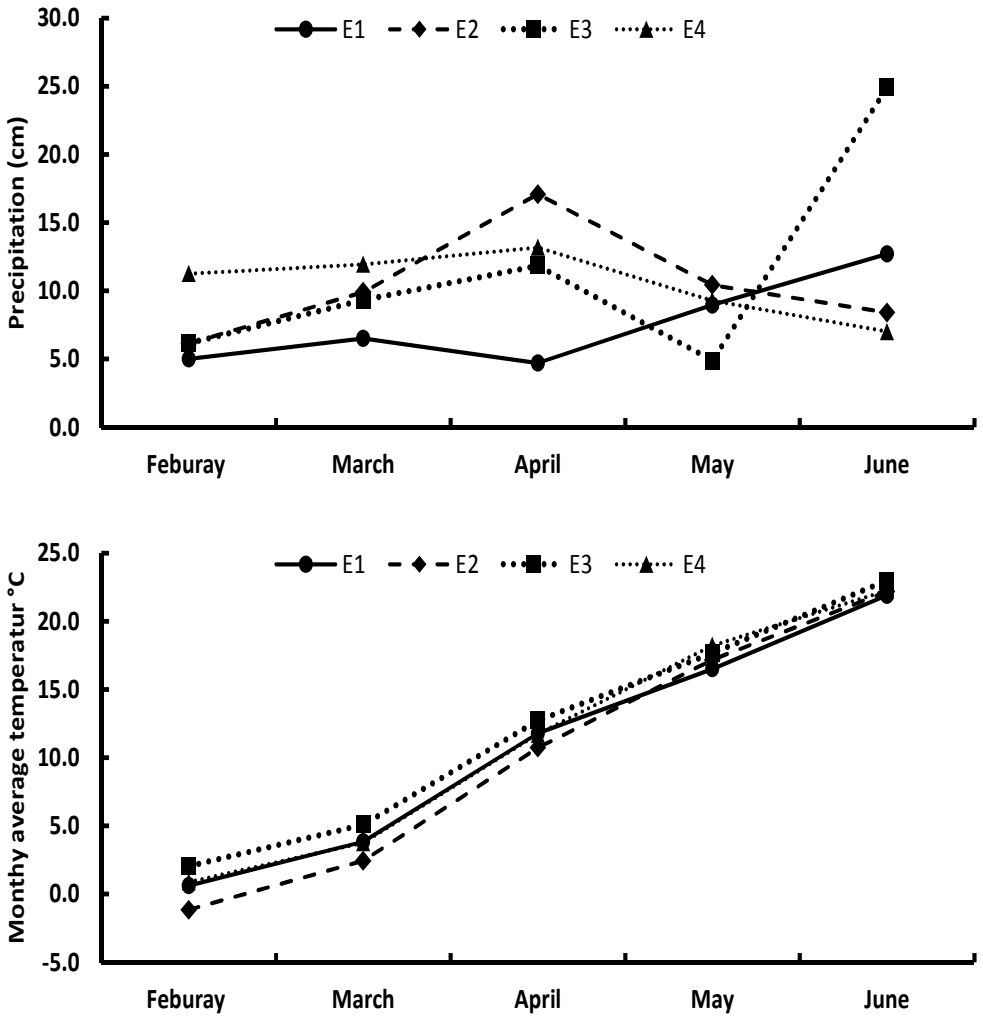


Figure 3.1 Precipitation (unit: cm) and monthly average temperature (unit: °C) during growing season at four field environments: E1, Clarksville, 2013; E2, Clarksville, 2014; E3, Queenstown 2013; E4, Queenstown 2014.

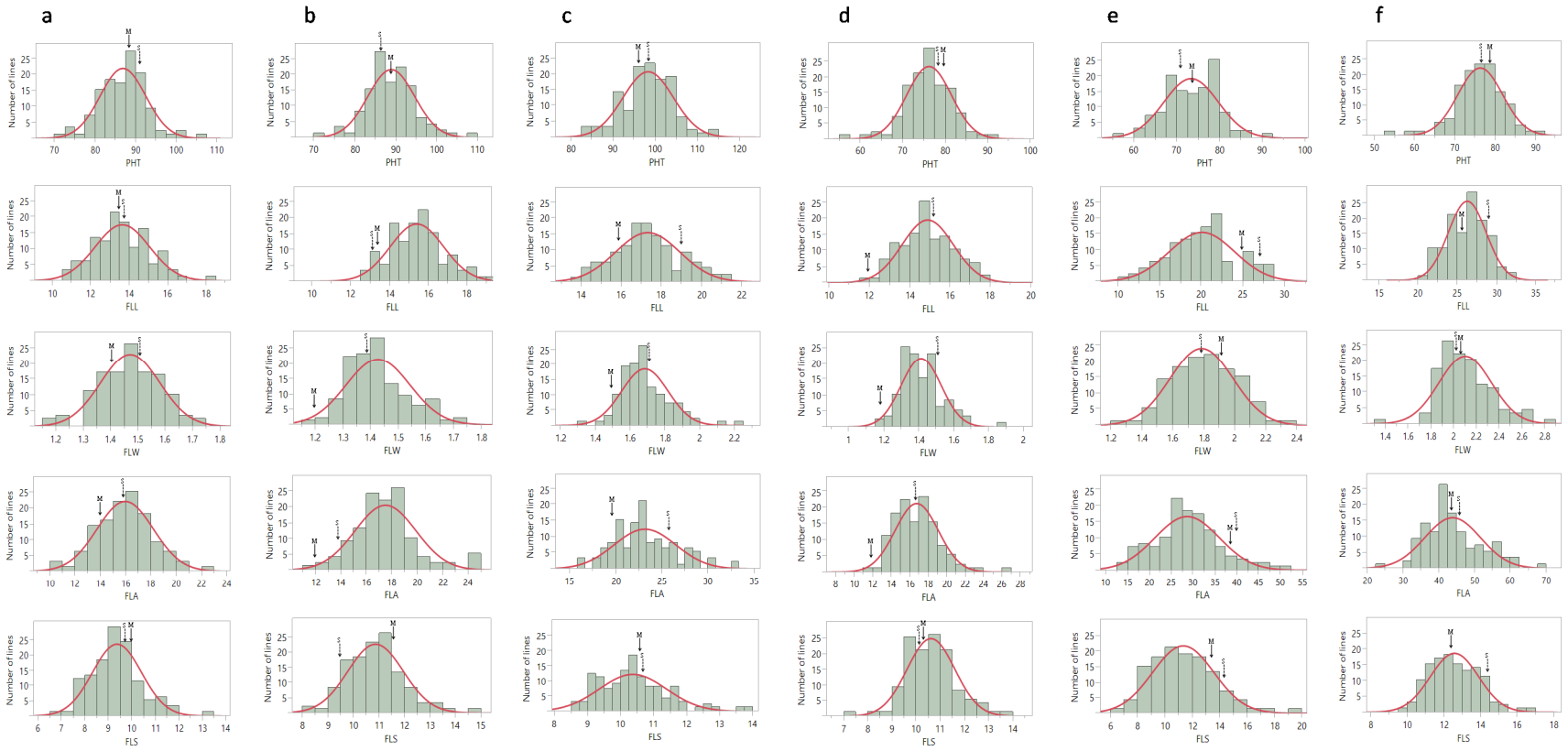


Figure 3.2 Frequency distribution of plant height (PHT, cm), flag leaf length (FLL, cm), flag leaf width (FLW, cm), flag leaf area (FLA, cm^2), and flag leaf shape (FLS) of the double haploid lines in a) Clarksville 2013, b) Clarksville 2014, c) Queenstown 2013, d) Queenstown 2014, e) Greenhouse 2012, f) Greenhouse 2013.

Table 3.1 Pooled analyses of variance and heritability estimates for plant height (PHT, cm), flag leaf length (FLL, cm), flag leaf width (FLW, cm), flag leaf area (FLA, cm^2), and flag leaf shape (FLS) in four field trials from 2013 to 2014

		Mean Squares				
Source of Variation	df	PH	FLL	FLW	FLA	FLS
Environment	3	20508.86*	578.47*	3.92*	2648.79*	107.89*
Rep(environment)	4	312.84*	23.69*	0.06*	65.26*	3.73*
Genotype	123	212.04*	11.22*	0.08*	38.38*	6.41*
genotype × environment	369	14.70*	1.65*	0.01*	5.42*	0.72*
R^2		0.95	0.88	0.89	0.90	0.86
Heritability (h^2) †		0.93(0.01)	0.85(0.02)	0.90(0.2)	0.86 (0.02)	0.89(0.02)

* Significant at the 0.001 probability level.
† Values in parenthesis are standard errors for h^2

Table 3.2 Pearson correlation coefficients among plant height (PHT, cm), flag leaf length (FLL, cm), flag leaf width (FLW, cm), flag leaf area (FLA, cm^2), and flag leaf shape (FLS, cm) in six trials from 2012 to 2014.

Environments	Traits	FLL	FLW	FLA	FLS
Clarksville 2013	PHT	0.24***	-0.07	0.14	0.28***
	FLL		0.26***	0.87***	0.76***
	FLW			0.70***	-0.41***
	FLA				0.35
Clarksville 2014	PHT	0.03	-0.27***	-0.13	0.22*
	FLL		0.29***	0.82***	0.67***
	FLW			0.78***	-0.51***
	FLA				0.12
Queenstown 2013	PHT	0.14	-0.19*	-0.01	0.29***
	FLL		0.38***	0.85***	0.65***
	FLW			0.81***	-0.44***
	FLA				0.16
Queenstown 2014	PHT	0.30***	-0.06	0.16	0.31***
	FLL		0.37***	0.84***	0.60***
	FLW			0.82***	-0.51***
	FLA				0.06
Greenhouse 2012	PHT	-0.19*	-0.13	-0.19*	-0.13
	FLL		0.35***	0.90***	0.81***
	FLW			0.71***	-0.25***
	FLA				0.48***
Greenhouse 2013	PHT	0.21*	-0.06	0.07	0.25***
	FLL		0.50***	0.81***	0.36***
	FLW			0.90***	-0.60***
	FLA				-0.19*

* Significant at the 0.05 probability level.
** Significant at the 0.01 probability level.
*** Significant at the 0.001 probability level.

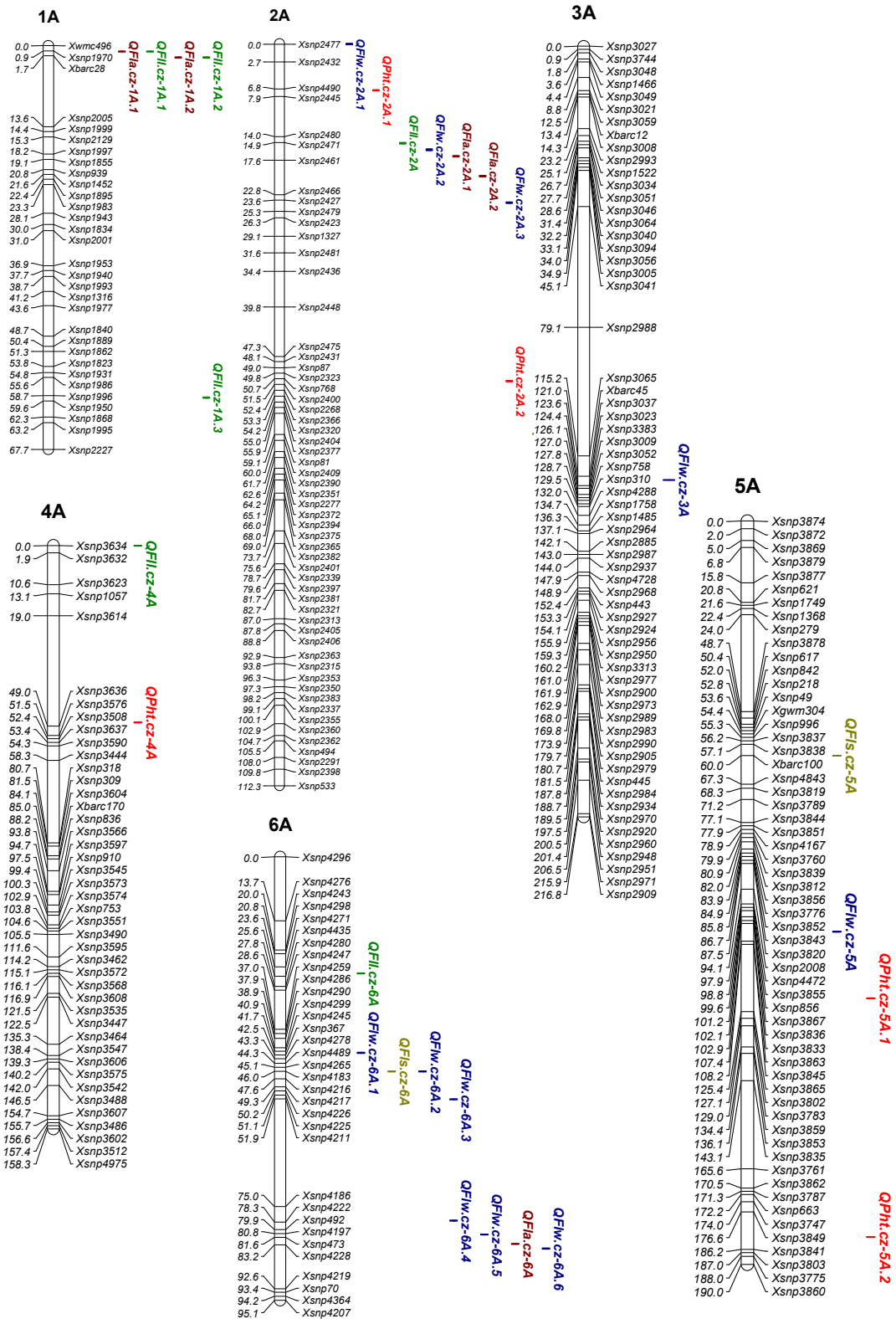
QTLs with additive and additive × environment interaction effects

Significant QTLs were detected for all traits evaluated, as summarized in Table 3.3. A total of seventy-four QTLs with additive effects were identified including twenty QTLs for PHT, thirteen for FLL, eighteen for FLW, twelve for FLA, and eleven for FLS. These QTLs were unevenly distributed in the wheat genome. Among them, 35 (47.3%) were in the A genome, 21 (28.4%) were in the B genome, and 18 (24.3%) were in the D genome. The phenotypic variance explained by each QTL ranged from 5.7 to 22% for PHT, 6.4 to 20.7% for FLL, 5.4 to 31.2% for FLW, 6.8 to 24.1% for FLA, and 7.3 to 19.6% for FLS. Both parents contributed favorable alleles (35 from MDW233 and 39 from SS8641). In general, these QTLs had low to moderate genetic effects common for quantitative traits. Additionally, QTL co-localization was found in nine marker intervals suggesting the possible presence of pleiotropy. Mapping QTLs with additive × environment interaction effects was conducted based on the data from the four field trials only. A total of four intervals were detected with significant Q×E interaction for PHT, FLL, and FLA (Table 3.4). Among them, the loci flanked by *XPpdD1-Xsnp2869* and *Xsnp1970-Xbarc28* were detected with significant additive effects and other two marker intervals were insignificant for additive effects. The heritability of Q×E interaction ranged from 1% to 2%. Queenstown 2013 had three Q×E interactions and the other three environments each had one.

QTLs with epistatic and epistatic × environment interaction effects

A total of 12 pairs of significant epistatic interactions ($p<0.001$) were detected for all five plant architecture traits (Table 3.5). These epistatic interactions involved loci

from within and across chromosomes with heritability values ranging from 0.6% to 4.3%. Among the twenty four epistatic intervals/loci, five were significant for additive effects and the rest were significant only in digenic epistatic interactions. Additionally, an epistatic × environment interaction was detected between chromosome regions flanked by *Xsnp4061-Xsnp4027* on 5B and *Xsnp4860-Xsnp4831* on 7B at Queenstown 2013 for FLW. However, none of these two intervals were significant for additive main effects.


1A
0.0 Xwmc496
0.9 Xsnp1970
1.7 Xbarc28
13.6 Xsnp2005
14.4 Xsnp1999
15.3 Xsnp2129
18.2 Xsnp1997
19.1 Xsnp1855
20.8 Xsnp939
21.6 Xsnp1452
22.4 Xsnp1895
23.3 Xsnp1983
28.1 Xsnp1943
30.0 Xsnp1834
31.0 Xsnp2001
36.9 Xsnp1953
37.7 Xsnp1940
38.7 Xsnp1993
41.2 Xsnp1316
43.6 Xsnp1977
48.7 Xsnp1840
50.4 Xsnp1889
51.3 Xsnp1862
53.8 Xsnp1823
54.8 Xsnp1931
55.6 Xsnp1986
58.7 Xsnp1996
59.6 Xsnp1950
62.3 Xsnp1868
63.2 Xsnp1995
67.7 Xsnp2227
QFla.cz-1A.1
QFll.cz-1A.1
QFla.cz-1A.2
QFll.cz-1A.2
QFll.cz-1A.3
2A
0.0 Xsnp2477
2.7 Xsnp2432
6.8 Xsnp4490
7.9 Xsnp2445
14.0 Xsnp2480
14.9 Xsnp2471
17.6 Xsnp2461
22.8 Xsnp2466
23.6 Xsnp2427
25.3 Xsnp2479
26.3 Xsnp2423
29.1 Xsnp1327
31.6 Xsnp2481
34.4 Xsnp2436
39.8 Xsnp2448
47.3 Xsnp2475
48.1 Xsnp2431
49.0 Xsnp87
49.8 Xsnp2323
50.7 Xsnp768
51.5 Xsnp2400
52.4 Xsnp2268
53.3 Xsnp2366
54.2 Xsnp2320
55.0 Xsnp2404
55.9 Xsnp2377
59.1 Xsnp81
60.0 Xsnp2409
61.7 Xsnp2390
62.6 Xsnp2351
64.2 Xsnp2277
65.1 Xsnp2372
66.0 Xsnp2394
68.0 Xsnp2375
69.0 Xsnp2365
73.7 Xsnp2382
75.6 Xsnp2401
78.7 Xsnp2339
79.6 Xsnp2397
81.7 Xsnp2381
82.7 Xsnp2321
87.0 Xsnp2313
87.8 Xsnp2405
88.8 Xsnp2406
92.9 Xsnp2363
93.8 Xsnp2315
96.3 Xsnp2353
97.3 Xsnp2350
98.2 Xsnp2383
99.1 Xsnp2337
100.1 Xsnp2355
102.9 Xsnp2360
104.7 Xsnp2362
105.5 Xsnp494
108.0 Xsnp2291
109.8 Xsnp2398
112.3 Xsnp533
QFlw.cz-2A.1
QPht.cz-2A.1
QFll.cz-2A
QFlw.cz-2A.2
QFla.cz-2A.1
QFla.cz-2A.2
QFlw.cz-2A.3
3A
0.0 Xsnp3027
0.9 Xsnp3744
1.8 Xsnp3048
3.6 Xsnp1466
4.4 Xsnp3049
8.8 Xsnp3021
12.5 Xsnp3059
13.4 Xbarc12
14.3 Xsnp3008
23.2 Xsnp2993
25.1 Xsnp1522
26.7 Xsnp3034
27.7 Xsnp3051
28.6 Xsnp3046
31.4 Xsnp3064
32.2 Xsnp3040
33.1 Xsnp3094
34.0 Xsnp3056
34.9 Xsnp3005
45.1 Xsnp3041
79.1 Xsnp2988
115.2 Xsnp3065
121.0 Xbarc45
123.6 Xsnp3037
124.4 Xsnp3023
126.1 Xsnp3383
127.0 Xsnp3009
127.8 Xsnp3052
128.7 Xsnp758
129.5 Xsnp310
132.0 Xsnp4288
134.7 Xsnp1758
136.3 Xsnp1485
137.1 Xsnp2964
142.1 Xsnp2885
143.0 Xsnp2987
144.0 Xsnp2937
147.9 Xsnp4728
148.9 Xsnp2968
152.4 Xsnp443
153.3 Xsnp2927
154.1 Xsnp2924
155.9 Xsnp2956
159.3 Xsnp2950
160.2 Xsnp3313
161.0 Xsnp2977
161.9 Xsnp2900
162.9 Xsnp2973
168.0 Xsnp2989
169.8 Xsnp2983
173.9 Xsnp2990
179.7 Xsnp2905
180.7 Xsnp2979
181.5 Xsnp445
187.8 Xsnp2984
188.7 Xsnp2934
189.5 Xsnp2970
197.5 Xsnp2920
200.5 Xsnp2960
201.4 Xsnp2948
206.5 Xsnp2951
215.9 Xsnp2971
216.8 Xsnp2909
QPht.cz-2A.2
QFlw.cz-3A
4A
0.0 Xsnp3634
1.9 Xsnp3632
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53.4 Xsnp3637
54.3 Xsnp3590
58.3 Xsnp3444
80.7 Xsnp318
81.5 Xsnp309
84.1 Xsnp3604
85.0 Xbarc170
88.2 Xsnp836
93.8 Xsnp3566
94.7 Xsnp3597
97.5 Xsnp910
99.4 Xsnp3545
100.3 Xsnp3573
102.9 Xsnp3574
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104.6 Xsnp3551
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115.1 Xsnp3572
116.1 Xsnp3568
116.9 Xsnp3608
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135.3 Xsnp3464
138.4 Xsnp3547
139.3 Xsnp3606
140.2 Xsnp3575
142.0 Xsnp3542
146.5 Xsnp3488
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20.8 Xsnp4298
23.6 Xsnp4271
25.6 Xsnp4435
27.8 Xsnp4280
28.6 Xsnp4247
37.0 Xsnp4259
37.9 Xsnp4286
38.9 Xsnp4290
40.9 Xsnp4299
41.7 Xsnp4245
42.5 Xsnp367
43.3 Xsnp4278
44.3 Xsnp4489
45.1 Xsnp4265
46.0 Xsnp4183
47.6 Xsnp4216
49.3 Xsnp4217
50.2 Xsnp4226
51.1 Xsnp4225
51.9 Xsnp4211
75.0 Xsnp4186
78.3 Xsnp4222
79.9 Xsnp492
80.8 Xsnp4197
81.6 Xsnp473
83.2 Xsnp4228
92.6 Xsnp4219
93.4 Xsnp70
94.2 Xsnp4364
95.1 Xsnp4207
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QFls.cz-6A
QFlw.cz-6A.2
QFlw.cz-6A.3
QFlw.cz-6A.4
QFlw.cz-6A.5
QFla.cz-6A
QFlw.cz-6A.6
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2.0 Xsnp3872
5.0 Xsnp3869
6.8 Xsnp3879
15.8 Xsnp3877
20.8 Xsnp621
21.6 Xsnp1749
22.4 Xsnp1368
24.0 Xsnp279
48.7 Xsnp3878
50.4 Xsnp617
52.0 Xsnp842
52.8 Xsnp218
53.6 Xsnp49
54.4 Xgwm304
55.3 Xsnp996
56.2 Xsnp3837
57.1 Xsnp3838
60.0 Xbarc100
67.3 Xsnp4843
68.3 Xsnp3819
71.2 Xsnp3789
77.1 Xsnp3844
77.9 Xsnp3851
78.9 Xsnp4167
79.9 Xsnp3760
80.9 Xsnp3839
82.0 Xsnp3812
83.9 Xsnp3856
84.9 Xsnp3776
85.8 Xsnp3852
86.7 Xsnp3843
87.5 Xsnp3820
94.1 Xsnp2008
97.9 Xsnp4472
98.8 Xsnp3855
99.6 Xsnp856
101.2 Xsnp3867
102.1 Xsnp3836
102.9 Xsnp3833
107.4 Xsnp3863
108.2 Xsnp3845
125.4 Xsnp3865
127.1 Xsnp3802
129.0 Xsnp3783
134.4 Xsnp3859
136.1 Xsnp3853
143.1 Xsnp3835
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171.3 Xsnp3787
172.2 Xsnp663
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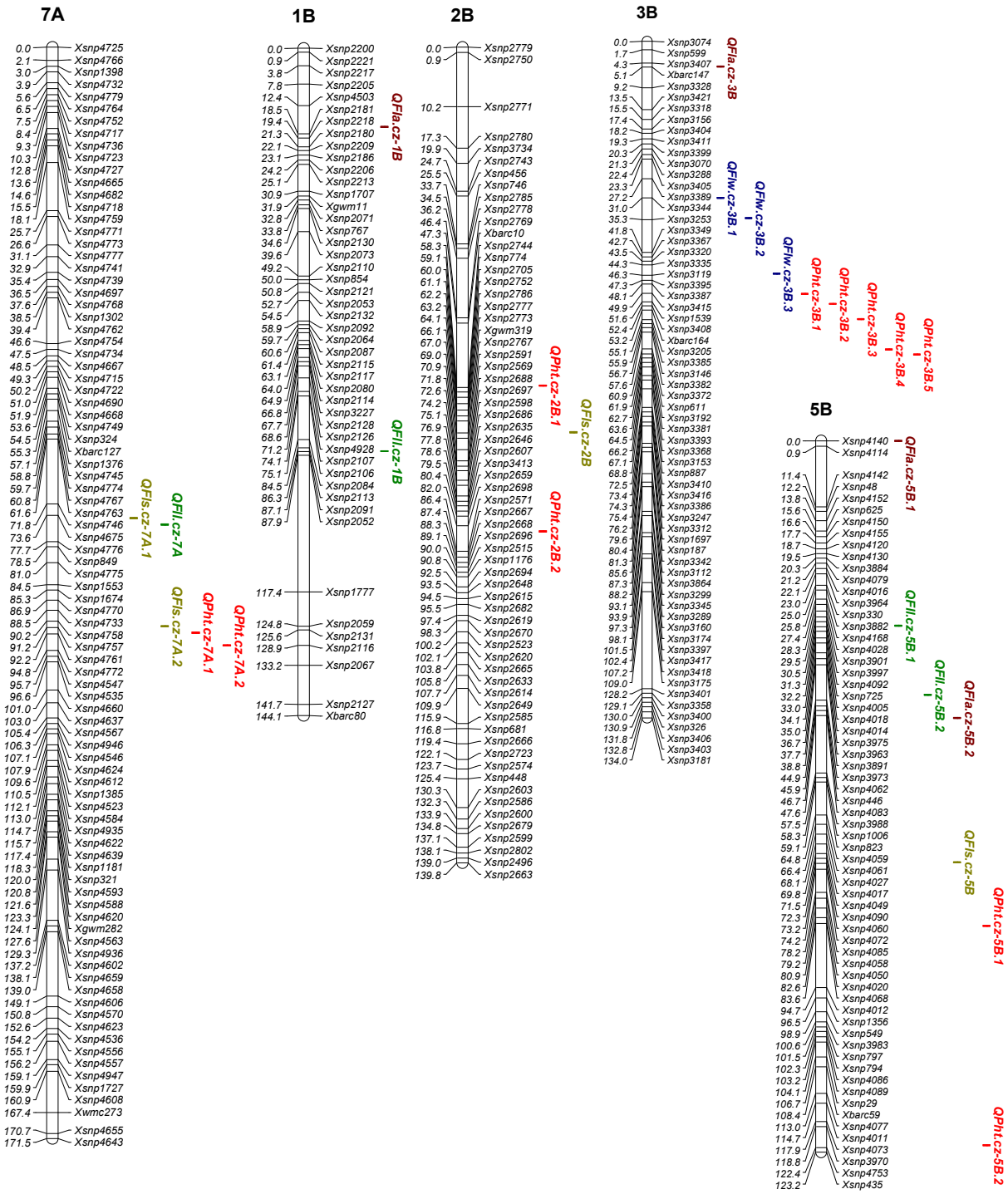
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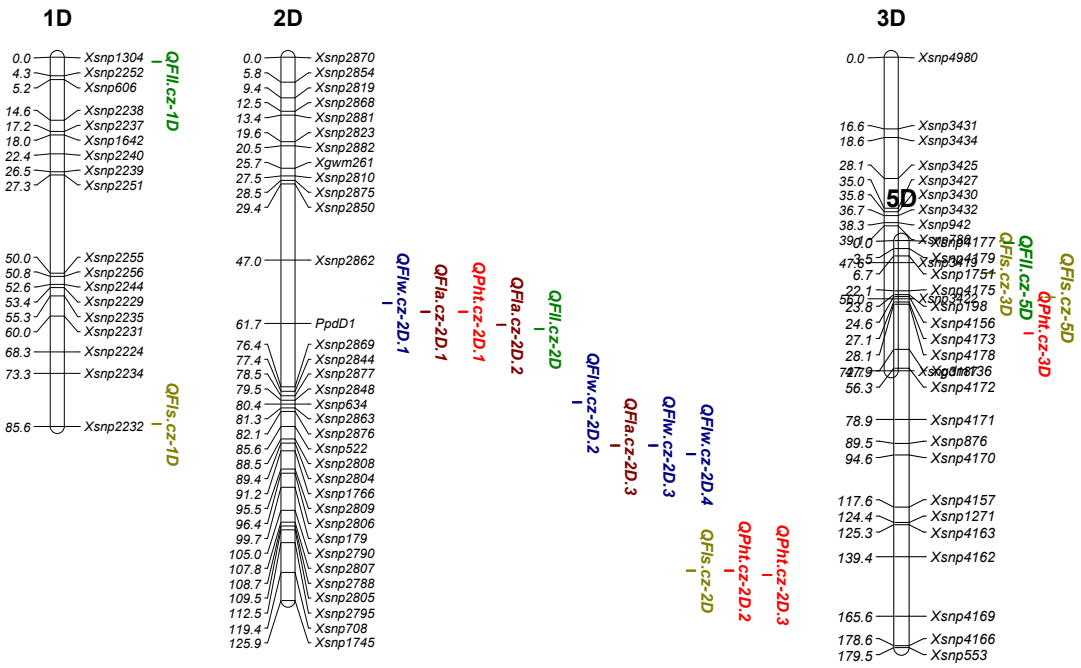


Figure 3.3 Position of quantitative trait loci (QTLs) detected in a doubled haploid mapping population derived from MD01W233-06-1 × SS8641. Locus marker names are shown on the right side of the chromosomes and values to the left of chromosomes show the genetic distance (cM) for each marker. QTLs are labeled with trait abbreviations and the QTL number for each trait. QTLs for the same trait are in the same color.

Table 3.3 Quantitative trait loci (QTLs) for plant height (PHT, cm), flag leaf length (FLL, cm), flag leaf width (FLW, cm), flag leaf area (FLA, cm^2), and flag leaf shape (FLS, cm) in six environments from 2012 to 2014.

QTL	Trait	Environment	Position (cM)	Marker interval	LOD score	PVE (%)	Additive effect
QPht.cz-2A.1	PHT	Clarksville 2013	7	*Xsnp4490-Xsnp2445*	3.9	5.7	-1.35
QPht.cz-2A.2	PHT	Queenstown 2014	51	*Xsnp768-Xsnp2400*	3.8	7.6	-1.46
QPht.cz-4A	PHT	Clarksville 2013	48	*Xsnp3614-Xsnp3636*	4.6	7.0	1.49
QPht.cz-5A.1	PHT	Greenhouse 2012	122	*Xsnp3845-Xsnp3865*	4.6	10.5	-2.06
QPht.cz-5A.2	PHT	Queenstown 2014	183	*Xsnp3849-Xsnp3841*	3.3	7.1	1.40
QPht.cz-7A.1	PHT	Clarksville 2013	92	*Xsnp4757-Xsnp4761*	6.2	9.6	-1.79
QPht.cz-7A.1	PHT	Clarksville 2014	92	*Xsnp4757-Xsnp4761*	4.6	11.1	-1.95
QPht.cz-7A.2	PHT	Queenstown 2014	94	*Xsnp4761-Xsnp4772*	5.3	10.8	-1.78
QPht.cz-2B.1	PHT	Clarksville 2013	58	*Xbarc10-Xsnp2744*	5.2	7.9	1.58
QPht.cz-2B.2	PHT	Queenstown 2013	83	*Xsnp2698-Xsnp2571*	4.1	9.8	1.86
QPht.cz-3B.1	PHT	Clarksville 2014	50	*Xsnp3415-Xsnp1539*	6.5	16.0	-2.29
QPht.cz-3B.2	PHT	Clarksville 2013	52	*Xsnp1539-Xsnp3408*	9.3	15.2	-2.20
QPht.cz-3B.3	PHT	Queenstown 2014	55	*Xbarc164-Xsnp3205*	4.1	8.0	-1.50
QPht.cz-3B.4	PHT	Greenhouse 2013	61	*Xsnp3372-Xsnp611*	5.1	13.8	-2.07
QPht.cz-3B.5	PHT	Queenstown 2013	62	*Xsnp611-Xsnp3192*	4.6	11.1	-1.98
QPht.cz-5B.1	PHT	Greenhouse 2012	84	*Xsnp4068-Xsnp4012*	9.3	20.1	2.86
QPht.cz-5B.2	PHT	Greenhouse 2012	122	*Xsnp3970-Xsnp4753*	3.9	7.7	-1.77
QPht.cz-2D.1	PHT	Queenstown 2014	59	*Xsnp2862-XPpdD1*	7.4	16.6	-2.16
QPht.cz-2D.1	PHT	Clarksville 2013	60	*Xsnp2862-XPpdD1*	4.9	7.8	-1.58
QPht.cz-2D.2	PHT	Greenhouse 2012	119	*Xsnp2795-Xsnp708*	9.1	19.5	2.81
QPht.cz-2D.2	PHT	Queenstown 2013	119	*Xsnp2795-Xsnp708*	8.4	22.0	2.79
QPht.cz-2D.2	PHT	Clarksville 2013	119	*Xsnp2795-Xsnp708*	6.5	10.2	1.80
QPht.cz-2D.2	PHT	Clarksville 2014	119	*Xsnp2795-Xsnp708*	3.6	8.6	1.68
QPht.cz-2D.3	PHT	Queenstown 2014	120	*Xsnp708-Xsnp1745*	7.9	17.1	2.17
QPht.cz-2D.3	PHT	Greenhouse 2013	120	*Xsnp708-Xsnp1745*	5.8	15.8	2.21
QPht.cz-3D	PHT	Greenhouse 2013	64	*Xsnp3422-Xsnp3187*	3.3	9.6	1.75
QFlw.cz-2A.1	FLW	Greenhouse 2012	0	*Xsnp2477-Xsnp2432*	4.3	9.5	0.06
QFlw.cz-2A.2	FLW	Greenhouse 2013	16	*Xsnp2471-Xsnp2461*	13.3	31.2	0.13
QFlw.cz-2A.3	FLW	Queenstown 2013	24	*Xsnp2427-Xsnp2479*	4.8	11.2	0.04
QFlw.cz-2A.3	FLW	Clarksville 2014	24	*Xsnp2427-Xsnp2479*	3.8	7.1	0.03
QFlw.cz-2A.3	FLW	Queenstown 2014	24	*Xsnp2427-Xsnp2479*	3.6	7.0	0.03
QFlw.cz-2A.3	FLW	Clarksville 2013	24	*Xsnp2427-Xsnp2479*	3.4	7.3	0.03
QFlw.cz-3A	FLW	Greenhouse 2012	122	*Xbarc45-Xsnp3037*	5.8	13.4	-0.07
QFlw.cz-5A	FLW	Clarksville 2014	105	*Xsnp3833-Xsnp3863*	5.2	10.4	0.04
QFlw.cz-6A.1	FLW	Clarksville 2014	42	*Xsnp4245-Xsnp367*	3.0	5.4	-0.03
QFlw.cz-6A.2	FLW	Queenstown 2014	46	*Xsnp4183-Xsnp4216*	4.7	9.1	-0.03
QFlw.cz-6A.3	FLW	Clarksville 2013	52	*Xsnp4211-Xsnp4186*	4.4	9.5	-0.03
QFlw.cz-6A.4	FLW	Queenstown 2013	78	*Xsnp4186-Xsnp4222*	5.0	11.9	-0.05
QFlw.cz-6A.5	FLW	Greenhouse 2013	81	*Xsnp4197-Xsnp473*	3.3	6.4	-0.06
QFlw.cz-6A.6	FLW	Clarksville 2014	84	*Xsnp4228-Xsnp4219*	3.4	6.4	-0.03
QFlw.cz-3B.1	FLW	Clarksville 2014	31	*Xsnp3389-Xsnp3344*	5.9	11.3	0.04
QFlw.cz-3B.2	FLW	Queenstown 2014	35	*Xsnp3344-Xsnp3253*	3.6	6.9	0.03
QFlw.cz-3B.3	FLW	Queenstown 2013	46	*Xsnp3335-Xsnp3119*	3.0	6.9	0.03
QFlw.cz-2D.1	FLW	Clarksville 2013	57	*Xsnp2862-XPpdD1*	7.0	17.2	-0.05
QFlw.cz-2D.1	FLW	Greenhouse 2013	59	*Xsnp2862-XPpdD1*	6.5	13.6	-0.09
QFlw.cz-2D.2	FLW	Queenstown 2013	80	*Xsnp2848-Xsnp634*	3.3	7.5	-0.04
QFlw.cz-2D.3	FLW	Queenstown 2014	90	*Xsnp2804-Xsnp1766*	9.3	19.9	-0.05
QFlw.cz-2D.3	FLW	Clarksville 2014	91	*Xsnp2804-Xsnp1766*	4.2	7.7	-0.03
QFlw.cz-2D.4	FLW	Greenhouse 2012	92	*Xsnp1766-Xsnp2809*	4.5	9.9	-0.06
QFls.cz-2A	FLS	Greenhouse 2013	59	*Xsnp2377-Xsnp81*	4.5	11.1	-0.44
QFls.cz-5A	FLS	Queenstown 2013	60	*Xbarc100-Xsnp4843*	4.7	11.7	-0.35
QFls.cz-5A	FLS	Clarksville 2014	61	*Xbarc100-Xsnp4843*	6.6	19.6	-0.49
QFls.cz-6A	FLS	Greenhouse 2013	46	*Xsnp4183-Xsnp4216*	4.9	12.3	0.46
QFls.cz-7A.1	FLS	Queenstown 2014	74	*Xsnp4675-Xsnp4776*	6.3	17.4	-0.41
QFls.cz-7A.2	FLS	Clarksville 2013	91	*Xsnp4758-Xsnp4757*	7.0	18.2	-0.46
QFls.cz-7A.2	FLS	Queenstown 2013	91	*Xsnp4758-Xsnp4757*	5.4	13.7	-0.38
QFls.cz-2B	FLS	Greenhouse 2013	66	*Xsnp2773-Xgwm319*	5.0	12.8	-0.47
QFls.cz-2B	FLS	Clarksville 2013	66	*Xsnp2773-Xgwm319*	3.4	8.3	-0.30
QFls.cz-5B	FLS	Greenhouse 2012	73	*Xsnp4090-Xsnp4060*	3.8	11.3	-0.75
QFls.cz-1D	FLS	Queenstown 2013	85	*Xsnp2234-Xsnp2232*	4.6	11.5	0.35
QFls.cz-2D	FLS	Greenhouse 2013	119	*Xsnp2795-Xsnp708*	3.0	7.3	0.35
QFls.cz-3D	FLS	Queenstown 2014	50	*Xsnp3419-Xsnp3422*	3.2	8.5	0.29
QFls.cz-3D	FLS	Greenhouse 2012	56	*Xsnp3419-Xsnp3422*	3.8	11.1	0.76
QFls.cz-5D	FLS	Clarksville 2014	25	*Xsnp4156-Xsnp4173*	4.7	12.7	0.39

Table 3.3 Continued

QTL	Trait	Environment	Position (cM)	Marker interval	LOD score	PVE (%)	Additive effect
QFll.cz-1A.1	FLL	Queenstown 2013	1	*Xsnp1970-Xbarc28*	7.5	18.5	0.69
QFll.cz-1A.1	FLL	Greenhouse 2013	1	*Xsnp1970-Xbarc28*	4.5	10.0	0.76
QFll.cz-1A.1	FLL	Clarksville 2014	1	*Xsnp1970-Xbarc28*	3.9	11.5	0.46
QFll.cz-1A.2	FLL	Queenstown 2014	2	*Xbarc28-Xsnp2005*	6.4	16.0	0.51
QFll.cz-1A.3	FLL	Clarksville 2013	59	*Xsnp1996-Xsnp1950*	3.1	6.4	0.36
QFll.cz-2A	FLL	Greenhouse 2013	15	*Xsnp2471-Xsnp2461*	5.2	11.7	0.83
QFll.cz-2A	FLL	Queenstown 2013	16	*Xsnp2471-Xsnp2461*	3.5	8.2	0.46
QFll.cz-4A	FLL	Greenhouse 2012	0	*Xsnp3634-Xsnp3632*	3.3	10.2	1.26
QFll.cz-6A	FLL	Greenhouse 2013	25	*Xsnp4271-Xsnp4435*	4.4	9.7	0.75
QFll.cz-7A	FLL	Clarksville 2013	75	*Xsnp4675-Xsnp4776*	6.4	14.5	-0.54
QFll.cz-1B	FLL	Queenstown 2014	87	*Xsnp2113-Xsnp2091*	3.9	9.2	0.39
QFll.cz-5B.1	FLL	Greenhouse 2012	32	*Xsnp4092-Xsnp725*	5.0	16.3	-1.58
QFll.cz-5B.2	FLL	Clarksville 2013	44	*Xsnp3891-Xsnp3973*	5.4	12.0	-0.49
QFll.cz-1D	FLL	Greenhouse 2013	1	*Xsnp1304-Xsnp2252*	3.8	8.5	0.71
QFll.cz-2D	FLL	Queenstown 2013	63	*XPpdD1-Xsnp2869*	6.2	15.3	-0.63
QFll.cz-2D	FLL	Clarksville 2013	66	*XPpdD1-Xsnp2869*	7.8	19.6	-0.63
QFll.cz-2D	FLL	Queenstown 2014	70	*XPpdD1-Xsnp2869*	7.5	20.7	-0.58
QFll.cz-5D	FLL	Clarksville 2014	1	*Xsnp4177-Xsnp4179*	4.7	14.6	0.53
QFla.cz-1A.1	FLA	Queenstown 2013	1	*Xsnp1970-Xbarc28*	8.3	16.8	1.36
QFla.cz-1A.2	FLA	Queenstown 2014	2	*Xbarc28-Xsnp2005*	4.3	9.1	0.70
QFla.cz-2A.1	FLA	Greenhouse 2013	17	*Xsnp2471-Xsnp2461*	13.1	28.7	4.18
QFla.cz-2A.2	FLA	Queenstown 2013	20	*Xsnp2461-Xsnp2466*	6.5	13.4	1.23
QFla.cz-6A	FLA	Clarksville 2014	83	*Xsnp473-Xsnp4228*	3.2	10.1	-0.76
QFla.cz-1B	FLA	Queenstown 2014	17	*Xsnp4503-Xsnp2181*	4.1	9.4	0.71
QFla.cz-3B	FLA	Greenhouse 2013	5	*Xsnp3407-Xbarc147*	3.8	6.8	2.03
QFla.cz-5B.1	FLA	Clarksville 2013	0	*Xsnp4140-Xsnp4114*	3.3	7.9	-0.63
QFla.cz-5B.2	FLA	Greenhouse 2012	48	*Xsnp4083-Xsnp3988*	3.2	11.4	-2.47
QFla.cz-2D.1	FLA	Queenstown 2013	59	*Xsnp2862-XPpdD1*	9.5	20.9	-1.53
QFla.cz-2D.2	FLA	Greenhouse 2013	62	*XPpdD1-Xsnp2869*	5.2	9.7	-2.43
QFla.cz-2D.2	FLA	Queenstown 2014	62	*XPpdD1-Xsnp2869*	5.0	10.6	-0.77
QFla.cz-2D.2	FLA	Clarksville 2013	63	*XPpdD1-Xsnp2869*	8.7	24.1	-1.10
QFla.cz-2D.3	FLA	Queenstown 2014	90	*Xsnp2804-Xsnp1766*	4.6	9.6	-0.72

Table 3.4 QTL × Environment interactions influencing plant height (PHT, cm), flag leaf length (FLL, cm), flag leaf width (FLW, cm), flag leaf area (FLA, cm^2), and flag leaf shape (FLS, cm) in four field environments during 2013 and 2014.

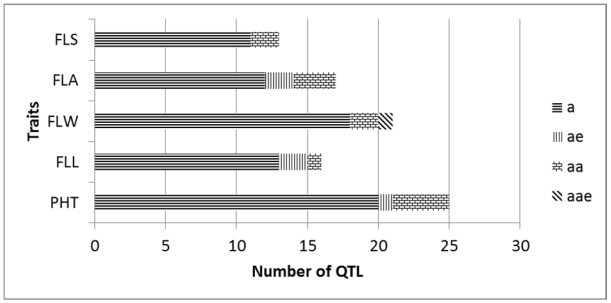
Trait	Chr.	Position	Interval	AE1†	AE2†	AE3†	AE4†	$h^2(ae)$ ‡
PHT	3B	49.9	*Xsnp3415-Xsnp1539*				0.61*	1.0%
FLL	1A	0.9	*Xsnp1970-Xbarc28*§			0.16*		1.1%
FLL	2D	66.7	*XPpd-D1-Xsnp2869*§		0.23*			1.4%
FLA	1A	0	*Xwmc496-Xsnp1970*§	-0.31*		0.45***		2.0%
FLA	2D	65.7	*XPpd-D1-Xsnp2869*			-0.33*		1.2%

† AE is the additive × environment interaction effect at each environment. E1: Clarksville 2013; E2: Clarksville 2014; E3: Queenstown 2013; E4: Queenstown 2014.
‡ h^2(ae) is heritability estimate of the additive × environment interaction effect across four field trails.
§ Interval with significant additive effect.
* Significant at 0.05 probability level.
***Significant at 0.001 probability level.

Table 3.5 Digenetic epistatic QTLs for plant height (PHT, cm), flag leaf length (FLL, cm), flag leaf width (FLW, cm), flag leaf area (FLA, cm^2), and flag leaf shape (FLS) in four field trails during 2013 and 2014.

Trait	Interval†	Chr.†	Position†	Interval‡	Chr.‡	Position‡	AA§	E1¶	E2¶	E3¶	E4¶	h^2(aa)#	h^2(aae)††
PHT	*Xsnp4757-Xsnp4761*‡‡	7A	91.2	*Xsnp3754-Xsnp4981*	4D	28	0.72***					1.3%	0.2%
PHT	*Xsnp3064-Xsnp3040*	3A	31.4	*Xsnp849-Xsnp4775*	7A	80.5	-1.05***					4.3%	0.1%
PHT	*Xsnp3734-Xsnp2743*	2B	19.9	*Xsnp786-Xsnp3419*	3D	39.1	-0.99***					4.7%	0.3%
PHT	*Xsnp3389-Xsnp3344*‡‡	3B	30.2	*Xsnp3417-Xsnp3418*	3B	102.4	1.04***					4.8%	0.2%
FLL	*Xsnp2362-Xsnp494*	2A	104.7	*Xsnp3444-Xsnp318*	4A	73.3	-0.30***					3.4%	0.7%
FLW	*Xsnp4763-Xsnp4746*	7A	71.6	*Xsnp2117-Xsnp2080*	1B	63.1	0.02***					2.7%	0.2%
FLW	*Xsnp4061-Xsnp4027*	5B	66.4	*Xsnp4860-Xsnp4831*	7B	137.3	0.02***			0.012*		3.5%	0.9%
FLA	*Xwmc496-Xsnp1970*	1A	0	*Xsnp2471-Xsnp2461*‡‡	2A	15.9	0.27***					0.8%	0.6%
FLA	*Xsnp2471-Xsnp2461*‡‡	2A	15.9	*Xsnp4177-Xsnp4179*‡‡	5D	1	0.29***					1.0%	0.3%
FLA	*Xsnp1995-Xsnp2227*	1A	63.2	*Xsnp2885-Xsnp2987*	3A	142.1	-0.41***					2.3%	0.3%
FLS	*Xsnp2351-Xsnp2277*	2A	62.6	*Xsnp4444-Xsnp4453*	6B	5.6	0.14***					0.6%	1.4%
FLS	*Xsnp2401-Xsnp2339*	2A	75.6	*Xsnp4444-Xsnp4453*	6B	5.6	-0.29***					2.7%	1.0%

† The flanking markers, chromosome and position of the first interval involved in the epistasis.
‡ The flanking markers, chromosome and position of the second interval involved in the epistasis.
§ The additive × additive effect.
¶ The epistasis × environment effect at each environment. E1: Clarksville 2013; E2: Clarksville 2014; E3: Queenstown 2013; E4: Queenstown 2014;
# The heritability estimate for additive × additive interaction effects across five environment.
†† The heritability estimate for epistasis × environment interaction effects across four field trials.
‡‡ Interval with significant additive effect.
* Significant at the 0.05 probability level
*** Significant at the 0.001 probability level



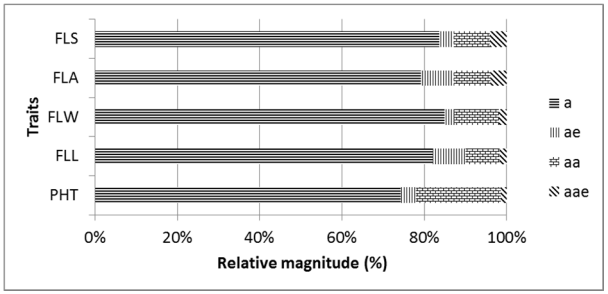


Figure 3.4 Distribution of genetic and non-genetic components for yield and yield related traits: plant height (PHT, cm), Flag leaf length (FLL, cm), Flag leaf width (FLW, cm), Flag leaf area (FLA, cm^2), Flag leaf shape (FLS). a) total number of QTLs detected for additive (a), additive × environment (ae), epistasis (aa), and epistasis × environment interactions (aae) effects. b) relative magnitude of a, ae, aa, aae effects.

Discussion

Plant architecture is important for grain yield potential in cereal crops. Understanding the genetic control of plant architecture can lay the foundation for further genetic improvement. In this study, a winter wheat DH population was used to study plant architecture traits including PHT, FLL, FLW, FLA, and FLS with the aim of locating the underlying QTLs and to provide targets for marker-assisted selection (MAS) in breeding programs.

QTLs for plant architecture traits

Twenty QTLs for plant height were mapped to chromosomes 2A, 4A, 5A, 7A, 1B, 2B, 5B, 2D, and 3D. A major QTL (*QPht.cz-2D.1*) flanked by *Xsnp2862* and *Ppd-D1* was detected in two environments with high LOD score and PVE (Table 3.3). This region also co-localized with QTLs for FLW and FLA and was closely linked with QTLs for FLL (Figure 3.3). The multiple effects of this region were possibly due to the pleiotropic effects of *Ppd-D1* which is one of the two major genes controlling photoperiod-sensitivity in wheat. Among all alleles of the *Ppd-D1* gene, *Ppd-D1b* is the intact allele and is photoperiod sensitive (Guo et al., 2010) which is also carried by MDW233. *Ppd-D1b* is known to reduce the dates to heading and plant height in many wheat cultivars worldwide (Wilhelm et al., 2013). Similarly, the MDW233 allele of *QPht.cz-2D.1* reduced plant height by an average of 1.87 cm in Queenstown 2014 and Clarksville 2013. Additionally, two other major QTLs (*QPht.cz-2D.2* and *QPht.cz-2D.3*) were detected for PHT, which were about 60 cM downstream of *Ppd-D1b* on chromosome 2D (Table 3.3). *QPht.cz-2D.2* was detected in four

environments with an average PVE=10.2%. *QPht.cz-2D.3* was detected in two environments with an average PVE of 16.5%. The favorable alleles for these were contributed by SS8641 and both of their additive effects were greater than that of *QPht.cz-2D.1.* In previous studies, Wang et al. (2010) reported a QTL for PHT on 2DS using a winter wheat population and McCartney et al. (2005) detected a QTL on 2DS for PHT using a population generated from the spring wheat cross RL4452 × 'AC Domain' to study the inheritance of multiple agronomic traits. The location of these two QTLs was very close to the well-known *Rht8* gene which is upstream of *Ppd-D1*(Gasperini et al., 2012). Thus, it is possible that QTLs *QPht.cz-2D.2* and *QPht.cz-2D.2*, identified in the present study, are novel loci for PHT. Moreover, *QPht.cz-2D.2* was found to co-localize with *QFll.cz-2D*, a QTL detected for FLS with LOD=4.7 and PVE=12.7 in the 2013 greenhouse study, suggesting the presence of pleiotropy in this loci. Based on these results, *QPht.cz-2D.2* and *QPht.cz-2D.3* are good candidates for fine mapping and gene cloning to get further understanding of their genetic function and develop gene-specific markers for MAS. Additionally, a cluster of five PHT QTLs was detected in a 12.6 cM region on chromosome 3B. Four of them were major QTLs explaining an average of 14% of the phenotypic variation and all their favorable alleles were from MDW233. In this region, QTLs for agronomic traits such as grain yield, thousand grain weight and plant height as well as QTL co-localizations have been reported by several independent studies (Bennett et al., 2012a; Cuthbert et al., 2008; Kumar et al., 2007; Rebetzke et al., 2008). Furthermore, a 2 cM region that contained two QTLs (*QPht.cz-7A.1* and *QPht.cz-7A.2*) on chromosome 7A was significant for PHT. *QPht.cz-7A.1* was detected in

Clarksville 2013 and Clarksville 2014 with an average PVE=10.35%. The interaction of *QPht.cz-7A.1* with another loci flanked by *Xsnp3754-Xsnp4981* on chromosome 4D explained 1.3% of the phenotypic variation of PHT. *QPht.cz-7A.2* was detected in Queenstown 2014 explaining 10.8% of the phenotypic variation. Both favorable alleles in these two loci were from MDW233. McCartney et al. (2005) mapped a QTL, *QHt.crc-7A*, in the same region for PHT but with a smaller PVE and LOD score. All three QTLs were located around 30 cM downstream of SSR marker *barc127* suggesting that *QHt.crc-7A* may be *QPht.cz-7A.1* or *QPht.cz-7A.2*. Another major QTL, *QPht.cz-5B.1* (LOD=9.3, PVE=20.1%), detected in the present study was comparable to the one identified by Zanke et al. (2014) in a whole genome association mapping of plant height. Previous studies also identified QTLs for plant height or other agronomic traits in the same or nearby region with *QPht.cz-2A.1* (Jia et al., 2013a; Zanke et al., 2014) *QPht.cz-2A.2* (Li et al., 2007b; McCartney et al., 2005), *QPht.cz-2B.1* (Jia et al., 2013a), *QPht.cz-2B.2* (McCartney et al., 2005), *QPht.cz-3D* (Hai et al., 2008), *QPht.cz-4A* (Hai et al., 2008), *QPht.cz-5A.1* (Jia et al., 2013a), *QPht.cz-5A.2* (Huang et al., 2006), *QPht.cz-5B.2* (Zanke et al., 2014).

Although considerable progress has been made in the genetic understanding of grain yield and yield components, reports of QTLs for flag leaf morphology in wheat are still limited. In this study, FLW data was collected from six environments for QTL analysis. *QFlw.cz-2A.2* on chromosome 2A associated with FLW had the largest effect and explained 31.2% of the phenotypic variation in the 2013 greenhouse study. In addition, *QFlw.cz-2A.2* had significant large effects on FLL and FLA with PVE

ranging from 8.2% to 28.7% and also interacted with the loci flanked by *Xsnp4177-Xsnp4179* on chromosome 5D to increase FLA. The favorable alleles for FLW, FLL, and FLA at this locus came from SS8641. Given its significant pleiotropic effects, additional markers are needed in order to resolve the QTL position more precisely and to develop reliable diagnostic markers for MAS. In a previous study, Jia et al. (2013a) found this region to be involved in epistatic interactions and contributed to FLL in the Nanda2419×Wangshuibai population. Similarly, in my study, *QFlw.cz-2A.2* interacted with locus *Xsnp4177-Xsnp4179* on chromosome 5D and locus *Xwmc496-Xsnp1970* on chromosome 1A to contribute to the expression of FLA. In the nearby region of *QFlw.cz-2A.2*, a consistent QTL *QFlw.cz-2A.3* was detected. *QFlw.cz-2A.3* was significant for FLW in all four field environments with LOD score ranging from 3.4 to 4.8 and was related to the QTLs associated with plant height (Kulwal et al., 2003) and yield components (Zhang et al., 2010). On chromosome 2D, there were two major QTLs: *QFlw.cz-2D.1* and *QFlw.cz-2D.3*. *QFlw.cz-2D.1* co-localized with *QPht.cz-2D.1*. *QFlw.cz-2D.3* was co-located with *QFla.cz-2D.3* for FLA with favorable alleles from MDW233. In the same region with *QFlw.cz-2D.3/ QFla.cz-2D*, a QTL with additive effects for FLL, FLW, and heat susceptibility index (HIS) was reported by Mason et al. (2013) where its Halberd allele was favorable for a longer or wider flag leaf and also improved heat tolerance. It was noticeable that FLW QTLs on chromosome 6A had same direction additive effects as well as the ones on 3B but the direction associated with QTLs on 6A was opposite to that of QTLs on 3B suggesting an antagonistic relationship. Other major QTLs associated with FLW, such as *QFlw.cz-3A* and *QFlw.cz-5A*, were related to grain yield, grains

m^{-2}, spikes m^{-2}, and grains per spike as reported by Dilbirligi et al. (2006) and Kato et al. (2000).

Thirteen QTLs were detected for FLL. The MDW233 alleles increased FLL at four loci located on chromosomes 7A, 5B, and 2D accounting for 14.4-20.7% of the phenotypic variation whereas SS8641 increased FLL at the other nine loci on 1A, 2A, 4A, 6A, 1B, 1D, and 5D, accounting for 6.4-18.5% of the phenotypic variation. Among them, two QTLs (*QFll.cz-1A.1* and *QFll.cz-1A.2*) on chromosome 1A overlapped at *Xbarc28* which also flanked *QFla.cz-1A.1* and *QFla.cz-1A.2* for FLA. At these four loci, favorable alleles were from SS8641 and explained 9.1-18.5% of the phenotypic variation. In previous studies, *Xbarc28* was also linked to QTLs for spike length (Marza et al., 2006). Additionally, the same region was also associated with QTLs and meta-QTLs for yield components (Zhang et al., 2010). These results suggested the existence of important genes/QTLs and that high resolution mapping would be necessary to determine if the effects were due to pleiotropy or closely linked QTLs. Two major QTLs on chromosome 4A and 5B contributed more than 1 cm to FLL in the 2012 greenhouse study. The SS8641 allele increased FLL at *QFll.cz-4A* but decreased FLL at *QFll.cz-5B.1*. Both of these two QTLs were located in the same region associated with agronomic traits such as spike length, spike compactness, and plant height (Sourdille et al., 2003). Moreover, major QTL *QFll.cz-5D* was significant for both additive and epistatic interaction effects. This same region was also reported to contain QTLs for grain quality traits related to dough physical properties (Huang et al., 2006) and epistatic QTLs for yield related traits

such as grains spike^{-1} and 100-grain weight (Jia et al., 2013a). Furthermore, a PHT QTL on chromosome 7A (McCartney et al., 2005) was located in the same region as *QFll.cz-7A* identified in this study. This region, flanked by *Ppd-D1-Xsnp2869*, was associated with both FLL and FLA explaining an average of 16.6% of the phenotypic variation across four environments. This is possibly due to the pleiotropic effects of *Ppd-D1* which accelerates wheat development in long days and affects the number of leaf and spikelet primordia number (Borràs-Gelonch et al., 2012; Foulkes et al., 2004).

QTLs for the derived traits FLS and FLA were also identified. Of the eleven QTLs detected for FLS, nine (81.8%) explained more than 10% of the phenotypic variation and QTLs on 5A, 7A, 2B, and 3D were detected in more than one environment. In addition, the twelve QTLs identified for FLA explained, on average, 13.5% of the phenotypic variation. To my knowledge, these are some of the first QTLs reported for these leaf morphology traits in wheat.

Genetic complexity of plant architecture

Compared with studies involving only additive QTLs (Bian et al., 2014; Xue et al., 2008a), I also examined epistatic effects and their interactions with environment revealing additional information on the genetic composition of plant architecture traits. In the six environments included in this study, seventy four additive QTLs and twelve pairs of epistatic QTLs were identified. Among them four additive QTLs and one pair of epistatic QTLs interacted with the environment. The results showed that both additive and epistatic effects were essential genetic bases of wheat plant

architecture and their effects were subject to environment modifications. The relative magnitude of these effects is shown in Figure 3.4. This indicated that, among all genetic effects, additive effects were the main contributors (>70%) to plant architecture variation in this DH population. It is interesting to note that only four significant additive QTLs were involved in epistatic interactions suggesting that epistasis can contribute to quantitative traits expression through the interactions of non-significant loci. Similarly, Zhang et al. (2008) found that 25% of additive-effect QTLs were involved in the epistatic interactions in wheat plant height. Additionally, I found that the locus flanked by *Xsnp3389-Xsnp3344* (significant additive effect for FLW) on 2B and the locus flanked by *Xsnp4177-Xsnp4179* (significant additive effect for FLL) on 5D, contributed to PHT and FLA respectively, when they were involved in epistatic interactions. This suggests that QTLs may express pleiotropic effects through their interactions with other loci. Furthermore, the additive effect of *QPht.cz-7A.1* was reduced after taking into account its epistatic interaction with the locus flanked *by Xsnp3754-Xsnp4981* and that the additive effect of *QFla.cz-2A.1* was enhanced by interacting with *QFll.cz-5D*. These antagonistic and synergistic epistatic interactions not only added complexity to the genetic control of plant architecture traits but also provides important information for designing schemes to pyramid beneficial alleles in breeding programs.

Conclusion

This study is one of the few dedicated to QTL mapping of plant architecture traits in hexaploid wheat. I identified several new QTLs and QTL clusters that were shown to affect the expression of PHT, FLL, FLW, FLA, and FLS such as *QPht.cz-2D.2* for

PHT, *QFll.cz-1A.1* for FLL, and the QTL clusters on chromosome 6A and 3B for FLW. Those QTLs could be used for marker assisted selection in breeding programs to modify plant architecture traits.

Chapter 4: Quantitative trait loci mapping of spike characteristics in a doubled haploid population of soft red winter wheat

Abstract

Understanding the genetic basis of spike characteristics in wheat is important for breeding wheat cultivars with higher yield potential. In this study, a doubled haploid population of 124 lines was used to evaluate six spike traits 1) spike length (SL), 2) fertile spikelet number per spike (FSN), 3) sterile spikelet number per spike (SSN), 4) total spikelet number per spike (TSN), 5) spike compactness (SC), and 6) grains per spikelet (GSP). Quantitative trait loci (QTL) mapping was conducted based on the data collected from five year-location trials. A total of 109 QTLs were detected for all traits. In addition, 13 QTL-by-environment and 20 epistatic interactions were also identified. Major QTLs *QSl.cz-1A*/ *QFsn.cz-1A* for SL and FSN explained up to 30.9% of the phenotypic variation, *QGsp.cz-2B*.1 for GSP explained up to 15.6% of the phenotypic variation, and *QSc.cz-5A.3* for SC explained up to 80.2% of the phenotypic variation. When combining the digenic interaction effect, the average contribution of *QFsn.cz-1A* to FSN in each environment was enhanced by 19%. QTLs for correlated traits in the same genomic region formed QTL clusters on chromosomes 1A, 5A, 2B, 3B, 5B, 1D, and 5D.The findings of this study will aid in the improvement of wheat spike characteristics and hence the grain yield potential in breeding programs.

Introduction

Wheat (*Triticum aestivum* L.) is a major food crop across the globe. Improving its yield potential has irrefutable importance in meeting the food demand from increasing population worldwide. The grain yield of wheat is largely determined by yield components out of which the three most important are spikes per unit area, grains per spike, and grain weight (Dilbirligi et al., 2006; Mengistu et al., 2012). Previous studies have shown that grain yield variation is mostly associated with grain number changes where grain number, expressed as grains m^{-2}, is the product of spikes m^{-2} and grains per spike and that there appears to be less opportunity for genetic yield improvement by selecting heavier grains (Fischer, 2011; Frederick and Bauer, 1999). Increases in grains per spike or/and spikes m^{-2} have contributed to wheat yield improvement in the past decades (Ma et al., 2007b). Spike characteristics including spike length (SL), total spikelet number per spike (TSN), fertile spikelet number per spike (FSN), sterile spikelet number per spike (SSN), spike compactness (SC), and grains per spikelet (GSP) determine the number of grains per spike, and thus, to a certain extent, determine the yield potential.

Spike characteristics are quantitative traits under quantitative trait loci (QTL) control and subject to environmental influence (Cui et al., 2012; Ma et al., 2007b). Genetic dissection of spike characteristics could facilitate improving grain yield potential of wheat. Several domestication genes, such as *Q*, compactum *(C)*, and sphaerococcum (*S1)* are related to wheat spike morphology and have been identified on chromosomes 5A, 2D, and 3D respectively (Faris et al., 2003; Faris and Gill, 2002; Johnson et al.,

2007a; Rao, 1977). The *Q* gene confers a free-threshing spike and pleiotropically influences many other domestication related traits, including plant height, glume keeledness, rachis toughness, spike type and spike emergence time, resulting in tougher stems and higher yields (Faris et al., 2003; Simons et al., 2006; Sormacheva et al., 2014). The *C* gene is located on the long arm of chromosome 2D near the centromere and affects spike compactness, grain size, grain shape, and grain number per spike (Johnson et al., 2007a). The *S1* gene confers rigid short culms, straight flag leaves, dense spikes, hemispherical glumes, and small spherical grains (Rao, 1977). In addition to these loci, previous studies have identified genomic regions associated with spike-related traits on all twenty one wheat chromosomes (Borner et al., 2002; Cui et al., 2012; Deng et al., 2011; Kumar et al., 2007; Ma et al., 2007b; Marza et al., 2006; Wang et al., 2011). For example, Cui et al. (2012) detected 190 QTLs across all wheat chromosomes for seven spike-related traits in two recombinant inbred line populations. Eighteen of the detected QTLs were major QTLs and were significant across multiple environments. Ma et al. (2007b) investigated the additive, dominant and epistatic effects of QTLs for SL, FSN, SSN, TSN, and SC in a recombinant inbred line population and also from an immortalized F_2 population derived from the same parents and found 18 genomic regions on chromosomes 1A, 1B, 2D, 3B, 4A, 5A, 5B, and 7A to be associated with spike characteristics. Additionally, Kumar et al. (2007) identified QTLs for SL on chromosomes 1A, 1B, 1D, 2B, 2D, 4A, 5A, and 5D and QTLs for TSN on 2D, 4A, 4D, 5A, and 6A. These results demonstrated that multiple loci with unequal effects can affect spike traits and that epistasis and dominance effects are also indisputable components of genetic architecture of spike

characteristics. Furthermore, mapping agronomically important QTLs as Mendelian factors in wheat was also reported by Uauy et al. (2006) after rice (Ashikari et al., 2005) and tomato (Frary et al., 2000). Similarly, Deng et al. (2011) investigated wheat spike traits in a F_2 population, derived from the cross between an elite cultivar Laizhou953 and an introgression line 05210 (in Laizhou953 background). This population showed a clear 3:1 segregation ratio for spike number per plant, spike length, and grain number per spike. The underlying QTL was mapped to chromosome 4B and explained 30.1 to 67.6% of the phenotypic variation in two environments. Fine mapping and molecular characterization of this region have not been reported yet.

In this study, I used a doubled haploid population derived from two soft red winter wheat cultivars that showed a wide range of phenotypic variation for spike characteristics. A previously constructed linkage map that spanned 1978 cM was used to study the genetic basis of six spike traits (Chapter 2 of this dissertation). The objectives of this study were to identify QTLs affecting spike characteristics as well as their closely linked markers for use by breeding programs and future fine mapping.

Materials and Methods

Genetic resources and phenotypic traits evaluation

A doubled-haploid (DH) population derived from a cross between a soft red winter wheat germplasm line MD01W233-06-1 (MDW233) (Costa et al., 2010) and a soft red winter wheat cultivar SS8641 (Johnson et al., 2007b) was used. MDW233 carries the *Rht-D1b* dwarfing gene the *Ppd-D1b* photoperiod sensitive allele as well as the

1RS/1AL translocation. A genetic linkage map with single nucleotide polymorphism (SNPs), simple sequence repeats (SSRs), and a morphological marker (coleoptile color) was previously constructed with an average interval length of 2.3 cM .

The DH population, comprised of 124 lines, and its two parents were evaluated at five year-location environments in Maryland and North Carolina: Clarksville, MD 2013 (E1), Clarksville, MD 2014 (E2), Queenstown, MD 2013 (E3), Queenstown, MD 2014 (E4), and Kinston, NC 2014 (E5). The population was grown in field plots arranged in a randomized complete block design with two replications. Each field plot consisted of seven rows separated by 15.2 cm. Seed density was 22 seeds per 0.305 m in each row. Soil fertility management followed recommended management practices for each location. All trials were sprayed with the metconazole fungicide (Caramba®, BASF Corporation) at anthesis to reduce potential infection by *Fusarium graminearum* and other diseases.

Ten plants in the middle rows from each plot were randomly selected for spike traits evaluation. Traits examined included spike length (SL) in centimeters, measured from the base of the rachis to the top of the uppermost spikelet, fertile spikelet number per spike (FSN), and sterile spikelet number per spike (SSN). Total spikelet number per spike (TSN) was equal to FSN plus SSN. Spike compactness (SC) was derived by dividing TSN by SL and grains per spikelet (GSP) was derived by dividing grain number per spike by FSN.

Phenotypic data analysis

Phenotypic data analysis was performed using SAS version 9.3 (SAS Institute, Raleigh, NC 2013) to compare differences among DH lines and environments. Phenotypic value for SL, FSN, SSN, TSN, SC, and GSP for 10 plants from each DH line in each replication was averaged before analyses. Simple summary statistics for six spike traits were calculated by the PROC MEANS procedure of SAS. Analysis of variance (ANOVA) for SL, FSN, SSN, TSN, SC, and GSP was performed separately for each environment and for five environments combined by the PROC GLM procedure. The linear model for ANOVA for single environment analysis was $Y_{ij}=\mu + g_i+ r_j+\varepsilon_{ij}$, where μ is the overall mean, Y_{ij} is the phenotypic value of the i^{th} DH line in j^{th} replication, g_i is the fixed effect of the i^{th} DH line, r_j is the fixed effects of j^{th} replication, and ε_{ij} is the random effects of error associated with Y_{ij} and for combined analysis $Y_{ijk}=\mu + g_i+ r_{jk} + e_k + \varepsilon_{ijk}$, where μ is the overall mean, Y_{ijk} is the phenotypic value of the i^{th} DH line in j^{th} replication of k^{th} environment, g_i is the fixed effect of the i^{th} DH line, r_{jk} is the fixed effects of j^{th} replication of k^{th} environment, e_k is the fixed effect of the k^{th} environment, and ε_{ijk} is the random effect of error associated with Y_{ijk}. Pearson's correlation coefficients were calculated by the PROC CORR procedure to detect the association among spike traits. Broad-sense heritability (h^2) (defined as $h^2= \sigma_G^2/(\sigma_G^2+(\sigma_{GE}^2/e)+ (\sigma_E^2/re))$, where σ_G^2 is the variance of genotypic effect, σ_{GE}^2 is the genotype × environment variance, and e and r are the number of environments and replicates, respectively) for each trait was calculated on a family mean basis by the PROC MIXED procedure, as described by Holland et al. (2003).

QTL detection

Mapping QTLs for spike characteristics was performed using two methods. First, inclusive composite interval mapping (ICIM) was conducted to detect QTLs with additive effects by the ICIM-ADD module of IciMapping version 4.0 (Li et al., 2008). The walking speed for all traits was 1 cM. Reference LOD values were determined by 1, 000 permutations (Doerge, 2002). Type I error to determine the LOD from the permutation test was 0.05 and the LOD threshold to declare the presence of a significant QTL was 3.0. Secondly, QTL epistasis (Q×Q), QTL× environment (Q×E) and epistasis × environment (QQ×E) interaction effects were detected by QTLNetwork version 2.1 using a mixed-model based composite interval mapping (MCIM) (Wang et al., 1999; Yang et al., 2007). Q×E, Q×Q, and QQ×E effects were estimated by the Monte Carlo Markov Chain method with a scanning speed of 1 cM step with the experiment-wise type I error for putative QTL detection of 0.05. In both methods, the position at which the LOD score curve reached its maximum was used as the estimate of the QTL location.

Results

Phenotypic analysis

Five different field trials were conducted at three locations over two years to evaluate spike characteristics of the DH population as well as the parental genotypes MDW233 and SS8641. Mean values of traits at each trial are shown in Table 4.1. SS8641 had longer spikes, also more fertile and total spikelets per spike as well as more grains per spikelet; MDW233 had more sterile spikelets per spike. The compactness was similar between the parents. In all trials, the DH population showed

significant variation and transgressive segregation was obvious with data distributed beyond the parental values, suggesting polygenic inheritance of the investigated traits (Table 4.1). ANOVA results showed that significant differences existed between DH lines and between environments at $p<0.001$ level in the performance of six spike traits (Table 4.2). Estimates of heritability (on a family mean basis) of the traits varied from trait to trait, ranging from 88% to 95%. The TSN had the highest heritability of 95% whereas GSP had the lowest (Table 4.2). Correlation coefficients among the spike traits in different trials are presented in Table 4.3. SL showed a significant positive correlation with FSN and TSN but a negative correlation with SC across all five environments. There was a positive correlation between TSN and FSN. A positive correlation was also found between TSN and SC. SC was positively correlated with SSN, FSN and TSN in almost all of the environments. GSP was negatively correlated with SSN and had no significant relationships with both SL and FSN except in E3. Significant negative correlations were also observed between GSP and TSN in E1 and E2 so was GSP and SC in E1, E2, and E3. The strongest correlation was observed between TSN and FSN.

Table 4.1 Phenotypic values for spike characteristics: spike length (SL, cm), sterile spikelet number per spike (SSN), fertile spikelet number per spike (FSN), total spikelet number per spike (TSN), spikelet compactness (SC), and grain number per spikelet (GSP) in the MD01W233-06-1 × SS8641 doubled haploid population evaluated in five field trials from 2013 to 2014: Clarksville 2013 (E1), Clarksville 2014 (E2), Queenstown 2013 (E3), Queenstown 2014 (E4), Kinston 2014 (E5).

		Parents		DH lines				
Traits	Environments	MDW233	SS8641	Mean	Std. Dev.	Minimum	Maximum	CV[§]
SL	E1	6.6	7.3	7.0	0.5	5.7	8.4	7.5%
	E2	6.9	7.7	7.3	0.5	6.3	8.5	6.9%
	E3	7.0	8.0	7.2	0.5	6.0	8.6	7.3%
	E4	6.1	6.9	6.8	0.5	5.6	8.3	7.5%
	E5	7.1	8.4	7.5	0.5	6.2	9.0	7.1%
FSN	E1	13.0	15.7	14.3	1.1	11.8	17.3	7.6%
	E2	14.4	16.5	15.2	0.9	13.0	17.6	6.0%
	E3	14.6	16.3	14.9	1.0	12.5	17.4	6.8%
	E4	12.5	13.8	14.0	0.9	11.5	16.2	6.3%
	E5	14.8	17.0	16.1	1.2	13.7	20.2	7.4%
SSN	E1	2.1	1.8	1.8	0.5	0.8	3.1	25.4%
	E2	1.9	1.8	2.2	0.4	1.3	3.6	20.3%
	E3	1.6	1.1	1.7	0.5	0.3	3.5	31.8%
	E4	1.6	1.5	1.2	0.4	0.3	2.5	34.1%
	E5	2.5	1.8	2.4	0.6	1.2	4.1	23.0%
TSN	E1	15.1	17.5	16.2	1.1	14.1	19.2	6.6%
	E2	16.2	18.3	17.4	1.0	15.2	20.2	5.6%
	E3	16.1	17.4	16.6	1.1	14.3	19.4	6.5%
	E4	14.0	15.3	15.2	0.9	13.0	17.7	6.0%
	E5	17.2	18.8	18.5	1.3	16.1	22.3	6.9%
SC	E1	2.3	2.4	2.3	0.2	2.0	2.9	6.5%
	E2	2.4	2.4	2.4	0.1	2.0	2.8	5.5%
	E3	2.3	2.2	2.3	0.1	1.9	2.7	6.4%
	E4	2.3	2.2	2.3	0.1	2.0	2.6	5.3%
	E5	2.4	2.2	2.5	0.2	2.1	3.0	6.7%
GSP	E1	2.7	2.9	2.8	0.2	2.1	3.3	8.5%
	E2	2.3	2.4	2.2	0.2	1.8	2.6	8.1%
	E3	3.0	3.1	2.8	0.3	2.2	3.4	9.2%
	E4	2.8	2.8	2.8	0.2	2.3	3.3	7.1%
	E5	2.4	2.7	2.6	0.2	2.3	3.2	7.2%

§ coefficient of variation

Table 4.2 Pooled analysis of variance and heritability estimates for spike characteristics: spike length (SL, cm), sterile spikelet number per spike (SSN), fertile spikelet number per spike (FSN), total spikelet number per spike (TSN), spikelet compactness (SC), and grain number per spikelet (GSP) in the MD01W233-06-1 × SS8641 doubled haploid population evaluated in five field trials from 2013 to 2014.

		Mean square					
Source of Variation	df	SL	SSN	FSN	TSN	SC	SSP
Environment	4	20.82***	55.20***	161.70***	388.27***	1.71***	17.08***
Rep (environment)	5	0.89***	2.74***	4.41***	4.68***	0.05***	3.62***
Genotype	123	2.25***	1.65***	7.94***	8.92***	0.17***	0.31***
Genotype × environment	492	0.11***	0.18***	0.64***	0.63***	0.01***	0.04***
R^2		0.91	0.87	0.89	0.95	0.91	0.91
Heritability (h^2)		0.95 (0.01)	0.89 (0.02)	0.92 (0.01)	0.92 (0.01)	0.94 (0.01)	0.88 (0.02)

* Significant at the 0.05 probability level.
** Significant at the 0.01 probability level.
*** Significant at the 0.001 probability level.

Table 4.3 Pearson correlation coefficients among spike characteristics: spike length (SL, cm), sterile spikelet number per spike (SSN), fertile spikelet number per spike (FSN), total spikelet number per spike (TSN), spikelet compactness (SC) in the MD01W233-06-1 × SS8641 the doubled haploid population evaluated in five field trials from 2013 to 2014.

Environments		SSN	FSN	TSN	SC	GSP
Clarksville 2013	SL	-0.26**	0.68***	0.58***	-0.55***	0.14
	SSN		-0.26**	0.17	0.47***	-0.39***
	FSN			0.91***	0.15	-0.05
	TSN				0.36***	-0.22*
	SC					-0.38***
Clarksville 2014	SL	0.00	0.66***	0.61***	-0.60***	0.07
	SSN		-0.09	0.37***	0.36***	-0.62***
	FSN			0.89***	0.10	0.05
	TSN				0.25**	-0.23*
	SC					-0.31***
Queenstown 2013	SL	-0.18*	0.71***	0.58***	-0.56***	0.25**
	SSN		-0.14	0.37***	0.56***	-0.62***
	FSN			0.87***	0.07	0.23**
	TSN				0.35***	-0.09
	SC					-0.36***
Queenstown 2014	SL	0.03	0.71***	0.71***	-0.60***	0.06
	SSN		-0.19*	0.27**	0.27**	-0.39***
	FSN			0.90***	0.01	0.15
	TSN				0.13	-0.03
	SC					-0.12
Kinston 2014	SL	-0.05	0.62***	0.55***	-0.50***	0.13
	SSN		-0.06	0.38***	0.45***	-0.40***
	FSN			0.90***	0.27**	0.16
	TSN				0.44***	-0.03
	SC					-0.16

* Significant at the 0.05 probability level.
** Significant at the 0.01 probability level.
*** Significant at the 0.001 probability level.

QTL detection

Up to 109 putative additive QTLs for the six spike traits were detected by ICIM (Table 4.4) and their map positions are shown in Figure 4.1. The number of QTLs detected for each trait ranged from 16 to 22, specifically, 20 for FSN, 12 for SC, 20 for SL, 19 for SSN, 16 for GSP, and 22 for TSN. These QTLs were located on 15 chromosomes and formed QTL clusters. In addition, 21 regions were detected to be associated with more than one trait.

Spike length

Twenty chromosome regions were identified to govern SL in the present study. Chromosome 1A and 1D each had one QTL. Chromosome 3A and 6A each had two QTLs. Three QTLs were detected on each of the chromosomes 3B, 2D, and 5D, and five QTLs were detected on 5A. Major QTLs (PVE >10%) for SL were identified on chromosomes 1A, 5A, 6A, 3B, and 5D. SS8641 alleles were associated with longer spikes at seventeen (85%) loci whereas MDW233 alleles were associated with longer spike at the other three loci on chromosome 2D. QTL *QSl.cz-1A* was detected in four environments (E1, E2, E3, and E5) and mapped to the interval *Xsnp1970- Xbarc28* on chromosome 1A (Figure 4.1), explaining 9.2-23.6% of the phenotypic variation of SL. This QTL was also significantly associated with FSN and TSN explaining 16.7 to 30.9% and 8.4 to 20.2% of the phenotypic variation of FSN and TSN, respectively. In all cases, the favorable alleles were contributed by SS8641 and the additive effects of *QSl.cz-1A* were the largest among all QTLs for SL, FSN, and TSN suggesting an essential region for spike characteristics. Major SL QTL *QSl.cz-3B.1* localized in the

same interval with FSN QTL *QFsn.cz-3B.1*. QTLs formed clusters on chromosomes 5D, 3B, and 5A.

Spike compactness

Twelve QTLs, distributed on six chromosomes, were significantly associated with SC. The major QTL *QSc.cz-5A.3* was detected in E2, E3, and E5 and had mostly large additive effects explaining up to 80.2% of the phenotypic variation. *QSc.cz-5A.1* also explained a large portion of the observed variation (26.7%) in E1. Additionally, *QSc.cz-5A.3* clustered with *QSc.cz-5A.1* and *QSc.cz-5A.2*. Clustering of consistent major QTLs was also identified on chromosome 2B and 5D. MDW233 contributed positive alleles at clusters on 5A and 5D whereas SS8641 increased SC at loci on chromosome 3A, 2B, 5B, and 6D.

Grains per spikelet

Sixteen QTLs were detected for GSP. They were distributed on chromosomes 1A, 5A, 6A, 7A, 2B, 3B, 5B, 6B, 1D, and 2D. QTL *QGsp.cz-2B.1* was detected in E1, E3, E4, and E5 accounting for 6.0-15.6% of the phenotypic variation and mapped to a position close to the major QTL *QGsp.cz-2B*.2 (LOD=7.4, PVE=13.7%). Four major QTLs mapped to similar positions and overlapped along the short arm of chromosome 5B explaining 11.6 to 14.5% of the phenotypic variation. Another two major QTLs *QGsp.cz-1A.2* and *QGsp.cz-2D* explained 14.2 to 15.5% of the phenotypic variation, respectively. SS8641 contributed favorable alleles for QTLs on chromosomes 1A, 3B, 6B, and 2D.

Fertile spikelet number per spike

Twenty QTLs significantly influenced FSN and mapped to nine chromosomes. QTLs on chromosomes 2D and 2A favored high FSN through MDW233 alleles and the rest were associated with high FSN through SS8641 alleles except for QTL *QFsn.cz-5A.1*.The QTL on chromosome 1A, mapped to the interval *Xsnp1970-Xbarc28*, consistently showed a large effect on FSN. Another consistent QTL *QFsn.cz-2D.2* was mapped to chromosome 2D with a LOD score of 3.3 to 5.3. For *QFsn.cz-2D.2*, the MDW233 allele increased FSN. The remaining QTLs were detected in only one environment. There were six major QTLs for FSN and the phenotypic variation explained by each individual QTL ranged from 10.4 to 30.9%.

Sterile spikelet number per spike

Nineteen QTLs were associated with SSN. For the QTLs located on chromosome 2A, 2B, 5B, and 3D, the SS8641 allele increased SSN, whereas for the QTLs on 1A, 3A, 2D, and 6D, the MDW233 alleles increased SSN. The phenotypic variation explained by these individual QTLs ranged from 3.7 to 30%. QTL *QSsn.cz-2B.2* was identified in E1, E2, E3, and E4 as a major QTL, sharing this interval with *QTsn.cz-2B.3* and *QSc.cz-2B.3*. QTL *QSsn.cz-1A* was coincident with *QGsp.cz-1A.2*. At locus *Ppd-D1*, *QSsn.cz-2D.1* and *QSsn.cz-2D.2* overlapped, each explaining 30% and 7.5% of the phenotypic variation, respectively.

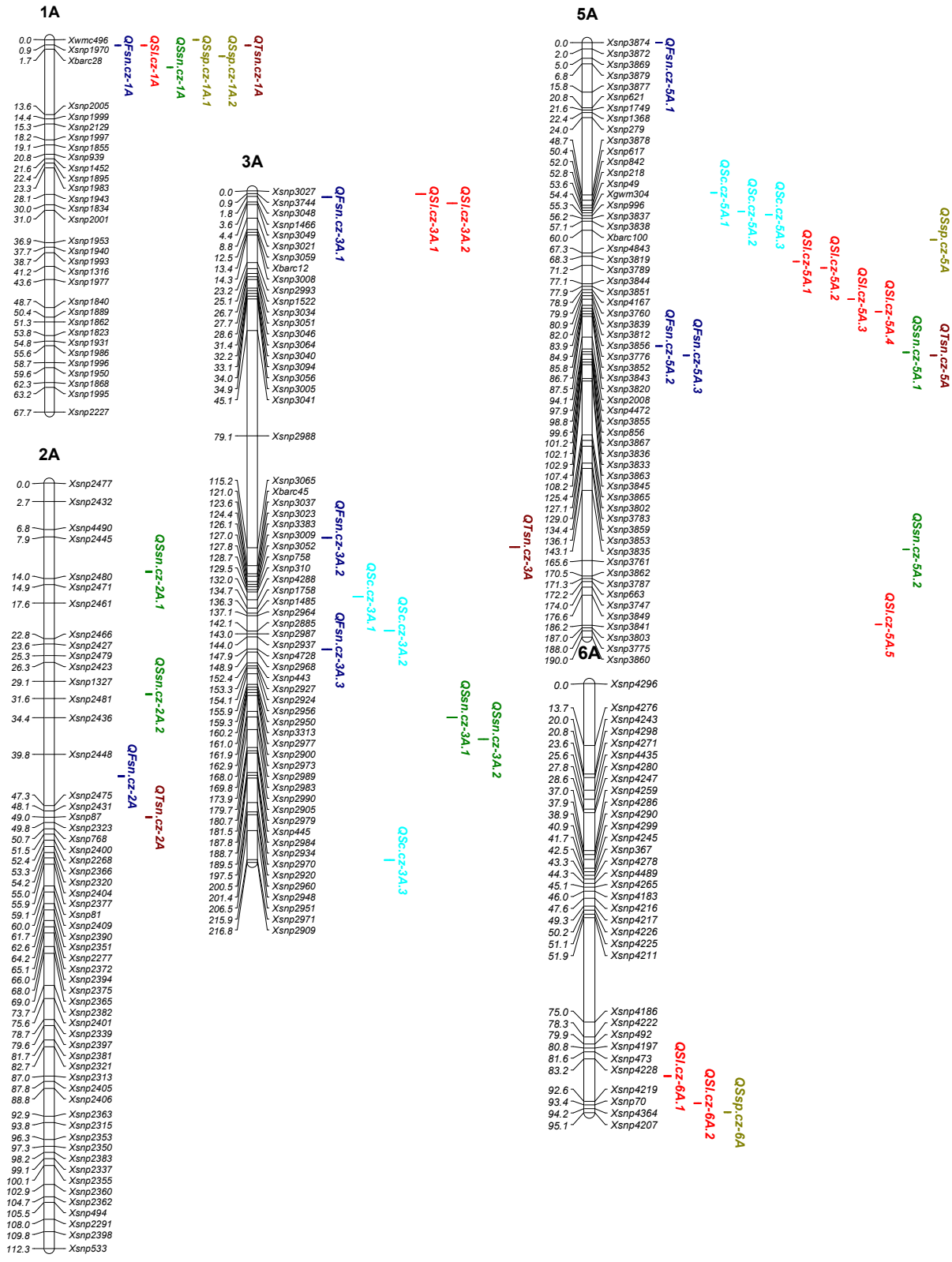
Total spikelet number per spike

Twenty-two chromosome regions were associated with TSN. However, seventeen of them were only detected once. Consistent QTLs included *QTsn.cz-1A, QTsn.cz-2D.2*, *QTsn.cz-2D.3*, *QTsn.cz-2D.4* and *QTsn.ca-5D.1* explaining 8.4 to 20.9% of the

phenotypic variation. For QTLs detected on chromosome 2A, 6B, and 2D, MDW233 alleles decreased TSN. SS8641alleles increased TSN at the remaining loci. QTL clusters were found on chromosomes 2B, 2D, and 5D and the genetic effects of QTLs in each cluster were in the same direction.

QTL× environment, epistasis, and epistasis× environment interactions

In this study, I used a mixed-model based composite interval mapping method to estimate the QTL× environment (Q×E), epistasis (Q×Q), and epistasis× environment (QQ×E) interactions. Thirteen Q×E interactions were detected for SSN, FSN, and TSN, out of which eleven involved intervals associated with significant additive effects. The other two were non-significant QTLs (LOD<3) for additive effects. E4, E5, and E3 each had six, five, and two Q×E interactions, respectively. No Q×E interaction was detected in E1 and E2. The contribution of Q×E interactions ranged from 0.6-2.2%. Twenty pairs of Q×Q interactions were detected for all six traits in the DH population and three QQ×E interactions were also identified (Table 4.6). Twelve intervals involved in Q×Q interactions were significant for additive effects. The heritability estimates of Q×Q and QQ×E interactions ranged from 0.3 to 4.9% and 0.9 to 1.4%.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37.7 Xsnp1940
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58.7 Xsnp1996
59.6 Xsnp1950
62.3 Xsnp1868
63.2 Xsnp1995
67.7 Xsnp2227
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QSl.cz-1A
QSsn.cz-1A
QSsp.cz-1A.1
QSsp.cz-1A.2
QTsn.cz-1A
2A
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7.9 Xsnp2445
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17.6 Xsnp2461
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34.4 Xsnp2436
39.8 Xsnp2448
47.3 Xsnp2475
48.1 Xsnp2431
49.0 Xsnp87
49.8 Xsnp2323
50.7 Xsnp768
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52.4 Xsnp2268
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55.9 Xsnp2377
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60.0 Xsnp2409
61.7 Xsnp2390
62.6 Xsnp2351
64.2 Xsnp2277
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66.0 Xsnp2394
68.0 Xsnp2375
69.0 Xsnp2365
73.7 Xsnp2382
75.6 Xsnp2401
78.7 Xsnp2339
79.6 Xsnp2397
81.7 Xsnp2381
82.7 Xsnp2321
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87.8 Xsnp2405
88.8 Xsnp2406
92.9 Xsnp2363
93.8 Xsnp2315
96.3 Xsnp2353
97.3 Xsnp2350
98.2 Xsnp2383
99.1 Xsnp2337
100.1 Xsnp2355
102.9 Xsnp2360
104.7 Xsnp2362
105.5 Xsnp494
108.0 Xsnp2291
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QSsn.cz-2A.2
QFsn.cz-2A
QTsn.cz-2A
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3.6 Xsnp1466
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8.8 Xsnp3021
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13.4 Xbarc12
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23.2 Xsnp2993
25.1 Xsnp1522
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27.7 Xsnp3051
28.6 Xsnp3046
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32.2 Xsnp3040
33.1 Xsnp3094
34.0 Xsnp3056
34.9 Xsnp3005
45.1 Xsnp3041
79.1 Xsnp2988
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121.0 Xbarc45
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124.4 Xsnp3023
126.1 Xsnp3383
127.0 Xsnp3009
127.8 Xsnp3052
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143.0 Xsnp2987
144.0 Xsnp2937
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148.9 Xsnp2968
152.4 Xsnp443
153.3 Xsnp2927
154.1 Xsnp2924
155.9 Xsnp2956
159.3 Xsnp2950
160.2 Xsnp3313
161.0 Xsnp2977
161.9 Xsnp2900
162.9 Xsnp2973
168.0 Xsnp2989
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QSl.cz-3A.2
QSl.cz-3A.1
QFsn.cz-3A.2
QSc.cz-3A.1
QSc.cz-3A.2
QFsn.cz-3A.3
QSsn.cz-3A.1
QSsn.cz-3A.2
QSc.cz-3A.3
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5.0 Xsnp3869
6.8 Xsnp3879
15.8 Xsnp3877
20.8 Xsnp621
21.6 Xsnp1749
22.4 Xsnp1368
24.0 Xsnp279
48.7 Xsnp3878
50.4 Xsnp617
52.0 Xsnp842
52.8 Xsnp218
53.6 Xsnp49
54.4 Xgwm304
55.3 Xsnp996
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57.1 Xsnp3838
60.0 Xbarc100
67.3 Xsnp4843
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71.2 Xsnp3789
77.1 Xsnp3844
77.9 Xsnp3851
78.9 Xsnp4167
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80.9 Xsnp3839
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188.0 Xsnp3775
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QFsn.cz-5A.2
QFsn.cz-5A.3
QTsn.cz-3A
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20.8 Xsnp4298
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80.8 Xsnp4197
81.6 Xsnp473
83.2 Xsnp4228
92.6 Xsnp4219
93.4 Xsnp70
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QSc.cz-5A.3
QSc.cz-5A.2
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QSl.cz-5A.4
QSsp.cz-5A
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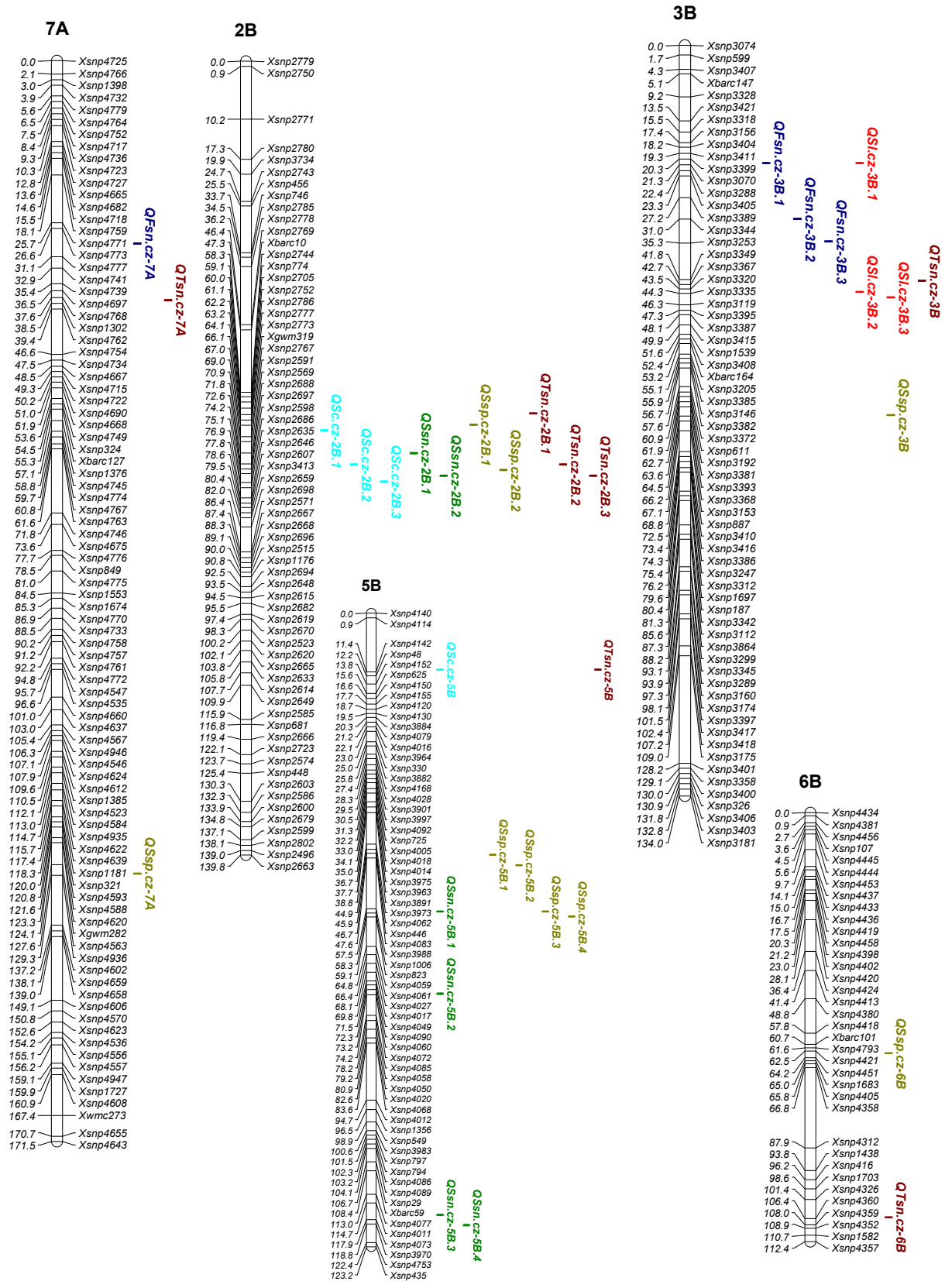
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78.5 Xsnp849
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QTsn.cz-7A
QSsp.cz-7A
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102.1 Xsnp2620
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109.9 Xsnp2649
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QSc.cz-2B.2
QSc.cz-2B.3
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QTsn.cz-2B.2
QTsn.cz-2B.3
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59.1 Xsnp823
64.8 Xsnp4059
66.4 Xsnp4061
68.1 Xsnp4027
69.8 Xsnp4017
71.5 Xsnp4049
72.3 Xsnp4090
73.2 Xsnp4060
74.2 Xsnp4072
78.2 Xsnp4085
79.2 Xsnp4058
80.9 Xsnp4050
82.6 Xsnp4020
83.6 Xsnp4068
94.7 Xsnp4012
96.5 Xsnp1356
98.9 Xsnp549
100.6 Xsnp3983
101.5 Xsnp797
102.3 Xsnp794
103.2 Xsnp4086
104.1 Xsnp4089
106.7 Xsnp29
108.4 Xbarc59
113.0 Xsnp4077
114.7 Xsnp4011
117.9 Xsnp4073
118.8 Xsnp3970
122.4 Xsnp4753
123.2 Xsnp435
QSc.cz-5B
QSsn.cz-5B.1
QSsn.cz-5B.2
QSsn.cz-5B.3
QSsn.cz-5B.4
QSsp.cz-5B.1
QSsp.cz-5B.2
QSsp.cz-5B.3
QSsp.cz-5B.4
QTsn.cz-5B
3B
0.0 Xsnp3074
1.7 Xsnp599
4.3 Xsnp3407
5.1 Xbarc147
9.2 Xsnp3328
13.5 Xsnp3421
15.5 Xsnp3318
17.4 Xsnp3156
18.2 Xsnp3404
19.3 Xsnp3411
20.3 Xsnp3399
21.3 Xsnp3070
22.4 Xsnp3288
23.3 Xsnp3405
27.2 Xsnp3389
31.0 Xsnp3344
35.3 Xsnp3253
41.8 Xsnp3349
42.7 Xsnp3367
43.5 Xsnp3320
44.3 Xsnp3335
46.3 Xsnp3119
47.3 Xsnp3395
48.1 Xsnp3387
49.9 Xsnp3415
51.6 Xsnp1539
52.4 Xsnp3408
53.2 Xbarc164
55.1 Xsnp3205
55.9 Xsnp3385
56.7 Xsnp3146
57.6 Xsnp3382
60.9 Xsnp3372
61.9 Xsnp611
62.7 Xsnp3192
63.6 Xsnp3381
64.5 Xsnp3393
66.2 Xsnp3368
67.1 Xsnp3153
68.8 Xsnp887
72.5 Xsnp3410
73.4 Xsnp3416
74.3 Xsnp3386
75.4 Xsnp3247
76.2 Xsnp3312
79.6 Xsnp1697
80.4 Xsnp187
81.3 Xsnp3342
85.6 Xsnp3112
87.3 Xsnp3864
88.2 Xsnp3299
93.1 Xsnp3345
93.9 Xsnp3289
97.3 Xsnp3160
98.1 Xsnp3174
101.5 Xsnp3397
102.4 Xsnp3417
107.2 Xsnp3418
109.0 Xsnp3175
128.2 Xsnp3401
129.1 Xsnp3358
130.0 Xsnp3400
130.9 Xsnp326
131.8 Xsnp3406
132.8 Xsnp3403
134.0 Xsnp3181
QFsn.cz-3B.1
QFsn.cz-3B.2
QFsn.cz-3B.3
QSl.cz-3B.1
QSl.cz-3B.2
QSl.cz-3B.3
QSsp.cz-3B
QTsn.cz-3B
6B
0.0 Xsnp4434
0.9 Xsnp4381
2.7 Xsnp4456
3.6 Xsnp107
4.5 Xsnp4445
5.6 Xsnp4444
9.7 Xsnp4453
14.1 Xsnp4437
15.0 Xsnp4433
16.7 Xsnp4436
17.5 Xsnp4419
20.3 Xsnp4458
21.2 Xsnp4398
23.0 Xsnp4402
28.1 Xsnp4420
36.4 Xsnp4424
41.4 Xsnp4413
48.8 Xsnp4380
57.8 Xsnp4418
60.7 Xbarc101
61.6 Xsnp4793
62.5 Xsnp4421
64.2 Xsnp4451
65.0 Xsnp1683
65.8 Xsnp4405
66.8 Xsnp4358
87.9 Xsnp4312
93.8 Xsnp1438
96.2 Xsnp416
98.6 Xsnp1703
101.4 Xsnp4326
106.4 Xsnp4360
108.0 Xsnp4359
108.9 Xsnp4352
110.7 Xsnp1582
112.4 Xsnp4357
QSsp.cz-6B
QTsn.cz-6B

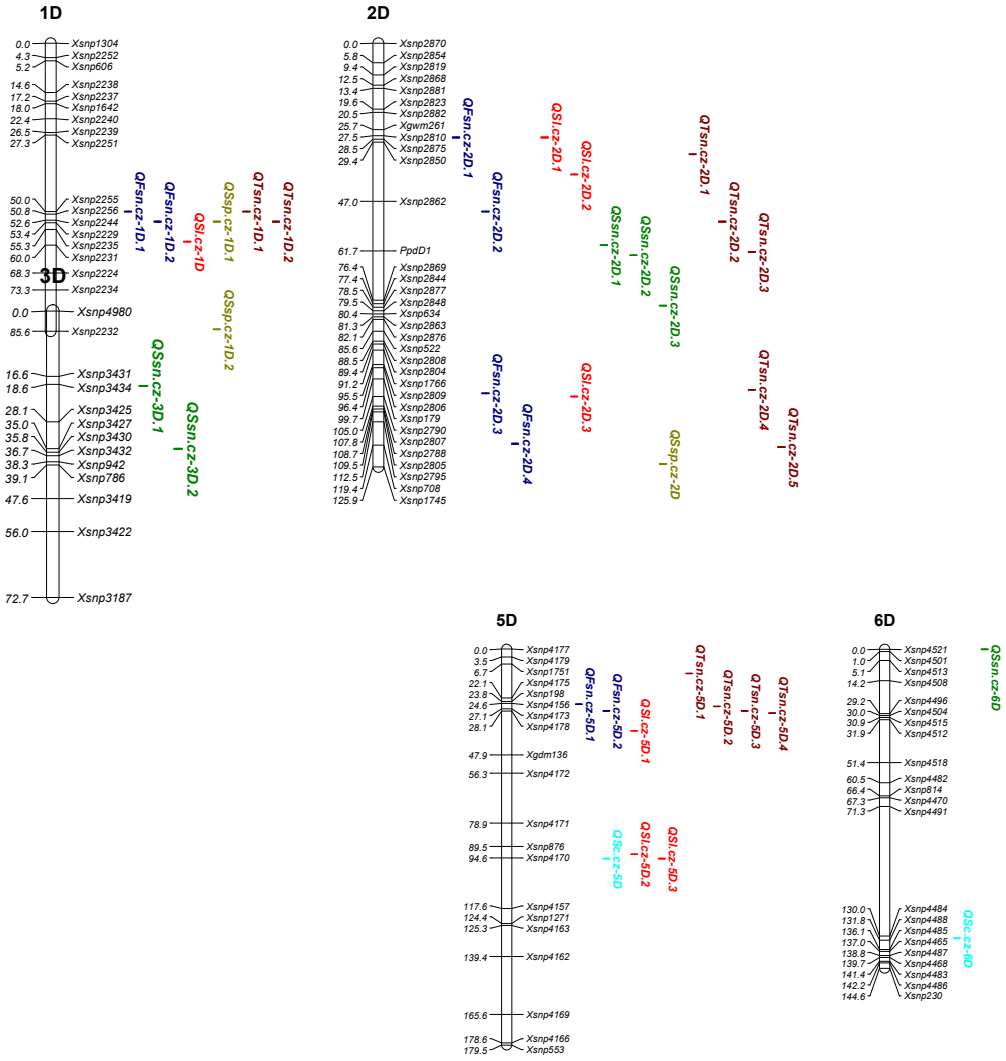


Figure 4.1 Position of quantitative trait loci (QTLs) detected in a doubled haploid mapping population derived from MD01W233-06-1 × SS8641. Locus marker names are shown on the right side of the chromosomes and values to the left of chromosomes show the genetic distance (cM) for each marker. QTLs are labeled with trait abbreviations and the QTL number for each trait. QTLs for the same trait are in the same color.

Table 4.4 Quantitative trait loci (QTLs) for spike characteristics: spike length (SL, cm), sterile spikelet number per spike (SSN), fertile spikelet number per spike (FSN), total spikelet number per spike (TSN), spikelet compactness (SC), and grain number per spikelet (GSP) in the MD01W233-06-1 × SS8641 doubled haploid population evaluated in five field trials from 2013 to 2014.

QTL	Trait	Environment	Position (cM)	Marker interval	LOD score	PVE (%)	Additive effect
QSl.cz-1A	SL	Clarksville 2013	1	*Xsnp1970-Xbarc28*	11.6	23.6	0.25
QSl.cz-1A	SL	Clarksville 2014	1	*Xsnp1970-Xbarc28*	5.7	11.1	0.17
QSl.cz-1A	SL	Kinston 2014	1	*Xsnp1970-Xbarc28*	6.1	9.2	0.16
QSl.cz-1A	SL	Queenstown 2013	1	*Xsnp1970-Xbarc28*	9.3	22.4	0.25
QSl.cz-3A.1	SL	Clarksville 2013	1	*Xsnp3744-Xsnp3048*	3.7	6.5	0.13
QSl.cz-3A.2	SL	Kinston 2014	4	*Xsnp1466-Xsnp3049*	5.0	7.3	0.15
QSl.cz-5A.1	SL	Kinston 2014	70	*Xsnp3819-Xsnp3789*	8.2	13.0	0.20
QSl.cz-5A.1	SL	Queenstown 2013	71	*Xsnp3819-Xsnp3789*	5.0	11.0	0.18
QSl.cz-5A.2	SL	Clarksville 2014	72	*Xsnp3789-Xsnp3844*	6.2	12.5	0.18
QSl.cz-5A.3	SL	Queenstown 2014	82	*Xsnp3812-Xsnp3856*	4.0	9.7	0.16
QSl.cz-5A.4	SL	Clarksville 2013	86	*Xsnp3852-Xsnp3843*	7.0	13.1	0.19
QSl.cz-5A.5	SL	Queenstown 2014	186	*Xsnp3849-Xsnp3841*	2.8	6.7	0.13
QSl.cz-6A.1	SL	Queenstown 2013	87	*Xsnp4228-Xsnp4219*	3.4	7.8	0.15
QSl.cz-6A.2	SL	Clarksville 2013	93	*Xsnp4219-Xsnp70*	6.0	11.0	0.17
QSl.cz-3B.1	SL	Queenstown 2014	21	*Xsnp3399-Xsnp3070*	5.5	13.9	0.19
QSl.cz-3B.2	SL	Clarksville 2013	44	*Xsnp3320-Xsnp3335*	5.3	9.5	0.16
QSl.cz-3B.2	SL	Kinston 2014	44	*Xsnp3320-Xsnp3335*	6.6	9.9	0.17
QSl.cz-3B.3	SL	Clarksville 2014	45	*Xsnp3335-Xsnp3119*	3.0	6.0	0.12
QSl.cz-3B.3	SL	Queenstown 2013	45	*Xsnp3335-Xsnp3119*	5.4	12.1	0.18
QSl.cz-1D	SL	Kinston 2014	59	*Xsnp2235-Xsnp2231*	4.4	6.5	0.14
QSl.cz-2D.1	SL	Kinston 2014	28	*Xsnp2810-Xsnp2875*	2.7	3.7	-0.11
QSl.cz-2D.2	SL	Clarksville 2013	39	*Xsnp2850-Xsnp2862*	2.9	5.5	-0.12
QSl.cz-2D.3	SL	Clarksville 2014	105	*Xsnp179-Xsnp2790*	3.0	5.6	-0.12
QSl.cz-5D.1	SL	Clarksville 2014	37	*Xsnp4178-Xgdm136*	6.1	13.5	0.18
QSl.cz-5D.2	SL	Queenstown 2014	93	*Xsnp876-Xsnp4170*	4.7	12.0	0.17
QSl.cz-5D.3	SL	Kinston 2014	95	*Xsnp4170-Xsnp4157*	4.0	5.8	0.13
QFsn.cz-1A	FSN	Clarksville 2013	1	*Xsnp1970-Xbarc28*	14.2	30.9	0.60
QFsn.cz-1A	FSN	Clarksville 2014	1	*Xsnp1970-Xbarc28*	9.4	16.7	0.37
QFsn.cz-1A	FSN	Kinston 2014	1	*Xsnp1970-Xbarc28*	20.6	30.0	0.65
QFsn.cz-1A	FSN	Queenstown 2013	1	*Xsnp1970-Xbarc28*	11.2	23.9	0.49
QFsn.cz-2A	FSN	Clarksville 2014	43	*Xsnp2448-Xsnp2475*	4.2	7.2	-0.25
QFsn.cz-3A.1	FSN	Kinston 2014	2	*Xsnp3048-Xsnp1466*	3.9	4.1	0.24
QFsn.cz-3A.2	FSN	Clarksville 2013	112	*Xsnp2988-Xsnp3065*	6.1	12.4	0.39
QFsn.cz-3A.3	FSN	Kinston 2014	148	*Xsnp4728-Xsnp2968*	5.0	5.3	0.27
QFsn.cz-5A.1	FSN	Kinston 2014	0	*Xsnp3874-Xsnp3872*	4.3	4.5	-0.25
QFsn.cz-5A.2	FSN	Clarksville 2014	97	*Xsnp2008-Xsnp4472*	2.8	4.5	0.20
QFsn.cz-5A.3	FSN	Queenstown 2014	100	*Xsnp856-Xsnp3867*	3.2	9.3	0.27
QFsn.cz-7A	FSN	Clarksville 2014	29	*Xsnp4773-Xsnp4777*	4.1	6.9	0.24
QFsn.cz-3B.1	FSN	Queenstown 2014	21	*Xsnp3399-Xsnp3070*	2.8	8.1	0.25
QFsn.cz-3B.2	FSN	Kinston 2014	31	*Xsnp3389-Xsnp3344*	4.1	4.3	0.25
QFsn.cz-3B.3	FSN	Queenstown 2013	35	*Xsnp3344-Xsnp3253*	4.7	8.9	0.30
QFsn.cz-1D.1	FSN	Clarksville 2013	50	*Xsnp2251-Xsnp2255*	3.6	6.3	0.27
QFsn.cz-1D.2	FSN	Kinston 2014	53	*Xsnp2244-Xsnp2229*	10.4	12.4	0.41
QFsn.cz-2D.1	FSN	Kinston 2014	28	*Xsnp2810-Xsnp2875*	3.2	3.3	-0.22
QFsn.cz-2D.2	FSN	Clarksville 2013	50	*Xsnp2862-XPpdD1*	3.3	6.3	-0.28
QFsn.cz-2D.2	FSN	Queenstown 2013	56	*Xsnp2862-XPpdD1*	5.3	10.4	-0.33
QFsn.cz-2D.3	FSN	Clarksville 2014	104	*Xsnp179-Xsnp2790*	6.7	11.6	-0.31
QFsn.cz-2D.4	FSN	Kinston 2014	119	*Xsnp2795-Xsnp708*	3.6	3.7	-0.23
QFsn.cz-5D.1	FSN	Queenstown 2014	25	*Xsnp4156-Xsnp4173*	2.7	7.7	0.25
QFsn.cz-5D.2	FSN	Clarksville 2014	28	*Xsnp4173-Xsnp4178*	7.4	12.6	0.33

Table 4.4 Continued

QTL	Trait	Environment	Position (cM)	Marker interval	LOD score	PVE (%)	Additive effect
QSsn.cz-1A	SSN	Clarksville 2013	5	*Xbarc28-Xsnp2005*	2.6	7.0	-0.12
QSsn.cz-2A.1	SSN	Kinston 2014	13	*Xsnp2445-Xsnp2480*	3.8	5.4	0.13
QSsn.cz-2A.2	SSN	Queenstown 2014	31	*Xsnp1327-Xsnp2481*	4.8	7.7	0.11
QSsn.cz-3A.1	SSN	Queenstown 2014	170	*Xsnp2983-Xsnp2990*	8.1	13.8	-0.15
QSsn.cz-3A.2	SSN	Clarksville 2013	177	*Xsnp2990-Xsnp2905*	3.9	9.8	-0.15
QSsn.cz-5A.1	SSN	Kinston 2014	99	*Xsnp3855-Xsnp856*	5.8	8.4	-0.16
QSsn.cz-5A.2	SSN	Kinston 2014	162	*Xsnp3835-Xsnp3761*	3.2	4.8	0.12
QSsn.cz-2B.1	SSN	Kinston 2014	69	*Xsnp2767-Xsnp2591*	8.5	13.0	0.20
QSsn.cz-2B.2	SSN	Clarksville 2014	73	*Xsnp2697-Xsnp2598*	5.3	14.4	0.17
QSsn.cz-2B.2	SSN	Clarksville 2013	74	*Xsnp2697-Xsnp2598*	5.2	12.9	0.17
QSsn.cz-2B.2	SSN	Queenstown 2013	74	*Xsnp2697-Xsnp2598*	6.3	18.3	0.23
QSsn.cz-2B.2	SSN	Queenstown 2014	74	*Xsnp2697-Xsnp2598*	3.2	5.1	0.09
QSsn.cz-5B.1	SSN	Clarksville 2014	58	*Xsnp3988-Xsnp1006*	2.9	7.5	0.12
QSsn.cz-5B.2	SSN	Queenstown 2014	74	*Xsnp4060-Xsnp4072*	4.5	7.5	0.11
QSsn.cz-5B.3	SSN	Kinston 2014	117	*Xsnp4011-Xsnp4073*	4.8	6.8	0.15
QSsn.cz-5B.4	SSN	Queenstown 2014	119	*Xsnp3970-Xsnp4753*	6.0	10.0	0.13
QSsn.cz-2D.1	SSN	Kinston 2014	60	*Xsnp2862-XPpdD1*	16.3	30.0	-0.31
QSsn.cz-2D.2	SSN	Queenstown 2014	63	*XPpdD1-Xsnp2869*	4.5	7.5	-0.11
QSsn.cz-2D.3	SSN	Clarksville 2013	78	*Xsnp2844-Xsnp2877*	5.6	14.4	-0.18
QSsn.cz-2D.3	SSN	Queenstown 2013	78	*Xsnp2844-Xsnp2877*	3.6	10.2	-0.17
QSsn.cz-3D.1	SSN	Kinston 2014	19	*Xsnp3434-Xsnp3425*	2.7	3.7	0.11
QSsn.cz-3D.2	SSN	Clarksville 2014	35	*Xsnp3427-Xsnp3430*	2.7	6.8	0.12
QSsn.cz-6D	SSN	Queenstown 2014	0	*Xsnp4521-Xsnp4501*	3.1	4.8	-0.09
QTsn.cz-1A	TSN	Clarksville 2013	1	*Xsnp1970-Xbarc28*	9.5	19.7	0.47
QTsn.cz-1A	TSN	Clarksville 2014	1	*Xsnp1970-Xbarc28*	5.9	8.4	0.28
QTsn.cz-1A	TSN	Kinston 2014	1	*Xsnp1970-Xbarc28*	13.2	20.0	0.57
QTsn.cz-1A	TSN	Queenstown 2013	1	*Xsnp1970-Xbarc28*	9.3	14.1	0.40
QTsn.cz-2A	TSN	Clarksville 2014	49	*Xsnp87-Xsnp2323*	6.2	8.8	-0.29
QTsn.cz-3A	TSN	Clarksville 2013	115	*Xsnp2988-Xsnp3065*	5.4	10.3	0.34
QTsn.cz-5A	TSN	Queenstown 2014	100	*Xsnp856-Xsnp3867*	2.8	7.4	0.25
QTsn.cz-7A	TSN	Clarksville 2014	38	*Xsnp4768-Xsnp1302*	5.2	7.4	0.27
QTsn.cz-2B.1	TSN	Clarksville 2014	62	*Xsnp2752-Xsnp2786*	2.8	3.8	0.19
QTsn.cz-2B.2	TSN	Queenstown 2013	71	*Xsnp2569-Xsnp2688*	3.5	4.8	0.24
QTsn.cz-2B.3	TSN	Clarksville 2013	73	*Xsnp2697-Xsnp2598*	3.5	6.4	0.27
QTsn.cz-3B	TSN	Queenstown 2013	42	*Xsnp3349-Xsnp3367*	3.5	4.6	0.23
QTsn.cz-5B	TSN	Kinston 2014	11	*Xsnp4114-Xsnp4142*	2.9	3.6	0.24
QTsn.cz-6B	TSN	Queenstown 2013	106	*Xsnp4326-Xsnp4360*	3.2	4.4	-0.23
QTsn.cz-1D.1	TSN	Clarksville 2013	50	*Xsnp2251-Xsnp2255*	3.1	5.7	0.25
QTsn.cz-1D.2	TSN	Kinston 2014	53	*Xsnp2244-Xsnp2229*	5.7	7.4	0.35
QTsn.cz-2D.1	TSN	Kinston 2014	33	*Xsnp2850-Xsnp2862*	3.8	5.2	-0.29
QTsn.cz-2D.2	TSN	Clarksville 2013	53	*Xsnp2862-XPpdD1*	5.4	11.2	-0.36
QTsn.cz-2D.2	TSN	Queenstown 2013	59	*Xsnp2862-XPpdD1*	9.4	14.7	-0.42
QTsn.cz-2D.3	TSN	Clarksville 2014	62	*XPpdD1-Xsnp2869*	4.2	5.9	-0.24
QTsn.cz-2D.3	TSN	Kinston 2014	63	*XPpdD1-Xsnp2869*	8.1	11.5	-0.43
QTsn.cz-2D.3	TSN	Queenstown 2014	68	*XPpdD1-Xsnp2869*	6.5	20.9	-0.41
QTsn.cz-2D.4	TSN	Clarksville 2014	103	*Xsnp179-Xsnp2790*	4.9	7.4	-0.27
QTsn.cz-2D.4	TSN	Queenstown 2013	105	*Xsnp179-Xsnp2790*	3.8	5.1	-0.24
QTsn.cz-2D.5	TSN	Kinston 2014	120	*Xsnp708-Xsnp1745*	4.8	6.5	-0.33
QTsn.cz-5D.1	TSN	Clarksville 2013	11	*Xsnp1751-Xsnp4175*	2.6	5.0	0.24
QTsn.cz-5D.1	TSN	Kinston 2014	12	*Xsnp1751-Xsnp4175*	3.6	5.0	0.28
QTsn.cz-5D.2	TSN	Queenstown 2014	26	*Xsnp4156-Xsnp4173*	4.6	12.6	0.32
QTsn.cz-5D.3	TSN	Clarksville 2014	28	*Xsnp4173-Xsnp4178*	11.6	18.4	0.42
QTsn.cz-5D.4	TSN	Queenstown 2013	29	*Xsnp4178-Xgdm136*	5.0	7.1	0.29

Table 4.4 Continued

QTL	Trait	Environment	Position (cM)	Marker interval	LOD score	PVE (%)	Additive effect
QSc.cz-3A.1	SC	Clarksville 2013	131	*Xsnp310-Xsnp4288*	4.1	7.7	0.04
QSc.cz-3A.2	SC	Clarksville 2014	142	*Xsnp2964-Xsnp2885*	5.0	8.8	0.04
QSc.cz-3A.2	SC	Queenstown 2013	142	*Xsnp2964-Xsnp2885*	3.6	7.4	0.04
QSc.cz-3A.3	SC	Kinston 2014	216	*Xsnp2971-Xsnp2909*	3.7	6.5	0.04
QSc.cz-5A.1	SC	Kinston 2014	48	*Xsnp279-Xsnp3878*	12.7	26.7	0.09
QSc.cz-5A.2	SC	Clarksville 2013	54	*Xsnp49-Xgwm304*	6.3	12.7	-0.05
QSc.cz-5A.2	SC	Queenstown 2014	54	*Xsnp49-Xgwm304*	3.8	9.3	-0.04
QSc.cz-5A.3	SC	Clarksville 2014	55	*Xgwm304-Xsnp996*	10.9	21.9	-0.06
QSc.cz-5A.3	SC	Kinston 2014	55	*Xgwm304-Xsnp996*	27.7	80.2	-0.15
QSc.cz-5A.3	SC	Queenstown 2013	55	*Xgwm304-Xsnp996*	6.0	13.0	-0.05
QSc.cz-2B.1	SC	Queenstown 2014	65	*Xsnp2773-Xgwm319*	5.8	15.4	0.05
QSc.cz-2B.1	SC	Clarksville 2013	66	*Xsnp2773-Xgwm319*	8.7	18.3	0.06
QSc.cz-2B.1	SC	Queenstown 2013	66	*Xsnp2773-Xgwm319*	9.3	21.6	0.07
QSc.cz-2B.2	SC	Kinston 2014	71	*Xsnp2569-Xsnp2688*	9.4	18.2	0.07
QSc.cz-2B.3	SC	Clarksville 2014	74	*Xsnp2697-Xsnp2598*	7.2	13.2	0.05
QSc.cz-5B	SC	Clarksville 2014	11	*Xsnp4114-Xsnp4142*	3.1	5.3	0.03
QSc.cz-5D	SC	Clarksville 2014	95	*Xsnp4170-Xsnp4157*	3.3	5.7	-0.03
QSc.cz-5D	SC	Kinston 2014	95	*Xsnp4170-Xsnp4157*	7.4	13.9	-0.06
QSc.cz-5D	SC	Queenstown 2014	95	*Xsnp4170-Xsnp4157*	6.6	16.8	-0.05
QSc.cz-5D	SC	Clarksville 2013	99	*Xsnp4170-Xsnp4157*	2.8	5.6	-0.04
QSc.cz-5D	SC	Queenstown 2013	100	*Xsnp4170-Xsnp4157*	3.5	8.1	-0.04
QSc.cz-6D	SC	Clarksville 2013	131	*Xsnp4484-Xsnp4488*	3.1	5.8	0.04
QGsp.cz-1A.1	GSP	Clarksville 2013	0	*Xwmc496-Xsnp1970*	3.6	6.7	0.06
QGsp.cz-1A.2	GSP	Queenstown 2013	3	*Xbarc28-Xsnp2005*	5.6	14.2	0.10
QGsp.cz-1A.2	GSP	Clarksville 2014	5	*Xbarc28-Xsnp2005*	6.1	13.3	0.06
QGsp.cz-5A	GSP	Queenstown 2014	63	*Xbarc100-Xsnp4843*	3.8	9.7	-0.06
QGsp.cz-6A	GSP	Kinston 2014	95	*Xsnp4364-Xsnp4207*	2.9	7.4	-0.05
QGsp.cz-7A	GSP	Queenstown 2014	129	*Xsnp4563-Xsnp4936*	3.8	9.0	-0.06
QGsp.cz-2B.1	GSP	Clarksville 2013	64	*Xsnp2777-Xsnp2773*	3.2	6.0	-0.06
QGsp.cz-2B.1	GSP	Kinston 2014	64	*Xsnp2777-Xsnp2773*	5.8	15.6	-0.08
QGsp.cz-2B.1	GSP	Queenstown 2013	64	*Xsnp2777-Xsnp2773*	5.4	12.9	-0.09
QGsp.cz-2B.1	GSP	Queenstown 2014	64	*Xsnp2777-Xsnp2773*	4.2	9.9	-0.06
QGsp.cz-2B.2	GSP	Clarksville 2014	72	*Xsnp2688-Xsnp2697*	7.4	13.7	-0.07
QGsp.cz-3B	GSP	Clarksville 2014	66	*Xsnp3393-Xsnp3368*	4.3	7.7	0.05
QGsp.cz-5B.1	GSP	Queenstown 2014	47	*Xsnp446-Xsnp4083*	4.8	11.6	-0.07
QGsp.cz-5B.2	GSP	Clarksville 2013	49	*Xsnp4083-Xsnp3988*	5.7	12.0	-0.08
QGsp.cz-5B.3	GSP	Clarksville 2014	58	*Xsnp3988-Xsnp1006*	7.7	14.5	-0.07
QGsp.cz-5B.4	GSP	Kinston 2014	59	*Xsnp1006-Xsnp823*	4.7	12.5	-0.07
QGsp.cz-5B.4	GSP	Queenstown 2013	59	*Xsnp1006-Xsnp823*	3.4	7.9	-0.07
QGsp.cz-6B	GSP	Clarksville 2013	63	*Xsnp4421-Xsnp4451*	2.7	5.3	0.05
QGsp.cz-1D.1	GSP	Queenstown 2013	53	*Xsnp2244-Xsnp2229*	2.7	6.0	-0.06
QGsp.cz-1D.2	GSP	Clarksville 2014	85	*Xsnp2234-Xsnp2232*	4.1	7.1	-0.05
QGsp.cz-2D	GSP	Clarksville 2013	125	*Xsnp708-Xsnp1745*	7.5	15.5	0.09

Table 4.5 QTL × Environment interactions influencing spike characteristics: spike length (SL, cm), sterile spikelet number per spike (SSN), fertile spikelet number per spike (FSN), total spikelet number per spike (TSN), spikelet compactness (SC) and grain number per spikelet (GSP) in the MD01W233-06-1 × SS8641 doubled haploid population evaluated in five field trials from 2013 to 2014.

Trait	QTL	Interval	Position	AE1†	AE2†	AE3†	AE4†	AE5†	$h^2(ae)$‡
SSN	5A	*Xsnp3820-Xsnp2008*	92.5				0.05*		0.9%
SSN	2B	*Xsnp2591-Xsnp2569*	69				-0.05*		0.7%
SSN	2D	*Ppd-D1-Xsnp2869*§	67.7					-0.12***	2.0%
FSN	1A	*Xsnp1970-Xbarc28*§	0.9				-0.22***	0.14**	2.2%
FSN	2A	*Xsnp2448-Xsnp2475*§	44.8			0.10*			0.6%
FSN	1D	*Xsnp2244-Xsnp2229*§	52.6				-0.10*	0.11*	0.9%
TSN	1A	*Xsnp1970-Xbarc28*§	0.9				-0.15***	0.13*	1.2%
TSN	2D	*Xsnp2850-Xsnp2862*§	34.4			-0.12*	0.19**	-0.16**	1.8%

† AE is the additive × environment interaction effect at each environment. E1: Clarksville 2013; E2: Clarksville 2014; E3: Queenstown 2013; E4: Queenstown 2014.
‡ h^2(ae) is heritability estimate of the additive × environment interaction effect across four field trails.
§ Interval with significant additive effect. * Significant at the 0.05 probability level **Significant at the 0.01 probability level ** *Significant at the 0.001 probability level

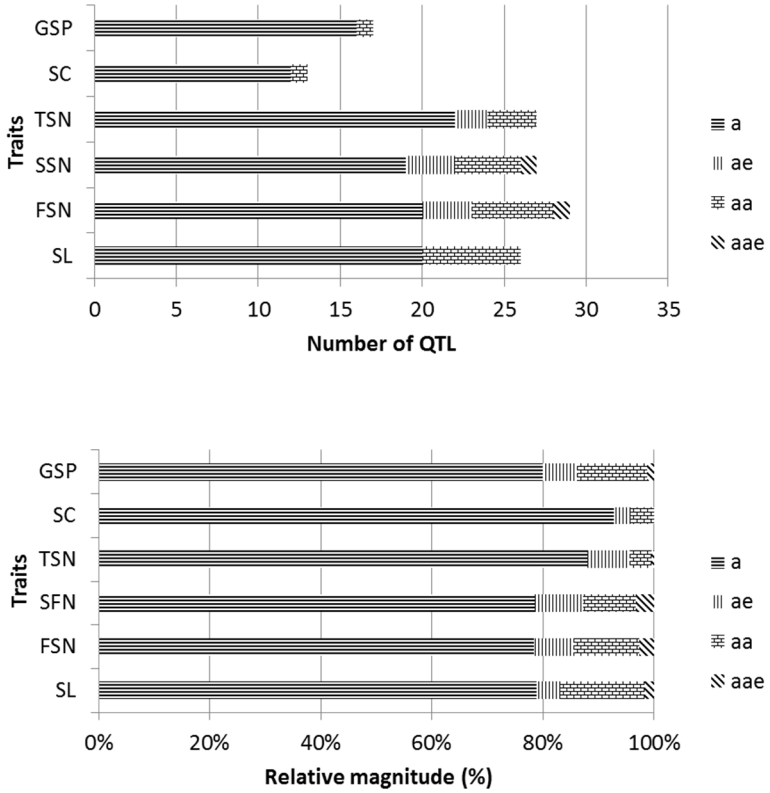


Figure 4.2 Distribution of genetic and non-genetic components for yield and yield related traits: spike length (SL, cm), sterile spikelet number per spike (SSN), fertile spikelet number per spike (FSN), total spikelet number per spike (TSN), spikelet compactness (SC), and grain number per spikelet (GSP). a) total number of QTLs detected for additive (*a*), additive × environment (*ae*), epistasis (*aa*), and epistasis × environment interactions (*aae*) effects. b) relative magnitude of *a*, *ae*, *aa*, *aae* effects.

Table 4.6 Digenic epistatic QTLs for spike characteristics: spike length (SL, cm), sterile spikelet number per spike (SSN), fertile spikelet number per spike (FSN), total spikelet number per spike (TSN), spikelet compactness (SC) and grain number per spikelet (GSP) in the "MD01W233-06-1 × SS8641" doubled haploid population evaluated in five field trials from 2013 to 2014.

Trait	Chr†	Position†	Interval†	Chr‡	Position‡	Interval‡	AA§	E1¶	E2¶	E3¶	E4¶	E5¶	$h^2(aa)$#	$h^2(aae)$††
SL	1A	0	*Xwmc496-Xsnp1970*‡‡	5A	78.9	*Xsnp4167-Xsnp3760*	0.07***						2.0%	0.2%
SL	5A	78.9	*Xsnp4167-Xsnp3760*	2D	118.5	*Xsnp2795-Xsnp708*‡‡	-0.04**						0.9%	0.2%
SL	5A	78.9	*Xsnp4167-Xsnp3760*	5D	44.1	*Xsnp4178-Xgdm136*‡‡	0.07***						2.3%	0.0%
SL	2D	28.5	*Xsnp2875-Xsnp2850*	2D	118.5	*Xsnp2795-Xsnp708*§	0.05***						0.6%	0.1%
SL	3A	148.9	*Xsnp2968-Xsnp443*	3A	58.8	*Xsnp4745-Xsnp4774*	-0.07***						3.1%	0.4%
SL	3B	93.1	*Xsnp3345-Xsnp3289*	3B	64.2	*Xsnp3737-Xsnp3751*	0.07***						2.9%	0.2%
SSN	3A	169.8	*Xsnp2983-Xsnp2990*‡‡	2B	69	*Xsnp2591-Xsnp2569*	-0.05***						1.0%	0.1%
SSN	1A	51.3	*Xsnp1862-Xsnp1823*	2D	101.7	*Xsnp179-Xsnp2790*§	-0.07***						2.5%	0.3%
SSN	5A	1	*Xsnp3874-Xsnp3872*‡‡	1B	87.1	*Xsnp2091-Xsnp2052*	0.01	0.07*					0.0%	1.4%
SSN	7A	169.4	*Xwmc273-Xsnp4655*	5D	0	*Xsnp4177-Xsnp4179*	-0.08***						2.6%	0.2%
FSN	1A	0.9	*Xsnp1970-Xbarc28*‡‡	5D	28.1	*Xsnp4178-Xgdm136*‡‡	0.10***						1.8%	0.0%
FSN	2A	44.8	*Xsnp2448-Xsnp2475*‡‡	3A	173.9	*Xsnp2990-Xsnp2905*‡‡	0.08***						0.7%	0.2%
FSN	3A	173.9	*Xsnp2990-Xsnp2905*‡‡	5D	28.1	*Xsnp4178-Xgdm136*‡‡	-0.12***						0.6%	0.3%
FSN	1A	38.7	*Xsnp1993-Xsnp1316*	6D	60.4	*Xsnp4482-Xsnp814*	0.12***				-0.12**	0.10*	1.6%	0.9%
FSN	1B	137.2	*Xsnp2067-Xsnp2127*	2B	88.3	*Xsnp2668-Xsnp2696*	0.21***						4.9%	0.3%
TSN	2B	49.8	*Xsnp2323-Xsnp768*	2D	119.4	*Xsnp708-Xsnp1745*‡‡	-0.08**						0.3%	0.2%
TSN	5B	81.9	*Xsnp4050-Xsnp4020*	1D	52.6	*Xsnp2244-Xsnp2229*‡‡	-0.11***						0.8%	0.0%
TSN	2D	34.4	*Xsnp2850-Xsnp2862*‡‡	2D	119.4	*Xsnp708-Xsnp1745*‡‡	0.15***						1.3%	0.1%
SC	6A	0	*Xsnp4296-Xsnp4276*	5B	103.2	*Xsnp4086-Xsnp4089*	0.02***						2.0%	0.0%
GSP	7A	15.5	*Xsnp4718-Xsnp4759*	5B	12.2	*Xsnp48-Xsnp4152*	0.05***						4.2%	0.4%

† The flanking markers, chromosome and position of the first interval involved in the epistasis.
‡ The flanking markers, chromosome and position of the second interval involved in the epistasis.
§ The additive × additive effect.
¶ The epistasis × environment effect at each environment. E1: Clarksville 2013; E2: Clarksville 2014; E3: Queenstown 2013; E4: Queenstown 2014;
# The heritability estimate for additive × additive interaction effects across five environment.
†† The heritability estimate for epistasis × environment interaction effects across four field trials.
‡‡ Interval with significant additive effect.
* Significantly different from zero at the 0.05 probability level
**Significant different from zero at the 0.01 probability level
** *Significant different from zero at the 0.001 probability level

Discussion

There are very few QTL mapping studies on wheat spike characteristics that integrate additive, epistasis, additive × environment interaction, and epistasis × environment interaction effects. In this study, I evaluated a soft red winter wheat DH population to identify QTLs influencing six spike traits and to investigate their interactions.

QTLs for spike characteristics

In the present study, major QTLs for SL, FSN, TSN, and GSP were co-localized and clustered in the 5cM- region on chromosome 1A in three marker intervals: *Xwmc496-Xsnp1970*, *Xsnp1970-Xbarc28* and *Xbarc28-Xsnp2005*. In previous studies, *Xbarc28* was also found to flank QTLs for spike length that explained 10.8% of the phenotypic variation (Marza et al., 2006). Similarly, QTLs for canopy temperature (Shukla et al., 2014), QTLs for pre-harvest sprouting (Munkvold et al., 2009) and QTLs and meta-QTLs for yield components (Zhang et al., 2010) have also been detected in this region. These results indicate the existence of large-effect genes in this interval and thus, high resolution mapping would be recognized to determine if the effects are due to pleiotropy or closely linked QTLs. Five QTLs for SL were identified on chromosomes 5A. Among them, two QTLs with large effects, *QSl.cz-5A.1* and *QSl.cz-5A.2*, overlapped at *Xsnp3789*. At 10 cM downstream were *QSl.cz-5A.2* and *QSl.cz-5A.3*. QTL *QSl.cz-5A.5* was at the distal end of the long arm of 5A. Previous studies have reported vernalization response genes (*Vrn* genes) and the major wheat domestication gene *Q* on chromosome 5A (Kato et al., 1998). *Vrn* genes together with photoperiod response genes (*Ppd* genes) and earliness per se genes (*Eps* genes)

determine flowering time of wheat and hence, in part, confer wheat wide adaptation to diverse regions around the world (Snape et al., 2001). The *Q* gene is a well-known domestication locus conferring the free-threshing character and is responsible for many other domestication-related traits such as rachis fragility, glume shape and tenacity, spike length, plant height, and spike emergence time (Faris et al., 2003; Simons et al., 2006; Sormacheva et al., 2014). The five SL QTLs on chromosome 5A were in the same regions where *Vrn-A1* and *Q* are located. Diagnostic markers will be employed to further verify the existence of *Vrn-A1* and *Q* in this DH population. QTL fine mapping is also necessary to determine if one or both of these two genes contributed to SL in this study and if new locus other than *Vrn-A1* and *Q* was detected. Additionally, consistent QTLs for SL (*QSl.cz-3B.2* and *QSl.cz-3B.3*) were identified on chromosome 3B in E1, E2, E4, and E5. *QSl.cz-3B.2* and *QSl.cz-3B.3* overlapped at locus *Xsnp3335* and were located in a region harboring QTLs for FSN, TSN, and GSP. In the same region, Li et al. (2007b) detected QTLs for grain yield and grain number per spike in two environments using a population of recombinant inbred lines derived from two winter wheat cultivars. Wang et al. (2009) also found this region significant for grain filling rate and yield-related traits over multiple environments. Three QTLs on 2D (Table 4.4) were of special interest because these were the only three loci where MDW233 alleles were associated with a longer spike. In a QTL mapping study for spike-related traits, Ma et al. (2007b) detected two QTLs on chromosome 2B flanked by marker *Xgwm261* for SL and SC in the cross of winter genotypes Nanda 2419 and Wangshuibai where the QTLs linked to *Xgwm261* explained 8.8 to 23.2% of the phenotypic variation. In my study, *Xgwm261* was 2.3

cM and 13.3 cM away from *QSl.cz-2D.1*/*QFsn.cz-2D.1* and *QSl.cz-2D.2*, respectively. In addition, *Xgwm261* was reported to flank co-localized QTLs and a QTL cluster for yield related traits including plant height, harvest index, days to maturity, thousand grain weight, and grain weight per spike (Mason et al., 2013). These results suggest that these regions on chromosome 2D may be the same. Furthermore, *QSl.cz-2D.3* mapped to the long arm of chromosome 2D and shared the same interval with major QTL *QFsn.cz-2D.3* and *QTsn.cz-2D.4* which coincided with the QTLs for FSN and TSN in Ma et al. (2007). The same position and genetic effects suggested the possibiligy of similar underlying QTLs.

A few studies have documented QTLs/genes for SSN, FSN, and TSN (Cui et al., 2012; Ma et al., 2007b). Some previously reported QTLs were confirmed in the present study. A minor QTL, *QSsn.cz-6D*, is consistent with the QTL detected by Cui et al. (2012) who also located a cluster of QTLs for spike characteristics on chromosome 2B corresponding with the major QTL clusters identified in the present study. QTLs in this cluster were repeatedly detected in almost all environments evaluated. At these loci, SS8641 contributed positive additive effects for SSN, TSN, and SC, whereas MDW233 was associated with positive GSP suggesting that the SS8641 allele of this cluster may lower spikelet fertility and increase TSN and SC by increasing the number of sterile spikelets. The SS8641 allele of this region should be avoided in breeding programs. In addition, a QTL cluster for FSN and TSN was identified on chromosome 5D flanked by *Xsnp4156*-*Xgdm136* and was located in the same region of previously reported QTLs detected by Li et al. (2007b) and Cui et al.

(2012). Cuthbert et al. (2008) reported a QTL cluster for grain numbers per spike, grain yield, thousand grain weight, grain filling time, and days to heading on chromosome 2D which may correspond to the region of major QTL *QSsn.cz-2D.3* identified in this study (Table 4.4). At the distal end of chromosome 2D, I detected three closely linked QTLs *QFsn.cz-2D.4*, *QTsn.cz-2D.5*, and *QGsp.cz-2D*. These QTLs were not located at the region of the *compactum* (*C*) locus, a spike-compacting gene on the long arm of chromosome 2D (Johnson et al., 2007a). The SS8641 alleles in this region decreased FSN and TSN but increased GSP. The association of this region with spike traits has not been reported elsewhere. Furthermore, I found that the major QTL *QFsn.cz-2D.2* shared the interval with *QTsn.cz-2D.2* and *QSsn.cz-2D.1* and overlapped with *QSn.cz-2D.2* and *QTsn.cz-2D.3* at the locus *Ppd-D1*. The effects of these QTLs were possibly caused by the locus *Ppd-D1* which is a member of the *Ppd1* genes known to confer photoperiod sensitivity and influence agronomic traits such as plant height, days to heading and thousand grain weight (Guo et al., 2010). Recently, the *Ppd-D1* locus was shown to control photoperiod-dependent floral induction and that it has a major inhibitory effect on paired spikelet formation by regulating the expression of the *FLOWERING LOCUS T* (*FT*) (Boden et al., 2015).

The QTL cluster on chromosome 5A for SC included the locus *Xgwm304* that is neither close to the *Q* gene nor the *Vrn-A1* gene but it has been related to grain yield and thousand grain weight by Cuthbert et al. (2008) and SL and SC by Ma et al. (2007b). In these two studies, this region was identified as harboring major QTLs because of high PVE values similar to my results. Thus, it is possible that this region

may contribute to grain yield by increasing spikelet numbers and grain weight. Sourdille et al. (2003) used a DH population derived from the cross Courtot × Chinese Spring to study wheat development traits and detected one QTL on the long arm of chromosome 5D for SC. This QTL explained 13.6% of the phenotypic variation and was similar to the genomic region *Xsnp876-Xsnp4157* where two major QTLs for SL and SC were identified in the present study. Another QTL cluster comprising of four major QTLs for GSP on chromosome 5B (Table 4.4) coincided with the interval of the SL QTL *QSl.ccsu-5B.2* identified by Kumar et al. (2007).

Chromosome 3A of wheat is known to contain QTLs for grain yield and other important agronomic traits. Using a recombinant inbred line population derived from the winter wheat cultivar Cheyenne (CNN) and its single chromosome substitution line CNN (WI3A) where chromosome 3A of CNN was substituted for Wichita (WI) chromosome 3A, Mengistu et al. (2012) and Dilbirligi et al. (2006) detected QTLs for grain yield, plant height, spikes per square meter, and grain number per spike and found that most of the detected QTLs on 3A were co-localized in two regions. In the present study, I detected five QTLs on chromosome 3A for SC and SSN among which *QSsn.cz-3A.1* explained 13.8% of the phenotypic variation while the rest were minor QTLs. Based on the mapping positions of SSR markers used in the current and previous studies (Somers et al., 2004), these five QTLs were similar to the QTLs previously identified by Dilbirligi et al. (2006) and Mengistu et al. (2012).

Genetic complexity of spike characteristics

Most important agronomic traits are quantitative in nature controlled by polygenes and influenced by the environment. Understanding the genetic and environmental factors causing the phenotypic variation of quantitative traits is essential for the genetic improvement of crops via knowledge-based breeding (Mackay, 2001; Würschum, 2012). In the present study, the effects of major, minor, and epistatic QTLs as well as their interactions with the environment and their relative contributions to spike characteristics were estimated (Figure 4.2). The QTLs with additive effects were the largest in total number and had the largest genetic contribution to phenotypic variation. This agreed with previous QTL studies involving epistasis, Q×E and QQ×E interactions (Kuchel et al., 2007a; Wu et al., 2012; Xing et al., 2002; Zhang et al., 2014). In addition, QTLs for spike characteristics were not evenly distributed within and across chromosomes and tended to cluster (Figure 4.1). I identified QTL clusters on chromosome 1A, 5A, 2B, 3B, 5B, 1D, 2D, and 5D where QTLs for multiple spike characteristics were co-localized or closely linked within a 10-cM region. In most cases, each cluster contained at least one major QTL. The clustering of QTLs also partially explained the correlation between spike characteristics. In this study, SL was highly correlated with FSN across environments (Table 4.3). This could be caused by the co-localization of *QSl.cz-1A* and *QFsn.cz-1A* plus the effects of closely linked QTLs *QSl.cz-3A.1*, *QSl.cz-3A.2* and *QFsn.cz-3A.1*. Despite of the slight difference in interpretation, characterizing the interaction at two or more loci or epistasis is as important in quantitative genetics as in classical genetics. I found that interactions (Q×E, Q×Q and

QQ×E) served as modifiers for spike characteristics determination in my DH population. For example, the interval *Xsnp4167-Xsnp3760* on chromosome 5A was not detected with significant additive effects but contributed to SL through its interactions with *Xsnp2795-Xsnp708*, *Xwmc496-Xsnp1970*, and *Xsnp4178-Xgdm136*, which were associated with significant additive effects for FSN, GSP, and SL, respectively. Significant epistasis was also detected between non-significant intervals such as *Xsnp2067-Xsnp2127* and *Xsnp2668-Xsnp2696* which increased FSN and accounted for 4.9% of the phenotypic variation. Similar results were reported by Ma et al. (2007b) where the interaction of two non-significant loci on chromosome 3D decreased TSN and FSN. These results confirmed that loci without main effects may contribute to trait determination through epistasis (Li et al., 2001). Additionally, I found that the SS8641 allele at the interval *Xsnp1970-Xbarc28* increased FSN and TSN in E5 and these effects was enhanced by 21.5% through the Q×E interaction. Although the effects and contribution from Q×E, Q×Q and QQ×E interactions were relatively smaller compared to additive main effects, they were important terms fine-tuning the expression of spike traits. This is valuable information for pyramiding QTLs in breeding programs.

Conclusion

Spike characteristics determine the number of grains produced on each spike. Genetically improving grain number per spike is widely accepted as one of the key paths towards higher grain yield. In this study, QTL mapping in a bi-parental population was performed and detected a total of 109 QTLs among which consistent QTLs such as *QSl.cz-1A* or *QFsn.cz-1A* for SL and FSN, *QGsp.cz-2B*.1 for GSP, and

QSc.cz-5A.3 for SC, explained up to 30.9%, 15.6%, and 80.2% of the phenotypic variation, respectively. I also found that the average contribution of *QFsn.cz-1A* to FSN at each trial was enhanced by 19% via interaction with the interval *Xsnp4178-Xgdm136*. In addition, QTLs clusters on chromosomes 1A, 5A, 2B, 3B, 5B, 1D, and 5D with synergistic or antagonistic genetic effects partially explained the phenotypic correlation between spike traits. These results provide valuable information for manipulating spike morphology for breeding purposes.

Chapter 5: Multivariate analysis of grain yield and yield related traits in a doubled haploid population of soft red winter wheat

Abstract

To study the interrelationships among grain yield and yield contributing traits, a series of statistical analyses including correlation, multiple linear regression, cluster analysis, principal component analysis and structural equation modeling were conducted in a soft red winter wheat doubled haploid population derived from the cross MD01W233-06-1 by SS8641. Six structural equation models with feedback loops were constructed and showed that spikes per square meter had the highest positive contribution to grain yield followed by grain weight per spike and that grains per spikelet and fertile spikelet number per spike were compensatory targets that mediate yield component compensation. In addition, DH84 and DH96 which yielded 24.13% and 22.64% higher than the mean performance of the whole population, respectively, may have potential as new cultivars.

Introduction

Wheat (*Triticum aestivum* L.) is one of the most important food crops, occupying 17% of the world's crop acreage, feeding about 40% of the world's population and providing 20% of total food calories and protein in human nutrition (Gupta et al., 2005). Continuous genetic improvement of wheat yield potential via breeding is essential to securing a stable food supply. In a wheat breeding program, a breeder usually records a number of agronomic characters on which statistical analyses are made to get a better understanding of the germplasm. The information is then utilized to make selections. Therefore, analytical methods that can extract the most

information from large datasets and provide insights into the nature and magnitude of association of plant traits are needed, especially when clear experimental control of the inter-correlated traits is difficult.

Several statistical methods have been utilized to investigate wheat grain yield and its related characters. For example, phenotypic correlation analysis is an important way to evaluate the association between plant characters. However, simple correlation does not necessarily imply a cause-and-effect relationship. The observed correlation could be due to unknown environmental or genetic factors. Genetic correlation is a measure of the extent to which plant characters are associated at the genetic level (Waitt and Levin, 1998) and is used as a supplement to phenotypic correlation when making selection decisions (Holland, 2006). Alternatively, multiple regression analysis can be useful when the main interest is the prediction of the response variable from a set of predictor variables or to select candidate variables for further analyses. Using multiple linear regression analysis, Leilah and Al-Khateeb (2005) reported that grain weight per spike, harvest index, biological yield, spike number per square meter and spike length were major contributors to wheat grain yield. Additionally, cluster and principal component analyses are often used separately or combined to group cultivars or agronomic variables into main groups or subgroups based on similarity, which is also useful for parental selection in breeding programs and crop modeling (Khodadadi et al., 2011; Leilah and Al-Khateeb, 2005). Furthermore, path analysis divides the correlation coefficients into direct and indirect effects and has been employed to study yield formation in cereal crops by separating

the direct influence of each yield component on grain yield from the indirect effects caused by mutual relationships among yield components themselves (Kashif and Khaliq, 2003; Li et al., 2006; Moral et al., 2003). Most path analysis studies on yield formation, however, have two main general limitations: 1) researchers assume bidirectional causal pathways between yield components and yield related traits; and 2) grain yield is modeled as a resultant variable and all other traits as causal variables with direct path toward grain yield (Kashif and Khaliq, 2003; Li et al., 2006). Additionally, whether a yield component can influence others that develop earlier is questionable given that yield components develop sequentially (Dofing and Knight, 1992). Furthermore, path analysis assumes that all variables are measured without error and that no correlation between the error terms and causal loops exist (Meehl and Waller, 2002).

Structural equation modeling (SEM) is a powerful multivariate approach to model complex relationships between latent and measured variables while accounting for measurement error (Ullman, 2006). SEM is an extension of general linear modeling (GLM) procedures, such as the ANOVA and multiple regression analysis. Its main goal is to determine if a specified theory about the causal pattern of multiple inter-correlated variables, usually represented by a path diagram, is consistent with empirical data. This consistency is evaluated through data-model fit indices that measure the extent to which the proposed network of relations is plausible. Four most commonly used fit indices are 1) standardized root mean squared residual (SRMR), 2) root mean squared error of approximation (RMSEA), 3) normed fit index (NFI),

and 4) nonnormed fit index (NNFI) (Hooper et al., 2008). Similar to classic path analysis, SEM is capable of conveying casual relationships among mutually inter-correlated dependent and independent variables (Kline, 2011). One of the primary advantages of SEM (vs. other applications of GLM such as ANOVA and path analysis) is that less restrictive assumptions exist in SEM which makes SEM a popular confirmatory and exploratory approach in social sciences (Marsh et al., 2014). SEM has been adapted to the quantitative genetics mixed-effects models settings by Gianola and Sorensen (2004) and promoted by Lamb et al. (2011) in plant sciences to study yield components, complex multi-site field trails etc. However, no applications have been reported in major crop plants.

The present study was undertaken to investigate and model the phenotype network regarding wheat grain yield formation through multivariate analyses. The novelty of this research is twofold: 1) it provides an overall view on grain yield formation by including yield components, spike morphology and plant architecture traits and 2) it introduces SEM as a supplement to traditional multivariate approaches to resolve the interrelationships among yield contributing traits. Data used in this study was collected at the end of growing seasons and, thus, phenotype network constructed in this study did not represent dynamic regulating network or mimic any developmental processes.

Materials and Methods

Field trials and data collection

Data used in this chapter was collected from a doubled haploid population of soft red winter evaluated in five field environments (refer to the chapter 2, 3, and 4 of this dissertation for details).

Statistical analyses

Phenotypic correlation analysis was performed by PROC CORR procedure of SAS, Version 9.3 (SAS Institute, Cary, NC 2013). Genetic correlation coefficients were estimated using MANOVA method (Liu et al., 1997) by PROC GLM procedure of SAS. Multiple linear regression and stepwise multiple linear regression was conducted using PROC REG procedure of SAS. Cluster analysis (using standardized data and Ward method) and principal component analysis (using correlation matrix and REML method) were performed by JMP® Pro, Version 11 (SAS Institute, Cary, NC, 2014). Structural equation modeling was based on correlation matrix and performed using LISREL, Version 9.1 (Joreskog and Sorbom, 2012).

Results and Discussion

Phenotypic and genetic correlation analyses

According to quantitative genetics theory, genetic and environmental causes of correlation combine together to produce phenotypic correlations. The magnitude and sign of phenotypic and genetic correlations, however, are not necessarily related (Waitt and Levin, 1998). It is important to know for breeders if the phenotypic correlation is due to heritable genetic factors or external environmental conditions. In

this study, a matrix of pairwise phenotypic and genetic correlation coefficients were computed and are presented in Table 5.1. GYLD was positively associated with SPSM and TGW but was negatively correlated with FLL, FLW, FLA, SL, FSN, TSN, and HD. SPSM and TGW had the highest positive phenotypic and genotypic association with GYLD implying that improving these traits could result in higher grain yield and this effect would be highly heritable. A significant positive correlation between GWPS and GYLD was not found in pooled correlation analysis but was detected in two environments: E4 and E5, which was similar with the results reported by Marza et al. (2006) and Heidari et al. (2011). The negative correlations between GYLD and FLL, FLW, FLA, SL, FSN, TSN, and HD suggested that early heading genotypes with smaller flag leaves, shorter spikes, and less fertile spikelets, and thus with lower grain number and lighter grain weight would contribute to higher grain yield. This was true in E1, E2, E3, and E4 where these unfavorable traits were compensated by higher SPSM but not in E5 where the compensation from SPSM was not enough, probably due to higher temperatures during the growing season. In a study to evaluate wheat yield formation under Mediterranean conditions, Moral et al. (2003) reported that durum wheat yielded less in warmer environments than in cooler regions mainly due to reduced SPSM and TGW. Similarly, Hou et al. (2012) found that winter wheat grew faster and produced more tillers but tended to decrease SPSM under warmer conditions also resulting in lower grain yield.

Cluster and principal component analysis

Cluster analysis has been used to classify wheat ecotypes and to evaluate genetic diversity in wheat germplasm collections. Cluster analysis groups genotypes into

clusters where genotypes in the same cluster exhibit high homogeneity but have high heterogeneity among clusters. In this study, I clustered the 124 DH lines into five clusters (Figure 5.21~5.26). Membership of each line is presented in Appendix D. The means of dendrogram clusters at each environment are presented in Table 5.6. The cluster with the highest grain yield at each environment was consistently associated with higher SPSM, smaller FLA, less GPS, lighter GWPS, shorter SL, fewer FSN and TSN, which also agreed with the results from phenotypic and genetic correlation analysis of this study.

Principal component analysis (PCA) is a standard multivariate technique for complex dataset analysis where observations are described by multiple inter-correlated variables. Its objective is to extract the most important information from the original inter-correlated variables by maximizing the variance of a set of new orthogonal variables called principal components, and to display the pattern of similarity of the observations and of the variables in maps (Abdi and Williams, 2010). Principal components are linear combinations of original variables. The first principal component has the maximal variance. The second principal component has maximal variance in a direction orthogonal to the first principal component, and so on. In this study, PCA grouped the investigated wheat variables into five main components explaining more than 80% of the total variation (Table 5.4). Specifically, the first two principal components explained more than half of the total variance. The first principal component accounted for 30.6%, 27.1%, 32.5%, 30.7%, 34.5%, and 33.1% of the total variation and second principal component for 20.2%, 18.1%, 22%, 18.7%,

and 23.7% of the total variation at E1, E2, E3, E4, and E5 trials, respectively. The first principal component was related to yield components and yield contributing traits whereas the second principal component was related to vegetative growth and spikelet fertility across trials (Table 5.5). The traits with largest loadings to the first principal component were GWPS, GPS, SPSM, SL and FSN, suggesting these were indicative of yield potential. The first two principal components and wheat variables were plotted in biplots (Figure 5.1). From the biplots, vectors representing uncorrelated traits formed right angles (90°) (e.g. GPS vs. HD, SSN vs. FSN), whereas highly correlated traits formed either acute (positive correlation; e.g. SPSM vs. GYLD) or obtuse (negative correlation; e.g. GYLD vs. FLA) angles. In general, three observations were made from the biplots: 1) SPSM and TGW were mostly positively associated with GYLD, 2) SSN, SC, GSP, and FLS were independent of GYLD, 3) HD, FLW, FSN, FLA, FLL, and GPS were negatively associated with GYLD. GWPS showed a slightly positive to no correlation with GYLD, which agreed with the results of previous phenotypic correlation analyses.

Additionally, cluster analysis coupled with PCA was used to select high yielding DH lines in this study. The first two principal components from each environment were plotted with DH cluster membership as labels (Figure 5.21~5.26). At E1, the highest yielding cluster (Cluster 1) was separated from the lowest yielding cluster (Cluster 4) as was Cluster 2 from Cluster 4 at E2, Cluster 5 from Cluster 3 at E3, Cluster 1 from Cluster 4 at E4, and Cluster 1 from Cluster 4 at E5. The extracted principal components were able to distinguish different clusters and, thus, largely confirmed

the generated cluster membership. Two DH lines, DH96 and DH84, stayed in the highest yielding clusters across all five environments. Furthermore, when data from the five environments were averaged, DH96 and DH84 ranked second and third among all lines, increasing grain yield by 24.13% and 22.64% respectively. Thus, DH96 and DH84 could be candidates to be new cultivars with a stable performance across these environments.

Multiple linear regression analysis

Regression coefficients and the associated probability values for each variable in predicting wheat grain yield are presented in Table 5.2 and 5.3. The final models from stepwise linear regression analyses explained more than 95% of the total variation in grain yield. Although the variables remaining in the models varied at different environments, GWPS and SPSM were shared by all, suggesting the importance of SPSM and GWPS as selection criteria in wheat breeding for grain yield. Similarly, Leilah and Al-Khateeb (2005) also observed that SPSM and GWPS were the most effective variables influencing wheat grain yield.

Structure equation modeling (SEM)

Phenotypic traits can have causal effects on each other (Rosa et al., 2011). Information regarding phenotype networks describing the cause-and-effect relationships and feedback between traits is very helpful to predict the performance of biological systems. In this study, a phenotype network regarding grain yield and yield contributing traits was modeled under the frame of SEM. The purpose was to quantify the relative contributions of correlated causal sources of variation once a certain

network of interrelated variables with biological significance has been accepted (Shipley, 2004). Initial models were constructed separately for grain yield and yield components and spike characteristics based on the results obtained from previous multivariate analyses and published results on the interrelationships among grain yield and yield contributing traits (Dofing and Knight, 1992; Moral et al., 2003). The initial models were then integrated into one. I included paths from GPS and TGW to GYLD at my first attempt to integrate initial models. The path coefficients were not significant and overall model fitting failed although this seemed meaningful biologically. LISREL suggested a list of paths that could improve fit indices. Based this list, the modification of paths was performed to obtain the best combination of four fit indices. Final models are shown in Figure 5.3.

All the path coefficients in the phenotype network were highly significantly different from zero (Figure 5.3). Across six models, GWPS and SPSM had direct causal influence on GYLD. The loadings for the path from SPSM to GYLD were higher than that for the path from GWPS suggesting that SPSM had a relatively more direct contribution to GYLD. No direct contribution from GPS or TGW to GYLD was established. However, GPS and TGW had an indirect effect on GYLD via GWPS. Additionally, FSN and GSP were feedback targets where depressing effect from GWPS, SPSM, TGW and GYLD were observed. GSP had more feedback effect than FSN. Previous studies found that SPSM had a direct negative effect on GPS and TGW (Moral et al., 2003) and that this compensation arose from the fact that these traits develop sequentially with later-developing traits under control of earlier-

developing ones (Slafer, 2007). However, in this study, a direct negative effect on GWPS from SPSM was significant only in Clarksville 2014 and Queenstown 2014. Although a direct path from SPSM to GWPS was absent in the other three trials, SPSM negatively affected GWPS by depressing GSP and FSN and hence GPS (Figure 5.3) suggesting GSP and FSN as mediators in yield component compensation. To my knowledge, this is the first report of GSP and FSN as direct feedback regulating targets in wheat.

Direct genetic evidence of feedback paths in SEM

The results of the QTL analyses of the set of agronomic traits involved in the present study (Chapter 2, 3, and 5 of this dissertation) were used to evaluate the validity of feedback paths in the structural equation models at each trial. The feedback path from **SPSM to GSP** in the model at Clarksville 2013 and Queenstown 2013 could be partially explained by the interval *Xwmc496-Xsnp1970* where QTL *QSsm.cz-1A.1* and QTL *QGsp.cz-1A.1* co-localized and the interval *Xbar28-Xsnp2005* where QTL *QSsm.cz-1A.3* and QTL *QGsp.cz-1A.2* also co-localized. The MDW233 allele at these two loci increased SPSM but decreased GSP. The feedback path from **GYLD to GSP** in the model at Clarksville 2014 could be associated with the region *Xsnp3382-Xsnp3368* on chromosome 3B where QTLs with opposite genetic effects on GYLD and GSP were located closely. The feedback path from **GYLD to FSN** in the model at Clarksville 2013 could be supported by the genomic region *Xwmc496-Xbar28* on chromosome 1A where QTL *QGld.cz-1A* and QTL *QFsn.cz-1A* co-localized but showed opposite genetic effects on GYLD and FSN. Another genetic evidence might be the interval *Xsnp2862-XPpd1* on chromosome 2D where its SS8641 allele

increased grain yield but decreased FSN. Additionally, the interval *Xsnp1970-Xbar28* on chromosome 1A and *Xsnp3389-Xsnp3344* on chromosome 3B may be the underlying genetic factors for the feedback path from **SPSM to FSN** in the model at Kinston 2014, where the MDW233 allele increased SPSM but decreased FSN. No QTLs were found to directly support the feedback paths from **GWPS to GSP and FSN** and from **TGW to FSN**. This could be due to two reasons: 1) the threshold level set to detect a significant QTL was too high so that QTLs with minor effects were overlooked. A consequence of this is that researchers would miss QTLs that could explain the feedback paths and 2) the causal relations could be due to methylation quantitative trait loci (meQTLs) in addition to DNA sequence changes (Koch, 2014) which are not detected in conventional QTL analyses.

Conclusion

Multivariate analyses were used to construct a phenotype network involving grain yield and yield related traits. Results showed that SPSM (spikes per square meter) was the most important trait that directly and positively contributed to grain yield followed by GWPS (grain weight per spike). In addition, GPS (grains per spike) had more weight on GWPS (grain weight per spike) than TGW (thousand grain weight) and GSP (grains per spikelet) had more weight on GPS (grains per spike) than FSN (fertile spikelet number). Therefore, high SPSM and GSP and moderate TGW and FSN could be the targets for breeding for higher grain yield in the Mid-Atlantic region.

Table 5.1 Genotypic (r_g) and phenotypic (r_p) correlation coefficients among the grain yield and yield contributing traits in the MD01W233-06-1 × SS8641 doubled haploid population. r_p is shown in the upper triangular and r_g in the lower triangular. Traits evaluated include grain yield (GYLD), grains per spike (GPS), grain weight per spike (GWPS), spikes per square meter (SPSM), and thousand-grain-weight (TGW), plant height (PHT), flag leaf length (FLL), flag leaf width (FLW), flag leaf area (FLA), flag leaf shape (FLS), spike length (SL), sterile spikelet number per spike (SSN), fertile spikelet number per spike (FSN), total spikelet number per spike (TSN), spike compactness (SC), grain number per spikelet (GSP), and dates to heading (HD). r_g and r_p were estimated from all five trials' data. Significance was not tested for r_g.

	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
GYLD		-0.17	0.12	0.70***	0.37***	0.13	-0.25**	-0.43***	-0.41***	0.09	-0.24**	-0.14	-0.40***	-0.44***	-0.15	0.11	-0.46***
GPS	-0.15		0.66***	-0.58***	-0.38***	0.06	0.45***	0.19*	0.40***	0.26**	0.49***	-0.36***	0.71***	0.51***	-0.06	0.76***	0.03
GWPS	0.14	0.66		-0.60***	0.36***	0.29***	0.36***	0.16	0.33***	0.21*	0.56***	-0.25**	0.41***	0.28**	-0.36***	0.56***	-0.24***
SPSM	0.69	-0.59	-0.63		0.02	-0.11	-0.45***	-0.45***	-0.56***	-0.08	-0.56***	0.07	-0.58***	-0.52***	0.13	-0.30***	-0.19*
TGW	0.36	-0.37	0.38	-0.01		0.36***	-0.11	0.02	-0.05	-0.12	0.08	0.21*	-0.35***	-0.24***	-0.34***	-0.24**	-0.29**
PHT	0.08	0.08	0.31	-0.17	0.33		0.24**	-0.21*	0.04	0.37***	0.12	0.18*	-0.01	0.07	-0.07	0.07	0.01
FLL	-0.36	0.47	0.40	-0.57	-0.10	0.27		0.31***	0.82***	0.66***	0.42**	0.19*	0.45***	0.50***	0.02	0.22*	0.36***
FLW	-0.59	0.17	0.20	-0.59	0.08	-0.23	0.30		0.79***	-0.51***	0.30***	0.18*	0.39***	0.45***	0.09	-0.09	0.54***
FLA	-0.57	0.40	0.38	-0.72	-0.01	0.05	0.82	0.80		0.12	0.45***	0.23*	0.52**	0.59**	0.06	0.09	0.55***
FLS	0.12	0.28	0.20	-0.07	-0.15	0.41	0.65	-0.52	0.10		0.16	0.01	0.11	0.10	-0.06	0.27**	-0.11
SL	-0.30	0.47	0.56	-0.62	0.12	0.13	0.45	0.31	0.48	0.17		-0.03	0.65***	0.60***	-0.58***	0.10	0.08
SSN	-0.26	-0.38	-0.27	-0.02	0.23	0.20	0.21	0.17	0.23	0.04	-0.02		-0.09	0.34***	0.38***	-0.47***	0.51***
FSN	-0.42	0.69	0.42	-0.61	-0.31	-0.03	0.47	0.44	0.57	0.09	0.64	-0.12		0.90***	0.15	0.09	0.35***
TSN	-0.51	0.49	0.28	-0.59	-0.20	0.06	0.54	0.49	0.64	0.10	0.61	0.32	0.90		0.30***	-0.11	0.55***
SC	-0.13	-0.08	-0.39	0.16	-0.34	-0.09	-0.01	0.10	0.05	-0.09	-0.62	0.33	0.10	0.24		-0.22*	0.46***
GSP	0.15	0.78	0.55	-0.29	-0.26	0.11	0.22	-0.15	0.06	0.31	0.07	-0.47	0.09	-0.12	-0.20		-0.28**
HD	-0.58	0.02	-0.25	-0.27	-0.29	-0.01	0.41	0.61	0.63	-0.12	0.12	0.47	0.39	0.58	0.41	-0.31	

* Significant at 0.05 probability level
** Significant at 0.01 probability level
*** Significant at 0.001 probability level

Table 5.2 Multiple linear regression of the MD01W233-06-1 × SS8641 doubled haploid population. Grain yield (GYLD) as dependent variable and grains per spike (GPS), grain weight per spike (GWPS), spikes per square meter (SPSM), and thousand-grain-weight (TGW), plant height (PHT), flag leaf length (FLL), flag leaf width (FLW), flag leaf area (FLA), flag leaf shape (FLS), spike length (SL), sterile spikelet number per spike (SSN), fertile spikelet number per spike (FSN), spike compactness (SC), grain number per spikelet (GSP), and heading date (HD) as independent variables. Total spikelet number per spike (TSN) was not included in the analysis because of its multicollinearity with SSN and FSN. Estimates of regression coefficients and the associated *p* values are shown.

	Clarksville 2013		Clarksville 2014		Queenstown 2013		Queenstown 2014		Kinston 2014†		Overall	
Variable	Estimate	P value	Estimate	P value	Estimate	P value	Estimate	P value	Estimate	P value	Estimate	P value
Intercept	-1233.71	0.0213	-520.30	0.2398	221.20	0.5448	-994.20	<.0001	-232.08	0.3173	-188.71	0.6140
GPS	-13.60	0.0472	-10.51	0.0213	1.28	0.5790	-13.96	<.0001	-2.15	0.5470	-9.94	0.0340
GWPS	412.69	<.0001	767.35	<.0001	484.42	<.0001	483.40	<.0001	446.89	<.0001	517.05	<.0001
SPSM	1.19	<.0001	0.93	<.0001	1.29	<.0001	1.05	<.0001	1.10	<.0001	1.08	<.0001
TGW	0.97	0.5116	1.20	0.3731	-0.56	0.6868	2.01	0.0092	0.64	0.4663	1.49	0.3043
PHT	0.83	0.0184	0.05	0.8966	0.05	0.8722	0.46	0.0145	--	--	-83.71	0.0132
FLL	23.39	0.2645	8.59	0.6147	5.08	0.7402	20.00	0.0318	--	--	32.65	0.0294
FLW	156.64	0.2374	117.05	0.3538	-68.27	0.6104	130.07	0.0648	--	--	58.11	0.0051
FLA	-16.81	0.2006	-8.48	0.3928	0.74	0.9313	-13.88	0.0077	--	--	-234.26	0.0212
FLS	-2.62	0.8495	1.55	0.9075	-10.10	0.4558	-4.00	0.6037	--	--	-0.16	0.5415
SL	-45.07	0.2789	-100.51	0.0319	-87.00	0.0218	-52.81	0.0168	-50.26	0.0380	12.11	0.3927
SSN	16.84	0.3571	39.68	0.0487	25.74	0.1169	17.15	0.1000	16.35	0.1014	-116.24	0.3442
FSN	55.92	0.0164	66.72	0.0030	33.69	0.0585	62.31	<.0001	24.84	0.0949	-0.33	0.9676
SC	-149.28	0.2291	-290.59	0.0411	-240.23	0.0370	-158.32	0.0166	-141.71	0.0524	-14.75	0.2511
GSP	208.35	0.0403	151.10	0.0367	-24.48	0.4378	202.47	<.0001	27.72	0.6457	144.65	0.0406
HD	1.25	0.3804	-0.32	0.8399	-0.59	0.4884	-0.10	0.8936	0.25	0.5540	-0.22	0.8005
R sq	0.9669		0.9620		0.9838		0.9848		0.9827		0.9722	
R sq (adj)	0.9623		0.9568		0.9815		0.9827		0.9812		0.9683	

† PHT, FLL, FLW, FLA, FLS were not evaluated in Kinston 2014.

Table 5.3 Stepwise multiple linear regression of the MD01W233-06-1 × SS8641 doubled haploid population. Grain yield (GYLD) as dependent variable and grains per spike (GPS), grain weight per spike (GWPS), spikes per square meter (SPSM), and thousand-grain-weight (TGW), plant height (PHT), flag leaf length (FLL), flag leaf width (FLW), flag leaf area (FLA), flag leaf shape (FLS), spike length (SL), sterile spikelet number per spike (SSN), fertile spikelet number per spike (FSN), spikelet compactness (SC), grain number per spikelet (GSP), and heading date (HD) as independent variables. Total spikelet number per spike (TSN) was not included in the analysis because of its multicollinearity with SSN and FSN. Variables kept in the final model, their regression coefficients, and the associated *p* values are shown.

	Clarksville 2013		Clarksville 2014		Queenstown 2013		Queenstown 2014		Kinston 2014†		Overall	
Variable	Estimate	P value	Estimate	P value	Estimate	P value	Estimate	P value	Estimate	P value	Estimate	P value
Intercept	-613.72	<.0001	-732.93	<.0001	-662.59	<.0001	-599.60	<.0001	-497.80	<.0001	-518.98	<.0001
GPS												
GWPS	436.68	<.0001	769.62	<.0001	475.04	<.0001	493.77	<.0001	430.65	<.0001	520.18	<.0001
SPSM	1.19	<.0001	0.93	<.0001	1.30	<.0001	1.08	<.0001	1.10	<.0002	1.10	<.0001
TGW							1.18	0.0171	0.85	0.0436		
PHT	0.95	0.0031					0.49	0.0131				
FLL												
FLW												
FLA												
FLS												
SL												
SSN					-9.71	0.0083	-7.82	0.0029				
FSN											-4.62	0.0019
SC					25.42	0.0447						
GSP												
HD												
R sq	0.9607		0.9545		0.9825		0.9783		0.9816		0.9676	
R sq (adj)	0.9598		0.9537		0.9819		0.9774		0.9812		0.9668	

† PHT, FLL, FLW, FLA, FLS were not evaluated in Kinston 2014.

Table 5.4 Principal component analysis of the MD01W233-06-1 × SS8641 doubled haploid population based on sixteen agronomic traits including grain yield (GYLD), grains per spike (GPS), grain weight per spike (GWPS), spikes per square meter (SPSM), and thousand-grain-weight (TGW), plant height (PHT), flag leaf length (FLL), flag leaf width (FLW), flag leaf area (FLA), flag leaf shape (FLS), spike length (SL), sterile spikelet number per spike (SSN), fertile spikelet number per spike (FSN), total spikelet number per spike (TSN), spikelet compactness (SC), and grain number per spikelet (GSP). Eigen values for each extracted principle component (PC), percentage (Per.) explained by each PC and cumulative percentage (Cum. Per.) are shown.

	Clarksville 2013			Clarksville 2014			Queenstown 2013			Queenstown 2014			Kinston 2014†			Overall		
	Eigen value	Per.	Cum. Per.	Eigen value	Per.	Cum. Per.	Eigen value	Per.	Cum. Per.	Eigen value	Per.	Cum. Per.	Eigen value	Per.	Cum. Per.	Eigen value	Per.	Cum. Per.
PC1	5.21	30.62	30.62	4.61	27.13	27.13	5.52	32.49	32.49	5.22	30.68	30.68	4.14	34.53	34.53	5.62	33.07	33.07
PC2	3.44	20.22	50.84	3.08	18.13	45.26	3.74	21.98	54.46	3.18	18.71	49.40	2.85	23.71	58.24	3.35	19.71	52.78
PC3	2.06	12.13	62.97	2.30	13.55	58.80	1.83	10.74	65.20	2.19	12.88	62.28	1.87	15.57	73.80	2.02	11.87	64.65
PC4	1.70	9.99	72.96	1.98	11.64	70.44	1.55	9.12	74.32	1.73	10.19	72.46	1.36	11.30	85.11	1.85	10.91	75.56
PC5	1.30	7.67	80.62	1.41	8.29	78.73	1.20	7.08	81.40	1.23	7.24	79.70	0.84	7.03	92.14	1.08	6.34	81.89
PC6	0.99	5.81	86.43	1.06	6.24	84.97	1.02	6.02	87.42	1.15	6.77	86.47	0.54	4.53	96.67	0.98	5.77	87.67
PC7	0.88	5.16	91.60	0.95	5.59	90.56	0.92	5.41	92.83	0.87	5.13	91.61	0.32	2.68	99.35	0.86	5.06	92.72
PC8	0.52	3.07	94.67	0.78	4.57	95.12	0.48	2.83	95.67	0.62	3.67	95.27	0.07	0.56	99.90	0.52	3.05	95.77
PC9	0.44	2.61	97.27	0.41	2.40	97.52	0.35	2.06	97.73	0.42	2.50	97.77	0.01	0.06	99.96	0.44	2.56	98.33
PC10	0.34	1.98	99.26	0.27	1.57	99.09	0.28	1.62	99.35	0.28	1.63	99.40	0.00	0.03	99.99	0.21	1.21	99.54
PC11	0.10	0.59	99.84	0.13	0.75	99.84	0.08	0.49	99.83	0.08	0.50	99.90	0.00	0.01	100.00	0.06	0.35	99.89
PC12	0.01	0.08	99.92	0.01	0.07	99.91	0.01	0.07	99.91	0.01	0.04	99.94	0.00	0.00	100.00	0.01	0.06	99.94
PC13	0.01	0.05	99.97	0.01	0.04	99.94	0.01	0.04	99.95	0.01	0.03	99.97				0.00	0.02	99.96
PC14	0.00	0.02	99.98	0.01	0.03	99.98	0.01	0.03	99.98	0.00	0.01	99.98				0.00	0.02	99.98
PC15	0.00	0.01	99.99	0.00	0.01	99.99	0.00	0.02	99.99	0.00	0.01	99.99				0.00	0.01	99.99
PC16	0.00	0.01	100.00	0.00	0.01	100.00	0.00	0.01	100.00	0.00	0.01	100.00				0.00	0.01	100.00
PC17	0.00	0.00	100.00				0.00	0.00	100.00	0.00	0.00	100.00				0.00	0.00	100.00

† PHT, FLL, FLW, FLA, FLS were not evaluated in Kinston 2014.

Table 5.5 Principle component analysis of the MD01W233-06-1 × SS8641 doubled haploid population based on sixteen agronomic traits including grain yield (GYLD), grains per spike (GPS), grain weight per spike (GWPS), spikes per square meter (SPSM), and thousand-grain-weight (TGW), plant height (PHT), flag leaf length (FLL), flag leaf width (FLW), flag leaf area (FLA), flag leaf shape (FLS), spike length (SL), sterile spikelet number per spike (SSN), fertile spikelet number per spike (FSN), total spikelet number per spike (TSN), spike compactness (SC), grain number per spikelet (GSP), and heading date (HD). Eigenvectors of the first two principle components (PC) are shown.

	Clarksville 2013		Clarksville 2014		Queenstown 2013		Queenstown 2014		Kinston 2014†		Overall	
	PC1	**PC2**	**PC1**	**PC2**	**PC1**	**PC2**	**PC1**	**PC2**	**PC1**	**PC2**	**PC1**	**PC2**
GYLD	-0.197	-0.293	-0.086	-0.042	-0.241	-0.196	-0.045	-0.303	-0.187	-0.152	-0.230	0.227
GPS	0.374	-0.118	0.349	-0.262	0.298	-0.302	0.343	-0.227	0.439	-0.149	0.311	0.255
GWPS	0.315	-0.254	0.302	-0.250	0.215	-0.375	0.302	-0.321	0.250	-0.314	0.230	0.367
SPSM	-0.355	-0.081	-0.312	0.174	-0.332	0.039	-0.286	0.013	-0.356	0.075	-0.338	-0.080
TGW	-0.046	-0.264	0.046	0.095	-0.135	-0.109	-0.079	-0.098	-0.215	-0.172	-0.094	0.114
PHT	0.086	-0.165	-0.013	0.010	-0.003	0.029	0.149	-0.070	--	--	0.043	0.138
FLL	0.277	-0.025	0.277	0.148	0.307	0.099	0.317	0.119	--	--	0.311	0.029
FLW	0.156	0.177	0.262	0.207	0.246	0.172	0.189	0.378	--	--	0.247	-0.233
FLA	0.281	0.075	0.339	0.220	0.335	0.162	0.309	0.293	--	--	0.347	-0.119
FLS	0.166	-0.140	0.046	-0.028	0.098	-0.045	0.132	-0.217	--	--	0.089	0.212
SL	0.341	-0.060	0.354	-0.012	0.299	-0.183	0.344	-0.063	0.321	-0.163	0.295	0.163
SSN	-0.144	0.291	-0.051	0.449	-0.011	0.413	-0.019	0.273	-0.046	0.423	0.031	-0.346
FSN	0.334	0.191	0.361	0.087	0.363	-0.046	0.375	0.001	0.450	0.101	0.356	-0.016
TSN	0.279	0.322	0.314	0.283	0.336	0.161	0.359	0.125	0.397	0.279	0.349	-0.164
SC	-0.104	0.394	-0.114	0.301	-0.002	0.365	-0.078	0.234	0.070	0.462	0.005	-0.351
GSP	0.192	-0.322	0.158	-0.445	0.137	-0.402	0.154	-0.327	0.218	-0.335	0.112	0.379
HD	0.076	0.433	0.152	0.369	0.221	0.347	0.108	0.439	0.137	0.449	0.196	-0.396

† PHT, FLL, FLW, FLA, FLS were not evaluated in Kinston 2014.

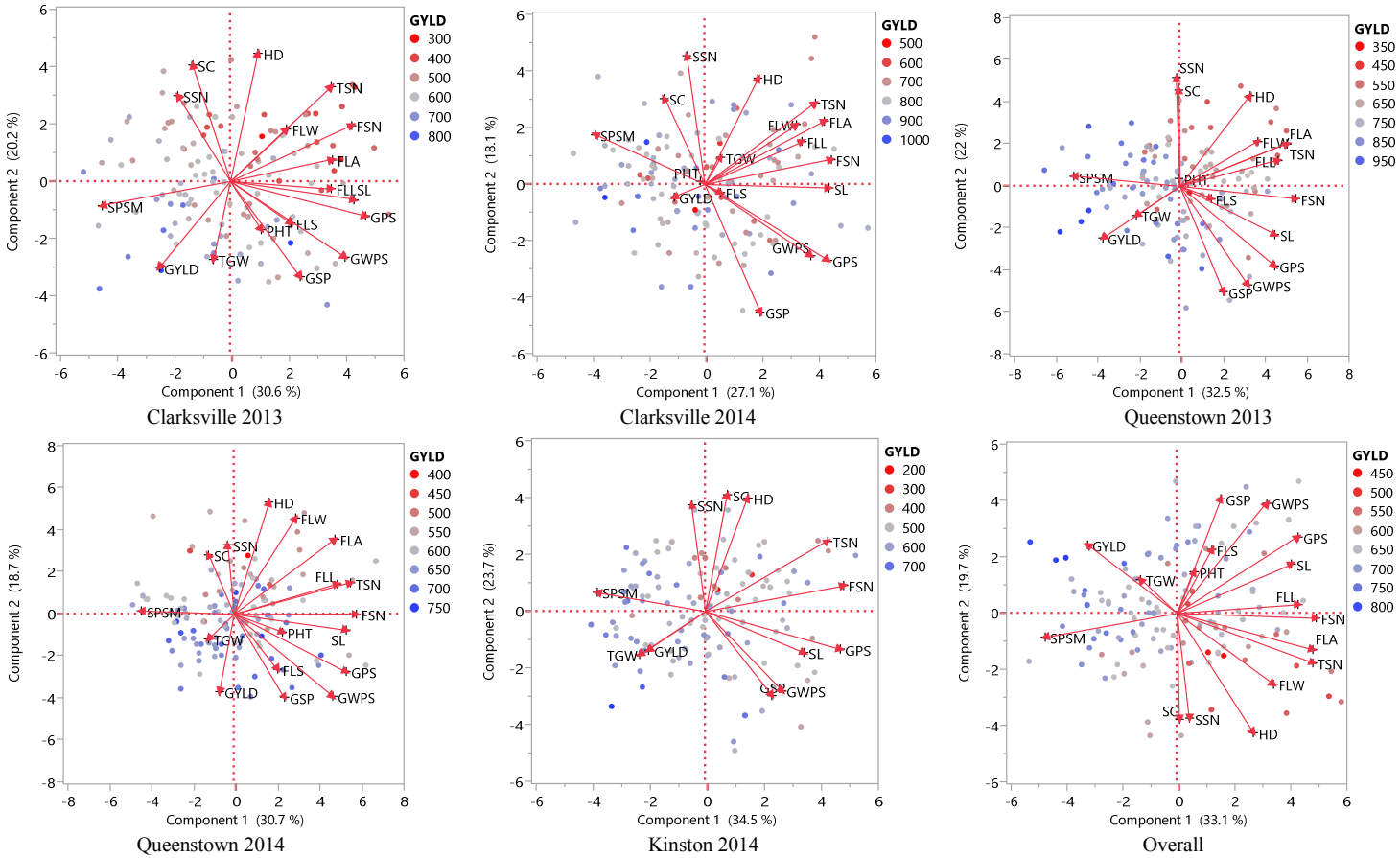


Figure 5.1 Principal component analysis: biplot summarizing the relationship among grain yield components, plant architecture, and spike morphology for the MD01W233-06-1 × SS8641doubled haploid population evaluated in five trials from 2013 to 2014. Traits are grain yield (GYLD), grains per spike (GPS), grain weight per spike (GWPS), spikes per square meter (SPSM), and thousand-grain-weight (TGW), plant height (PHT), flag leaf length (FLL), flag leaf width (FLW), flag leaf area (FLA), flag leaf shape (FLS), spike length (SL), sterile spikelet number per spike (SSN), fertile spikelet number per spike (FSN), total spikelet number per spike (TSN), spikelet compactness (SC), and grain number per spikelet (GSP). PHT, FLL, FLW, FLA, FLS were not evaluated at Kinston 2014.

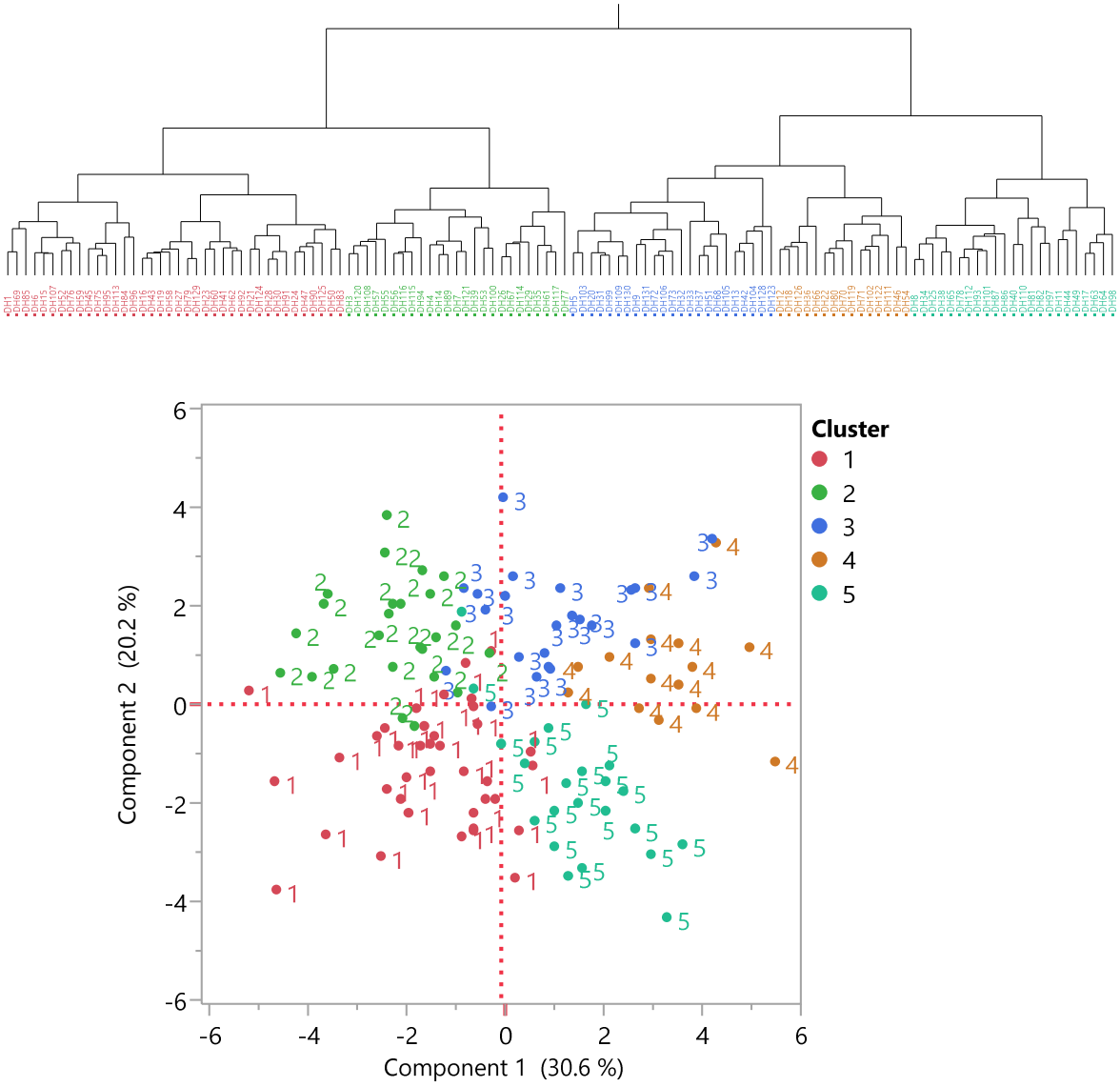


Figure 5.21 Dendrogram of cluster analysis and scatter diagram of the doubled-haploid lines for the first two principal components at Clarksville 2013 (E1).

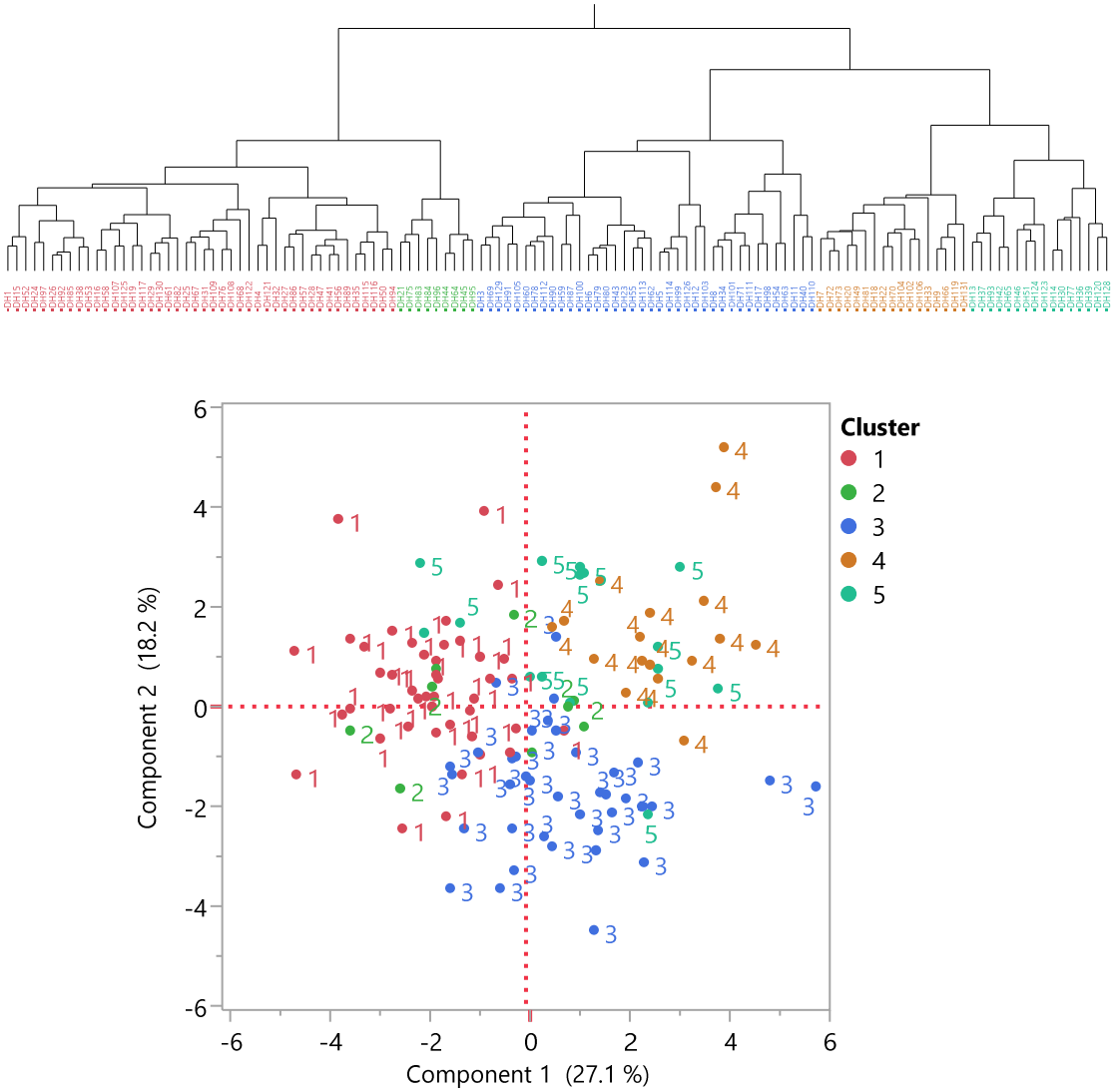


Figure 5.22 Dendrogram of cluster analysis and scatter diagram of the doubled-haploid lines for the first two principal components at Clarksville 2014 (E2).

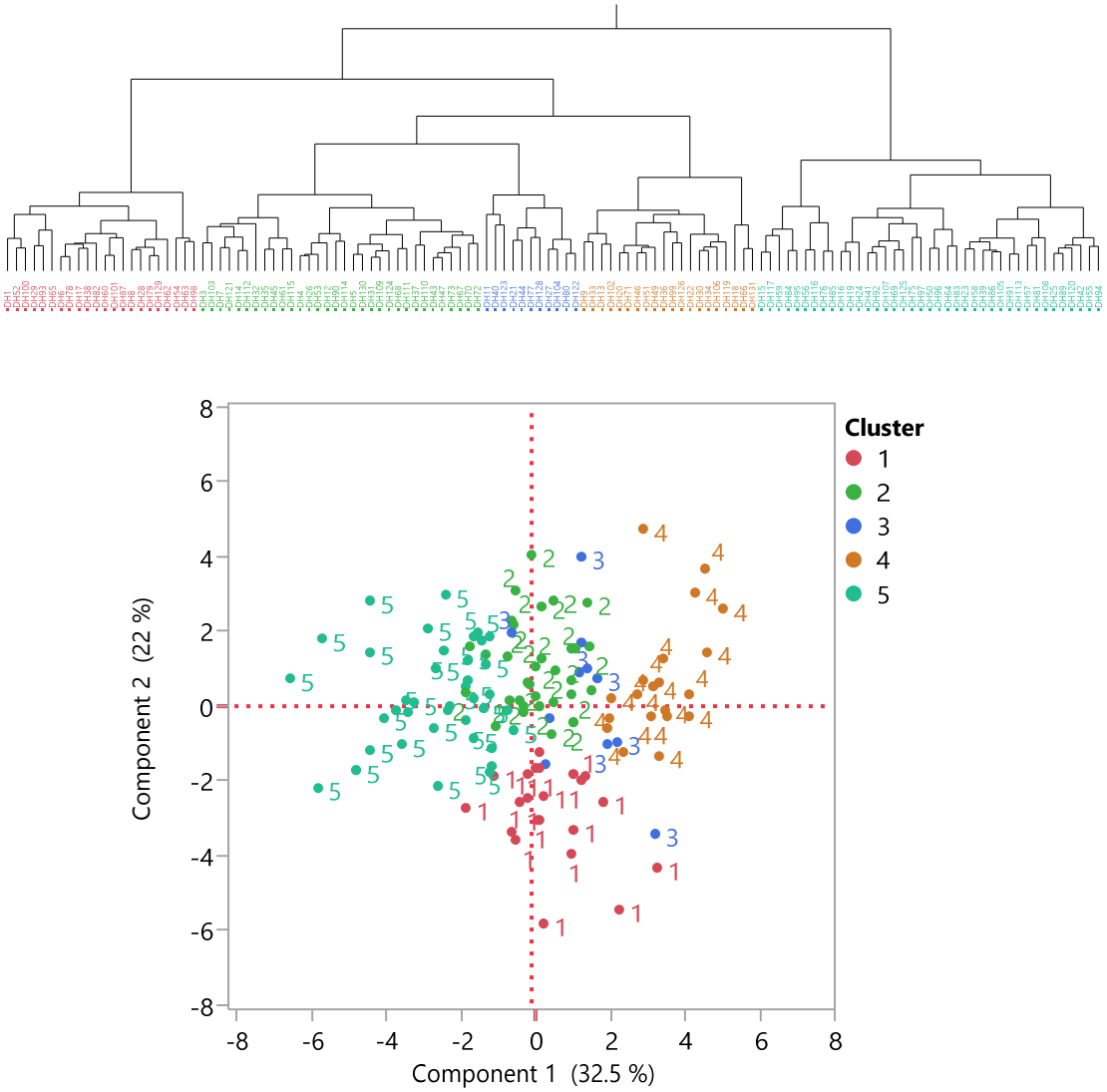


Figure 5.23 Dendrogram of cluster analysis and scatter diagram of the doubled-haploid lines for the first two principal components at Queenstown 2013 (E3).

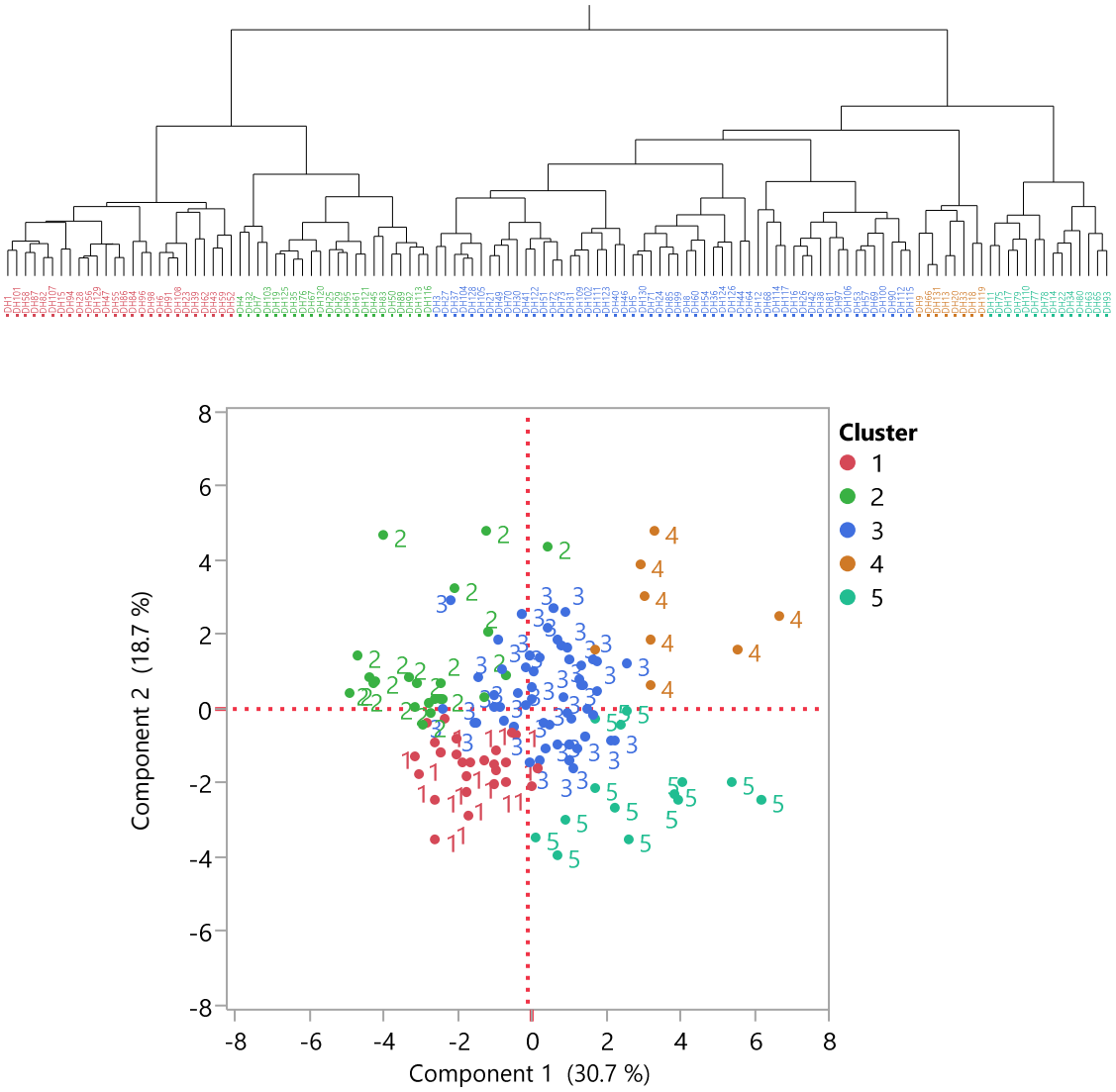


Figure 5.24 Dendrogram of cluster analysis and scatter diagram of the doubled-haploid lines for the first two principal components at Queenstown 2014 (E4).

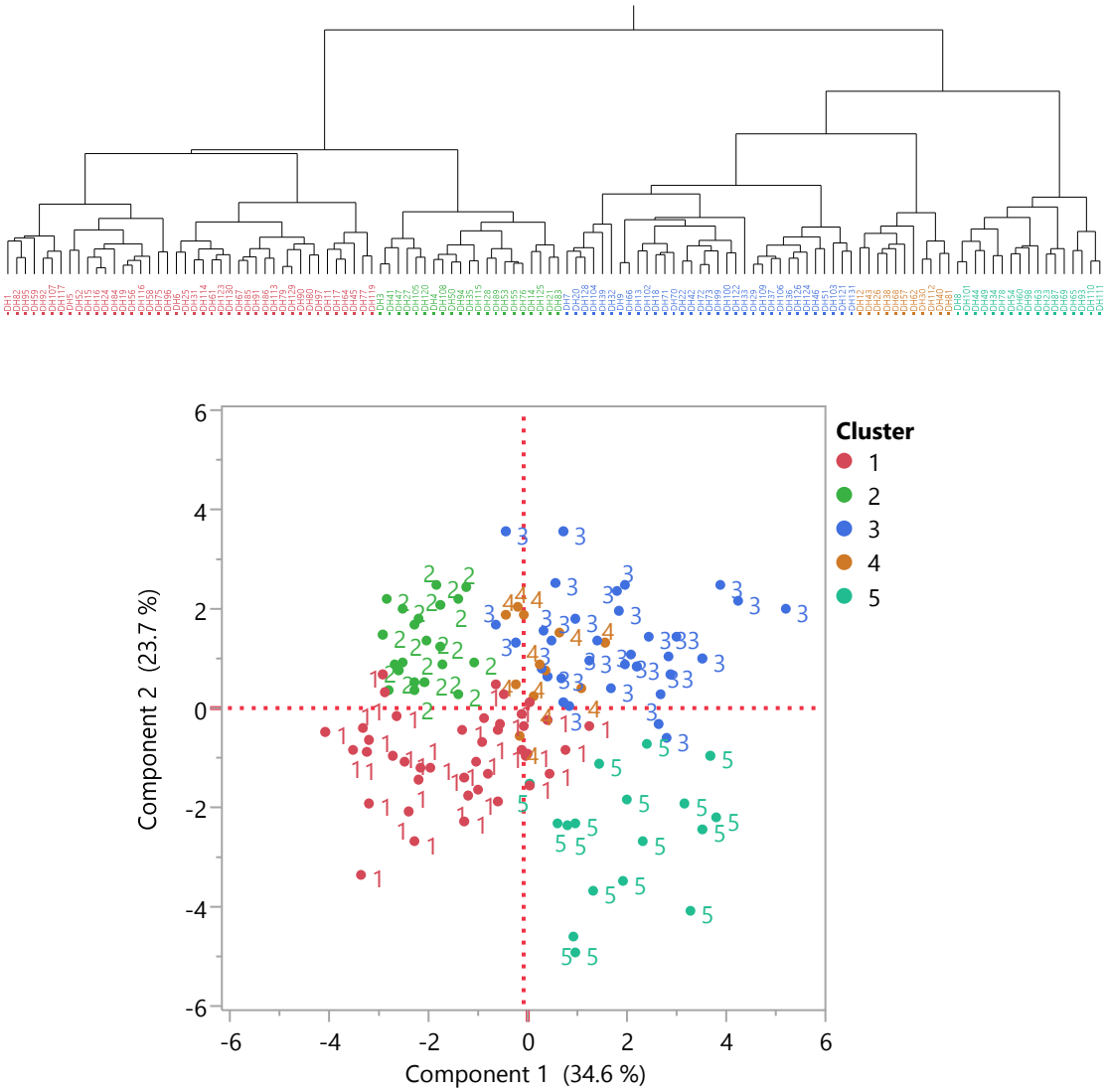


Figure 5.25 Dendrogram of cluster analysis and scatter diagram of the doubled-haploid lines for the first two principal components at Kinston 2014 (E5).

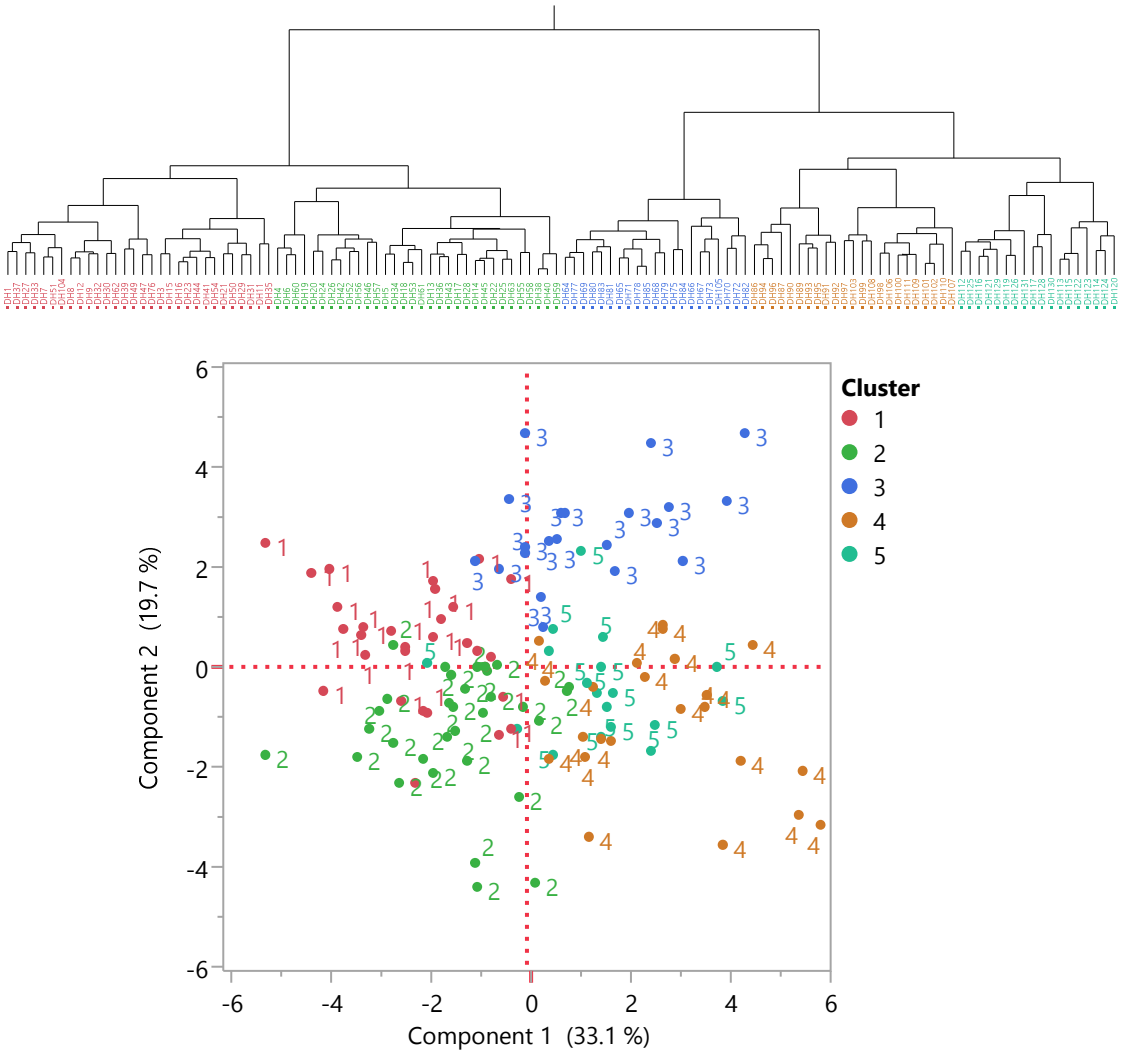


Figure 5.26 Dendrogram of cluster analysis and scatter diagram of the doubled-haploid lines for the first two principal components based on the average of E1, E2, E3, and E4.

Table 5.6 Mean and standard error for five clusters based on seventeen yield related traits evaluated at Clarksville 2013 (E1), Clarksville 2014 (E2), Queenstown 2013 (E3), Queenstown 2014 (E4), Kinston 2014 (E5), and average of five environments.

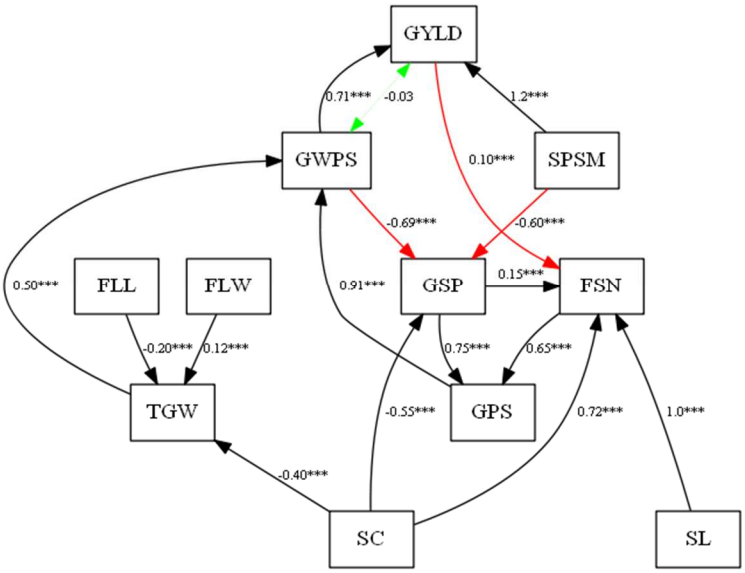
Environments	Traits	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
E1	GYLD	639.64 ± 6.40	561.74 ± 4.83	493.13 ± 6.07	484.99 ± 7.49	578.20 ± 8.01
	GPS	38.15 ± 0.26	35.19 ± 0.20	40.82 ± 0.26	45.10 ± 0.24	43.81 ± 0.30
	GWPS	1.19 ± 0.01	1.08 ± 0.01	1.16 ± 0.01	1.38 ± 0.01	1.37 ± 0.01
	SPSM	540.92 ± 6.65	527.62 ± 5.15	428.18 ± 5.67	359.14 ± 6.16	426.97 ± 5.01
	TGW	32.34 ± 0.18	31.29 ± 0.16	29.19 ± 0.14	31.31 ± 0.14	32.36 ± 0.18
	PHT	87.82 ± 0.41	83.68 ± 0.54	85.28 ± 0.37	87.12 ± 0.45	89.57 ± 0.57
	FLL	13.52 ± 0.09	12.45 ± 0.09	14.51 ± 0.13	14.54 ± 0.10	13.59 ± 0.13
	FLW	1.44 ± 0.01	1.46 ± 0.01	1.53 ± 0.01	1.54 ± 0.01	1.44 ± 0.01
	FLA	15.47 ± 0.17	14.46 ± 0.14	17.55 ± 0.18	17.77 ± 0.13	15.53 ± 0.19
	FLS	9.48 ± 0.06	8.61 ± 0.08	9.61 ± 0.12	9.56 ± 0.08	9.54 ± 0.10
	SL	6.66 ± 0.03	6.67 ± 0.04	7.02 ± 0.03	7.64 ± 0.04	7.41 ± 0.04
	SSN	1.81 ± 0.04	2.18 ± 0.04	1.99 ± 0.03	1.70 ± 0.04	1.40 ± 0.03
	FSN	13.38 ± 0.05	13.96 ± 0.07	14.80 ± 0.08	15.84 ± 0.07	14.90 ± 0.04
	TSN	15.19 ± 0.05	16.14 ± 0.07	16.80 ± 0.08	17.54 ± 0.07	16.30 ± 0.05
	SC	2.29 ± 0.01	2.43 ± 0.01	2.40 ± 0.01	2.31 ± 0.01	2.21 ± 0.01
	GSP	2.85 ± 0.02	2.52 ± 0.01	2.76 ± 0.01	2.85 ± 0.01	2.94 ± 0.02
	HD	132.22 ± 0.13	133.90 ± 0.11	135.11 ± 0.11	134.47 ± 0.06	131.57 ± 0.11
E2	GYLD	789.07 ± 7.10	888.68 ± 5.20	770.68 ± 6.44	756.12 ± 5.43	797.80 ± 9.01
	GPS	32.94 ± 0.18	33.31 ± 0.15	38.17 ± 0.21	38.13 ± 0.22	35.97 ± 0.33
	GWPS	0.91 ± 0.01	1.06 ± 0.01	1.08 ± 0.01	1.05 ± 0.01	0.97 ± 0.01
	SPSM	882.49 ± 8.33	852.99 ± 6.89	722.89 ± 6.07	729.60 ± 6.08	844.23 ± 9.17
	TGW	28.79 ± 0.18	33.14 ± 0.07	29.03 ± 0.16	30.59 ± 0.19	28.30 ± 0.23
	PHT	87.62 ± 0.45	95.30 ± 0.49	88.50 ± 0.60	89.37 ± 0.42	88.67 ± 0.29
	FLL	14.58 ± 0.09	15.38 ± 0.06	15.28 ± 0.12	16.10 ± 0.07	17.21 ± 0.08
	FLW	1.40 ± 0.01	1.42 ± 0.01	1.40 ± 0.01	1.59 ± 0.01	1.39 ± 0.01
	FLA	16.21 ± 0.14	17.35 ± 0.11	17.06 ± 0.21	20.33 ± 0.17	18.97 ± 0.18
	FLS	10.44 ± 0.07	10.89 ± 0.07	10.94 ± 0.09	10.18 ± 0.06	12.47 ± 0.08
	SL	6.95 ± 0.03	7.33 ± 0.04	7.33 ± 0.05	7.56 ± 0.03	7.52 ± 0.05
	SSN	2.23 ± 0.03	2.40 ± 0.03	1.84 ± 0.03	2.48 ± 0.04	2.42 ± 0.03
	FSN	14.68 ± 0.06	14.35 ± 0.08	15.36 ± 0.06	16.14 ± 0.05	15.97 ± 0.08
	TSN	16.91 ± 0.06	16.75 ± 0.07	17.20 ± 0.06	18.62 ± 0.06	18.39 ± 0.07
	SC	2.44 ± 0.01	2.29 ± 0.01	2.36 ± 0.01	2.47 ± 0.01	2.46 ± 0.01
	GSP	2.09 ± 0.01	2.14 ± 0.01	2.34 ± 0.01	2.19 ± 0.01	2.08 ± 0.02
	HD	141.42 ± 0.11	141.50 ± 0.07	140.92 ± 0.12	143.59 ± 0.13	142.00 ± 0.10

Table 5.6 Continued

Environments	Traits	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
E3	GYLD	804.35 ± 5.83	672.72 ± 8.33	612.83 ± 8.42	659.55 ± 8.19	825.29 ± 9.62
	GPS	49.36 ± 0.27	41.67 ± 0.24	43.34 ± 0.39	47.65 ± 0.30	39.51 ± 0.27
	GWPS	1.61 ± 0.01	1.33 ± 0.01	1.39 ± 0.02	1.51 ± 0.01	1.33 ± 0.01
	SPSM	506.02 ± 4.75	507.85 ± 5.63	446.12 ± 6.34	438.93 ± 4.67	629.89 ± 9.94
	TGW	32.2 ± 0.17	31.32 ± 0.15	31.92 ± 0.20	31.66 ± 0.16	33.22 ± 0.19
	PHT	96.11 ± 0.50	94.86 ± 0.47	104.28 ± 0.41	98.66 ± 0.53	100.31 ± 0.43
	FLL	16.87 ± 0.11	17.11 ± 0.09	19.57 ± 0.12	18.96 ± 0.09	16.22 ± 0.10
	FLW	1.64 ± 0.01	1.71 ± 0.01	1.59 ± 0.01	1.87 ± 0.01	1.62 ± 0.01
	FLA	21.89 ± 0.20	23.21 ± 0.18	24.73 ± 0.26	28.08 ± 0.21	20.78 ± 0.18
	FLS	10.37 ± 0.07	10.06 ± 0.06	12.41 ± 0.07	10.22 ± 0.08	10.09 ± 0.07
	SL	7.48 ± 0.04	7.20 ± 0.03	7.35 ± 0.04	7.69 ± 0.03	6.70 ± 0.03
	SSN	1.11 ± 0.04	1.92 ± 0.04	1.62 ± 0.05	1.84 ± 0.05	1.75 ± 0.04
	FSN	15.26 ± 0.05	14.88 ± 0.05	14.99 ± 0.06	16.26 ± 0.05	13.96 ± 0.07
	TSN	16.38 ± 0.06	16.80 ± 0.06	16.61 ± 0.04	18.09 ± 0.07	15.71 ± 0.08
	SC	2.20 ± 0.01	2.34 ± 0.01	2.27 ± 0.01	2.36 ± 0.01	2.36 ± 0.01
	GSP	3.13 ± 0.01	2.66 ± 0.01	2.76 ± 0.02	2.79 ± 0.02	2.66 ± 0.02
	HD	124.84 ± 0.21	128.91 ± 0.18	129.41 ± 0.17	130.5 ± 0.21	125.96 ± 0.22
E4	GYLD	657.02 ± 3.15	601.17 ± 3.10	595.94 ± 6.01	553.28 ± 2.13	655.64 ± 4.44
	GPS	39.42 ± 0.20	34.50 ± 0.21	39.97 ± 0.24	42.94 ± 0.28	44.83 ± 0.36
	GWPS	1.12 ± 0.01	1.00 ± 0.01	1.11 ± 0.01	1.20 ± 0.01	1.32 ± 0.01
	SPSM	591.24 ± 5.10	603.86 ± 2.58	539.76 ± 4.95	465.42 ± 3.43	500.91 ± 4.10
	TGW	28.97 ± 0.16	30.14 ± 0.20	28.57 ± 0.15	29.02 ± 0.21	30.16 ± 0.17
	PHT	76.85 ± 0.34	73.53 ± 0.36	75.55 ± 0.52	78.16 ± 0.34	79.49 ± 0.49
	FLL	13.99 ± 0.08	13.93 ± 0.08	15.25 ± 0.10	16.66 ± 0.09	15.59 ± 0.08
	FLW	1.32 ± 0.00	1.41 ± 0.01	1.44 ± 0.01	1.61 ± 0.01	1.36 ± 0.01
	FLA	14.60 ± 0.09	15.65 ± 0.17	17.47 ± 0.15	21.39 ± 0.22	16.86 ± 0.13
	FLS	10.67 ± 0.07	9.92 ± 0.06	10.64 ± 0.09	10.35 ± 0.05	11.55 ± 0.09
	SL	6.47 ± 0.03	6.38 ± 0.03	6.84 ± 0.04	7.19 ± 0.03	7.47 ± 0.04
	SSN	1.02 ± 0.03	1.51 ± 0.04	1.14 ± 0.03	1.51 ± 0.04	1.13 ± 0.03
	FSN	13.58 ± 0.05	13.09 ± 0.05	14.15 ± 0.05	15.21 ± 0.05	15.07 ± 0.07
	TSN	14.61 ± 0.06	14.60 ± 0.06	15.29 ± 0.06	16.72 ± 0.04	16.20 ± 0.06
	SC	2.26 ± 0.01	2.30 ± 0.01	2.25 ± 0.01	2.33 ± 0.01	2.18 ± 0.01
	GSP	2.90 ± 0.01	2.62 ± 0.01	2.81 ± 0.02	2.81 ± 0.01	2.96 ± 0.02
	HD	138.46 ± 0.10	140.07 ± 0.13	140.30 ± 0.12	142.25 ± 0.09	138.54 ± 0.12

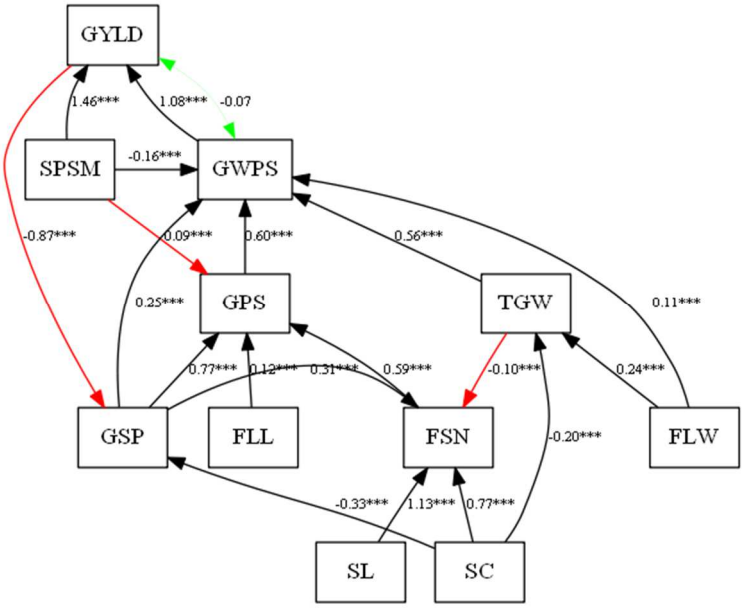
Table 5.6 Continued

Environment	Traits	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
E5	GYLD	591.65 ± 5.44	585.89 ± 5.01	545.90 ± 4.71	400.65 ± 6.28	544.87 ± 5.99
	GPS	40.11 ± 0.22	37.55 ± 0.15	45.84 ± 0.35	40.47 ± 0.20	48.73 ± 0.19
	GWPS	1.17 ± 0.01	1.10 ± 0.01	1.20 ± 0.01	1.03 ± 0.01	1.35 ± 0.01
	SPSM	508.88 ± 5.51	534.13 ± 3.68	458.08 ± 4.65	388.77 ± 5.29	404.32 ± 3.96
	TGW	28.91 ± 0.23	29.26 ± 0.20	25.74 ± 0.14	24.52 ± 0.26	27.27 ± 0.21
	SL	7.46 ± 0.04	7.07 ± 0.03	7.76 ± 0.04	7.42 ± 0.03	8.05 ± 0.05
	SSN	2.21 ± 0.04	2.96 ± 0.04	2.74 ± 0.04	2.30 ± 0.04	1.82 ± 0.03
	FSN	15.40 ± 0.08	15.09 ± 0.05	17.25 ± 0.08	16.15 ± 0.05	16.70 ± 0.08
	TSN	17.61 ± 0.09	18.05 ± 0.05	19.99 ± 0.08	18.45 ± 0.05	18.52 ± 0.09
	SC	2.37 ± 0.01	2.56 ± 0.01	2.59 ± 0.01	2.50 ± 0.01	2.31 ± 0.01
	GSP	2.60 ± 0.01	2.48 ± 0.01	2.65 ± 0.01	2.51 ± 0.02	2.92 ± 0.01
	HD	113.25 ± 0.23	116.81 ± 0.12	119.03 ± 0.22	114.95 ± 0.17	112.26 ± 0.32
All five trials	GYLD	692.85 ± 5.00	654.56 ± 4.01	677.91 ± 3.08	589.85 ± 5.71	627.68 ± 5.26
	GPS	38.68 ± 0.18	37.06 ± 0.19	44.33 ± 0.23	42.53 ± 0.27	40.68 ± 0.30
	GWPS	1.15 ± 0.00	1.1 ± 0.01	1.34 ± 0.01	1.22 ± 0.01	1.18 ± 0.01
	SPSM	617.91 ± 5.00	612.58 ± 4.18	519.57 ± 3.94	497.52 ± 4.10	547.24 ± 3.53
	TGW	30.1 ± 0.18	29.9 ± 0.15	30.56 ± 0.19	29.43 ± 0.14	29.56 ± 0.23
	PHT	88.28 ± 0.30	84.37 ± 0.43	89.45 ± 0.46	85.89 ± 0.48	91.36 ± 0.31
	FLL	14.65 ± 0.08	14.66 ± 0.07	15.73 ± 0.07	15.8 ± 0.11	16.39 ± 0.10
	FLW	1.44 ± 0.01	1.49 ± 0.01	1.47 ± 0.01	1.64 ± 0.01	1.46 ± 0.01
	FLA	16.86 ± 0.14	17.43 ± 0.11	18.44 ± 0.12	20.72 ± 0.22	19.12 ± 0.17
	FLS	10.22 ± 0.06	9.89 ± 0.06	10.77 ± 0.06	9.7 ± 0.06	11.31 ± 0.08
	SL	6.67 ± 0.03	7.03 ± 0.03	7.52 ± 0.03	7.44 ± 0.03	7.36 ± 0.04
	SSN	1.73 ± 0.03	2.04 ± 0.03	1.51 ± 0.02	1.93 ± 0.04	2.11 ± 0.03
	FSN	14.09 ± 0.04	14.52 ± 0.05	15.31 ± 0.06	15.8 ± 0.06	15.41 ± 0.07
	TSN	15.82 ± 0.05	16.56 ± 0.05	16.81 ± 0.05	17.73 ± 0.07	17.51 ± 0.06
	SC	2.38 ± 0.01	2.36 ± 0.01	2.24 ± 0.01	2.39 ± 0.01	2.39 ± 0.01
	GSP	2.69 ± 0.01	2.49 ± 0.01	2.84 ± 0.01	2.63 ± 0.01	2.57 ± 0.01
	HD	130.29 ± 0.14	131.92 ± 0.16	129.42 ± 0.12	133.44 ± 0.16	132.94 ± 0.12



a) Phenotype network at 2013 Clarksville, MD (E1).

Model fit indices:
SRMR=0.04
RMSEA=0.06
NNFI=0.97
CFI=0.98



b) Phenotype network at 2014 Clarksville, MD (E2).

Model fit indices:
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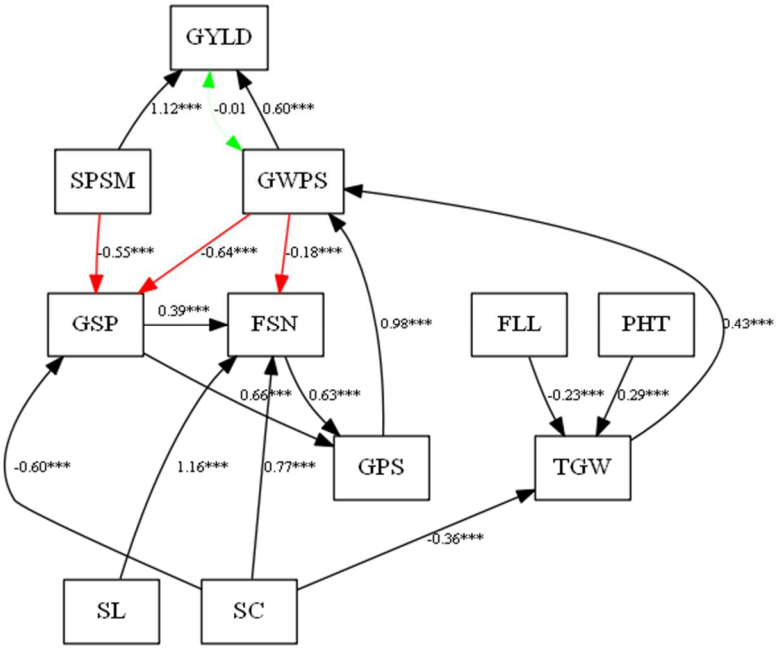
CFI=0.99



c) Phenotype network at 2013 Queenstwon, MD (E3).

Model fit indices:
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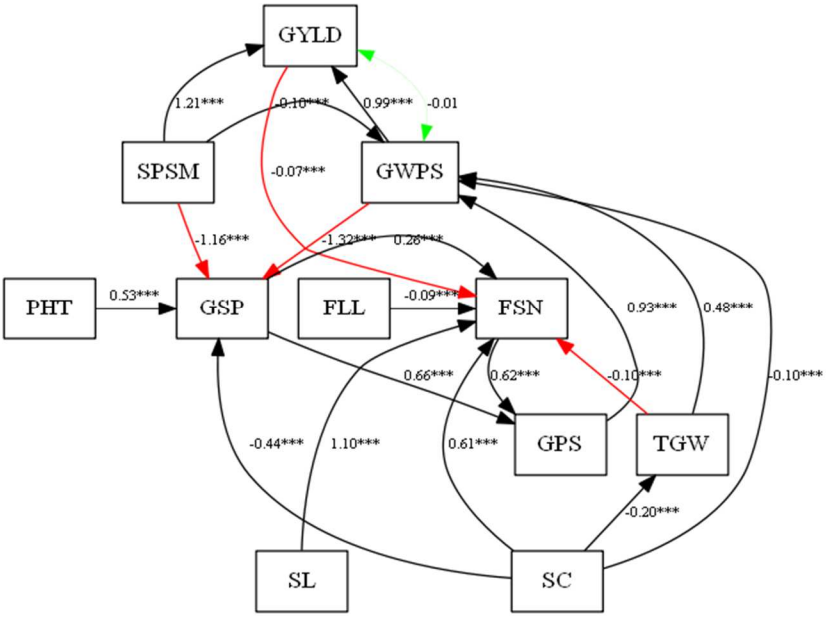
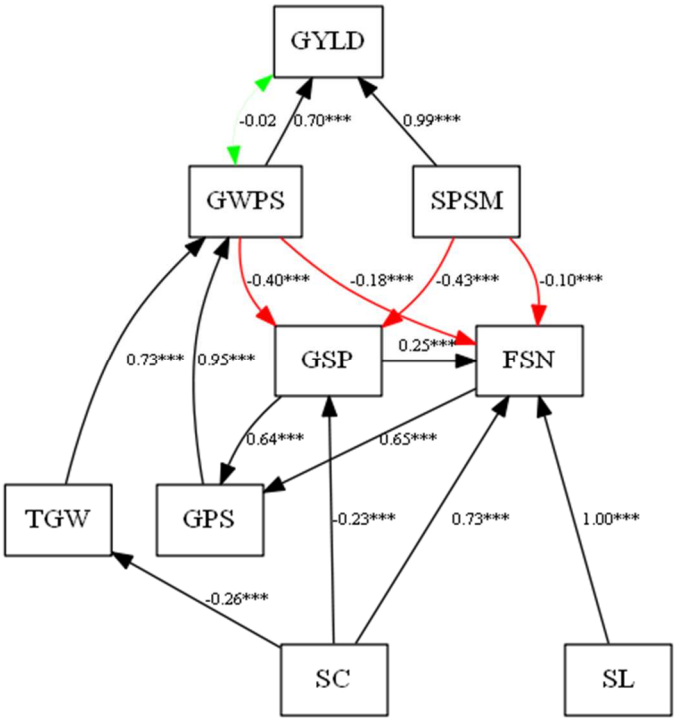
RMSEA=0.06
NNFI=0.97
CFI=0.98



d) Phenotype network at 2014 Queenstwon, MD (E4).

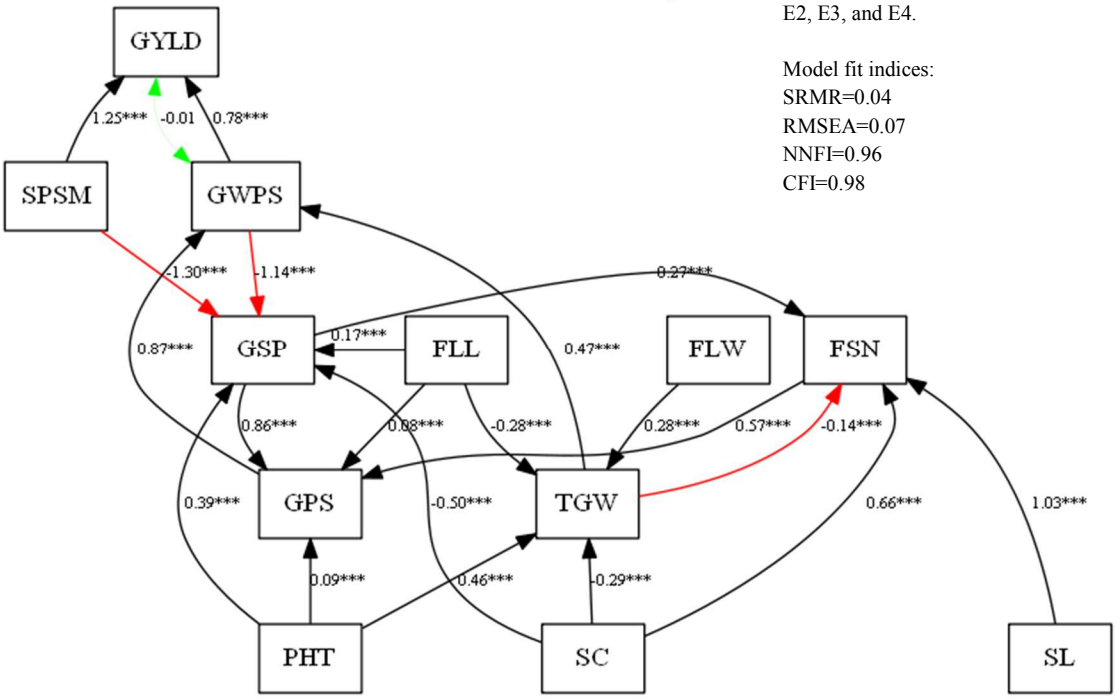
Model fit indices:
SRMR=0.03
RMSEA=0.07
NNFI=0.96
CFI=0.98



e) Phenotype network at 2014 Kinston, NC (E4).

Model fit indices:
SRMR=0.08
RMSEA=0.06
NNFI=0.98
CFI=0.99

Plant architecture traits were not evaluated in E4.



f) Phenotype network based on E1, E2, E3, and E4.

Model fit indices:
SRMR=0.04
RMSEA=0.07
NNFI=0.96
CFI=0.98

Figure 5.3 Graphical representaion of the structural equation modeling for the phenotypic network based on data from a) Clarksville 2013, b) Clarksville 2014, c) Queenstown 2013, d) Queenstown 2014, f) Kinston 2014, and g) First four environments averaged. Red arrows indicate negative contribution. Green arrows indicate error covariance.

Appendix A.

Table A.1 Source of simple sequence repeats (SSRs) on the linkage map constructed in this study

SSR Marker	Source	Reference
Xbarc100	USDA-ARS Beltsville Agricultural Research Center	(Song et al., 2005) Theor Appl Genet 110: 550–560
Xbarc101	USDA-ARS Beltsville Agricultural Research Center	(Song et al., 2005) Theor Appl Genet 110: 550–560
Xbarc10	USDA-ARS Beltsville Agricultural Research Center	(Song et al., 2005) Theor Appl Genet 110: 550–560
Xbarc127	USDA-ARS Beltsville Agricultural Research Center	(Song et al., 2005) Theor Appl Genet 110: 550–560
Xbarc12	USDA-ARS Beltsville Agricultural Research Center	(Song et al., 2005) Theor Appl Genet 110: 550–560
Xbarc147	USDA-ARS Beltsville Agricultural Research Center	(Song et al., 2005) Theor Appl Genet 110: 550–560
Xbarc163	USDA-ARS Beltsville Agricultural Research Center	(Song et al., 2005) Theor Appl Genet 110: 550–560
Xbarc164	USDA-ARS Beltsville Agricultural Research Center	(Song et al., 2005) Theor Appl Genet 110: 550–560
Xbarc170	USDA-ARS Beltsville Agricultural Research Center	(Song et al., 2005) Theor Appl Genet 110: 550–560
Xbarc28	USDA-ARS Beltsville Agricultural Research Center	(Song et al., 2005) Theor Appl Genet 110: 550–560
Xbarc45	USDA-ARS Beltsville Agricultural Research Center	(Song et al., 2005) Theor Appl Genet 110: 550–560
Xbarc59	USDA-ARS Beltsville Agricultural Research Center	(Song et al., 2005) Theor Appl Genet 110: 550–560
Xbarc80	USDA-ARS Beltsville Agricultural Research Center	(Song et al., 2005) Theor Appl Genet 110: 550–560
Xgdm136	Gatersleben D-genome Microsatellite	(Pestsova et al.,2000) Genome 43: 689–697
Xgwm111	Gatersleben wheat microsatellite	(Roder et al., 1998) Genetics 149: 2007–2024
Xgwm11	Gatersleben wheat microsatellite	(Roder et al., 1998) Genetics 149: 2007–2025
Xgwm261	Gatersleben wheat microsatellite	(Roder et al., 1998) Genetics 149: 2007–2026
Xgwm282	Gatersleben wheat microsatellite	(Roder et al., 1998) Genetics 149: 2007–2027
Xgwm304	Gatersleben wheat microsatellite	(Roder et al., 1998) Genetics 149: 2007–2028
Xgwm319	Gatersleben wheat microsatellite	(Roder et al., 1998) Genetics 149: 2007–2029
Xwmc273	Wheat Microsatellite Consortium	Somers and Isaac, 2004. SSRs from the Wheat Microsatellite Consortium http://wheat.pw.usda.gov/ggpages/SSR/WMC/
Xwmc496	Wheat Microsatellite Consortium	

Appendix B.

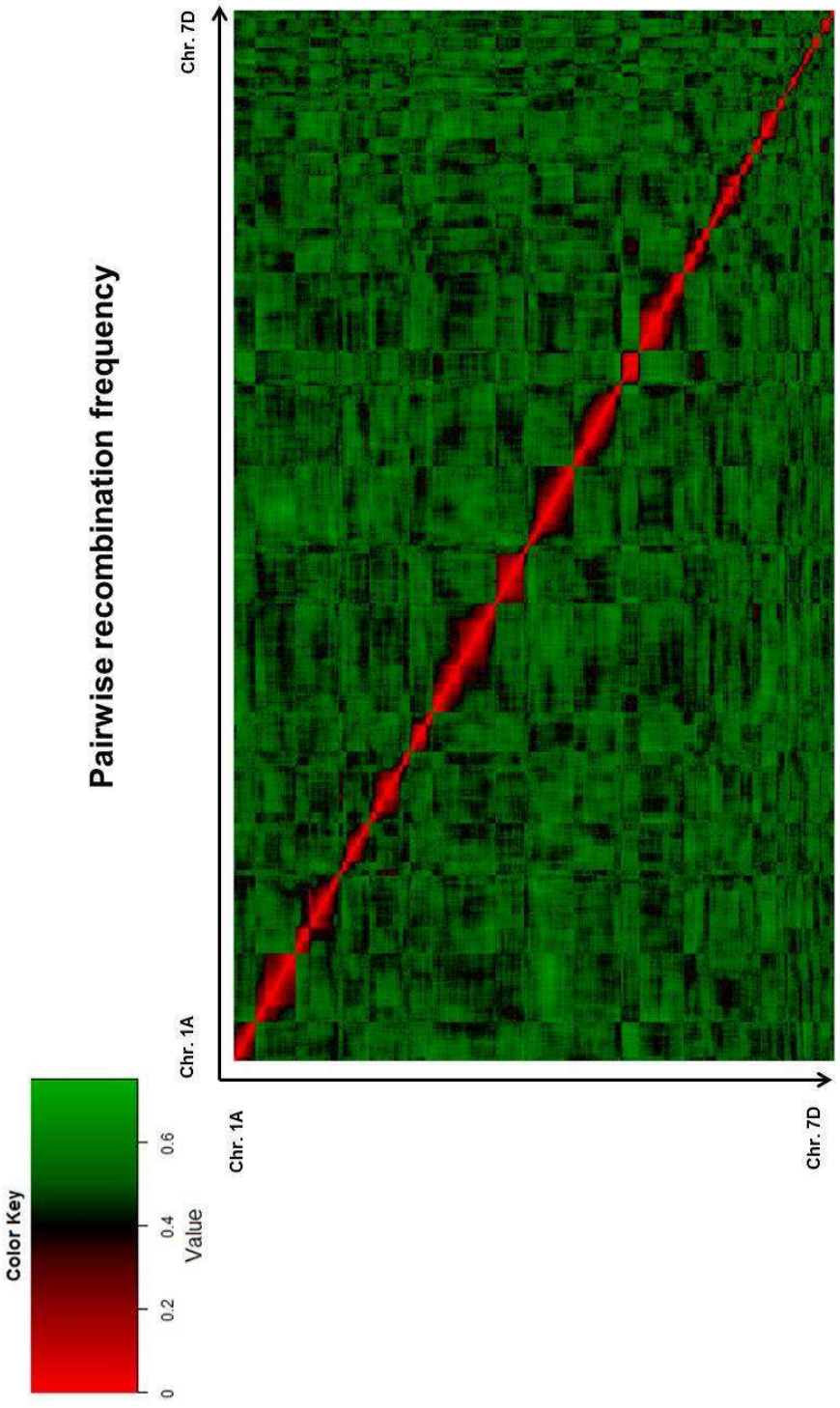


Figure B.1 Heat map of the genetic linkage map based on recombination frequencies among 859 DNA markers. Markers are aligned along each chromosome from 1A to 7D.

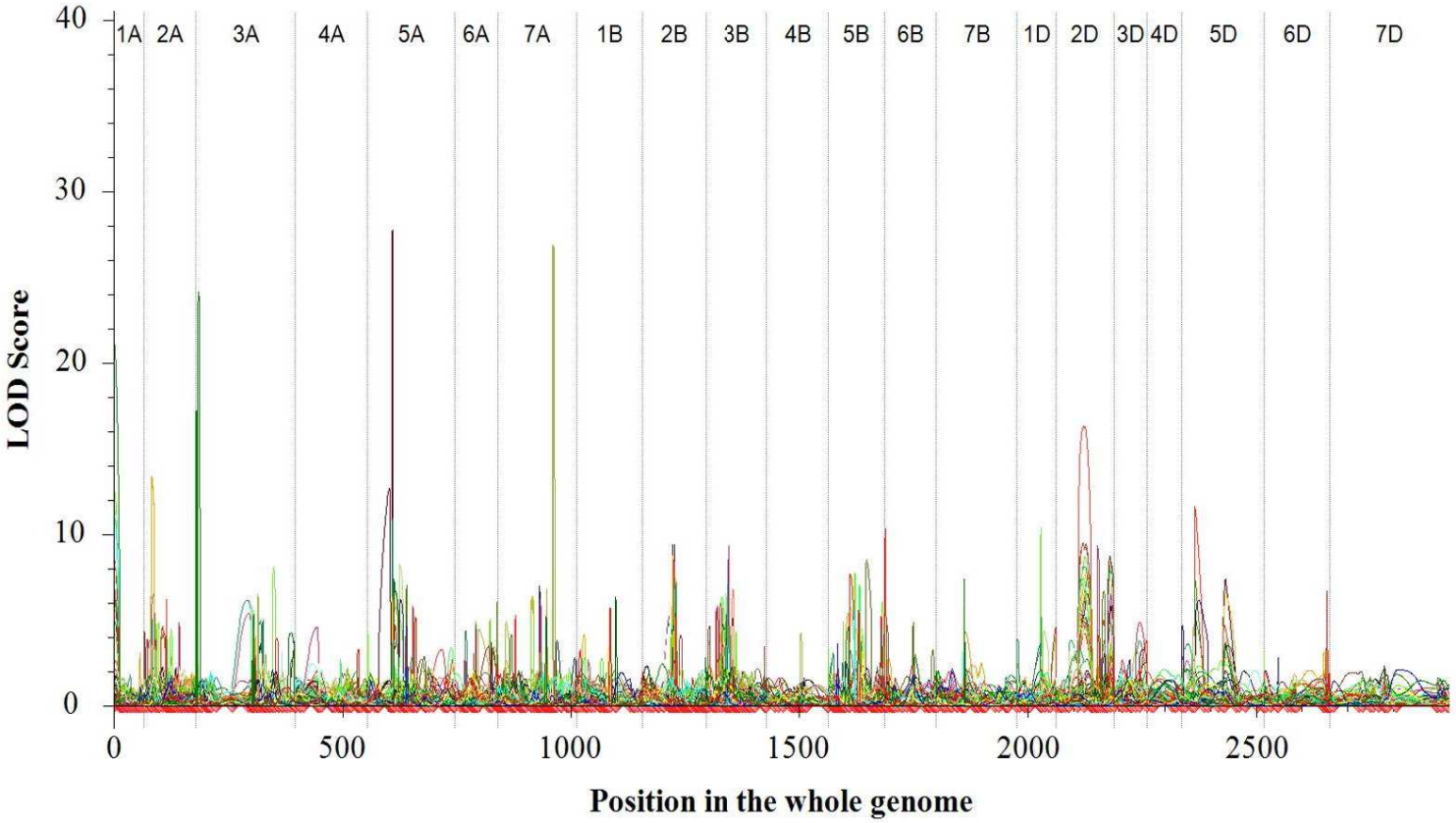


Figure B.2 Genome-wide distribution of LOD score. Markers are aligned along each chromosome from 1A to 7D according to their order on each chromosome. Unit of X-axis: cM.

Appendix C.

Table C.1 Summary of major and possible new QTLs identified in the present study. QTLs detected in multiple environments were indicated by asterisk.

QTL	Trait	Marker interval	LOD	PVE	Additive effect		
QFlw.cz-2A.2	FLW	*Xsnp2471-Xsnp2461*	13.3	31.2%	0.13	Major	
QFsn.cz-1A	FSN	*Xsnp1970-Xbarc28*	20.6	30.0%	0.65	Major	*
QGps.cz-1A.1	GPS	*Xsnp1970-Xbarc28*	14.2	26.5%	2.44	Major	
QGps.cz-1A.2	GPS	*Xbarc28-Xsnp2005*	21.2	44.1%	2.95	Major	*
QGps.cz-3A.2	GPS	*Xsnp3049-Xsnp3021*	24.1	52.0%	-3.20	Major	
QGws.cz-1A.1	GWPS	*Xwmc496-Xsnp1970*	12.2	28.6%	0.08	Major	
QGws.cz-1A.2	GWPS	*Xsnp1970-Xbarc28*	11.5	33.2%	0.06	Major	*
QPht.cz-5B.1	PHT	*Xsnp4068-Xsnp4012*	9.3	20.1%	2.86	Major	
QSc.cz-5A.3	SC	*Xgwm304-Xsnp996*	27.7	80.2%	-0.15	Major	*
QSc.cz-2B.1	SC	*Xsnp2773-Xgwm319*	9.3	21.6%	0.07	Major	*
QSc.cz-5A.1	SC	*Xsnp279-Xsnp3878*	12.7	26.7%	0.09	Major	
QSl.cz-1A	SL	*Xsnp1970-Xbarc28*	9.3	22.4%	0.25	Major	*
QSsm.cz-1A.1	SPSM	*Xwmc496-Xsnp1970*	13.9	30.1%	-50.85	Major	*
QSsm.cz-1A.2	SPSM	*Xsnp1970-Xbarc28*	15.6	22.1%	-34.04	Major	
QSsm.cz-1A.3	SPSM	*Xbarc28-Xsnp2005*	8.3	23.0%	-51.60	Major	*
QSsn.cz-2D.1	SSN	*Xsnp2862-XPpdD1*	16.3	30.0%	-0.31	Major	
QTgw.cz-7A.5	TGW	*Xsnp4588-Xsnp4620*	26.8	71.2%	-1.77	Major	
QTsn.cz-1A	TSN	*Xsnp1970-Xbarc28*	13.2	20.0%	0.57	Major	
QTsn.cz-2D.3	TSN	*XPpdD1-Xsnp2869*	6.5	20.9%	-0.41	Major	
QFla.cz-1A.1	FLA	*Xsnp1970-Xbarc28*	8.3	16.8%	1.36	New	
QFla.cz-1A.2	FLA	*Xbarc28-Xsnp2005*	4.3	9.1%	0.70	New	
QFla.cz-1B	FLA	*Xsnp4503-Xsnp2181*	4.1	9.4%	0.71	New	
QFla.cz-2A.1	FLA	*Xsnp2471-Xsnp2461*	13.1	28.7%	4.18	New	
QFla.cz-2A.2	FLA	*Xsnp2461-Xsnp2466*	6.5	13.4%	1.23	New	
QFla.cz-2D.1	FLA	*Xsnp2862-XPpdD1*	9.5	20.9%	-1.53	New	
QFla.cz-2D.2	FLA	*XPpdD1-Xsnp2869*	8.7	24.1%	-1.10	New	*
QFla.cz-2D.3	FLA	*Xsnp2804-Xsnp1766*	4.6	9.6%	-0.72	New	
QFla.cz-3B	FLA	*Xsnp3407-Xbarc147*	3.8	6.8%	2.03	New	
QFla.cz-5B.1	FLA	*Xsnp4140-Xsnp4114*	3.3	7.9%	-0.63	New	
QFla.cz-5B.2	FLA	*Xsnp4083-Xsnp3988*	3.2	11.4%	-2.47	New	
QFla.cz-6A	FLA	*Xsnp473-Xsnp4228*	3.2	10.1%	-0.76	New	
QFll.cz-1A.1	FLL	*Xsnp1970-Xbarc28*	4.5	10.0%	0.76	New	*
QFll.cz-2D	FLL	*XPpdD1-Xsnp2869*	7.5	20.6%	-0.58	New	*
QGws.cz-5B	GWPS	*Xsnp4130-Xsnp3884*	3.6	7.3%	-0.04	New	
QGws.cz-7B	GWPS	*Xsnp4927-Xsnp489*	3.1	7.5%	0.03	New	
Qyld.cz-2A	GYLD	*Xsnp2477-Xsnp2432*	4.3	9.9%	25.21	New	
QYld.cz-5B.2	GYLD	*Xsnp4011-Xsnp4073*	4.5	10.3%	25.67	New	
QPht.cz-2D.2	PHT	*Xsnp2795-Xsnp708*	8.4	22.0%	2.79	New	
QSl.cz-5A.1	SL	*Xsnp3819-Xsnp3789*	8.2	13.0%	0.20	New	
QSl.cz-5A.2	SL	*Xsnp3789-Xsnp3844*	6.2	12.5%	0.18	New	
QSl.cz-5A.3	SL	*Xsnp3812-Xsnp3856*	4.0	9.7%	0.16	New	
QSl.cz-5A.4	SL	*Xsnp3852-Xsnp3843*	7.0	13.1%	0.19	New	
QSl.cz-5A.5	SL	*Xsnp3849-Xsnp3841*	2.8	6.7%	0.13	New	
QTgw.cz-3A.6	TGW	*Xsnp2951-Xsnp2971*	4.2	6.7%	-0.57	New	

Appendix D.

Table D.1 Cluster membership of 124 doubled haploid lines based on data from: Clarksville 2013 (E1), Clarksville 2014 (E2), Queenstown 2013 (E3), Queenstown 2014 (E4), Kinston 2014 (E5), and average of five environments.

No.	Name	E1	E2	E4	E4	E5	five average
1	DH1	1	1	1	1	1	1
2	DH3	2	3	2	3	2	1
3	DH4	2	1	2	2	2	2
4	DH5	3	3	2	3	1	2
5	DH6	1	3	1	1	1	3
6	DH7	2	4	2	2	3	2
7	DH8	5	3	1	3	5	3
8	DH9	3	4	4	4	3	4
9	DH11	5	3	3	5	1	3
10	DH12	4	3	2	3	4	4
11	DH13	3	5	4	4	3	5
12	DH14	2	5	2	5	2	5
13	DH15	1	1	5	1	1	1
14	DH16	1	1	5	3	1	1
15	DH17	5	3	1	5	1	3
16	DH18	4	4	4	4	3	4
17	DH19	1	1	5	2	1	1
18	DH20	3	4	4	4	3	4
19	DH21	1	2	3	3	2	5
20	DH22	4	4	4	5	3	4
21	DH23	1	3	5	1	5	1
22	DH24	1	1	5	3	1	1
23	DH25	5	1	5	2	1	2
24	DH26	2	1	2	3	4	2
25	DH27	1	1	3	3	2	1
26	DH28	1	1	1	1	2	1
27	DH29	2	1	1	2	3	2
28	DH30	1	5	4	3	4	5
29	DH31	3	1	2	3	1	2
30	DH32	3	1	2	2	3	2
31	DH33	3	4	4	4	3	4
32	DH34	5	3	4	5	5	3
33	DH35	2	1	2	2	2	2
34	DH36	4	5	4	3	3	4
35	DH37	3	5	2	3	3	5
36	DH38	5	1	1	3	4	3
37	DH39	2	5	5	1	3	1
38	DH40	5	3	3	3	4	5
39	DH41	1	1	5	3	2	2
40	DH42	3	5	5	3	3	5
41	DH43	1	3	2	1	4	1
42	DH44	5	2	3	3	5	5
43	DH45	1	2	2	2	1	2
44	DH46	4	5	4	3	3	4
45	DH47	1	1	2	1	2	2
46	DH49	5	4	4	3	5	4
47	DH50	1	1	5	2	2	2
48	DH51	3	5	4	3	3	5
49	DH52	1	1	1	1	1	1
50	DH53	2	1	2	3	2	2
51	DH54	4	3	1	3	5	3
52	DH55	2	3	5	1	2	1
53	DH56	2	1	5	1	1	1
54	DH57	2	1	5	3	4	1
55	DH58	1	1	5	1	1	1
56	DH59	1	3	5	1	1	1
57	DH60	1	3	1	3	5	3
58	DH61	2	1	2	2	1	2
59	DH62	1	3	1	1	4	1
60	DH63	5	3	1	5	5	3
61	DH64	5	2	5	3	1	3
62	DH65	5	5	1	5	5	3

Table D.1 Continued.

No.	Name	E1	E2	E4	E4	E5	five average
63	DH66	4	4	4	4	3	4
64	DH67	2	1	2	2	1	2
65	DH68	3	1	2	3	4	4
66	DH69	1	3	5	3	5	1
67	DH70	4	4	2	3	3	5
68	DH71	4	3	4	3	3	4
69	DH72	3	4	2	3	3	4
70	DH73	3	4	2	3	3	4
71	DH75	1	2	5	5	1	1
72	DH76	1	1	5	2	2	2
73	DH77	2	5	3	5	1	5
74	DH78	5	3	1	5	5	3
75	DH79	1	3	1	5	1	3
76	DH80	4	3	3	5	1	3
77	DH81	5	4	5	3	4	4
78	DH82	5	1	1	1	1	1
79	DH83	1	2	5	2	2	5
80	DH84	1	2	5	1	1	1
81	DH85	1	1	5	3	1	2
82	DH86	5	1	5	1	1	1
83	DH87	5	3	1	1	5	3
84	DH89	2	1	5	2	2	2
85	DH90	1	3	2	3	1	2
86	DH91	1	3	5	1	1	1
87	DH92	1	1	5	2	1	2
88	DH93	5	5	1	5	5	3
89	DH94	2	1	5	1	2	2
90	DH95	1	2	5	2	1	1
91	DH96	1	2	5	1	1	1
92	DH97	5	1	5	3	1	3
93	DH98	5	3	1	1	5	3
94	DH99	3	3	4	3	3	4
95	DH100	2	3	1	3	3	4
96	DH101	5	3	1	1	5	3
97	DH102	4	4	4	3	3	5
98	DH103	3	3	2	2	3	4
99	DH104	3	4	3	3	3	5
100	DH105	3	3	5	3	2	1
101	DH106	3	4	4	3	3	4
102	DH107	1	1	5	1	1	1
103	DH108	2	1	5	1	2	2
104	DH109	3	1	2	3	3	2
105	DH110	5	3	2	5	5	5
106	DH111	4	3	2	3	5	3
107	DH112	5	3	2	3	4	4
108	DH113	1	3	5	2	1	1
109	DH114	2	3	2	3	1	2
110	DH115	2	1	2	3	2	2
111	DH116	2	1	5	2	1	2
112	DH117	2	1	5	3	1	2
113	DH119	4	4	4	4	1	4
114	DH120	2	5	5	2	2	2
115	DH121	2	1	2	2	3	2
116	DH122	4	1	3	3	3	5
117	DH123	3	5	3	3	1	5
118	DH124	1	5	2	3	3	2
119	DH125	1	1	5	2	2	1
120	DH126	4	3	4	3	3	4
121	DH128	3	5	3	3	3	5
122	DH129	1	3	1	1	1	3
123	DH130	3	1	2	3	1	2
124	DH131	3	4	4	4	3	4

Appendix E.

Table E.1 Phenotypic data for yield contributing traits evaluated at Clarksville 2013 (E1), Clarksville 2014 (E2), Queenstown 2013 (E3), Queenstown 2014 (E4), and Kinston 2014 (E5). Two replications at each environment. Missing data is indicated by dot.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
1	E1	1	DH1	658.7	34.7	1.0	646.4	29.6	86.5	10.9	1.2	10.2	9.3	6.2	1.5	13.3	14.8	2.4	2.6	131
2	E1	1	DH3	696.5	35.3	1.1	636.7	32.7	91.2	15.5	1.6	19.7	9.6	6.1	2.0	12.8	14.8	2.4	2.8	134
3	E1	1	DH4	494.4	31.9	1.0	477.2	33.5	78.2	12.9	1.6	16.0	8.3	6.5	2.2	14.3	16.5	2.6	2.2	136
4	E1	1	DH5	499.8	35.1	1.0	483.8	30.3	74.5	15.6	1.6	20.3	9.6	6.9	2.1	13.5	15.6	2.3	2.6	136
5	E1	1	DH6	697.4	40.4	1.3	543.6	32.7	90.0	13.7	1.4	15.2	9.7	6.8	1.3	14.2	15.5	2.3	2.8	129
6	E1	1	DH7	564.1	32.5	1.0	560.1	29.9	81.2	13.4	1.5	16.1	8.9	6.3	2.9	13.9	16.8	2.7	2.3	135
7	E1	1	DH8	640.2	42.3	1.2	520.5	30.5	93.9	14.2	1.5	17.1	9.5	7.3	2.2	14.4	16.6	2.3	2.9	132
8	E1	1	DH9	354.9	39.4	1.1	335.4	29.9	79.6	15.9	1.6	20.4	9.9	7.2	2.3	15.8	18.1	2.5	2.5	133
9	E1	1	DH11	720.7	44.8	1.5	475.4	35.1	110.9	16.1	1.4	18.4	11.2	8.4	1.7	15.0	16.7	2.0	3.0	131
10	E1	1	DH12	416.1	41.3	1.2	341.6	30.7	82.3	13.0	1.4	15.0	9.0	7.1	1.8	14.6	16.4	2.4	2.8	132
11	E1	1	DH13	482.5	42.5	1.2	389.5	28.0	88.5	15.0	1.4	16.8	10.6	7.1	2.0	15.8	17.8	2.5	2.7	137
12	E1	1	DH14	632.4	38.7	1.3	503.1	32.7	87.0	12.6	1.6	15.9	8.1	6.7	2.0	14.7	16.7	2.5	2.6	137
13	E1	1	DH15	640.0	35.3	1.1	579.1	31.8	80.7	12.9	1.4	14.1	9.3	6.6	1.5	13.3	14.8	2.2	2.7	130
14	E1	1	DH16	601.1	39.7	1.2	513.8	31.6	87.5	13.2	1.5	16.0	8.6	6.4	1.8	13.5	15.3	2.4	2.9	133
15	E1	1	DH17	596.6	40.7	1.4	417.2	34.7	87.4	15.2	1.4	16.4	11.3	7.5	1.3	14.0	15.3	2.0	2.9	130
16	E1	1	DH18	424.7	43.8	1.4	307.7	31.0	81.3	13.8	1.7	18.7	8.0	7.4	1.7	16.1	17.8	2.4	2.7	135
17	E1	1	DH19	660.7	35.3	1.2	573.5	33.4	91.7	13.5	1.5	16.2	9.0	6.2	1.9	12.4	14.3	2.3	2.8	133
18	E1	1	DH20	500.7	47.7	1.3	371.2	28.8	73.8	13.7	1.6	17.2	8.7	6.7	1.3	15.0	16.3	2.4	3.2	134
19	E1	1	DH21	583.2	37.1	1.2	488.4	33.1	93.7	15.2	1.5	18.1	10.3	6.9	2.8	13.4	16.2	2.3	2.8	134
20	E1	1	DH22	611.5	39.5	1.2	500.0	33.4	95.3	14.6	1.6	18.4	9.2	7.1	2.5	15.7	18.2	2.6	2.5	134
21	E1	1	DH23	663.0	41.2	1.3	522.5	31.1	87.4	16.1	1.4	17.4	11.8	6.3	1.2	13.2	14.4	2.3	3.1	131
22	E1	1	DH24	748.8	33.4	1.0	744.3	31.0	93.6	12.1	1.5	14.6	7.9	6.0	1.8	12.4	14.2	2.4	2.7	132
23	E1	1	DH25	672.5	44.1	1.3	515.4	33.8	79.2	13.7	1.4	15.4	9.6	7.4	1.9	14.8	16.7	2.3	3.0	130
24	E1	1	DH26	644.8	33.1	1.1	609.4	33.1	79.5	12.7	1.5	15.4	8.4	6.6	2.4	13.7	16.1	2.4	2.4	132
25	E1	1	DH27	586.9	41.1	1.2	479.5	30.5	91.3	15.0	1.4	16.9	10.5	6.3	1.4	12.9	14.3	2.3	3.2	134
26	E1	1	DH28	602.4	38.7	1.2	514.8	32.0	93.5	13.2	1.5	15.9	8.8	6.4	2.2	14.1	16.3	2.6	2.7	133
27	E1	1	DH29	442.6	30.9	1.0	428.0	33.7	70.8	12.1	1.4	13.3	8.9	6.9	1.8	13.6	15.4	2.2	2.3	135
28	E1	1	DH30	601.2	34.1	1.2	520.9	32.8	86.0	15.1	1.6	19.1	9.4	6.5	2.4	13.3	15.7	2.4	2.6	133
29	E1	1	DH31	488.3	36.8	1.0	487.3	29.0	83.2	14.5	1.5	17.1	9.7	6.9	2.0	13.7	15.7	2.3	2.7	136
30	E1	1	DH32	421.5	38.4	1.0	435.5	25.7	81.1	13.9	1.6	17.7	8.6	7.4	1.2	16.4	17.6	2.4	2.3	137
31	E1	1	DH33	415.1	48.6	1.0	400.7	28.9	90.0	16.0	1.7	21.6	9.4	7.1	2.0	16.3	18.3	2.6	3.0	137
32	E1	1	DH34	574.3	45.6	1.3	444.5	30.7	92.2	15.2	1.5	17.7	10.3	7.3	1.2	15.2	16.4	2.3	3.0	132
33	E1	1	DH35	576.1	37.9	1.2	480.1	33.7	85.8	11.4	1.9	17.0	6.1	7.1	1.9	13.6	15.5	2.2	2.8	134
34	E1	1	DH36	418.7	40.8	1.3	330.5	31.5	81.9	14.7	1.5	17.3	10.1	8.1	1.4	17.0	18.4	2.3	2.4	135
35	E1	1	DH37	553.4	42.1	1.1	504.0	29.7	92.2	15.6	1.6	19.4	10.1	7.1	2.4	14.4	16.8	2.4	2.9	134
36	E1	1	DH38	533.9	41.7	1.2	445.7	29.4	82.3	13.8	1.4	15.3	9.8	7.1	1.2	14.4	15.6	2.2	2.9	129
37	E1	1	DH39	576.6	39.7	1.2	499.6	30.1	89.7	10.4	1.1	9.4	9.2	6.1	2.1	15.4	17.5	2.9	2.6	137
38	E1	1	DH40	547.8	37.1	1.2	450.5	32.8	94.0	12.1	1.4	13.4	9.1	7.7	1.1	14.7	15.8	2.1	2.5	132
39	E1	1	DH41	601.8	39.5	1.1	544.1	30.3	86.3	16.6	1.4	18.4	12.0	6.6	1.3	13.5	14.8	2.2	2.9	130
40	E1	1	DH42	571.0	44.6	1.4	417.1	30.7	85.8	16.5	1.4	18.1	11.9	7.5	1.5	16.8	18.3	2.5	2.7	134
41	E1	1	DH43	615.0	34.9	1.0	608.3	31.9	89.7	13.7	1.5	16.6	9.0	6.1	2.3	12.3	14.6	2.4	2.8	134
42	E1	1	DH44	765.9	34.8	1.3	612.2	36.0	106.0	16.0	1.6	20.7	9.8	7.6	1.9	13.9	15.8	2.1	2.5	136
43	E1	1	DH45	641.7	35.9	1.3	505.7	35.3	90.6	11.5	1.5	13.5	7.7	7.1	1.9	13.9	15.8	2.2	2.6	133
44	E1	1	DH46	478.0	41.8	1.1	416.4	29.4	87.4	15.8	1.6	19.4	10.2	7.8	2.3	14.2	16.5	2.1	2.9	134
45	E1	1	DH47	699.0	37.0	1.1	618.6	32.3	86.7	13.8	1.4	15.8	9.6	6.8	2.1	13.5	15.6	2.3	2.7	135
46	E1	1	DH49	599.8	46.2	1.4	435.6	30.9	88.7	14.4	1.5	17.4	9.4	7.6	1.8	14.6	16.4	2.2	3.2	134
47	E1	1	DH50	669.3	34.4	1.1	585.6	34.4	88.7	15.1	1.6	19.5	9.3	6.2	2.1	12.5	14.6	2.3	2.8	131
48	E1	1	DH51	507.0	42.6	1.0	507.5	29.2	90.7	16.5	1.6	21.5	10.0	7.2	2.6	15.1	17.7	2.5	2.8	134
49	E1	1	DH52	748.9	37.9	1.1	709.9	28.6	78.4	13.3	1.4	15.2	9.5	6.5	1.5	14.1	15.6	2.4	2.7	131
50	E1	1	DH53	517.6	38.0	1.1	460.9	29.0	73.7	12.8	1.4	14.9	8.8	6.6	1.4	14.6	16.0	2.4	2.6	134
51	E1	1	DH54	487.7	41.0	1.3	370.0	33.7	77.2	14.7	1.6	18.3	9.6	7.3	1.9	13.8	15.7	2.2	3.0	133
52	E1	1	DH55	409.0	41.3	0.9	431.8	25.7	84.8	12.4	1.8	18.0	6.7	6.4	2.1	13.5	15.6	2.4	3.1	135
53	E1	1	DH56	447.3	34.6	1.0	470.4	29.5	85.3	12.1	1.5	14.8	8.0	6.1	2.1	12.7	14.8	2.4	2.7	132
54	E1	1	DH57	596.6	32.9	1.0	590.6	30.0	78.1	12.8	1.4	14.7	8.9	5.6	1.8	13.1	14.9	2.7	2.5	132
55	E1	1	DH58	595.2	38.0	1.1	528.2	32.5	90.7	14.8	1.5	17.7	9.9	6.4	2.0	12.7	14.7	2.3	3.0	132
56	E1	1	DH59	807.9	33.7	1.0	791.2	29.6	88.0	13.7	1.4	15.4	9.6	6.0	1.3	12.5	13.8	2.3	2.7	131
57	E1	1	DH60	653.8	39.8	1.2	536.8	31.2	81.8	14.3	1.4	16.4	10.0	6.7	2.0	12.9	14.9	2.2	3.1	132
58	E1	1	DH61	533.8	34.2	1.1	496.1	31.6	81.3	12.5	1.7	16.6	7.6	6.9	1.8	13.8	15.6	2.3	2.5	135
59	E1	1	DH62	507.1	41.8	1.2	437.1	28.5	81.9	14.2	1.5	17.4	9.3	6.6	0.7	13.3	14.0	2.1	3.1	132
60	E1	1	DH63	507.0	47.1	1.6	313.6	32.1	84.0	14.1	1.4	15.6	10.1	7.6	1.1	14.9	16.0	2.1	3.2	131
61	E1	1	DH64	586.2	39.4	1.4	428.9	36.3	91.1	14.4	1.5	16.9	9.8	7.4	0.9	13.7	14.6	2.0	2.9	131
62	E1	1	DH65	595.4	43.8	1.3	460.5	29.8	81.6	14.1	1.3	14.7	10.9	7.3	1.1	14.9	16.0	2.2	2.9	130

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
63	E1	1	DH66	354.2	40.0	1.4	250.2	34.0	87.6	14.8	1.7	19.5	8.9	7.8	2.9	16.5	19.4	2.5	2.4	134
64	E1	1	DH67	560.6	37.2	1.1	511.5	.	84.1	12.0	1.3	12.1	9.4	6.8	1.8	14.1	15.9	2.3	2.6	133
65	E1	1	DH68	455.1	37.5	1.1	428.2	28.5	80.5	15.2	1.6	18.7	9.8	6.7	2.0	13.1	15.1	2.3	2.9	133
66	E1	1	DH69	649.4	38.9	1.1	608.7	30.8	83.4	12.5	1.4	13.6	9.1	6.2	1.5	12.5	14.0	2.3	3.1	132
67	E1	1	DH70	633.5	36.6	1.2	544.2	32.5	89.7	15.5	1.5	18.6	10.3	6.9	2.0	14.2	16.2	2.3	2.6	136
68	E1	1	DH71	573.9	44.8	1.3	427.3	30.7	82.1	14.3	1.5	17.3	9.4	7.7	1.5	15.6	17.1	2.2	2.9	135
69	E1	1	DH72	578.3	43.3	1.2	469.4	30.5	87.0	14.8	1.6	18.4	9.4	7.2	1.6	15.8	17.4	2.4	2.7	137
70	E1	1	DH73	498.6	38.2	1.0	492.2	28.7	80.2	12.7	1.8	18.0	7.1	6.8	2.0	15.0	17.0	2.5	2.5	136
71	E1	1	DH75	614.6	36.6	1.2	500.1	34.3	89.9	12.2	1.3	12.6	9.7	6.8	1.9	12.9	14.8	2.2	2.8	130
72	E1	1	DH76	630.3	36.8	1.2	531.0	30.7	81.9	13.0	1.4	14.3	9.3	6.7	1.5	13.7	15.2	2.3	2.7	134
73	E1	1	DH77	688.1	35.1	1.2	556.7	33.7	89.9	16.1	1.4	18.5	11.1	8.1	2.1	16.0	18.1	2.2	2.2	133
74	E1	1	DH78	535.2	41.0	1.2	459.8	30.9	83.8	12.3	1.3	13.1	9.1	7.2	2.1	14.2	16.3	2.3	2.9	131
75	E1	1	DH79	562.7	42.6	1.3	432.2	30.3	89.5	14.2	1.5	17.1	9.3	7.0	2.0	13.9	15.9	2.3	3.1	133
76	E1	1	DH80	657.8	42.4	1.3	502.1	30.6	90.5	14.2	1.5	17.4	9.4	6.6	1.9	14.9	16.8	2.5	2.8	135
77	E1	1	DH81	400.0	27.2	0.9	433.4	32.6	88.6	11.8	1.5	13.7	8.1	6.6	0.9	16.0	16.9	2.6	1.7	132
78	E1	1	DH82	644.4	36.6	1.0	626.9	31.8	84.9	11.9	1.6	14.9	7.6	6.9	1.9	13.8	15.7	2.3	2.7	130
79	E1	1	DH83	646.3	39.5	1.3	499.9	35.1	99.7	13.8	1.4	15.5	9.8	6.9	2.2	12.6	14.8	2.1	3.1	133
80	E1	1	DH84	669.3	34.7	1.2	568.2	37.4	90.5	11.5	1.2	11.1	9.5	6.8	1.8	12.4	14.2	2.1	2.8	130
81	E1	1	DH85	658.5	32.0	1.1	617.7	31.9	74.4	12.9	1.2	12.3	10.8	6.2	2.4	12.4	14.8	2.4	2.6	133
82	E1	1	DH86	648.8	43.0	1.3	500.2	32.4	92.6	13.3	1.5	15.4	9.2	6.2	1.4	13.9	15.3	2.5	3.1	131
83	E1	1	DH87	435.7	41.7	1.1	383.2	27.8	85.5	14.1	1.3	14.3	12.3	6.6	1.6	14.5	16.1	2.4	2.9	133
84	E1	1	DH89	630.0	34.6	1.1	570.1	32.3	89.7	11.4	1.6	14.1	7.4	6.5	2.5	14.2	16.7	2.6	2.4	134
85	E1	1	DH90	553.3	35.3	1.1	484.9	32.2	82.7	14.7	1.5	17.9	9.5	6.6	2.0	13.1	15.1	2.3	2.7	131
86	E1	1	DH91	668.0	36.0	1.1	604.0	31.5	95.6	14.3	1.6	17.9	9.3	6.6	2.5	14.1	16.6	2.5	2.6	131
87	E1	1	DH92	612.1	37.6	1.2	518.3	32.2	84.9	14.8	1.5	18.1	9.7	6.6	1.7	13.0	14.7	2.2	2.9	132
88	E1	1	DH93	539.2	46.4	1.3	406.0	30.1	76.9	12.3	1.4	13.3	9.1	7.0	1.5	14.6	16.1	2.3	3.2	130
89	E1	1	DH94	698.3	31.1	0.9	759.9	30.9	88.7	10.6	1.3	11.0	8.1	6.8	2.8	13.5	16.3	2.4	2.3	134
90	E1	1	DH95	751.8	35.3	1.3	581.9	36.1	85.9	11.3	1.3	11.5	8.9	7.2	1.8	13.5	15.3	2.1	2.6	130
91	E1	1	DH96	646.4	30.9	1.1	610.4	34.5	92.0	13.6	1.2	13.2	11.3	5.8	2.6	11.0	13.6	2.3	2.8	133
92	E1	1	DH97	515.6	40.8	1.2	418.9	34.6	91.9	11.5	1.5	13.2	7.9	6.8	1.6	14.5	16.1	2.4	2.8	133
93	E1	1	DH98	573.3	41.4	1.4	402.9	34.5	81.1	12.6	1.6	16.2	7.8	7.3	1.0	13.3	14.3	2.0	3.1	130
94	E1	1	DH99	495.0	38.5	1.1	457.9	29.5	80.6	14.5	1.6	18.1	9.2	6.4	1.1	13.7	14.8	2.3	2.8	133
95	E1	1	DH100	624.2	40.8	1.0	611.3	27.9	75.1	11.5	1.4	12.5	8.4	6.7	2.1	14.8	16.9	2.5	2.7	132
96	E1	1	DH101	525.2	44.8	1.3	408.1	29.5	84.1	13.3	1.3	13.4	10.5	7.3	1.0	14.6	15.6	2.1	3.1	130
97	E1	1	DH102	620.0	42.5	1.2	518.4	29.5	89.8	14.5	1.4	16.7	10.0	7.6	2.4	16.0	18.4	2.4	2.7	133
98	E1	1	DH103	461.5	36.1	1.1	436.2	29.7	78.9	13.7	1.7	18.0	8.3	6.6	2.1	13.6	15.7	2.4	2.7	137
99	E1	1	DH104	713.4	41.1	1.2	617.1	27.9	90.3	14.6	1.3	15.7	10.9	6.8	1.9	15.6	17.5	2.6	2.6	136
100	E1	1	DH105	622.2	41.6	1.1	581.5	28.2	81.3	16.4	1.6	20.9	10.3	6.0	2.4	13.5	15.9	2.6	3.1	135
101	E1	1	DH106	448.2	39.5	1.2	372.6	29.8	85.4	14.3	1.6	18.8	8.7	7.0	2.1	15.5	17.6	2.5	2.5	135
102	E1	1	DH107	590.7	37.0	1.1	556.2	.	84.7	11.5	1.4	12.6	8.6	6.8	1.6	13.2	14.8	2.2	2.8	130
103	E1	1	DH108	457.5	33.0	1.0	475.6	29.4	92.2	12.5	1.4	13.7	9.1	6.3	2.4	13.1	15.5	2.5	2.5	132
104	E1	1	DH109	529.5	36.6	1.0	507.7	27.9	80.9	12.8	1.4	14.6	8.9	6.8	2.4	13.5	15.9	2.3	2.7	134
105	E1	1	DH110	361.3	37.3	0.9	393.1	29.4	92.3	13.1	1.5	15.4	9.1	7.7	2.0	14.7	16.7	2.2	2.5	133
106	E1	1	DH111	453.8	46.6	1.3	361.9	28.9	85.5	16.6	1.5	20.0	10.9	7.8	1.8	15.1	16.9	2.2	3.1	133
107	E1	1	DH112	621.1	38.9	1.1	561.6	30.5	87.7	11.7	1.3	11.6	9.5	7.1	2.0	14.3	16.3	2.3	2.7	133
108	E1	1	DH113	557.5	36.8	1.2	446.7	34.2	91.2	12.9	1.4	14.1	9.4	6.2	1.9	12.9	14.8	2.4	2.8	133
109	E1	1	DH114	571.5	36.2	1.1	521.4	31.7	68.0	12.5	1.4	14.4	8.6	7.0	1.3	14.1	15.4	2.2	2.6	133
110	E1	1	DH115	525.9	31.8	0.9	567.3	29.3	87.6	12.8	1.4	14.5	9.2	6.7	2.5	13.0	15.5	2.3	2.4	134
111	E1	1	DH116	525.5	31.4	0.9	605.4	30.8	86.5	12.1	1.4	13.7	8.5	6.5	2.9	12.3	15.2	2.3	2.6	133
112	E1	1	DH117	547.8	32.3	1.0	553.9	33.7	78.8	13.3	1.8	18.4	7.7	6.5	1.5	13.0	14.5	2.2	2.5	133
113	E1	1	DH119	588.6	44.1	1.5	392.1	32.5	92.2	16.7	1.5	19.3	12.9	7.6	2.4	15.3	17.7	2.3	2.9	133
114	E1	1	DH120	650.0	32.7	0.9	689.3	31.7	89.0	14.0	1.4	15.1	10.2	6.4	2.5	13.1	15.6	2.5	2.5	135
115	E1	1	DH121	621.1	36.9	1.2	537.8	29.9	81.5	13.3	1.4	14.5	9.7	6.9	3.0	14.4	17.4	2.5	2.6	137
116	E1	1	DH122	540.4	44.8	0.9	571.2	27.8	88.3	14.7	1.6	18.8	9.2	7.2	1.5	16.0	17.5	2.4	2.8	134
117	E1	1	DH123	405.6	44.0	1.2	339.7	26.8	96.0	13.3	1.2	12.2	11.9	7.7	1.7	15.5	17.2	2.2	2.8	135
118	E1	1	DH124	703.4	37.4	1.2	591.6	30.5	83.2	15.5	1.5	18.0	10.7	7.2	2.2	13.6	15.8	2.2	2.7	134
119	E1	1	DH125	679.9	37.8	1.1	597.5	30.0	79.0	14.4	1.7	18.9	8.7	6.4	1.6	13.3	14.9	2.3	2.8	133
120	E1	1	DH126	488.5	45.8	1.4	357.6	29.6	76.7	12.8	1.5	14.9	8.7	7.5	1.0	16.5	17.5	2.3	2.8	136
121	E1	1	DH128	478.5	42.0	1.1	428.4	27.0	93.1	17.7	1.5	20.5	12.5	6.9	2.2	15.5	17.7	2.6	2.7	136
122	E1	1	DH129	668.1	43.0	1.3	527.3	32.6	91.5	13.2	1.6	16.2	8.7	6.9	2.1	13.6	15.7	2.3	3.2	133
123	E1	1	DH130	620.1	35.3	1.0	599.7	30.0	85.2	13.9	1.5	16.7	9.2	6.8	2.3	13.4	15.7	2.3	2.6	134
124	E1	1	DH131	396.3	38.9	1.3	314.3	33.6	88.0	13.7	1.6	17.7	8.4	7.4	2.5	15.5	18.0	2.4	2.5	137

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
125	E1	2	DH1	581.7	34.8	1.0	567.5	30.3	84.8	11.4	1.2	10.9	9.5	6.0	1.3	12.3	13.6	2.3	2.8	132
126	E1	2	DH3	428.9	38.1	1.0	409.2	27.5	88.8	12.5	1.4	14.0	8.9	6.4	2.5	13.5	16.0	2.5	2.8	136
127	E1	2	DH4	525.7	36.5	1.2	433.1	32.9	78.7	11.3	1.6	14.2	7.1	7.0	2.0	15.0	17.0	2.4	2.4	133
128	E1	2	DH5	359.3	36.6	0.9	390.1	29.9	80.9	13.9	1.5	16.9	9.0	7.0	2.1	13.3	15.4	2.2	2.8	135
129	E1	2	DH6	559.5	40.3	1.2	460.5	31.4	86.7	13.8	1.4	15.1	10.0	6.8	1.2	13.8	15.0	2.2	2.9	130
130	E1	2	DH7	535.0	35.9	1.1	505.2	31.5	85.1	12.7	1.5	15.0	8.5	6.6	3.3	14.3	17.6	2.7	2.5	136
131	E1	2	DH8	564.3	50.1	1.5	368.1	30.8	91.9	14.7	1.4	16.6	10.3	7.4	1.4	15.5	16.9	2.3	3.2	132
132	E1	2	DH9	484.1	43.7	1.4	338.3	31.0	86.1	14.4	1.5	17.5	9.4	7.7	2.2	15.3	17.5	2.3	2.9	135
133	E1	2	DH11	668.8	43.9	1.5	446.8	35.4	99.3	16.6	1.5	19.2	11.3	8.0	1.6	13.9	15.5	1.9	3.2	131
134	E1	2	DH12	311.6	53.4	1.7	182.9	32.9	84.5	14.2	1.6	17.9	9.0	8.1	1.2	17.7	18.9	2.3	3.0	134
135	E1	2	DH13	515.0	45.5	1.4	378.1	28.5	92.2	15.9	1.5	18.3	11.0	7.0	2.4	15.5	17.9	2.6	2.9	136
136	E1	2	DH14	634.0	32.4	1.1	590.9	32.4	89.4	14.1	1.6	17.6	8.9	6.6	3.2	13.5	16.7	2.5	2.4	135
137	E1	2	DH15	647.9	37.2	1.2	553.3	31.9	82.8	13.6	1.4	15.4	9.5	7.2	1.7	14.2	15.9	2.2	2.6	130
138	E1	2	DH16	589.3	41.6	1.2	493.5	30.8	82.6	12.8	1.4	14.2	9.1	6.2	1.6	13.5	15.1	2.4	3.1	132
139	E1	2	DH17	535.7	45.9	1.5	349.0	34.4	88.8	16.3	1.6	20.9	10.1	8.0	1.4	15.3	16.7	2.1	3.0	130
140	E1	2	DH18	391.5	43.4	1.4	289.6	32.1	85.2	12.2	1.6	15.7	7.5	7.5	1.4	16.5	17.9	2.4	2.6	135
141	E1	2	DH19	372.0	38.5	1.3	286.6	32.1	87.4	12.8	1.5	15.2	8.5	6.6	1.5	13.6	15.1	2.3	2.8	132
142	E1	2	DH20	633.8	38.0	1.3	490.2	29.7	81.8	13.8	1.6	17.6	8.6	7.0	2.0	14.2	16.2	2.3	2.7	134
143	E1	2	DH21	642.3	36.8	1.2	523.0	33.6	90.4	14.3	1.5	16.8	9.7	7.0	2.7	12.9	15.6	2.2	2.8	135
144	E1	2	DH22	510.4	48.9	1.5	347.9	32.5	93.7	13.8	1.5	16.2	9.3	7.2	1.4	15.9	17.3	2.4	3.1	135
145	E1	2	DH23	640.2	45.4	1.4	466.6	31.6	93.7	14.9	1.4	16.3	10.9	6.4	1.1	13.5	14.6	2.3	3.4	130
146	E1	2	DH24	762.1	42.2	1.3	587.1	31.9	88.7	14.7	1.6	19.1	9.0	6.8	1.1	13.9	15.0	2.2	3.0	132
147	E1	2	DH25	662.4	48.3	1.3	508.7	34.2	84.3	14.0	1.5	16.6	9.3	7.8	1.6	15.7	17.3	2.2	3.1	132
148	E1	2	DH26	494.2	38.1	1.1	444.0	32.3	78.0	12.1	1.4	13.3	8.7	6.9	1.6	14.4	16.0	2.3	2.6	133
149	E1	2	DH27	575.2	39.9	1.2	483.8	28.3	92.9	13.5	1.5	15.9	9.1	6.4	2.3	13.4	15.7	2.5	3.0	136
150	E1	2	DH28	588.7	38.7	1.2	493.5	33.0	91.5	15.4	1.6	19.2	9.8	6.3	2.4	13.7	16.1	2.5	2.8	134
151	E1	2	DH29	402.3	37.1	1.2	348.9	31.9	75.9	14.0	1.4	15.5	10.0	7.5	2.2	14.9	17.1	2.3	2.5	133
152	E1	2	DH30	566.5	42.2	1.3	448.2	35.4	93.3	13.9	1.6	17.7	8.6	6.7	2.4	15.2	17.6	2.6	2.8	133
153	E1	2	DH31	466.8	46.8	1.4	340.2	29.1	83.0	12.5	1.5	15.2	8.2	7.6	1.5	15.1	16.6	2.2	3.1	134
154	E1	2	DH32	575.6	37.6	1.0	568.8	27.2	80.2	11.1	1.5	13.5	7.2	7.2	2.0	15.8	17.8	2.5	2.4	138
155	E1	2	DH33	436.3	48.7	1.1	391.7	29.7	90.4	17.1	1.7	23.8	9.8	7.2	2.0	16.2	18.2	2.5	3.0	136
156	E1	2	DH34	637.0	46.8	1.5	425.8	33.5	97.4	14.5	1.5	17.4	9.5	7.2	1.5	15.4	16.9	2.3	3.0	130
157	E1	2	DH35	527.6	36.1	1.2	438.9	34.0	83.5	10.9	1.5	12.9	7.3	7.0	2.2	13.6	15.8	2.3	2.6	134
158	E1	2	DH36	492.1	49.9	1.7	294.3	31.9	83.0	14.6	1.7	19.7	8.5	8.6	1.0	17.5	18.5	2.2	2.8	134
159	E1	2	DH37	555.4	33.6	1.1	516.6	30.5	84.9	16.0	1.5	19.3	10.5	6.9	2.1	13.6	15.7	2.3	2.5	134
160	E1	2	DH38	669.5	43.7	1.4	479.6	31.4	80.4	15.5	1.6	19.0	10.1	7.2	1.0	14.6	15.6	2.2	3.0	130
161	E1	2	DH39	504.3	37.2	1.1	460.2	31.0	89.0	11.7	1.3	12.4	8.8	6.2	2.5	14.8	17.3	2.8	2.5	135
162	E1	2	DH40	497.3	42.8	1.4	351.9	32.9	104.3	13.5	1.3	13.6	10.6	8.4	0.6	16.4	16.9	2.0	2.6	133
163	E1	2	DH41	666.8	41.2	1.2	573.8	30.0	87.7	13.3	1.4	14.7	9.7	7.0	1.1	14.6	15.7	2.2	2.8	135
164	E1	2	DH42	440.2	41.0	1.3	340.2	30.5	87.3	14.7	1.3	15.4	11.3	7.0	1.7	15.6	17.3	2.5	2.6	136
165	E1	2	DH43	622.4	41.6	1.4	458.3	31.8	84.5	12.8	1.4	14.6	8.9	7.0	1.7	14.0	15.7	2.3	3.0	134
166	E1	2	DH44	570.1	41.7	1.4	397.8	34.9	95.4	15.4	1.5	18.3	10.2	7.9	1.7	15.0	16.7	2.1	2.8	133
167	E1	2	DH45	598.4	36.4	1.3	450.9	35.8	89.1	11.4	1.4	12.7	8.1	7.4	2.0	14.4	16.4	2.2	2.5	132
168	E1	2	DH46	340.1	43.0	1.2	277.4	31.4	89.5	17.2	1.7	22.5	10.4	8.2	1.7	14.7	16.4	2.0	2.9	135
169	E1	2	DH47	807.0	36.5	1.2	676.4	32.7	91.7	13.6	1.6	17.3	8.5	7.2	1.5	14.0	15.5	2.2	2.6	133
170	E1	2	DH49	1091.6	48.2	1.6	699.7	32.0	92.8	15.1	1.5	18.5	9.9	7.9	1.9	15.1	17.0	2.2	3.2	134
171	E1	2	DH50	712.9	41.9	1.5	490.0	35.6	96.4	14.3	1.6	17.8	9.1	7.1	1.5	14.1	15.6	2.2	3.0	130
172	E1	2	DH51	480.2	41.2	1.0	461.7	28.8	88.5	15.5	1.5	18.4	10.3	7.2	2.5	13.9	16.4	2.3	3.0	134
173	E1	2	DH52	664.6	39.3	1.2	547.4	29.0	80.9	12.9	1.2	12.8	10.3	6.8	1.2	14.5	15.7	2.3	2.7	132
174	E1	2	DH53	786.5	30.3	1.0	816.8	30.3	73.5	10.5	1.3	11.1	8.0	6.4	2.4	14.7	17.1	2.7	2.1	134
175	E1	2	DH54	368.5	45.5	1.5	244.7	32.7	83.0	16.5	1.6	20.3	10.6	7.7	1.8	14.4	16.2	2.1	3.2	137
176	E1	2	DH55	620.6	35.4	1.0	593.9	28.7	91.8	11.3	1.4	12.3	8.3	6.1	2.6	12.9	15.5	2.5	2.7	134
177	E1	2	DH56	723.0	31.7	1.1	657.9	31.7	90.2	12.3	1.4	13.9	8.7	6.0	2.3	12.5	14.8	2.5	2.5	133
178	E1	2	DH57	508.5	31.8	0.9	535.8	29.3	84.7	14.0	1.5	16.2	9.6	5.8	2.0	13.3	15.3	2.6	2.4	136
179	E1	2	DH58	439.9	43.9	1.2	378.3	29.5	84.7	12.0	1.3	12.8	8.9	6.9	1.8	13.1	14.9	2.2	3.3	133
180	E1	2	DH59	858.9	43.7	1.4	599.0	32.7	83.2	14.3	1.4	15.6	10.3	6.8	1.0	14.2	15.2	2.3	3.1	130
181	E1	2	DH60	659.4	46.4	1.5	447.0	31.9	83.5	14.8	1.3	15.6	11.3	7.2	1.5	14.0	15.5	2.1	3.3	132
182	E1	2	DH61	583.5	35.6	1.1	522.8	31.5	84.8	12.8	1.6	16.3	8.1	6.9	1.4	14.2	15.6	2.3	2.5	136
183	E1	2	DH62	540.5	40.6	1.2	462.4	29.8	87.0	14.2	1.4	15.6	10.3	6.4	1.1	13.3	14.4	2.2	3.1	132
184	E1	2	DH63	631.4	48.3	1.6	398.1	33.2	87.0	15.6	1.6	19.4	10.0	7.8	1.4	15.1	16.5	2.1	3.2	131
185	E1	2	DH64	480.0	43.0	1.6	306.9	36.6	96.1	13.3	1.4	15.1	9.2	7.6	1.2	14.6	15.8	2.1	2.9	132
186	E1	2	DH65	519.6	50.3	1.5	342.7	30.8	85.4	15.9	1.4	17.9	11.1	7.6	1.0	15.5	16.5	2.2	3.2	130

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
187	E1	2	DH66	396.9	45.6	1.6	245.6	33.8	88.3	13.5	1.7	18.6	7.8	7.9	2.5	16.5	19.0	2.4	2.8	136
188	E1	2	DH67	628.9	36.6	1.2	518.4	32.8	83.1	12.8	1.4	14.4	9.0	7.0	1.6	14.4	16.0	2.3	2.6	131
189	E1	2	DH68	454.5	37.9	1.3	358.4	27.5	85.2	16.3	1.7	21.7	9.8	7.1	2.4	13.6	16.0	2.3	2.8	133
190	E1	2	DH69	487.0	37.4	0.9	532.2	30.1	83.3	12.1	1.2	12.1	9.8	6.0	1.7	12.9	14.6	2.4	2.9	133
191	E1	2	DH70	505.3	42.4	1.5	333.8	32.5	90.7	13.9	1.4	15.6	9.7	7.8	1.7	15.5	17.2	2.2	2.7	134
192	E1	2	DH71	625.7	45.9	1.4	437.9	30.5	90.7	13.4	1.6	16.7	8.6	8.0	1.1	16.3	17.4	2.2	2.8	134
193	E1	2	DH72	564.8	42.7	1.4	417.1	30.9	88.7	13.1	1.5	15.3	8.8	7.4	1.7	16.1	17.8	2.4	2.6	135
194	E1	2	DH73	549.0	43.0	1.3	413.4	29.6	90.0	11.7	1.4	13.4	8.1	7.2	1.7	15.5	17.2	2.4	2.8	136
195	E1	2	DH75	655.8	39.9	1.5	446.7	35.9	89.6	13.4	1.5	16.2	8.9	7.5	1.8	14.2	16.0	2.1	2.8	130
196	E1	2	DH76	721.4	35.4	1.1	637.8	32.8	79.0	13.2	1.4	14.3	9.7	6.4	2.0	12.8	14.8	2.3	2.8	134
197	E1	2	DH77	601.8	30.5	1.1	570.4	33.7	77.7	14.3	1.3	14.5	11.2	7.5	2.6	14.9	17.5	2.3	2.0	133
198	E1	2	DH78	608.0	47.6	1.4	445.4	30.5	89.0	13.8	1.4	15.1	10.0	7.5	1.2	16.6	17.8	2.4	2.9	133
199	E1	2	DH79	644.7	45.2	1.3	511.3	31.8	92.4	13.2	1.4	14.4	9.7	7.1	2.2	14.2	16.4	2.3	3.2	133
200	E1	2	DH80	611.0	46.4	1.4	443.4	30.7	91.0	15.1	1.4	16.5	11.1	6.9	1.6	16.2	17.8	2.6	2.9	135
201	E1	2	DH81	418.2	41.4	1.4	303.7	33.2	87.3	11.8	1.4	13.1	8.5	6.8	1.3	15.8	17.1	2.5	2.6	132
202	E1	2	DH82	563.9	45.0	1.6	357.6	32.8	85.1	9.8	1.4	10.9	7.1	7.8	2.3	16.7	19.0	2.4	2.7	133
203	E1	2	DH83	764.8	38.0	1.3	569.0	35.5	100.6	14.8	1.6	18.4	9.5	7.0	2.3	13.1	15.4	2.2	2.9	133
204	E1	2	DH84	834.4	32.8	1.2	694.1	37.4	87.7	10.2	1.2	9.6	8.6	6.9	2.1	12.6	14.7	2.1	2.6	130
205	E1	2	DH85	738.8	28.6	0.9	863.0	32.4	82.6	14.3	1.5	16.7	9.7	6.0	2.4	12.3	14.7	2.5	2.3	134
206	E1	2	DH86	607.3	53.8	1.7	352.1	32.6	94.7	12.1	1.4	13.1	8.9	6.9	0.7	15.1	15.8	2.3	3.6	132
207	E1	2	DH87	581.1	54.4	1.6	367.8	29.7	88.7	13.2	1.2	12.7	10.9	7.4	0.4	16.3	16.7	2.3	3.3	131
208	E1	2	DH89	624.2	35.2	1.2	520.6	33.9	88.4	12.7	1.5	15.1	8.4	6.5	2.4	13.7	16.1	2.5	2.6	133
209	E1	2	DH90	735.5	33.4	1.0	746.0	34.1	87.6	13.4	1.6	16.9	8.5	6.5	2.0	13.6	15.6	2.4	2.5	130
210	E1	2	DH91	607.4	36.3	1.2	525.9	33.1	95.8	13.7	1.4	15.1	9.8	6.4	2.1	13.0	15.1	2.4	2.8	133
211	E1	2	DH92	450.4	44.1	1.3	357.8	32.9	81.9	15.0	1.5	17.8	10.1	7.1	1.3	14.3	15.6	2.2	3.1	133
212	E1	2	DH93	484.6	43.9	1.2	391.8	30.2	83.6	12.6	1.3	13.2	9.4	7.0	1.5	14.9	16.4	2.3	3.0	130
213	E1	2	DH94	580.9	34.1	1.1	543.9	30.4	91.6	10.6	1.3	11.3	7.8	7.1	2.2	14.7	16.9	2.4	2.3	133
214	E1	2	DH95	528.3	32.9	1.2	452.7	36.3	86.7	14.1	1.5	17.1	9.1	7.2	2.3	13.3	15.6	2.2	2.5	130
215	E1	2	DH96	828.3	38.8	1.4	603.7	37.3	91.2	13.3	1.4	15.1	9.3	6.4	1.9	12.6	14.5	2.3	3.1	133
216	E1	2	DH97	476.8	47.3	1.6	300.6	34.0	88.6	10.9	1.5	13.1	7.2	7.1	1.2	15.2	16.4	2.3	3.1	133
217	E1	2	DH98	566.6	46.1	1.6	351.3	36.0	83.3	12.2	1.6	15.3	7.7	7.6	0.9	14.7	15.6	2.1	3.1	130
218	E1	2	DH99	438.9	44.2	1.3	350.0	29.6	86.7	13.3	1.6	16.6	8.4	7.1	1.4	14.9	16.3	2.3	3.0	135
219	E1	2	DH100	438.7	.	.	.	28.6	74.8	11.4	1.3	12.3	8.5	.	.	.	.	.	.	133
220	E1	2	DH101	645.3	42.7	1.3	480.5	31.4	92.8	12.2	1.5	14.5	8.1	7.2	1.1	14.5	15.6	2.2	2.9	132
221	E1	2	DH102	506.9	50.8	1.4	349.8	28.9	90.6	13.8	1.4	15.3	9.9	8.3	1.5	16.6	18.1	2.2	3.1	134
222	E1	2	DH103	416.2	36.4	1.1	367.7	30.8	85.4	12.8	1.6	15.9	8.1	6.6	2.3	13.1	15.4	2.3	2.8	136
223	E1	2	DH104	414.0	36.9	1.0	412.8	27.9	89.6	15.0	1.3	15.9	11.2	6.8	2.0	15.2	17.2	2.5	2.4	135
224	E1	2	DH105	543.5	41.6	1.1	495.9	27.9	81.1	14.2	1.4	16.1	9.9	6.2	2.6	14.4	17.0	2.8	2.9	134
225	E1	2	DH106	579.9	45.2	1.4	407.8	30.6	89.7	11.9	1.6	14.7	7.6	7.3	1.7	15.6	17.3	2.4	2.9	133
226	E1	2	DH107	603.5	39.9	1.2	492.6	31.7	90.8	13.0	1.3	13.6	9.9	7.0	1.5	13.4	14.9	2.1	3.0	132
227	E1	2	DH108	494.4	40.8	1.2	407.6	29.9	90.8	11.9	1.4	13.1	8.6	7.0	2.0	14.9	16.9	2.4	2.7	133
228	E1	2	DH109	595.6	39.3	1.2	496.0	30.1	79.7	14.0	1.4	16.0	9.7	7.1	2.3	13.6	15.9	2.2	2.9	133
229	E1	2	DH110	473.3	46.5	1.4	339.5	31.8	93.8	13.2	1.3	13.8	10.0	8.2	1.5	15.7	17.2	2.1	3.0	132
230	E1	2	DH111	495.5	54.8	1.7	294.1	30.2	89.4	15.7	1.4	17.4	11.3	8.7	1.0	16.9	17.9	2.1	3.2	133
231	E1	2	DH112	504.1	46.6	1.4	361.3	31.2	89.8	12.1	1.4	13.7	8.5	7.7	1.6	15.1	16.7	2.2	3.1	132
232	E1	2	DH113	555.9	39.6	1.3	427.9	34.7	95.2	12.0	1.3	12.1	9.4	6.7	1.7	14.1	15.8	2.3	2.8	132
233	E1	2	DH114	624.2	38.5	1.3	486.5	32.0	72.1	12.7	1.5	15.5	8.2	7.4	1.1	15.5	16.6	2.2	2.5	133
234	E1	2	DH115	509.0	32.7	1.0	503.4	31.6	93.7	10.8	1.3	11.2	8.2	6.8	2.1	12.9	15.0	2.2	2.5	133
235	E1	2	DH116	549.9	31.0	1.0	537.5	34.4	94.0	11.0	1.5	12.8	7.5	6.3	2.7	12.2	14.9	2.4	2.5	131
236	E1	2	DH117	552.4	35.2	1.2	452.0	34.8	79.5	12.6	1.4	14.0	9.0	6.9	1.4	13.5	14.9	2.2	2.6	133
237	E1	2	DH119	502.3	46.4	1.5	333.3	34.3	98.7	15.0	1.6	19.5	9.2	7.6	2.1	15.4	17.5	2.3	3.0	136
238	E1	2	DH120	399.1	36.8	1.1	365.1	28.3	83.9	13.1	1.5	15.1	9.0	6.7	2.2	14.5	16.7	2.5	2.5	135
239	E1	2	DH121	577.2	36.8	1.2	501.9	31.2	83.3	12.9	1.4	14.5	9.0	7.0	2.3	15.1	17.4	2.5	2.4	135
240	E1	2	DH122	347.9	49.3	1.4	242.8	28.7	90.6	14.5	1.4	16.2	10.3	7.5	1.1	16.4	17.5	2.3	3.0	135
241	E1	2	DH123	268.7	36.6	0.9	312.4	.	86.3	14.6	1.3	15.0	11.2	7.0	2.3	13.9	16.2	2.3	2.6	136
242	E1	2	DH124	515.3	33.0	0.9	548.8	29.9	87.3	14.1	1.5	16.4	9.7	7.0	2.2	13.0	15.2	2.2	2.5	135
243	E1	2	DH125	755.9	40.6	1.5	511.5	31.9	83.5	12.4	1.7	16.6	7.4	7.1	1.9	15.0	16.9	2.4	2.7	134
244	E1	2	DH126	396.6	51.5	1.5	265.6	30.9	76.8	12.3	1.6	15.2	7.9	7.9	0.8	17.2	18.0	2.3	3.0	135
245	E1	2	DH128	357.2	45.5	1.2	292.5	26.9	90.4	19.2	1.4	21.0	14.0	7.0	1.9	15.8	17.7	2.5	2.9	137
246	E1	2	DH129	643.8	42.6	1.4	472.7	32.2	91.3	12.7	1.4	13.9	9.2	6.9	1.8	13.4	15.2	2.2	3.2	132
247	E1	2	DH130	615.2	46.7	1.4	432.3	27.3	82.2	12.6	1.4	14.5	8.7	7.5	1.4	14.8	16.2	2.2	3.2	134
248	E1	2	DH131	442.8	38.4	1.3	347.1	34.4	85.7	13.3	1.6	17.1	8.1	6.6	1.7	14.0	15.7	2.4	2.7	136

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
249	E2	1	DH1	938.1	29.8	0.8	1175.6	26.8	94.3	14.6	1.3	15.5	10.9	6.7	2.3	14.3	16.6	2.5	1.8	141
250	E2	1	DH3	782.8	36.8	1.1	734.3	29.1	92.8	13.6	1.5	15.7	9.3	6.9	1.9	15.2	17.1	2.5	2.2	141
251	E2	1	DH4	798.0	32.7	0.9	866.5	30.3	84.6	13.8	1.5	16.3	9.3	7.2	2.7	16.0	18.7	2.6	1.7	143
252	E2	1	DH5	702.9	36.0	0.8	863.5	26.6	78.7	16.3	1.6	21.1	10.1	7.6	1.9	14.5	16.4	2.2	2.2	143
253	E2	1	DH6	885.5	36.0	0.9	936.1	30.3	97.6	16.4	1.4	17.9	11.9	7.3	2.2	15.5	17.7	2.4	2.0	142
254	E2	1	DH7	865.4	35.6	1.0	866.3	32.0	87.7	14.8	1.5	17.6	9.8	6.9	2.7	15.1	17.8	2.6	2.0	143
255	E2	1	DH8	888.0	38.6	1.1	805.0	30.3	99.8	16.4	1.4	18.7	11.4	7.5	2.3	15.2	17.5	2.3	2.2	140
256	E2	1	DH9	761.4	38.0	1.0	770.7	31.9	87.6	16.1	1.6	20.7	9.9	7.7	3.1	16.5	19.6	2.6	1.9	144
257	E2	1	DH11	817.9	38.4	1.3	651.7	32.3	107.9	15.1	1.3	15.1	11.9	8.3	1.7	15.8	17.5	2.1	2.2	142
258	E2	1	DH12	670.8	35.7	1.0	690.9	29.2	72.9	15.0	1.7	20.3	9.1	6.8	1.8	15.1	16.9	2.5	2.1	143
259	E2	1	DH13	807.1	35.6	0.9	899.8	26.9	89.7	18.9	1.4	21.6	13.1	7.5	2.8	17.0	19.8	2.7	1.8	142
260	E2	1	DH14	823.6	28.8	0.9	898.1	31.5	87.9	16.9	1.4	18.4	12.5	7.1	2.8	15.1	17.9	2.5	1.6	143
261	E2	1	DH15	900.7	29.1	0.8	1120.2	28.9	90.5	16.2	1.4	18.4	11.4	7.0	2.2	14.2	16.4	2.4	1.8	141
262	E2	1	DH16	752.6	36.7	1.0	739.3	28.3	89.3	14.0	1.5	16.6	9.3	7.0	1.7	14.7	16.4	2.4	2.2	142
263	E2	1	DH17	839.2	36.1	1.1	768.5	32.7	89.6	17.8	1.5	20.5	12.2	7.4	2.1	14.4	16.5	2.2	2.2	140
264	E2	1	DH18	793.3	39.1	1.1	730.5	31.1	81.6	17.6	1.9	26.6	9.3	7.6	1.7	15.8	17.5	2.3	2.2	145
265	E2	1	DH19	822.2	31.6	1.0	855.6	32.3	92.6	14.3	1.4	15.8	10.3	6.6	2.2	13.3	15.5	2.3	2.0	140
266	E2	1	DH20	810.2	40.0	1.0	775.3	.	88.0	15.3	1.6	19.4	9.5	7.1	2.5	15.7	18.2	2.6	2.2	144
267	E2	1	DH21	836.3	33.1	1.0	812.7	32.9	91.6	18.1	1.5	20.8	12.5	7.4	3.1	14.6	17.7	2.4	1.9	143
268	E2	1	DH22	849.6	34.1	0.9	923.4	31.8	97.1	16.7	1.5	19.6	11.2	7.6	3.0	15.9	18.9	2.5	1.8	143
269	E2	1	DH23	884.2	33.3	0.9	963.2	28.1	92.5	18.7	1.4	20.1	13.7	6.3	2.4	13.7	16.1	2.5	2.1	141
270	E2	1	DH24	909.7	33.9	0.9	1042.0	28.4	95.3	15.6	1.6	20.0	9.6	6.7	2.1	14.2	16.3	2.4	2.1	141
271	E2	1	DH25	836.0	34.1	0.9	973.3	30.5	83.2	16.0	1.3	17.0	11.9	7.3	2.5	15.2	17.7	2.4	1.9	139
272	E2	1	DH26	862.1	34.5	0.9	956.8	29.1	85.7	17.7	1.4	20.2	12.3	7.2	2.1	15.4	17.5	2.5	2.0	142
273	E2	1	DH27	975.6	30.8	0.9	1142.4	28.9	99.2	17.7	1.4	19.4	12.9	6.2	2.4	13.7	16.1	2.6	1.9	144
274	E2	1	DH28	895.4	36.8	1.0	927.9	29.7	96.9	15.4	1.4	17.0	11.1	7.1	2.2	15.5	17.7	2.5	2.1	143
275	E2	1	DH29	835.9	34.9	0.9	897.9	30.0	79.9	15.3	1.4	17.0	10.9	7.4	2.3	15.1	17.4	2.4	2.0	143
276	E2	1	DH30	876.8	31.6	1.1	780.8	34.1	86.5	18.3	1.4	20.8	12.7	7.0	2.2	15.9	18.1	2.6	1.7	142
277	E2	1	DH31	679.8	32.5	0.7	921.1	26.7	87.2	14.6	1.4	16.7	10.1	7.3	2.5	14.4	16.9	2.3	1.9	141
278	E2	1	DH32	780.3	30.8	0.8	1005.6	26.4	86.9	12.2	1.4	13.5	8.8	6.5	2.9	14.7	17.6	2.7	1.7	145
279	E2	1	DH33	644.6	41.5	0.8	799.7	26.9	96.2	15.8	1.5	19.4	10.3	7.3	3.1	17.1	20.2	2.8	2.0	147
280	E2	1	DH34	837.0	37.3	1.0	798.7	28.8	100.2	16.3	1.4	18.2	11.5	7.6	2.5	15.7	18.2	2.4	2.0	141
281	E2	1	DH35	867.5	25.7	0.8	1135.5	30.9	91.9	15.2	1.5	18.2	10.0	7.1	3.3	13.6	16.9	2.4	1.5	141
282	E2	1	DH36	862.0	33.4	0.9	909.5	29.3	83.5	18.9	1.7	25.7	11.0	7.8	2.5	15.6	18.1	2.3	1.7	142
283	E2	1	DH37	693.3	33.2	0.8	855.9	26.4	90.2	16.0	1.3	16.4	12.4	7.4	2.8	15.7	18.5	2.5	1.8	141
284	E2	1	DH38	805.7	34.2	0.9	883.4	27.3	86.5	16.3	1.4	18.6	11.3	7.2	2.2	15.6	17.8	2.5	1.9	141
285	E2	1	DH39	932.9	36.3	1.1	882.6	29.4	87.4	15.5	1.3	15.7	12.2	6.4	2.3	15.3	17.6	2.7	2.1	140
286	E2	1	DH40	760.5	33.5	1.0	780.0	30.6	100.8	14.9	1.3	15.3	11.5	7.8	2.0	15.8	17.8	2.3	1.9	142
287	E2	1	DH41	873.5	31.3	0.9	922.4	31.6	89.9	16.9	1.4	19.5	11.6	7.1	2.7	15.4	18.1	2.6	1.7	144
288	E2	1	DH42	905.8	35.3	0.9	1031.7	29.7	90.3	18.9	1.4	20.9	13.5	7.5	3.0	16.5	19.5	2.6	1.8	143
289	E2	1	DH43	934.0	36.6	1.1	879.5	32.0	90.6	16.3	1.4	18.5	11.4	7.3	2.5	14.5	17.0	2.3	2.2	142
290	E2	1	DH44	940.9	30.6	0.9	999.9	33.0	109.3	16.5	1.5	20.2	10.7	7.4	3.2	13.9	17.1	2.3	1.8	145
291	E2	1	DH45	927.1	32.1	1.1	868.8	33.2	97.8	14.8	1.5	18.0	9.7	7.8	2.4	15.6	18.0	2.3	1.8	143
292	E2	1	DH46	722.9	31.8	0.6	1147.5	28.8	94.3	17.8	1.5	21.8	11.5	7.7	3.5	14.7	18.2	2.4	1.7	145
293	E2	1	DH47	831.5	34.4	1.0	835.7	31.0	92.8	14.2	1.4	15.7	10.1	7.1	2.4	14.8	17.2	2.4	2.0	142
294	E2	1	DH49	774.5	39.3	1.0	771.5	30.8	91.6	18.7	1.7	25.3	10.9	7.5	2.7	15.3	18.0	2.4	2.2	145
295	E2	1	DH50	889.9	30.6	0.9	989.8	30.3	104.4	14.0	1.4	15.2	10.2	6.9	2.3	15.1	17.4	2.5	1.8	143
296	E2	1	DH51	725.8	38.1	0.8	917.6	26.4	91.4	17.7	1.4	20.2	12.3	7.6	2.8	15.8	18.6	2.4	2.0	144
297	E2	1	DH52	862.1	34.0	0.8	1123.9	25.7	83.0	14.0	1.2	13.7	11.3	6.8	2.1	14.7	16.8	2.5	2.0	141
298	E2	1	DH53	914.3	37.8	1.1	860.9	26.9	76.6	16.6	1.5	19.6	11.2	7.3	1.6	16.2	17.8	2.5	2.1	142
299	E2	1	DH54	881.7	37.6	1.2	723.9	31.9	95.4	19.5	1.6	25.5	11.8	8.6	1.8	15.9	17.7	2.1	2.1	142
300	E2	1	DH55	801.1	34.7	0.9	855.8	26.7	92.2	15.0	1.5	17.4	10.3	6.5	2.3	14.4	16.7	2.6	2.1	139
301	E2	1	DH56	959.7	29.0	0.9	1026.4	32.2	87.3	17.7	1.4	20.2	12.2	6.6	2.6	14.0	16.6	2.5	1.7	143
302	E2	1	DH57	892.0	34.0	1.0	938.9	27.2	93.8	15.6	1.5	18.4	10.4	6.6	2.3	15.7	18.0	2.7	1.9	142
303	E2	1	DH58	683.4	30.5	0.8	898.0	30.5	94.3	13.8	1.4	14.8	10.2	6.4	2.6	12.7	15.3	2.4	2.0	141
304	E2	1	DH59	910.8	37.1	0.9	961.8	26.6	91.7	13.6	1.2	13.4	11.0	6.8	1.7	15.0	16.7	2.5	2.2	140
305	E2	1	DH60	983.9	40.6	1.1	903.4	30.0	90.5	16.4	1.4	18.3	11.6	7.7	2.2	15.1	17.3	2.3	2.3	141
306	E2	1	DH61	870.6	32.5	0.8	1151.6	29.1	89.7	13.5	1.5	15.5	9.3	7.5	1.8	15.6	17.4	2.3	1.9	144
307	E2	1	DH62	838.3	38.7	1.1	753.8	28.2	92.0	17.3	1.4	19.4	12.2	6.8	1.1	14.7	15.8	2.3	2.5	140
308	E2	1	DH63	885.1	40.7	1.2	764.3	29.6	84.0	20.6	1.7	27.7	12.2	8.2	2.4	15.7	18.1	2.2	2.3	142
309	E2	1	DH64	857.5	37.9	1.2	719.4	34.3	100.2	15.6	1.5	17.9	10.7	7.8	2.1	15.2	17.3	2.2	2.2	141
310	E2	1	DH65	826.8	38.9	1.0	863.9	26.8	87.8	18.6	1.3	19.6	14.0	7.9	2.2	17.2	19.4	2.5	2.0	142

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
311	E2	1	DH66	740.2	34.8	1.0	746.9	34.3	92.6	16.5	1.7	22.2	9.7	7.9	3.4	15.8	19.2	2.4	1.8	145
312	E2	1	DH67	676.6	31.0	0.8	890.2	28.0	85.9	16.4	1.4	18.3	11.6	6.9	2.6	14.6	17.2	2.5	1.8	139
313	E2	1	DH68	600.8	33.7	0.8	717.8	26.2	77.4	15.8	1.5	18.8	10.6	7.3	1.5	15.0	16.5	2.3	2.0	141
314	E2	1	DH69	823.4	37.7	0.9	961.9	30.8	91.3	14.8	1.4	16.5	10.4	6.9	1.8	15.0	16.8	2.4	2.2	141
315	E2	1	DH70	911.0	35.4	1.0	891.3	31.8	90.3	16.8	1.5	20.1	11.2	7.7	2.7	16.5	19.2	2.5	1.8	144
316	E2	1	DH71	707.0	39.8	1.1	653.5	29.2	86.1	16.4	1.5	19.1	11.2	7.9	1.5	15.8	17.3	2.2	2.3	144
317	E2	1	DH72	835.5	36.8	0.8	985.3	30.7	85.1	14.4	1.6	17.8	9.3	7.5	2.7	16.2	18.9	2.5	1.9	144
318	E2	1	DH73	832.5	38.8	0.9	880.0	31.2	91.5	16.4	1.7	21.8	9.7	7.6	2.1	17.1	19.2	2.5	2.0	145
319	E2	1	DH75	901.8	33.2	0.9	971.7	33.5	97.3	18.0	1.4	19.6	13.2	7.3	2.4	15.1	17.5	2.4	1.9	142
320	E2	1	DH76	837.7	30.6	0.8	1035.5	28.7	84.5	17.1	1.4	19.8	11.8	6.8	2.6	14.2	16.8	2.5	1.8	142
321	E2	1	DH77	926.0	32.7	0.9	1007.7	31.9	94.0	18.3	1.4	20.0	13.4	8.5	3.2	16.9	20.1	2.4	1.5	141
322	E2	1	DH78	764.6	35.8	0.9	849.6	28.3	88.0	14.4	1.3	14.7	11.2	7.4	2.5	15.6	18.1	2.5	2.0	140
323	E2	1	DH79	776.5	35.5	1.0	785.1	30.2	92.9	16.9	1.3	17.8	12.7	6.9	2.2	14.4	16.6	2.4	2.1	141
324	E2	1	DH80	873.5	38.9	1.1	766.2	29.2	87.4	17.1	1.4	18.5	12.5	7.1	1.5	15.6	17.1	2.4	2.3	140
325	E2	1	DH81	711.7	37.6	1.1	639.9	30.8	90.9	15.0	1.4	17.4	10.6	7.0	2.0	15.9	17.9	2.6	1.9	141
326	E2	1	DH82	730.8	37.6	1.0	767.6	27.5	91.2	13.5	1.4	14.8	9.8	7.3	1.7	15.4	17.1	2.3	2.2	140
327	E2	1	DH83	986.3	30.4	1.0	971.8	35.8	98.2	16.3	1.7	22.4	9.5	6.8	3.2	13.5	16.7	2.5	1.8	143
328	E2	1	DH84	997.7	29.8	0.9	1111.0	31.0	87.0	16.6	1.4	17.8	12.3	7.0	2.7	12.8	15.5	2.2	1.9	140
329	E2	1	DH85	864.6	31.0	0.8	1026.8	29.5	87.5	15.7	1.4	17.9	11.1	7.1	2.9	14.9	17.8	2.5	1.7	141
330	E2	1	DH86	698.5	31.8	0.9	804.7	29.7	95.9	14.7	1.3	15.6	11.0	6.4	2.1	14.8	16.9	2.6	1.9	142
331	E2	1	DH87	978.5	36.6	0.9	1038.7	25.8	89.6	17.2	1.4	19.1	12.2	6.7	1.8	14.8	16.6	2.5	2.2	139
332	E2	1	DH89	829.1	29.3	0.9	937.9	32.2	93.6	14.8	1.5	17.3	10.0	7.0	2.7	15.1	17.8	2.6	1.6	143
333	E2	1	DH90	867.5	33.6	1.0	882.5	29.6	86.1	16.6	1.5	19.4	11.3	7.4	3.0	15.2	18.2	2.4	1.9	140
334	E2	1	DH91	809.0	36.2	1.0	803.4	29.5	92.8	17.1	1.4	18.3	12.6	7.0	2.5	15.1	17.6	2.5	2.1	141
335	E2	1	DH92	865.5	31.8	0.9	966.0	29.8	84.8	16.8	1.5	19.8	11.2	7.4	2.4	15.7	18.1	2.5	1.8	144
336	E2	1	DH93	877.7	39.8	1.0	853.8	.	86.1	17.7	1.4	19.7	12.6	7.6	2.0	16.7	18.7	2.5	2.1	140
337	E2	1	DH94	849.3	29.6	0.9	962.9	31.4	100.1	12.5	1.4	13.5	9.2	7.2	2.4	15.5	17.9	2.5	1.6	142
338	E2	1	DH95	839.4	35.3	1.0	803.2	33.2	88.1	14.9	1.5	17.6	10.0	7.7	2.0	14.8	16.8	2.2	2.1	140
339	E2	1	DH96	1089.0	31.8	1.1	1030.2	34.5	102.2	14.9	1.3	15.8	11.1	7.1	2.5	13.4	15.9	2.3	2.0	141
340	E2	1	DH97	879.3	34.9	1.0	881.0	32.4	88.0	15.3	1.6	19.3	9.6	7.0	2.0	15.3	17.3	2.5	2.0	141
341	E2	1	DH98	826.9	35.5	1.1	738.3	33.0	92.0	16.9	1.5	19.5	11.6	7.3	2.3	13.6	15.9	2.2	2.2	139
342	E2	1	DH99	751.5	40.5	1.1	703.0	28.7	85.5	14.9	1.6	18.9	9.4	7.5	1.3	16.0	17.3	2.3	2.3	143
343	E2	1	DH100	815.5	42.2	0.9	910.2	25.0	80.2	14.4	1.4	16.4	10.0	7.1	1.9	16.7	18.6	2.6	2.3	140
344	E2	1	DH101	844.9	39.2	1.0	855.2	26.5	94.4	13.4	1.4	14.6	9.8	7.4	1.6	15.7	17.3	2.3	2.3	142
345	E2	1	DH102	822.3	39.7	0.9	880.4	27.7	99.0	15.6	1.5	18.9	10.2	7.7	3.0	16.1	19.1	2.5	2.1	145
346	E2	1	DH103	630.4	32.3	0.9	677.8	30.1	85.2	14.6	1.7	19.5	8.7	7.4	2.1	15.2	17.3	2.4	1.9	146
347	E2	1	DH104	836.4	41.3	1.1	777.3	28.1	98.3	16.5	1.4	18.4	11.7	7.2	2.1	16.3	18.4	2.5	2.3	144
348	E2	1	DH105	740.2	33.0	0.9	850.8	27.5	86.2	15.4	1.4	16.8	11.2	6.2	2.2	14.8	17.0	2.7	1.9	141
349	E2	1	DH106	932.8	40.9	1.1	840.4	29.0	93.4	16.2	1.6	20.2	10.4	8.0	2.3	16.5	18.8	2.3	2.2	142
350	E2	1	DH107	908.7	31.2	0.8	1079.2	29.0	97.2	12.7	1.3	12.9	9.8	7.0	2.3	13.6	15.9	2.3	2.0	140
351	E2	1	DH108	855.0	29.7	0.7	1141.5	27.5	87.0	17.3	1.5	20.2	11.8	6.3	2.7	14.1	16.8	2.7	1.8	141
352	E2	1	DH109	834.3	34.7	0.9	897.1	26.9	91.0	16.2	1.4	18.2	11.5	7.7	2.5	15.5	18.0	2.4	1.9	143
353	E2	1	DH110	804.0	38.7	1.0	802.4	28.0	101.2	13.5	1.4	14.5	10.1	8.7	2.1	16.7	18.8	2.2	2.1	140
354	E2	1	DH111	680.8	38.3	1.0	684.3	27.7	93.3	17.2	1.4	18.8	12.4	8.0	1.7	16.1	17.8	2.2	2.2	140
355	E2	1	DH112	777.1	40.0	1.0	749.4	28.0	91.6	15.6	1.4	17.8	10.9	7.8	2.0	16.6	18.6	2.4	2.1	141
356	E2	1	DH113	821.5	32.3	0.9	885.2	29.7	99.0	16.1	1.4	17.7	11.5	6.6	1.7	14.8	16.5	2.5	1.9	141
357	E2	1	DH114	766.4	38.9	1.0	739.7	28.3	80.0	16.5	1.5	19.6	11.0	7.6	1.3	15.5	16.8	2.2	2.3	142
358	E2	1	DH115	897.9	27.2	0.8	1097.6	30.7	99.1	13.1	1.5	15.2	9.0	7.1	3.2	14.3	17.5	2.5	1.6	141
359	E2	1	DH116	800.6	25.0	0.8	1002.0	33.0	94.2	13.4	1.3	14.0	10.3	6.5	3.1	12.9	16.0	2.5	1.6	142
360	E2	1	DH117	962.3	32.4	1.0	997.2	30.1	87.1	15.7	1.5	18.5	10.6	7.2	1.6	14.3	15.9	2.3	2.0	141
361	E2	1	DH119	811.4	34.4	1.1	752.0	31.8	90.6	17.2	1.6	22.2	10.6	8.0	2.8	15.3	18.1	2.3	1.9	143
362	E2	1	DH120	821.1	28.4	0.7	1197.0	29.9	83.4	18.2	1.3	19.3	13.7	6.8	3.2	14.0	17.2	2.5	1.7	142
363	E2	1	DH121	678.5	30.7	0.8	807.7	30.0	81.8	16.1	1.5	18.7	11.0	7.1	3.6	15.0	18.6	2.6	1.6	142
364	E2	1	DH122	671.7	34.2	0.6	1088.7	15.8	99.1	16.7	1.5	19.7	11.2	6.4	2.5	13.8	16.3	2.6	2.1	146
365	E2	1	DH123	726.4	35.6	0.9	809.9	26.0	94.1	17.5	1.3	17.4	13.9	7.8	2.7	16.1	18.8	2.4	1.9	144
366	E2	1	DH124	849.0	36.5	0.9	907.1	28.3	85.4	17.8	1.4	20.1	12.4	8.0	2.3	15.8	18.1	2.3	2.0	144
367	E2	1	DH125	808.3	32.4	0.9	911.3	28.0	86.5	13.5	1.4	15.1	9.7	7.0	2.3	14.0	16.3	2.3	2.0	140
368	E2	1	DH126	.	39.2	0.9	.	26.2	81.5	14.4	1.5	16.9	9.8	7.3	1.4	15.8	17.2	2.3	2.3	142
369	E2	1	DH128	807.7	29.2	0.7	1115.5	26.7	94.2	19.4	1.3	19.1	15.6	6.7	3.0	14.3	17.3	2.6	1.7	142
370	E2	1	DH129	707.7	36.9	1.0	679.8	28.3	96.2	12.7	1.2	12.5	10.2	6.8	2.2	14.8	17.0	2.5	2.2	140
371	E2	1	DH130	913.9	36.0	1.0	908.5	29.6	89.3	14.8	1.5	17.4	10.0	7.8	2.3	15.3	17.6	2.3	2.0	141
372	E2	1	DH131	686.3	30.9	1.0	721.7	34.7	90.6	18.8	1.7	24.9	11.5	7.8	4.0	15.5	19.5	2.5	1.6	145

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
373	E2	2	DH1	929.6	38.8	1.0	914.1	26.6	93.1	15.2	1.3	16.1	11.4	7.3	1.4	15.6	17.0	2.3	2.5	141
374	E2	2	DH3	804.7	37.5	1.2	686.6	30.2	92.6	14.5	1.5	17.1	9.7	6.8	1.8	15.0	16.8	2.5	2.5	142
375	E2	2	DH4	693.9	29.3	0.8	898.9	29.4	80.2	15.7	1.6	19.9	9.7	7.0	3.2	15.0	18.2	2.6	1.9	144
376	E2	2	DH5	684.8	40.5	1.1	597.0	27.9	82.7	14.0	1.5	16.1	9.6	8.0	1.4	15.8	17.2	2.2	2.6	141
377	E2	2	DH6	773.9	38.1	1.1	714.6	29.4	90.4	14.1	1.3	14.6	10.8	7.2	1.7	15.3	17.0	2.4	2.5	140
378	E2	2	DH7	718.7	37.0	1.0	689.1	32.5	81.1	15.7	1.5	19.5	10.1	7.1	2.8	15.3	18.1	2.6	2.4	143
379	E2	2	DH8	695.1	41.0	1.2	575.4	27.7	85.8	14.8	1.4	16.0	10.8	7.5	1.7	15.0	16.7	2.2	2.7	141
380	E2	2	DH9	636.5	36.4	1.2	532.6	31.1	83.3	15.7	1.5	19.2	10.3	7.1	2.7	15.1	17.8	2.5	2.4	142
381	E2	2	DH11	977.2	39.4	1.3	742.6	33.6	108.5	15.2	1.2	14.9	12.3	8.7	1.5	16.3	17.8	2.0	2.4	141
382	E2	2	DH12	586.9	38.7	0.9	623.7	27.6	70.2	12.7	1.8	17.5	7.2	6.4	1.2	15.2	16.4	2.6	2.5	142
383	E2	2	DH13	577.5	44.0	1.1	512.9	25.0	82.1	15.0	1.3	15.4	11.6	7.6	1.6	17.5	19.1	2.5	2.5	141
384	E2	2	DH14	878.4	33.7	1.1	805.2	32.3	87.5	17.6	1.5	21.1	11.6	7.5	2.5	15.9	18.4	2.5	2.1	143
385	E2	2	DH15	813.8	31.2	0.9	940.8	28.0	87.3	14.4	1.3	15.2	10.8	7.1	1.9	14.6	16.5	2.3	2.1	141
386	E2	2	DH16	732.6	30.1	0.8	965.2	28.5	87.5	14.8	1.5	17.5	10.0	6.7	3.1	13.3	16.4	2.5	2.3	142
387	E2	2	DH17	730.2	39.1	1.3	567.8	33.1	89.6	16.0	1.4	17.6	11.5	7.7	2.0	15.2	17.2	2.2	2.6	139
388	E2	2	DH18	781.5	40.2	1.2	644.3	30.7	89.4	14.4	1.9	21.7	7.6	7.8	2.4	16.2	18.6	2.4	2.5	146
389	E2	2	DH19	738.5	34.5	1.1	661.8	30.3	78.4	14.5	1.3	15.3	10.8	6.5	1.6	13.3	14.9	2.3	2.6	139
390	E2	2	DH20	739.5	41.9	1.0	704.9	28.8	80.8	16.8	1.6	21.9	10.2	7.4	2.0	16.1	18.1	2.5	2.6	143
391	E2	2	DH21	822.5	31.6	1.0	790.1	31.8	90.6	15.1	1.4	16.3	11.1	7.2	3.2	14.0	17.2	2.4	2.3	142
392	E2	2	DH22	847.0	42.5	1.3	663.8	30.5	101.1	15.4	1.5	17.8	10.6	8.0	1.6	17.5	19.1	2.4	2.4	141
393	E2	2	DH23	820.1	39.4	1.1	765.0	27.0	91.8	17.0	1.3	17.4	13.3	6.6	1.7	14.6	16.3	2.5	2.7	141
394	E2	2	DH24	880.0	37.4	1.1	820.9	28.7	85.3	15.4	1.5	17.9	10.5	7.0	1.3	14.7	16.0	2.3	2.5	141
395	E2	2	DH25	705.3	36.2	0.9	768.3	29.3	78.5	13.5	1.3	13.9	10.3	7.0	2.2	15.3	17.5	2.5	2.4	138
396	E2	2	DH26	815.4	35.5	0.9	951.4	29.4	82.1	14.8	1.5	17.1	10.1	7.0	1.9	14.9	16.8	2.4	2.4	141
397	E2	2	DH27	667.1	34.9	1.0	650.2	30.2	87.2	13.8	1.2	13.4	11.2	6.4	1.8	14.0	15.8	2.5	2.5	141
398	E2	2	DH28	729.9	32.7	1.0	750.2	30.1	87.6	13.4	1.3	13.5	10.6	6.5	2.0	13.7	15.7	2.4	2.4	141
399	E2	2	DH29	816.7	31.0	0.8	970.0	28.7	81.4	12.9	1.4	13.9	9.5	7.1	2.5	15.0	17.5	2.5	2.1	141
400	E2	2	DH30	893.2	31.8	1.1	814.2	35.4	90.9	16.9	1.5	20.4	11.1	7.2	2.5	15.9	18.4	2.6	2.0	143
401	E2	2	DH31	632.8	36.3	1.0	664.8	26.0	82.7	14.9	1.4	16.2	10.9	7.4	1.7	15.1	16.8	2.3	2.4	140
402	E2	2	DH32	863.6	31.2	0.8	1131.8	26.2	87.8	14.0	1.4	15.5	10.0	6.6	3.1	14.8	17.9	2.7	2.1	146
403	E2	2	DH33	731.3	43.5	0.8	878.0	27.3	93.6	18.8	1.7	25.6	11.0	7.7	2.8	17.4	20.2	2.6	2.5	147
404	E2	2	DH34	733.0	42.8	1.2	588.3	28.5	95.3	15.3	1.4	17.0	10.8	7.7	1.5	16.9	18.4	2.4	2.5	141
405	E2	2	DH35	752.0	34.3	1.0	749.7	30.9	88.2	13.4	1.4	14.5	9.9	7.2	2.2	14.7	16.9	2.4	2.3	141
406	E2	2	DH36	867.6	37.0	1.0	844.8	29.3	84.3	17.6	1.7	23.0	10.6	8.4	2.3	16.9	19.2	2.3	2.2	143
407	E2	2	DH37	708.0	40.6	1.0	709.5	25.2	90.3	15.2	1.4	16.5	11.2	7.5	2.2	16.4	18.6	2.5	2.5	141
408	E2	2	DH38	995.7	37.4	1.0	994.7	27.1	82.9	14.8	1.4	16.2	10.8	7.4	2.2	16.2	18.4	2.5	2.3	141
409	E2	2	DH39	1098.1	31.6	0.9	1180.7	28.8	95.7	18.5	1.4	20.7	13.3	6.3	3.0	14.6	17.6	2.8	2.2	140
410	E2	2	DH40	744.0	36.5	1.1	674.6	29.3	100.4	12.8	1.2	12.6	10.4	8.2	2.0	17.0	19.0	2.3	2.1	143
411	E2	2	DH41	696.9	33.4	0.9	760.0	26.8	85.2	13.0	1.2	13.0	10.4	7.0	1.9	15.0	16.9	2.4	2.2	142
412	E2	2	DH42	918.7	43.5	1.3	696.0	29.6	94.3	16.1	1.3	17.1	11.9	7.9	1.4	18.0	19.4	2.4	2.4	142
413	E2	2	DH43	845.4	37.9	1.2	727.6	30.8	81.8	14.3	1.3	14.8	11.0	6.9	2.0	14.4	16.4	2.4	2.6	140
414	E2	2	DH44	815.7	39.0	1.4	604.2	32.6	100.0	15.4	1.5	18.1	10.3	7.9	1.4	15.4	16.8	2.1	2.5	141
415	E2	2	DH45	735.2	34.4	1.2	618.3	33.6	89.1	14.1	1.5	16.8	9.4	7.8	1.5	15.7	17.2	2.2	2.2	140
416	E2	2	DH46	591.8	37.8	0.9	624.2	26.6	89.0	17.0	1.5	20.8	11.0	8.1	2.3	15.4	17.7	2.2	2.5	142
417	E2	2	DH47	837.5	32.3	0.9	916.3	28.9	90.3	14.0	1.4	15.8	9.9	6.9	2.1	14.1	16.2	2.3	2.3	142
418	E2	2	DH49	642.3	36.3	1.1	588.7	31.5	81.6	15.5	1.5	18.6	10.2	7.2	2.2	14.8	17.0	2.4	2.4	141
419	E2	2	DH50	740.6	31.3	1.0	755.7	29.8	92.3	12.8	1.2	12.5	10.5	6.9	1.9	14.9	16.8	2.4	2.1	142
420	E2	2	DH51	717.5	44.4	1.1	666.2	25.5	90.0	16.3	1.4	18.3	11.5	8.0	1.6	16.6	18.2	2.3	2.7	142
421	E2	2	DH52	943.3	35.8	0.8	1257.7	24.3	88.2	14.4	1.3	14.8	11.2	6.9	1.8	15.1	16.9	2.4	2.4	142
422	E2	2	DH53	914.8	36.1	0.9	984.7	28.2	73.6	13.7	1.4	15.2	9.9	6.9	1.8	15.5	17.3	2.5	2.3	141
423	E2	2	DH54	786.2	39.6	1.3	620.5	32.4	84.2	19.3	1.5	22.7	12.9	8.2	1.6	15.0	16.6	2.0	2.6	142
424	E2	2	DH55	732.7	37.4	1.1	691.2	28.0	90.7	14.7	1.4	16.0	10.7	6.5	1.8	14.2	16.0	2.5	2.6	141
425	E2	2	DH56	665.9	35.8	1.0	640.3	28.5	85.3	11.9	1.3	12.4	9.1	7.0	2.1	15.0	17.1	2.4	2.4	141
426	E2	2	DH57	783.2	31.7	0.9	839.5	28.8	88.8	14.3	1.5	16.7	9.6	6.3	1.9	15.1	17.0	2.7	2.1	142
427	E2	2	DH58	736.4	35.7	0.9	776.0	30.3	89.2	14.7	1.4	16.8	10.2	6.8	2.0	14.0	16.0	2.4	2.5	141
428	E2	2	DH59	837.7	42.0	1.1	740.0	27.1	81.3	13.5	1.2	12.6	11.6	6.9	0.8	15.8	16.6	2.4	2.7	140
429	E2	2	DH60	613.1	38.6	1.2	520.9	29.5	81.2	11.8	1.3	11.9	9.4	7.3	2.5	15.0	17.5	2.4	2.6	137
430	E2	2	DH61	649.7	32.0	0.9	692.7	29.8	79.6	12.6	1.4	13.8	9.1	7.1	1.9	14.3	16.2	2.3	2.2	142
431	E2	2	DH62	675.4	36.5	1.0	649.4	28.3	82.9	15.6	1.3	16.5	11.7	6.5	1.9	13.7	15.6	2.4	2.7	139
432	E2	2	DH63	762.6	45.7	1.4	550.6	30.3	90.4	16.4	1.6	20.4	10.5	8.5	1.3	16.7	18.0	2.1	2.7	141
433	E2	2	DH64	903.8	34.4	1.0	864.9	33.1	103.1	16.0	1.5	18.5	10.9	7.7	2.3	15.4	17.7	2.3	2.2	142
434	E2	2	DH65	884.3	43.6	1.2	755.1	26.5	94.8	18.0	1.4	20.1	12.8	8.4	1.8	18.0	19.8	2.4	2.4	142

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
435	E2	2	DH66	628.1	38.3	1.3	490.3	32.8	83.8	15.6	1.5	18.7	10.3	8.0	2.0	16.6	18.6	2.3	2.3	143
436	E2	2	DH67	574.4	34.3	0.9	658.7	27.0	81.9	14.5	1.2	14.1	11.8	6.7	1.9	15.1	17.0	2.5	2.3	139
437	E2	2	DH68	473.2	32.5	0.9	551.5	27.2	78.7	16.2	1.4	17.6	12.0	6.9	1.7	14.3	16.0	2.3	2.3	141
438	E2	2	DH69	694.3	42.3	1.2	603.2	29.4	80.1	13.8	1.4	14.8	10.2	6.8	1.3	15.5	16.8	2.5	2.7	140
439	E2	2	DH70	788.9	35.5	1.0	795.3	31.3	91.4	14.9	1.5	17.4	10.1	7.7	2.7	16.2	18.9	2.5	2.2	143
440	E2	2	DH71	708.5	39.0	1.1	628.1	29.9	84.1	15.3	1.4	17.2	10.7	7.7	1.6	15.7	17.3	2.3	2.5	141
441	E2	2	DH72	610.0	35.5	1.0	597.4	28.7	84.1	14.2	1.5	17.1	9.4	7.3	1.9	16.2	18.1	2.5	2.2	143
442	E2	2	DH73	599.3	36.9	1.0	594.6	28.1	82.8	14.8	1.5	17.7	9.7	7.2	1.9	15.9	17.8	2.5	2.3	143
443	E2	2	DH75	822.2	32.3	0.9	871.9	32.3	89.2	13.1	1.3	13.0	10.4	6.8	2.4	13.7	16.1	2.4	2.4	141
444	E2	2	DH76	693.5	34.0	1.0	689.4	28.5	76.9	14.3	1.4	16.0	10.1	6.7	2.1	14.3	16.4	2.4	2.4	140
445	E2	2	DH77	827.4	32.6	1.0	823.3	30.3	88.0	18.0	1.3	18.1	14.2	8.0	2.8	15.9	18.7	2.4	2.0	139
446	E2	2	DH78	798.5	40.4	1.1	696.8	30.4	88.7	14.1	1.3	14.5	10.8	7.8	1.5	16.5	18.0	2.3	2.4	139
447	E2	2	DH79	847.6	37.5	1.1	774.8	29.3	96.4	15.2	1.4	16.4	11.1	7.2	2.1	14.9	17.0	2.4	2.5	142
448	E2	2	DH80	797.6	37.2	1.1	723.8	29.1	87.2	15.2	1.3	15.8	11.6	7.0	1.9	15.3	17.2	2.5	2.4	142
449	E2	2	DH81	690.7	35.6	1.1	646.7	30.6	79.2	17.2	1.7	23.6	9.9	7.2	1.1	16.5	17.6	2.4	2.2	141
450	E2	2	DH82	755.0	34.4	0.9	885.1	26.7	88.8	12.6	1.4	14.4	8.9	7.4	2.1	15.0	17.1	2.3	2.3	141
451	E2	2	DH83	733.4	33.3	1.1	652.0	32.4	96.6	13.1	1.3	13.1	10.4	6.6	2.6	13.3	15.9	2.4	2.5	140
452	E2	2	DH84	857.6	35.8	1.1	760.3	33.3	87.7	14.4	1.3	14.8	11.1	7.0	1.6	13.8	15.4	2.2	2.6	140
453	E2	2	DH85	764.3	37.1	1.1	683.7	27.4	79.8	14.8	1.3	15.6	11.3	7.0	1.4	15.1	16.5	2.4	2.5	141
454	E2	2	DH86	852.1	34.1	0.9	901.7	31.5	96.7	15.3	1.4	16.5	11.2	6.6	2.0	15.0	17.0	2.6	2.3	144
455	E2	2	DH87	822.5	43.2	1.3	650.7	27.2	89.7	13.5	1.3	13.5	10.7	7.0	1.0	15.3	16.3	2.3	2.8	138
456	E2	2	DH89	581.9	32.2	1.1	548.9	31.4	82.0	13.1	1.4	14.2	9.5	6.7	2.0	14.6	16.6	2.5	2.2	141
457	E2	2	DH90	676.0	36.9	1.2	575.8	30.1	77.2	14.9	1.3	15.7	11.2	7.5	2.5	15.5	18.0	2.4	2.4	139
458	E2	2	DH91	656.0	37.6	1.1	577.0	30.5	89.8	14.8	1.4	15.9	10.9	6.7	2.2	15.1	17.3	2.6	2.5	140
459	E2	2	DH92	715.0	34.3	0.9	753.5	26.9	81.9	15.9	1.4	17.1	11.8	6.9	1.8	14.8	16.6	2.4	2.3	140
460	E2	2	DH93	663.1	44.5	1.2	535.7	25.6	80.9	14.9	1.3	14.9	11.8	7.5	1.4	16.7	18.1	2.4	2.6	140
461	E2	2	DH94	795.2	28.4	0.9	903.7	30.1	90.3	12.5	1.3	13.3	9.4	6.9	2.3	14.6	16.9	2.5	1.9	140
462	E2	2	DH95	958.7	35.3	1.0	958.7	31.7	91.3	16.0	1.3	16.9	12.0	8.0	2.0	15.3	17.3	2.2	2.3	142
463	E2	2	DH96	971.1	29.2	1.0	944.6	34.6	96.0	14.0	1.3	14.5	10.7	6.7	2.6	12.8	15.4	2.3	2.3	141
464	E2	2	DH97	831.8	38.1	1.1	736.7	33.0	90.1	15.6	1.6	19.2	10.1	7.3	1.4	15.6	17.0	2.3	2.4	141
465	E2	2	DH98	729.1	44.4	1.4	519.3	32.1	84.3	13.6	1.4	14.8	10.0	7.8	1.0	15.2	16.2	2.1	2.9	138
466	E2	2	DH99	704.9	33.8	0.9	771.3	27.7	80.5	16.4	1.5	19.1	11.2	6.8	1.7	14.5	16.2	2.4	2.3	143
467	E2	2	DH100	648.2	48.0	1.2	544.7	25.3	74.6	12.5	1.4	13.4	9.2	7.3	1.1	16.9	18.0	2.5	2.8	140
468	E2	2	DH101	872.9	41.4	1.1	823.5	27.7	91.2	17.8	1.6	22.3	11.2	8.0	1.4	16.3	17.7	2.2	2.5	141
469	E2	2	DH102	650.9	43.5	1.1	589.1	28.3	88.5	15.4	1.6	19.7	9.6	8.1	1.8	17.0	18.8	2.3	2.6	144
470	E2	2	DH103	539.0	32.5	1.0	531.5	30.0	77.5	13.0	1.5	15.7	8.5	7.2	2.1	15.0	17.1	2.4	2.2	145
471	E2	2	DH104	762.3	37.7	1.0	798.2	27.6	95.6	15.6	1.4	17.7	10.9	7.0	2.8	15.5	18.3	2.6	2.4	145
472	E2	2	DH105	659.9	38.0	1.1	618.5	27.2	88.2	15.5	1.4	17.8	10.8	6.8	1.8	16.2	18.0	2.7	2.3	142
473	E2	2	DH106	810.6	42.4	1.2	656.3	29.4	81.7	14.9	1.5	17.6	10.0	7.7	2.1	16.6	18.7	2.4	2.6	141
474	E2	2	DH107	758.2	32.0	0.9	870.4	28.9	90.0	12.4	1.2	12.0	10.2	6.8	2.2	13.7	15.9	2.3	2.3	139
475	E2	2	DH108	672.9	34.7	1.0	689.4	27.0	87.9	15.1	1.4	16.4	11.2	6.6	2.3	14.6	16.9	2.6	2.4	139
476	E2	2	DH109	570.9	30.5	0.8	675.6	27.2	80.0	14.3	1.4	15.3	10.6	7.0	2.6	14.5	17.1	2.5	2.1	140
477	E2	2	DH110	617.6	38.8	1.1	554.4	27.2	90.4	12.2	1.0	9.2	12.8	8.0	1.9	16.1	18.0	2.3	2.4	139
478	E2	2	DH111	642.9	39.2	1.1	568.5	27.9	89.6	15.4	1.3	16.3	11.5	8.0	1.9	15.8	17.7	2.2	2.5	141
479	E2	2	DH112	574.3	38.7	1.1	500.3	27.8	78.7	13.8	1.4	15.1	10.0	7.4	2.2	15.8	18.0	2.4	2.5	140
480	E2	2	DH113	686.5	35.1	1.1	638.0	30.8	84.6	15.3	1.3	15.7	11.8	6.5	1.6	14.2	15.8	2.5	2.5	140
481	E2	2	DH114	773.9	36.5	1.0	765.5	28.4	74.0	14.6	1.5	17.0	9.9	7.3	1.3	15.2	16.5	2.3	2.4	141
482	E2	2	DH115	669.1	31.7	1.0	679.3	29.3	88.7	13.0	1.3	13.9	9.7	7.0	2.4	14.1	16.5	2.4	2.2	140
483	E2	2	DH116	730.3	30.2	0.9	772.8	30.4	91.2	13.3	1.4	14.8	9.4	6.5	2.4	13.1	15.5	2.4	2.3	141
484	E2	2	DH117	666.0	34.1	1.0	663.3	29.8	80.6	13.0	1.4	13.9	9.6	7.3	1.4	14.2	15.6	2.2	2.4	139
485	E2	2	DH119	761.8	39.3	1.3	608.5	31.8	99.4	17.3	1.6	21.9	10.8	8.3	2.4	16.7	19.1	2.3	2.3	143
486	E2	2	DH120	805.8	33.9	0.9	923.0	29.7	87.8	16.0	1.4	17.1	11.8	7.1	2.2	15.7	17.9	2.5	2.2	142
487	E2	2	DH121	759.2	35.5	1.1	712.9	29.0	89.1	13.4	1.4	15.4	9.3	7.2	2.8	15.4	18.2	2.5	2.3	141
488	E2	2	DH122	581.9	35.8	0.9	641.6	27.7	87.9	13.3	1.3	13.8	10.2	6.5	1.6	14.5	16.1	2.5	2.5	142
489	E2	2	DH123	555.1	34.4	0.9	602.1	25.4	91.4	14.1	1.1	12.9	12.2	7.5	2.5	14.9	17.4	2.3	2.3	143
490	E2	2	DH124	626.2	35.3	0.9	722.2	26.0	79.8	15.3	1.3	15.9	11.7	7.8	1.9	15.1	17.0	2.2	2.3	142
491	E2	2	DH125	863.3	31.1	0.9	978.7	28.7	84.7	12.5	1.4	13.8	9.0	6.7	2.7	13.8	16.5	2.5	2.2	141
492	E2	2	DH126	775.2	43.0	1.1	692.7	26.7	82.8	13.8	1.5	16.7	9.0	7.9	1.4	17.0	18.4	2.3	2.5	144
493	E2	2	DH128	731.9	37.1	1.0	721.8	27.4	84.5	17.9	1.3	18.3	13.8	6.6	2.2	14.8	17.0	2.6	2.5	142
494	E2	2	DH129	697.2	37.9	1.2	601.6	29.8	86.7	13.9	1.3	14.1	11.0	6.7	2.2	14.4	16.6	2.5	2.6	140
495	E2	2	DH130	794.7	32.0	0.9	893.9	28.8	83.3	13.6	1.4	14.6	10.0	7.3	2.5	14.8	17.3	2.4	2.2	141
496	E2	2	DH131	689.8	35.9	1.2	576.2	36.6	89.4	16.7	1.8	23.2	9.5	8.1	3.2	16.5	19.7	2.4	2.2	144

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
497	E3	1	DH1	662.5	47.7	1.5	439.9	31.3	98.3	14.6	1.5	17.0	9.9	7.0	0.4	15.5	15.9	2.3	3.1	126
498	E3	1	DH3	810.1	48.3	1.5	527.1	30.5	99.6	17.7	1.8	25.1	9.9	7.2	1.7	16.1	17.8	2.5	3.0	130
499	E3	1	DH4	794.3	44.1	1.4	561.8	29.9	90.3	18.3	1.9	28.2	9.4	7.1	1.6	15.0	16.6	2.4	2.9	129
500	E3	1	DH5	830.1	43.9	1.3	648.0	31.0	91.8	17.4	1.6	22.6	10.6	7.7	1.8	14.8	16.6	2.1	3.0	129
501	E3	1	DH6	847.7	47.5	1.5	557.0	32.6	99.2	17.5	1.6	22.8	10.6	7.3	1.1	15.4	16.5	2.3	3.1	123
502	E3	1	DH7	491.5	38.6	1.2	408.3	31.0	92.4	17.0	1.7	23.4	9.8	6.6	3.1	14.2	17.3	2.6	2.7	133
503	E3	1	DH8	614.6	51.5	1.6	373.6	30.7	103.1	18.7	1.7	24.5	11.3	7.7	1.5	15.2	16.7	2.2	3.4	127
504	E3	1	DH9	655.1	43.8	1.4	454.6	32.8	97.4	20.0	1.9	29.9	10.7	7.4	2.4	16.2	18.6	2.5	2.7	130
505	E3	1	DH11	611.3	49.4	1.9	330.1	35.1	115.5	19.7	1.6	24.3	12.8	8.6	1.4	15.5	16.9	2.0	3.2	125
506	E3	1	DH12	582.1	42.5	1.4	408.5	32.5	87.0	16.7	1.7	22.9	9.6	7.0	1.5	14.1	15.6	2.2	2.9	128
507	E3	1	DH13	548.3	47.8	1.4	387.4	.	93.9	20.0	1.7	27.2	11.6	7.1	2.2	15.9	18.1	2.6	2.6	130
508	E3	1	DH14	475.6	38.8	1.3	363.6	32.1	95.9	16.6	1.6	20.9	10.7	7.0	3.2	15.3	18.5	2.7	2.1	129
509	E3	1	DH15	774.6	37.5	1.3	597.7	31.9	91.0	14.8	1.5	17.3	10.0	7.1	1.8	13.8	15.6	2.2	2.4	122
510	E3	1	DH16	834.4	42.1	1.5	573.5	33.0	95.1	15.5	1.7	20.5	9.3	6.9	1.5	13.8	15.3	2.2	2.8	124
511	E3	1	DH17	790.0	42.5	1.5	516.3	32.7	98.9	17.8	1.6	22.7	11.0	7.4	1.8	14.3	16.1	2.2	2.6	124
512	E3	1	DH18	605.8	42.7	1.4	435.1	31.4	94.4	18.7	2.2	33.5	8.3	7.5	1.9	15.6	17.5	2.3	2.4	135
513	E3	1	DH19	469.2	41.2	1.4	334.7	34.6	99.2	16.4	1.8	23.3	9.2	6.6	1.5	13.3	14.8	2.3	2.8	127
514	E3	1	DH20	808.3	50.7	1.6	495.6	30.1	91.5	20.4	1.9	31.4	10.5	7.8	1.5	16.6	18.1	2.3	2.8	130
515	E3	1	DH21	651.0	36.8	1.3	512.2	32.3	105.2	18.9	1.6	23.7	11.9	6.8	3.1	13.4	16.5	2.4	2.2	131
516	E3	1	DH22	852.4	51.7	1.7	491.3	32.7	114.2	16.1	1.8	22.9	9.0	7.8	2.0	17.6	19.6	2.5	2.6	129
517	E3	1	DH23	817.3	42.1	1.3	607.2	30.7	103.8	18.6	1.5	22.2	12.3	6.5	1.9	13.8	15.7	2.4	2.7	126
518	E3	1	DH24	450.2	43.8	1.4	319.3	32.2	96.9	16.0	1.6	20.7	9.8	6.7	1.5	14.1	15.6	2.3	2.8	121
519	E3	1	DH25	1044.5	38.0	1.2	880.7	33.1	96.4	16.3	1.7	21.9	9.6	6.9	2.6	14.4	17.0	2.5	2.2	125
520	E3	1	DH26	671.9	44.4	1.4	465.0	31.1	94.5	16.2	1.8	22.5	9.2	7.0	1.8	15.1	16.9	2.4	2.6	128
521	E3	1	DH27	505.0	47.8	1.5	333.3	30.6	103.2	20.5	1.8	28.7	11.7	7.1	1.5	14.7	16.2	2.3	2.9	131
522	E3	1	DH28	804.5	52.1	1.5	532.1	32.2	98.1	17.5	1.6	22.6	10.7	7.1	0.9	15.3	16.2	2.3	3.2	129
523	E3	1	DH29	903.7	46.9	1.5	589.9	31.6	89.2	15.8	1.6	20.2	9.8	7.6	2.1	16.2	18.3	2.4	2.6	129
524	E3	1	DH30	779.4	45.7	1.6	498.0	34.1	99.7	18.0	1.8	25.5	10.1	7.3	2.1	16.3	18.4	2.5	2.5	129
525	E3	1	DH31	583.7	44.6	1.4	409.0	29.7	92.6	18.5	1.7	24.7	10.9	7.6	1.7	15.4	17.1	2.3	2.6	129
526	E3	1	DH32	612.5	42.2	1.2	505.4	25.9	95.7	15.4	1.7	20.5	9.1	7.5	1.7	16.5	18.2	2.4	2.3	134
527	E3	1	DH33	533.0	51.8	1.5	364.3	29.2	104.2	18.9	1.9	29.2	9.7	7.6	2.2	16.8	19.0	2.5	2.7	136
528	E3	1	DH34	629.3	47.2	1.5	412.6	32.1	99.5	18.3	1.7	24.4	10.9	7.4	2.2	15.6	17.8	2.4	2.7	126
529	E3	1	DH35	505.5	32.0	1.1	453.8	.	99.8	17.3	1.9	25.8	9.2	7.1	3.1	14.1	17.2	2.4	1.9	126
530	E3	1	DH36	832.9	48.7	1.6	533.6	31.4	96.7	20.6	2.0	32.3	10.4	9.0	1.1	18.3	19.4	2.2	2.5	130
531	E3	1	DH37	735.2	44.6	1.4	522.9	30.9	100.1	16.3	1.6	20.5	10.3	7.3	2.8	15.6	18.4	2.5	2.4	128
532	E3	1	DH38	824.3	42.3	1.4	568.9	31.5	95.4	17.2	1.6	21.9	10.7	7.5	0.9	15.5	16.4	2.2	2.6	121
533	E3	1	DH39	863.0	44.7	1.5	591.9	31.1	105.4	17.5	1.7	23.7	10.2	6.5	1.7	14.2	15.9	2.5	2.8	126
534	E3	1	DH40	363.4	38.1	1.3	280.6	33.3	107.7	15.6	1.5	18.2	10.7	7.5	0.7	15.2	15.9	2.1	2.4	130
535	E3	1	DH41	651.2	41.5	1.3	500.6	31.9	97.6	17.4	1.7	23.5	10.2	6.7	1.3	13.5	14.8	2.2	2.8	131
536	E3	1	DH42	953.4	38.1	1.1	848.7	31.9	103.4	16.3	1.6	20.2	10.4	7.0	2.9	15.5	18.4	2.6	2.1	130
537	E3	1	DH43	830.6	45.2	1.5	545.7	32.9	96.2	16.6	1.7	22.3	9.8	7.2	1.9	15.3	17.2	2.4	2.6	128
538	E3	1	DH44	720.3	37.6	1.4	531.2	36.0	109.5	21.3	1.8	29.9	12.0	7.7	2.1	14.2	16.3	2.1	2.3	132
539	E3	1	DH45	693.5	36.8	1.3	547.8	35.1	93.8	17.9	1.8	25.8	9.9	6.8	2.1	13.6	15.7	2.3	2.4	128
540	E3	1	DH46	581.9	48.3	1.5	390.0	30.8	99.2	19.8	1.7	26.8	11.5	8.1	1.5	15.5	17.0	2.1	2.8	131
541	E3	1	DH47	888.6	41.3	1.3	667.6	32.9	99.8	17.2	1.7	23.8	9.9	7.1	2.3	14.5	16.8	2.4	2.5	130
542	E3	1	DH49	682.3	55.8	1.8	384.9	31.7	97.5	19.7	1.8	28.6	10.8	7.9	1.3	15.9	17.2	2.2	3.2	130
543	E3	1	DH50	904.9	33.6	1.3	671.8	35.1	100.8	14.3	1.5	17.1	9.5	6.5	2.4	13.4	15.8	2.4	2.1	125
544	E3	1	DH51	632.7	50.0	1.5	434.2	29.9	98.6	20.3	1.8	28.8	11.4	7.9	1.4	15.9	17.3	2.2	2.9	131
545	E3	1	DH52	698.2	48.0	1.5	476.9	29.5	87.9	15.4	1.7	20.7	9.2	7.2	0.8	15.5	16.3	2.3	2.9	127
546	E3	1	DH53	768.8	46.1	1.6	491.6	31.0	83.6	18.7	1.8	27.0	10.3	7.2	0.9	15.2	16.1	2.2	2.9	129
547	E3	1	DH54	858.6	50.5	1.9	456.4	34.9	94.4	18.1	1.9	26.8	9.7	8.0	1.8	14.6	16.4	2.1	3.1	123
548	E3	1	DH55	875.1	40.5	1.2	707.4	28.5	101.3	16.3	1.6	20.2	10.4	6.3	2.4	14.4	16.8	2.7	2.4	129
549	E3	1	DH56	848.5	32.9	1.2	691.0	.	100.4	13.8	1.5	16.1	9.4	5.9	2.3	11.9	14.2	2.4	2.3	125
550	E3	1	DH57	874.6	42.2	1.4	638.8	30.6	98.3	14.3	1.7	19.7	8.2	6.3	2.2	15.2	17.4	2.8	2.4	129
551	E3	1	DH58	689.1	47.6	1.5	475.3	31.1	101.3	15.5	1.5	18.3	10.5	6.9	1.5	14.2	15.7	2.3	3.0	127
552	E3	1	DH59	1071.2	36.6	1.1	951.3	30.6	100.9	14.8	1.6	19.0	9.2	6.5	1.4	13.3	14.7	2.3	2.5	122
553	E3	1	DH60	880.1	54.3	1.7	519.8	31.3	95.7	18.9	1.7	26.2	10.9	8.0	1.4	16.5	17.9	2.2	3.0	126
554	E3	1	DH61	642.1	37.3	1.1	564.2	31.7	93.0	17.3	1.8	24.2	9.7	7.2	2.0	14.6	16.6	2.3	2.3	131
555	E3	1	DH62	771.7	52.6	1.7	462.7	.	103.1	19.5	1.7	26.3	11.4	7.2	0.4	15.5	15.9	2.2	3.3	126
556	E3	1	DH63	666.0	55.4	2.0	331.3	33.6	93.5	16.8	1.8	24.3	9.2	8.5	0.9	15.8	16.7	2.0	3.3	123
557	E3	1	DH64	830.2	42.6	1.6	515.7	36.1	111.8	16.2	1.6	20.3	10.2	7.5	1.6	14.7	16.3	2.2	2.6	123
558	E3	1	DH65	721.8	55.6	1.7	420.4	31.0	91.1	18.8	1.6	23.4	12.0	8.0	0.9	17.0	17.9	2.2	3.1	125

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
559	E3	1	DH66	652.4	42.7	1.5	421.7	34.8	105.2	18.7	2.1	30.4	9.1	8.1	3.7	17.1	20.8	2.6	2.1	132
560	E3	1	DH67	845.4	45.1	1.5	573.6	32.1	97.4	17.9	1.7	23.8	10.6	7.2	1.1	15.9	17.0	2.4	2.7	125
561	E3	1	DH68	609.3	43.3	1.2	503.1	27.4	97.0	18.3	1.8	25.8	10.2	7.4	1.0	15.3	16.3	2.2	2.7	127
562	E3	1	DH69	946.3	44.2	1.5	612.1	33.0	98.4	16.1	1.7	21.0	9.8	6.9	0.9	14.4	15.3	2.2	2.9	124
563	E3	1	DH70	661.2	46.8	1.3	490.2	31.7	98.6	16.8	1.8	23.8	9.5	8.0	1.8	17.0	18.8	2.3	2.5	132
564	E3	1	DH71	826.0	49.2	1.5	555.1	31.2	99.8	19.0	1.9	28.0	10.3	8.0	1.5	17.1	18.6	2.3	2.6	130
565	E3	1	DH72	835.7	41.7	1.4	617.7	31.8	98.1	14.2	1.7	18.6	8.5	6.9	2.8	15.2	18.0	2.6	2.3	129
566	E3	1	DH73	804.7	50.0	1.6	506.4	30.4	99.6	16.2	1.7	22.2	9.4	7.8	1.3	15.9	17.2	2.2	2.9	130
567	E3	1	DH75	941.7	36.5	1.3	723.8	36.1	103.5	17.1	1.8	24.6	9.5	6.9	1.9	13.5	15.4	2.2	2.3	122
568	E3	1	DH76	916.5	31.1	1.1	867.0	32.4	91.3	18.1	1.6	22.7	11.4	6.3	2.5	13.1	15.6	2.5	2.0	130
569	E3	1	DH77	746.8	37.5	1.3	581.2	33.7	105.3	18.1	1.6	22.3	11.6	7.8	2.6	15.8	18.4	2.4	2.0	127
570	E3	1	DH78	862.2	47.3	1.6	530.9	33.4	92.0	16.6	1.6	21.0	10.5	7.1	1.5	14.8	16.3	2.3	2.9	125
571	E3	1	DH79	670.1	52.0	1.7	399.1	32.0	101.2	15.8	1.5	19.1	10.4	7.5	1.3	15.2	16.5	2.2	3.1	126
572	E3	1	DH80	742.3	48.2	1.5	480.8	31.7	103.9	19.3	1.6	24.6	12.0	7.1	1.4	15.6	17.0	2.4	2.8	129
573	E3	1	DH81	719.8	36.1	1.2	584.8	31.6	101.0	15.3	1.6	19.5	9.5	6.1	1.6	15.4	17.0	2.8	2.1	127
574	E3	1	DH82	793.8	51.3	1.8	436.9	32.2	100.1	15.0	1.6	19.2	9.3	8.1	0.6	16.2	16.8	2.1	3.1	122
575	E3	1	DH83	828.1	40.2	1.4	584.0	35.6	110.5	18.3	1.6	23.2	11.4	7.2	2.6	14.2	16.8	2.3	2.4	126
576	E3	1	DH84	1017.3	34.9	1.3	786.2	37.2	102.4	15.5	1.5	18.2	10.4	7.1	1.7	12.8	14.5	2.0	2.4	122
577	E3	1	DH85	921.5	33.3	1.2	792.1	31.7	90.6	16.2	1.6	20.2	10.2	6.4	2.1	13.0	15.1	2.4	2.2	128
578	E3	1	DH86	787.1	40.3	1.4	571.2	32.0	104.8	17.3	1.6	21.4	11.1	6.1	1.8	14.5	16.3	2.7	2.5	128
579	E3	1	DH87	893.4	47.2	1.4	642.3	28.7	101.3	18.0	1.7	24.0	10.7	7.0	1.0	14.8	15.8	2.3	3.0	121
580	E3	1	DH89	804.8	40.5	1.4	591.8	33.5	99.8	17.2	1.7	22.6	10.3	7.1	2.2	14.8	17.0	2.4	2.4	127
581	E3	1	DH90	768.8	37.2	1.3	580.2	31.0	91.2	15.2	1.7	19.8	9.3	6.7	2.2	13.5	15.7	2.4	2.4	125
582	E3	1	DH91	714.4	42.8	1.4	498.9	31.7	109.0	17.0	1.5	20.5	11.1	7.1	1.9	14.6	16.5	2.4	2.6	125
583	E3	1	DH92	898.9	36.5	1.3	708.3	32.9	97.5	16.8	1.7	22.1	10.3	6.8	1.9	13.4	15.3	2.2	2.4	126
584	E3	1	DH93	888.8	50.2	1.7	523.8	31.1	87.8	16.5	1.8	23.2	9.3	7.8	1.3	15.6	16.9	2.2	2.9	126
585	E3	1	DH94	838.3	37.0	1.2	691.1	31.2	103.2	15.5	1.5	19.1	10.1	6.9	2.0	14.8	16.8	2.4	2.2	130
586	E3	1	DH95	1026.1	37.0	1.3	799.1	36.0	102.0	15.7	1.4	18.0	11.1	7.5	1.7	14.3	16.0	2.1	2.3	121
587	E3	1	DH96	759.0	35.8	1.3	564.3	.	105.1	16.0	1.6	19.6	10.3	6.4	2.4	12.5	14.9	2.3	2.4	128
588	E3	1	DH97	884.6	44.2	1.5	581.2	34.2	109.4	16.1	1.9	23.8	8.7	7.3	1.0	15.8	16.8	2.3	2.6	126
589	E3	1	DH98	712.6	48.5	1.8	404.2	38.0	91.5	16.4	1.6	20.6	10.3	7.8	0.2	15.1	15.3	2.0	3.2	120
590	E3	1	DH99	722.2	48.9	1.6	466.0	32.0	91.5	17.5	2.0	27.7	8.8	7.0	1.5	16.4	17.9	2.6	2.7	130
591	E3	1	DH100	877.3	47.9	1.4	620.9	30.5	80.5	14.6	1.7	19.7	8.6	6.9	1.5	15.3	16.8	2.4	2.8	125
592	E3	1	DH101	891.5	47.0	1.4	626.5	.	99.4	17.6	1.8	24.9	9.9	7.5	1.7	15.5	17.2	2.3	2.7	126
593	E3	1	DH102	669.8	53.4	1.4	462.2	29.2	99.7	20.3	1.8	28.7	11.7	8.1	1.9	16.9	18.8	2.3	2.8	131
594	E3	1	DH103	470.3	42.7	1.4	342.8	30.7	92.4	18.8	2.0	30.2	9.3	7.2	1.9	14.7	16.6	2.3	2.6	132
595	E3	1	DH104	714.7	42.7	1.3	551.0	29.6	104.0	19.8	1.7	26.2	11.9	6.9	1.7	14.6	16.3	2.4	2.6	132
596	E3	1	DH105	760.8	44.3	1.4	541.9	29.7	97.1	18.5	1.6	23.6	11.5	6.3	1.9	14.4	16.3	2.6	2.7	126
597	E3	1	DH106	873.8	48.0	1.5	592.4	31.1	99.6	16.2	1.8	22.7	9.2	7.6	2.0	16.3	18.3	2.4	2.6	128
598	E3	1	DH107	726.8	38.9	1.1	642.6	31.4	98.0	15.8	1.8	22.2	9.0	6.7	1.5	13.2	14.7	2.2	2.6	125
599	E3	1	DH108	488.1	40.1	1.3	367.2	30.5	106.8	17.4	1.6	22.7	10.6	6.4	2.4	14.7	17.1	2.7	2.3	125
600	E3	1	DH109	634.5	43.0	1.3	485.1	30.0	92.0	18.1	1.6	23.0	11.2	7.5	1.7	14.9	16.6	2.2	2.6	129
601	E3	1	DH110	545.4	41.5	1.4	391.8	32.1	109.2	16.0	1.5	19.3	10.5	7.9	2.1	16.0	18.1	2.3	2.3	127
602	E3	1	DH111	517.6	34.3	1.1	452.5	30.5	103.7	18.9	1.6	24.4	11.5	6.8	2.1	13.7	15.8	2.3	2.2	127
603	E3	1	DH112	608.4	41.0	1.3	458.8	30.2	90.2	16.0	1.6	20.4	9.9	7.2	2.5	15.2	17.7	2.5	2.3	128
604	E3	1	DH113	776.2	36.8	1.3	593.9	33.1	106.4	17.2	1.5	21.1	11.1	6.2	2.2	14.2	16.4	2.7	2.2	129
605	E3	1	DH114	622.4	41.2	1.3	492.0	31.7	78.4	17.1	1.7	23.7	9.9	7.3	0.9	14.4	15.3	2.1	2.7	128
606	E3	1	DH115	551.7	37.0	1.1	494.8	30.9	103.9	15.9	1.6	20.5	9.8	7.2	1.9	14.4	16.3	2.3	2.3	127
607	E3	1	DH116	780.0	30.9	1.1	740.0	35.2	103.3	12.9	1.6	16.0	8.4	6.5	3.0	12.4	15.4	2.4	2.0	123
608	E3	1	DH117	827.6	37.4	1.3	619.9	34.3	92.7	13.8	1.7	18.1	8.3	7.0	1.5	14.3	15.8	2.3	2.4	124
609	E3	1	DH119	715.5	44.8	1.5	475.1	32.5	104.0	20.8	2.0	33.0	10.3	7.5	1.8	15.7	17.5	2.3	2.5	128
610	E3	1	DH120	941.8	35.8	1.2	812.6	32.5	100.7	17.4	1.6	21.8	11.0	6.7	2.9	14.4	17.3	2.6	2.1	130
611	E3	1	DH121	737.3	39.8	1.3	547.4	30.0	92.1	16.6	1.7	22.2	9.8	6.7	2.7	13.8	16.5	2.4	2.4	131
612	E3	1	DH122	635.9	52.3	1.6	386.8	30.3	95.3	18.9	1.7	25.0	11.3	7.4	0.7	15.8	16.5	2.2	3.2	131
613	E3	1	DH123	571.2	49.3	1.5	379.6	29.2	103.0	17.5	1.2	16.0	15.2	7.8	1.2	14.9	16.1	2.1	3.1	128
614	E3	1	DH124	744.5	40.7	1.3	558.5	31.0	96.7	18.6	1.6	23.7	11.5	7.6	2.4	15.5	17.9	2.4	2.3	131
615	E3	1	DH125	789.9	38.8	1.4	577.0	33.2	89.8	15.7	1.8	22.0	8.9	6.5	1.5	13.9	15.4	2.4	2.5	128
616	E3	1	DH126	797.2	49.7	1.6	506.2	31.9	87.8	17.9	1.9	26.2	9.7	7.9	1.1	16.9	18.0	2.3	2.8	130
617	E3	1	DH128	567.3	40.2	1.1	510.1	29.4	103.3	21.3	1.7	28.9	12.5	6.8	2.0	15.2	17.2	2.5	2.3	131
618	E3	1	DH129	888.1	49.3	1.6	550.9	30.9	100.8	19.2	1.6	23.8	12.3	7.2	1.6	14.6	16.2	2.3	3.0	127
619	E3	1	DH130	698.6	38.7	1.2	565.7	32.4	96.0	16.2	1.7	21.6	9.6	7.0	2.0	14.3	16.3	2.3	2.4	128
620	E3	1	DH131	659.9	36.4	1.3	520.1	35.2	107.1	17.4	1.9	26.4	9.1	7.7	3.9	15.8	19.7	2.6	1.9	134

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
621	E3	2	DH1	854.9	45.4	1.4	590.4	30.8	99.1	14.1	1.5	16.2	9.7	6.5	0.6	14.9	15.4	2.4	3.1	124
622	E3	2	DH3	508.4	37.2	1.2	427.6	31.2	106.5	18.6	1.9	28.2	9.8	6.3	1.9	13.7	15.6	2.5	2.7	130
623	E3	2	DH4	763.1	41.2	1.3	607.5	31.8	90.5	16.4	1.7	22.4	9.5	6.6	1.9	14.9	16.8	2.5	2.8	129
624	E3	2	DH5	758.5	40.8	1.2	628.4	31.2	92.6	17.2	1.7	23.0	10.2	7.6	1.7	15.0	16.7	2.2	2.7	130
625	E3	2	DH6	818.4	49.7	1.6	500.2	32.1	99.1	16.4	1.6	20.7	10.3	7.5	0.8	15.6	16.4	2.2	3.2	122
626	E3	2	DH7	780.7	39.2	1.2	643.1	31.3	87.9	17.9	1.8	25.1	10.4	6.5	3.1	14.4	17.5	2.7	2.7	132
627	E3	2	DH8	731.5	47.9	1.4	535.9	31.7	101.8	17.8	1.5	21.6	11.8	7.2	1.8	14.7	16.4	2.3	3.3	127
628	E3	2	DH9	382.1	51.6	1.7	222.9	34.0	95.6	18.1	1.8	25.6	10.1	8.1	2.1	18.0	20.1	2.5	2.9	131
629	E3	2	DH11	548.8	48.1	1.8	310.2	36.1	113.3	19.4	1.5	23.6	12.6	8.6	1.6	15.5	17.1	2.0	3.1	127
630	E3	2	DH12	619.9	47.0	1.5	413.0	32.5	87.8	18.5	2.0	28.8	9.4	7.0	1.1	15.2	16.3	2.3	3.1	128
631	E3	2	DH13	668.9	53.1	1.5	437.2	28.4	97.2	18.3	1.7	25.0	10.6	7.4	1.9	17.1	19.0	2.6	3.0	129
632	E3	2	DH14	608.4	40.0	1.4	446.7	33.4	93.5	18.4	1.7	24.9	10.7	7.0	2.0	14.9	16.9	2.4	2.7	129
633	E3	2	DH15	853.9	38.6	1.3	668.1	33.1	96.3	14.1	1.6	18.2	8.9	7.3	1.0	14.6	15.6	2.2	2.6	122
634	E3	2	DH16	478.5	45.2	1.6	307.1	32.7	94.7	16.5	1.7	22.4	9.6	6.8	1.1	13.9	15.0	2.2	3.2	125
635	E3	2	DH17	707.3	48.0	1.7	410.5	35.2	100.3	16.9	1.6	22.0	10.3	8.1	1.1	15.2	16.3	2.0	3.1	125
636	E3	2	DH18	438.9	43.8	1.3	342.0	.	96.7	19.1	2.2	32.6	8.8	7.8	1.3	16.7	18.0	2.3	2.6	136
637	E3	2	DH19	788.0	41.7	1.5	527.8	34.1	106.5	15.9	1.7	21.6	9.2	6.5	0.9	13.1	14.0	2.2	3.2	127
638	E3	2	DH20	579.4	44.4	1.3	434.0	29.7	89.0	20.6	1.8	29.1	11.5	6.9	1.6	14.5	16.1	2.3	3.1	131
639	E3	2	DH21	777.6	40.3	1.3	577.7	32.7	104.1	19.5	1.7	25.8	11.7	7.2	1.9	13.9	15.8	2.2	2.9	129
640	E3	2	DH22	646.4	51.1	1.6	396.8	33.3	115.2	17.9	1.9	27.1	9.3	7.5	1.7	16.3	18.0	2.4	3.1	129
641	E3	2	DH23	855.6	41.0	1.3	654.6	31.7	104.1	17.6	1.7	23.4	10.5	6.3	1.8	12.7	14.5	2.3	3.2	124
642	E3	2	DH24	603.8	40.5	1.3	452.9	32.3	101.7	16.3	1.6	20.2	10.7	6.9	0.6	14.8	15.4	2.2	2.7	122
643	E3	2	DH25	744.2	44.0	1.3	573.8	32.6	97.3	18.1	1.6	23.4	11.1	7.1	1.8	15.3	17.1	2.4	2.9	126
644	E3	2	DH26	813.8	42.4	1.3	617.9	31.8	85.1	17.9	1.7	23.7	11.0	6.8	1.3	14.2	15.5	2.3	3.0	129
645	E3	2	DH27	754.6	42.3	1.3	581.8	30.2	105.3	20.5	1.7	27.3	12.1	6.6	1.9	14.0	15.9	2.4	3.0	130
646	E3	2	DH28	714.5	45.6	1.4	503.5	32.4	105.5	17.3	1.7	23.1	10.3	6.6	1.7	14.0	15.8	2.4	3.1	129
647	E3	2	DH29	892.5	53.0	1.8	496.4	32.1	82.3	15.7	1.7	20.8	9.4	8.1	1.3	16.2	17.5	2.2	3.2	128
648	E3	2	DH30	594.3	46.6	1.6	360.4	34.1	98.6	18.4	1.8	27.0	10.0	7.2	1.3	15.3	16.6	2.3	3.0	128
649	E3	2	DH31	809.0	42.2	1.3	623.2	30.6	97.4	17.2	1.7	23.2	10.1	7.5	1.9	15.2	17.1	2.3	2.8	131
650	E3	2	DH32	597.0	39.3	1.1	542.2	25.5	91.9	15.2	1.7	20.3	9.0	6.9	1.7	14.9	16.6	2.4	2.6	134
651	E3	2	DH33	510.1	51.6	1.4	354.0	29.6	99.3	18.9	1.9	29.0	9.8	7.2	2.4	16.5	18.9	2.6	3.1	136
652	E3	2	DH34	855.9	51.8	1.7	490.8	32.4	105.2	19.3	1.8	27.6	10.7	7.9	1.1	16.2	17.3	2.2	3.2	125
653	E3	2	DH35	610.7	37.6	1.3	476.7	33.4	101.2	17.5	1.9	25.8	9.4	7.2	1.9	14.1	16.0	2.2	2.7	128
654	E3	2	DH36	764.6	43.4	1.5	502.7	32.0	93.3	18.9	1.9	27.8	10.2	8.2	1.3	16.3	17.6	2.1	2.7	130
655	E3	2	DH37	484.1	50.4	1.5	320.6	31.7	98.6	18.4	1.6	23.1	11.6	7.5	1.7	15.8	17.5	2.3	3.2	128
656	E3	2	DH38	750.2	45.9	1.6	483.4	.	90.7	18.0	1.8	25.1	10.2	7.5	0.9	14.7	15.6	2.1	3.2	121
657	E3	2	DH39	765.8	40.3	1.3	592.3	31.3	104.0	15.7	1.7	21.0	9.4	6.0	1.8	13.8	15.6	2.6	2.9	128
658	E3	2	DH40	419.3	40.9	1.3	318.6	32.8	111.6	17.7	1.6	21.8	11.7	7.6	0.8	15.7	16.5	2.2	2.6	126
659	E3	2	DH41	861.3	41.2	1.3	671.3	31.8	99.6	17.4	1.7	22.8	10.5	6.9	1.5	14.5	16.0	2.3	2.8	130
660	E3	2	DH42	856.9	45.0	1.5	574.4	31.7	102.8	17.1	1.5	20.7	11.2	7.2	1.8	15.8	17.6	2.5	2.8	129
661	E3	2	DH43	673.8	43.4	1.4	471.9	32.1	98.8	17.4	1.6	22.6	10.5	7.0	2.2	14.4	16.6	2.4	3.0	129
662	E3	2	DH44	571.5	40.8	1.4	395.8	35.7	104.4	19.9	1.7	27.6	11.4	7.6	1.8	14.4	16.2	2.1	2.9	131
663	E3	2	DH45	578.9	36.9	1.4	410.9	35.5	96.9	15.2	1.7	20.6	8.8	7.1	2.0	14.4	16.4	2.3	2.6	127
664	E3	2	DH46	592.5	46.8	1.4	430.9	32.4	99.4	20.9	1.9	31.0	11.2	8.2	1.7	15.4	17.1	2.1	3.0	131
665	E3	2	DH47	649.0	45.0	1.4	478.3	33.7	90.4	17.4	1.6	22.7	10.7	7.4	1.6	15.1	16.7	2.3	2.9	130
666	E3	2	DH49	628.5	46.7	1.5	420.1	32.9	98.2	19.4	1.7	26.3	11.4	7.5	1.9	14.8	16.7	2.2	3.1	131
667	E3	2	DH50	641.7	41.5	1.6	411.9	37.8	108.0	15.7	1.6	19.5	10.0	6.8	1.5	13.8	15.3	2.2	3.0	125
668	E3	2	DH51	649.8	44.2	1.3	506.4	29.8	98.5	19.8	1.7	26.4	11.7	7.6	2.3	15.4	17.8	2.4	2.8	130
669	E3	2	DH52	847.6	45.9	1.4	621.9	31.8	88.4	14.6	1.4	16.7	10.3	7.0	1.3	14.4	15.7	2.2	3.2	128
670	E3	2	DH53	882.1	41.1	1.3	670.8	30.1	85.1	16.5	1.8	23.9	9.1	6.7	1.7	14.5	16.2	2.4	2.9	130
671	E3	2	DH54	720.2	47.1	1.7	425.9	35.9	100.4	16.0	1.9	23.6	8.6	7.6	1.1	14.5	15.6	2.0	3.2	124
672	E3	2	DH55	926.0	39.6	1.2	801.0	29.8	105.6	16.0	1.6	20.2	10.0	6.4	1.9	14.3	16.2	2.5	2.8	127
673	E3	2	DH56	984.3	35.4	1.2	847.8	35.1	101.4	13.9	1.5	16.8	9.1	6.1	1.6	13.0	14.6	2.4	2.7	125
674	E3	2	DH57	788.3	40.5	1.3	600.4	31.5	95.8	15.2	1.6	19.6	9.3	6.0	1.3	14.0	15.3	2.5	2.9	128
675	E3	2	DH58	880.2	38.0	1.3	694.7	33.2	101.2	16.0	1.5	19.0	10.6	6.3	2.3	12.8	15.1	2.4	3.0	126
676	E3	2	DH59	932.2	42.8	1.4	659.8	33.2	95.5	16.1	1.5	19.6	10.5	6.5	0.6	13.3	13.9	2.1	3.2	123
677	E3	2	DH60	809.4	49.9	1.6	518.2	.	102.0	17.4	1.7	23.0	10.6	7.6	1.5	14.6	16.1	2.1	3.4	127
678	E3	2	DH61	502.1	37.4	1.2	416.3	32.1	90.8	17.0	1.5	20.5	11.4	7.3	2.1	14.5	16.6	2.3	2.6	130
679	E3	2	DH62	746.0	39.8	1.2	597.8	32.6	93.5	19.4	1.7	25.5	11.8	6.4	1.6	12.9	14.5	2.3	3.1	127
680	E3	2	DH63	833.0	51.8	1.8	450.7	34.6	91.0	17.1	1.5	20.4	11.6	8.3	0.8	15.5	16.3	2.0	3.3	124
681	E3	2	DH64	923.7	42.7	1.5	603.7	38.6	109.5	16.7	1.7	22.3	9.9	7.5	1.6	14.9	16.5	2.2	2.9	126
682	E3	2	DH65	808.8	58.2	1.8	444.6	30.7	99.0	17.7	1.6	22.3	11.1	8.2	0.4	17.0	17.4	2.1	3.4	124

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
683	E3	2	DH66	510.4	42.2	1.4	355.2	35.4	102.0	20.4	2.2	35.1	9.4	7.9	2.2	15.7	17.9	2.3	2.7	133
684	E3	2	DH67	818.6	40.5	1.4	568.5	33.4	99.0	17.9	1.7	23.4	10.8	6.8	1.8	14.9	16.7	2.5	2.7	126
685	E3	2	DH68	570.4	38.9	1.2	460.4	28.3	93.1	18.7	1.7	25.0	11.1	7.0	2.0	14.0	16.0	2.3	2.8	127
686	E3	2	DH69	820.1	41.5	1.4	578.4	32.7	93.5	15.9	1.6	20.0	10.0	6.3	0.9	13.4	14.3	2.3	3.1	125
687	E3	2	DH70	687.0	43.1	1.1	607.9	32.3	99.8	17.2	1.7	23.6	9.9	7.4	2.0	15.8	17.8	2.4	2.7	131
688	E3	2	DH71	481.2	47.1	1.5	331.0	31.6	93.3	20.2	1.9	29.9	10.9	7.6	1.0	15.3	16.3	2.2	3.1	131
689	E3	2	DH72	824.6	43.9	1.4	569.8	32.4	96.9	15.7	1.7	21.7	9.0	7.5	1.7	16.0	17.7	2.4	2.7	130
690	E3	2	DH73	692.3	40.4	1.3	529.7	31.4	94.9	16.8	1.8	23.9	9.4	6.6	1.9	14.5	16.4	2.5	2.8	130
691	E3	2	DH75	877.8	37.0	1.3	685.7	35.5	96.7	15.5	1.9	23.5	8.1	6.9	1.6	13.7	15.3	2.2	2.7	121
692	E3	2	DH76	983.3	34.0	1.1	873.3	32.6	92.7	17.3	1.7	22.5	10.5	6.4	2.0	12.8	14.8	2.3	2.6	129
693	E3	2	DH77	550.0	40.8	1.3	426.3	32.6	102.9	24.4	1.6	30.0	15.8	7.2	1.7	15.0	16.7	2.3	2.7	127
694	E3	2	DH78	895.1	52.2	1.8	503.1	35.5	102.6	16.7	1.6	21.3	10.4	7.6	0.8	16.2	17.0	2.2	3.2	124
695	E3	2	DH79	974.9	46.5	1.6	620.5	.	104.5	16.7	1.5	19.8	11.0	7.0	1.8	14.3	16.1	2.3	3.2	126
696	E3	2	DH80	748.9	51.7	1.6	458.1	31.7	100.4	19.1	1.6	24.2	12.0	7.0	1.0	16.1	17.1	2.4	3.2	130
697	E3	2	DH81	593.1	41.4	1.3	454.5	32.6	90.2	17.8	1.8	25.5	9.9	6.3	0.7	14.5	15.2	2.4	2.9	128
698	E3	2	DH82	705.3	41.9	1.4	491.5	33.5	101.1	14.8	1.6	18.6	9.4	7.4	1.1	14.1	15.2	2.1	3.0	125
699	E3	2	DH83	847.2	46.9	1.6	516.3	34.9	95.0	17.9	1.6	22.3	11.4	7.4	1.7	14.6	16.3	2.2	3.2	127
700	E3	2	DH84	1031.6	37.0	1.4	752.4	37.6	97.4	13.8	1.4	15.1	10.1	7.2	1.5	13.0	14.5	2.0	2.8	122
701	E3	2	DH85	841.7	35.1	1.2	695.6	32.6	91.8	16.3	1.5	19.7	10.7	6.3	1.8	12.8	14.6	2.3	2.7	129
702	E3	2	DH86	795.7	42.4	1.4	556.0	33.3	100.4	18.0	1.5	21.6	11.9	6.2	1.4	14.0	15.4	2.5	3.0	125
703	E3	2	DH87	993.9	52.8	1.5	648.3	29.4	97.6	16.8	1.5	20.1	11.1	7.4	0.1	15.9	16.0	2.2	3.3	122
704	E3	2	DH89	751.7	35.4	1.2	615.7	33.1	102.6	17.1	1.7	22.8	10.2	6.5	2.3	14.0	16.3	2.5	2.5	127
705	E3	2	DH90	531.0	42.5	1.4	375.8	32.1	90.7	15.0	1.6	19.2	9.3	7.2	1.9	14.5	16.4	2.3	2.9	125
706	E3	2	DH91	738.6	42.0	1.4	523.4	32.9	101.5	16.7	1.5	19.8	11.2	6.4	1.8	14.0	15.8	2.5	3.0	128
707	E3	2	DH92	822.9	41.2	1.4	599.8	32.2	94.3	17.7	1.7	23.4	10.6	7.1	1.2	14.0	15.2	2.2	2.9	127
708	E3	2	DH93	966.8	58.1	1.9	520.1	31.2	91.5	15.2	1.6	19.1	9.6	7.5	0.9	15.9	16.8	2.2	3.6	124
709	E3	2	DH94	913.9	40.7	1.3	696.6	32.0	103.6	14.3	1.6	18.2	8.9	7.1	1.5	14.9	16.3	2.3	2.7	129
710	E3	2	DH95	984.6	36.4	1.2	791.5	36.6	96.7	15.0	1.6	19.1	9.8	7.4	1.7	13.9	15.6	2.1	2.6	122
711	E3	2	DH96	905.2	39.2	1.4	629.0	37.9	104.4	17.5	1.5	21.3	11.3	6.5	1.7	12.7	14.4	2.2	3.1	126
712	E3	2	DH97	714.0	39.5	1.3	534.1	35.4	105.4	15.7	1.8	22.5	8.7	6.9	1.5	14.9	16.4	2.4	2.6	126
713	E3	2	DH98	878.0	48.7	1.8	487.5	37.9	88.6	17.8	1.8	25.2	10.0	8.2	0.3	15.0	15.3	1.9	3.2	119
714	E3	2	DH99	657.1	49.9	1.5	435.1	31.1	91.5	17.9	1.9	27.4	9.3	7.2	0.9	16.2	17.1	2.4	3.1	131
715	E3	2	DH100	681.8	56.0	1.6	430.9	29.1	86.2	15.4	1.6	19.4	9.8	7.1	1.3	16.0	17.3	2.5	3.5	126
716	E3	2	DH101	685.4	53.2	1.6	434.6	30.7	96.9	17.5	1.7	23.6	10.2	7.7	0.5	16.0	16.5	2.1	3.3	124
717	E3	2	DH102	772.5	50.6	1.4	538.7	28.4	104.5	17.8	1.7	23.9	10.5	8.2	1.9	17.8	19.7	2.4	2.8	130
718	E3	2	DH103	552.8	37.5	1.2	453.8	30.0	88.0	17.7	1.9	26.0	9.5	6.6	2.3	13.8	16.1	2.4	2.7	132
719	E3	2	DH104	608.5	45.8	1.4	436.2	29.8	100.8	19.4	1.5	22.8	13.1	7.0	1.2	15.9	17.1	2.4	2.9	131
720	E3	2	DH105	964.3	42.5	1.3	721.2	30.4	102.7	17.4	1.6	22.6	10.7	6.2	2.2	14.3	16.5	2.7	3.0	127
721	E3	2	DH106	696.4	52.2	1.6	422.3	31.0	96.1	17.4	1.8	25.5	9.4	7.7	1.6	16.0	17.6	2.3	3.3	128
722	E3	2	DH107	848.7	37.8	1.2	702.0	30.6	103.3	15.6	1.5	18.9	10.2	6.7	1.7	13.4	15.1	2.3	2.8	125
723	E3	2	DH108	659.8	38.4	1.2	536.4	30.5	105.6	14.9	1.6	18.5	9.5	6.4	1.9	14.0	15.9	2.5	2.7	124
724	E3	2	DH109	724.0	40.3	1.2	588.6	29.1	95.5	17.1	1.6	21.6	10.7	7.4	1.9	14.7	16.6	2.3	2.7	128
725	E3	2	DH110	749.9	45.9	1.5	497.6	.	101.7	16.4	1.6	21.1	10.1	7.9	1.3	14.9	16.2	2.0	3.1	127
726	E3	2	DH111	696.0	50.1	1.6	436.9	30.1	104.5	19.2	1.7	25.6	11.5	8.1	1.2	15.9	17.1	2.1	3.1	127
727	E3	2	DH112	479.4	43.2	1.4	353.8	31.9	98.1	16.0	1.6	20.7	9.9	7.2	2.1	15.1	17.1	2.3	2.9	127
728	E3	2	DH113	856.8	46.8	1.7	499.0	36.5	113.5	16.2	1.5	19.1	11.2	7.1	1.7	14.7	16.4	2.3	3.2	127
729	E3	2	DH114	797.9	40.6	1.3	634.3	31.9	87.3	16.5	1.6	21.4	10.2	7.3	1.4	14.6	16.0	2.2	2.8	126
730	E3	2	DH115	544.1	37.0	1.1	508.0	32.3	101.0	16.5	1.6	20.5	10.6	7.0	2.0	13.7	15.7	2.2	2.7	127
731	E3	2	DH116	836.0	34.3	1.2	702.5	35.8	101.6	15.5	1.6	19.3	9.9	6.6	2.4	12.5	14.9	2.3	2.7	126
732	E3	2	DH117	932.5	34.0	1.2	775.8	35.4	91.8	14.8	1.7	19.5	9.0	7.1	1.2	14.0	15.2	2.2	2.4	124
733	E3	2	DH119	698.4	46.6	1.6	429.5	31.7	106.3	19.4	1.8	28.5	10.6	7.8	1.8	16.3	18.1	2.3	2.9	128
734	E3	2	DH120	863.9	38.5	1.2	691.7	33.3	94.7	17.9	1.6	22.9	11.1	6.6	2.4	14.2	16.6	2.5	2.7	129
735	E3	2	DH121	608.3	42.2	1.4	444.6	31.8	97.9	15.1	1.7	20.9	8.7	7.0	2.7	14.7	17.4	2.5	2.9	131
736	E3	2	DH122	620.7	46.0	1.3	477.5	31.5	97.1	19.4	1.5	22.8	13.5	7.2	1.3	15.8	17.1	2.4	2.9	131
737	E3	2	DH123	623.2	40.3	1.2	510.4	28.4	99.8	19.2	1.5	22.9	12.8	7.5	1.6	14.4	16.0	2.1	2.8	127
738	E3	2	DH124	637.1	40.1	1.4	466.8	31.4	90.3	19.5	1.7	26.0	11.7	7.7	1.9	14.9	16.8	2.2	2.7	131
739	E3	2	DH125	857.7	43.2	1.4	602.3	33.8	93.7	17.1	1.8	24.4	9.6	6.7	0.9	14.0	14.9	2.2	3.1	127
740	E3	2	DH126	794.6	43.7	1.4	583.8	31.1	85.8	18.1	1.7	24.1	11.2	7.5	1.2	16.3	17.5	2.3	2.7	130
741	E3	2	DH128	429.9	36.6	1.0	445.1	29.8	98.4	21.2	1.6	27.4	13.0	6.7	2.4	14.2	16.6	2.5	2.6	131
742	E3	2	DH129	854.7	46.5	1.5	568.3	32.8	104.2	16.4	1.5	19.9	10.8	7.2	1.8	14.7	16.5	2.3	3.2	126
743	E3	2	DH130	929.4	44.6	1.4	660.1	31.2	94.3	17.5	1.6	22.4	10.9	8.0	1.3	16.3	17.6	2.2	2.7	126
744	E3	2	DH131	402.2	41.3	1.4	283.0	34.3	99.1	18.9	2.1	31.0	9.2	7.8	3.0	15.8	18.8	2.4	2.6	132

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
745	E4	1	DH1	671.4	37.0	1.0	671.4	28.8	72.4	12.5	1.3	12.4	9.9	6.0	0.5	12.7	13.2	2.2	2.9	139
746	E4	1	DH3	523.2	36.3	1.0	519.0	28.5	76.0	16.8	1.5	19.6	11.5	6.0	1.2	12.7	13.9	2.3	2.8	142
747	E4	1	DH4	601.8	27.9	0.8	753.2	30.0	71.8	13.9	1.6	17.6	8.6	6.4	2.3	13.1	15.4	2.5	2.1	142
748	E4	1	DH5	633.9	38.6	1.0	608.9	29.0	75.1	15.1	1.5	17.9	10.1	7.5	1.4	13.7	15.1	2.0	2.8	142
749	E4	1	DH6	665.9	33.9	1.0	667.9	31.1	79.3	13.8	1.2	13.1	11.5	6.6	1.6	13.5	15.1	2.3	2.5	136
750	E4	1	DH7	554.1	34.0	0.9	592.6	30.0	67.4	15.4	1.5	18.3	10.3	6.1	2.2	12.7	14.9	2.4	2.7	142
751	E4	1	DH8	671.1	37.7	1.0	669.1	30.0	84.0	15.7	1.5	18.7	10.4	6.6	1.6	12.9	14.5	2.2	2.9	139
752	E4	1	DH9	572.6	38.9	1.1	529.2	31.0	75.7	15.2	1.5	17.8	10.3	6.6	2.0	14.1	16.1	2.4	2.7	142
753	E4	1	DH11	744.5	46.4	1.5	485.0	32.3	95.9	14.9	1.3	15.4	11.4	8.7	1.3	15.9	17.2	2.0	2.9	139
754	E4	1	DH12	538.7	37.9	1.0	527.1	28.4	62.0	11.5	1.7	15.6	6.7	5.7	0.6	14.1	14.7	2.6	2.7	141
755	E4	1	DH13	635.0	44.3	1.2	530.5	27.0	81.4	15.9	1.4	17.5	11.4	6.9	1.3	14.8	16.1	2.3	3.0	140
756	E4	1	DH14	677.1	42.3	1.4	491.8	31.2	81.3	15.1	1.5	18.4	9.8	7.3	0.9	15.4	16.3	2.2	2.8	139
757	E4	1	DH15	696.0	39.2	1.1	653.5	28.4	76.3	13.2	1.2	13.1	10.6	6.9	0.8	14.6	15.4	2.2	2.7	137
758	E4	1	DH16	489.9	35.4	0.9	544.3	28.9	70.1	16.1	1.3	17.1	12.0	6.2	1.5	13.2	14.7	2.4	2.7	139
759	E4	1	DH17	705.5	38.1	1.2	594.8	33.4	80.6	15.3	1.3	15.3	12.3	6.9	2.0	13.4	15.4	2.2	2.8	136
760	E4	1	DH18	621.3	45.5	1.3	475.8	29.1	78.5	17.4	1.9	25.6	9.4	7.7	1.1	16.2	17.3	2.2	2.8	142
761	E4	1	DH19	617.6	35.5	1.0	597.3	31.5	72.1	13.9	1.5	17.0	9.0	6.3	1.2	12.9	14.1	2.2	2.7	138
762	E4	1	DH20	483.6	40.9	1.1	448.2	26.2	73.9	18.1	1.6	22.2	11.7	6.4	1.3	14.1	15.4	2.4	2.9	143
763	E4	1	DH21	746.5	36.9	1.1	668.9	29.2	85.2	15.7	1.4	18.0	10.9	7.0	2.2	13.9	16.1	2.3	2.6	141
764	E4	1	DH22	696.7	40.9	1.2	581.5	29.6	87.7	14.8	1.5	17.5	9.9	6.8	0.9	14.5	15.4	2.3	2.8	141
765	E4	1	DH23	648.3	38.5	1.0	667.7	25.9	78.8	14.9	1.1	13.0	13.6	6.1	1.6	13.3	14.9	2.5	2.9	138
766	E4	1	DH24	615.4	34.6	0.9	672.6	27.1	74.4	16.1	1.6	20.9	9.8	6.1	1.2	12.8	14.0	2.3	2.7	138
767	E4	1	DH25	639.5	39.9	1.1	599.3	30.1	71.9	15.6	1.4	17.9	10.9	6.9	1.5	14.1	15.6	2.3	2.8	139
768	E4	1	DH26	707.5	40.8	1.1	643.8	27.9	73.2	13.6	1.4	14.6	10.0	6.6	0.2	14.3	14.5	2.2	2.9	139
769	E4	1	DH27	571.6	33.4	1.0	591.7	28.2	74.5	17.4	1.4	19.2	12.4	6.0	2.1	12.8	14.9	2.5	2.6	142
770	E4	1	DH28	621.1	38.6	1.1	558.5	28.9	80.5	15.5	1.4	17.0	11.1	6.2	1.4	13.5	14.9	2.4	2.8	141
771	E4	1	DH29	683.6	35.8	1.0	673.5	29.2	69.1	12.6	1.4	14.3	8.8	6.6	1.4	13.1	14.5	2.2	2.7	141
772	E4	1	DH30	568.5	32.5	1.0	544.5	31.6	73.8	17.1	1.5	19.9	11.7	6.8	1.6	13.9	15.5	2.3	2.3	142
773	E4	1	DH31	562.7	40.5	1.1	524.9	26.2	75.8	14.4	1.4	15.5	10.6	7.0	1.3	14.4	15.7	2.2	2.8	140
774	E4	1	DH32	570.6	34.2	0.9	657.3	24.5	75.5	15.3	1.4	17.7	10.6	6.1	1.9	13.1	15.0	2.5	2.6	143
775	E4	1	DH33	506.9	43.1	0.9	591.5	26.3	84.1	15.6	1.7	21.0	9.2	7.0	2.1	15.9	18.0	2.6	2.7	144
776	E4	1	DH34	765.8	48.6	1.4	544.7	28.1	83.4	18.3	1.5	22.3	11.9	7.8	1.0	16.0	17.0	2.2	3.0	140
777	E4	1	DH35	595.9	30.2	0.9	678.6	29.3	71.0	13.9	1.5	16.1	9.6	6.0	1.6	11.7	13.3	2.2	2.6	139
778	E4	1	DH36	741.5	37.5	1.1	679.7	28.6	79.2	16.0	1.6	20.2	10.1	7.3	1.3	14.4	15.7	2.1	2.6	141
779	E4	1	DH37	590.1	39.9	1.0	597.8	25.8	79.0	17.7	1.4	19.8	12.5	6.6	1.5	13.5	15.0	2.3	3.0	142
780	E4	1	DH38	553.7	41.5	1.2	471.2	29.9	76.0	14.1	1.4	15.1	10.4	7.1	0.6	16.0	16.6	2.4	2.6	138
781	E4	1	DH39	658.6	39.8	1.1	605.3	27.6	72.7	16.4	1.4	18.1	11.9	5.6	0.8	13.3	14.1	2.5	3.0	139
782	E4	1	DH40	542.7	33.6	1.0	546.5	28.3	87.5	12.9	1.3	13.5	10.0	6.8	1.1	13.6	14.7	2.2	2.5	140
783	E4	1	DH41	660.5	37.4	1.0	683.0	28.2	85.3	14.3	1.4	15.5	10.4	6.6	1.2	14.2	15.4	2.3	2.6	140
784	E4	1	DH42	637.9	43.5	1.3	492.9	29.5	80.3	15.6	1.3	16.4	11.7	6.9	0.3	15.3	15.6	2.3	2.8	139
785	E4	1	DH43	769.0	41.6	1.2	647.3	30.6	71.8	14.6	1.3	15.2	11.1	6.5	1.0	13.2	14.2	2.2	3.1	139
786	E4	1	DH44	724.6	32.6	1.1	685.5	33.8	89.4	17.5	1.5	21.5	11.3	7.0	2.1	12.8	14.9	2.2	2.5	142
787	E4	1	DH45	603.6	26.8	0.9	653.3	34.2	78.8	13.1	1.4	14.4	9.5	6.6	2.1	13.0	15.1	2.3	2.0	139
788	E4	1	DH46	579.0	40.7	1.1	538.1	29.0	85.9	14.9	1.5	17.4	10.1	7.9	1.4	15.1	16.5	2.1	2.7	141
789	E4	1	DH47	726.0	41.1	1.1	639.1	29.4	82.8	12.9	1.4	14.3	9.2	6.8	1.2	13.4	14.6	2.2	3.1	141
790	E4	1	DH49	634.1	37.3	1.0	624.8	29.5	83.2	15.7	1.5	19.0	10.3	7.0	2.2	14.1	16.3	2.4	2.6	142
791	E4	1	DH50	596.1	35.6	1.0	589.7	28.7	81.8	12.9	1.3	13.7	9.7	6.5	1.0	13.8	14.8	2.3	2.6	141
792	E4	1	DH51	602.5	42.6	1.0	601.3	26.3	77.4	15.1	1.4	16.9	10.7	6.7	1.7	13.5	15.2	2.3	3.1	141
793	E4	1	DH52	725.7	39.9	0.9	774.5	23.8	72.4	14.8	1.3	15.9	11.1	6.6	0.5	14.8	15.3	2.3	2.7	138
794	E4	1	DH53	647.2	37.8	1.0	618.8	27.9	70.4	13.7	1.4	15.1	9.9	6.8	0.8	14.5	15.3	2.3	2.6	139
795	E4	1	DH54	663.5	45.6	1.5	448.6	31.6	76.6	15.6	1.6	19.5	9.9	7.8	0.6	14.8	15.4	2.0	3.1	139
796	E4	1	DH55	695.3	40.0	1.1	624.7	27.9	81.4	13.4	1.3	14.2	10.1	6.3	1.1	13.6	14.7	2.3	2.9	138
797	E4	1	DH56	638.6	39.5	1.2	544.9	30.4	76.6	13.3	1.3	14.0	9.9	6.3	1.0	13.6	14.6	2.3	2.9	139
798	E4	1	DH57	577.7	36.9	1.0	565.2	27.7	66.4	14.0	1.3	14.1	11.1	5.9	0.5	13.8	14.3	2.4	2.7	140
799	E4	1	DH58	723.0	39.0	1.1	679.5	27.9	78.1	12.8	1.3	13.0	9.9	6.4	1.3	12.6	13.9	2.2	3.1	138
800	E4	1	DH59	720.6	36.5	1.0	743.7	28.0	73.4	14.6	1.3	15.5	11.0	5.8	1.0	13.4	14.4	2.5	2.7	139
801	E4	1	DH60	681.5	39.6	1.1	595.2	30.6	75.8	14.3	1.4	15.8	10.3	6.7	1.5	12.8	14.3	2.1	3.1	139
802	E4	1	DH61	640.7	32.0	0.9	701.0	27.8	74.9	13.1	1.5	15.1	8.9	6.8	1.7	13.2	14.9	2.2	2.4	141
803	E4	1	DH62	666.2	42.1	1.2	577.3	29.0	74.2	14.9	1.4	15.9	11.1	6.1	0.4	12.9	13.3	2.2	3.3	138
804	E4	1	DH63	638.5	49.9	1.5	436.1	29.5	81.0	15.8	1.6	20.2	9.7	8.2	1.3	15.5	16.8	2.1	3.2	139
805	E4	1	DH64	739.1	35.9	1.1	655.8	32.4	84.3	15.8	1.4	18.1	10.9	6.9	1.5	13.8	15.3	2.2	2.6	139
806	E4	1	DH65	529.2	44.6	1.1	475.9	27.6	74.9	17.3	1.4	18.9	12.6	7.4	1.1	15.4	16.5	2.2	2.9	139

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
807	E4	1	DH66	439.7	34.0	1.1	399.3	31.3	74.1	17.4	1.7	22.9	10.4	7.0	2.0	14.0	16.0	2.3	2.4	142
808	E4	1	DH67	588.6	35.7	1.0	586.3	31.4	71.5	14.3	1.4	16.0	10.4	6.1	0.9	13.5	14.4	2.3	2.6	138
809	E4	1	DH68	438.6	38.0	1.0	455.9	25.4	75.9	16.0	1.6	20.5	10.0	6.7	0.8	14.1	14.9	2.2	2.6	139
810	E4	1	DH69	642.1	42.4	1.0	652.6	28.6	69.9	15.0	1.5	17.8	10.0	6.0	0.8	13.6	14.4	2.4	3.1	140
811	E4	1	DH70	512.3	35.3	1.0	527.1	29.5	77.8	16.0	1.4	17.4	11.6	6.7	1.9	13.7	15.6	2.3	2.6	142
812	E4	1	DH71	683.9	39.6	1.1	605.2	30.2	76.9	14.0	1.5	16.3	9.5	7.5	0.9	14.9	15.8	2.1	2.6	141
813	E4	1	DH72	575.8	37.7	0.9	632.8	26.2	76.8	14.4	1.5	17.2	9.6	6.8	1.5	14.4	15.9	2.4	2.6	142
814	E4	1	DH73	479.5	34.2	0.9	524.1	26.6	72.7	16.4	1.4	18.7	11.5	6.4	1.6	13.7	15.3	2.4	2.5	142
815	E4	1	DH75	634.8	44.7	1.3	474.5	33.3	82.9	14.6	1.3	15.2	11.4	7.7	1.1	15.6	16.7	2.2	2.9	137
816	E4	1	DH76	659.1	34.1	1.0	690.2	29.3	72.1	14.3	1.4	15.9	10.2	6.2	1.2	13.0	14.2	2.3	2.6	139
817	E4	1	DH77	573.3	34.4	1.1	545.5	30.2	70.3	20.1	1.3	21.4	14.9	7.3	1.7	13.8	15.5	2.1	2.5	140
818	E4	1	DH78	659.7	40.0	1.2	566.8	30.4	75.5	17.9	1.3	19.0	13.3	7.1	1.7	14.3	16.0	2.3	2.8	137
819	E4	1	DH79	761.2	49.7	1.5	523.5	31.0	84.4	16.0	1.3	17.2	12.0	7.3	1.0	14.5	15.5	2.1	3.4	139
820	E4	1	DH80	733.9	52.6	1.4	511.8	28.2	82.4	15.6	1.4	17.2	11.2	7.0	0.3	15.4	15.7	2.2	3.4	139
821	E4	1	DH81	520.4	35.8	1.0	508.7	30.3	66.0	15.2	1.7	20.4	9.1	6.6	1.1	14.1	15.2	2.3	2.5	140
822	E4	1	DH82	659.4	34.0	0.9	740.8	26.6	77.1	12.9	1.4	14.2	9.3	6.4	1.7	12.5	14.2	2.2	2.7	139
823	E4	1	DH83	619.2	35.1	1.2	532.9	33.4	83.8	14.6	1.3	15.5	11.0	6.1	1.9	12.4	14.3	2.3	2.8	141
824	E4	1	DH84	747.9	36.0	1.1	661.3	30.7	81.0	11.6	1.2	11.3	9.5	6.7	1.4	13.2	14.6	2.2	2.7	136
825	E4	1	DH85	665.8	35.7	1.0	683.6	28.4	72.4	13.8	1.4	15.2	9.9	6.6	1.1	13.6	14.7	2.2	2.6	139
826	E4	1	DH86	635.8	39.8	1.1	572.2	29.2	79.4	13.2	1.3	13.2	10.4	6.1	0.8	13.8	14.6	2.4	2.9	139
827	E4	1	DH87	742.9	44.4	1.1	651.1	26.3	81.4	15.7	1.4	17.6	11.3	6.6	0.6	14.7	15.3	2.3	3.0	137
828	E4	1	DH89	587.0	37.6	1.1	526.0	30.8	77.3	13.4	1.3	14.2	10.1	6.5	1.4	14.7	16.1	2.5	2.6	139
829	E4	1	DH90	545.1	35.3	1.0	534.4	30.0	74.5	14.8	1.4	15.8	11.1	6.7	2.3	13.8	16.1	2.4	2.5	137
830	E4	1	DH91	559.8	40.4	1.1	497.6	28.8	82.1	15.2	1.3	15.6	11.9	6.3	1.4	13.9	15.3	2.4	2.9	139
831	E4	1	DH92	663.3	36.4	0.9	711.7	27.9	76.3	13.4	1.3	14.2	10.1	6.3	1.1	13.1	14.2	2.3	2.8	140
832	E4	1	DH93	635.5	50.9	1.3	486.6	27.3	72.6	16.5	1.4	18.6	11.5	7.5	0.6	16.1	16.7	2.2	3.2	139
833	E4	1	DH94	748.6	35.1	1.0	736.1	29.8	84.4	12.3	1.3	13.2	9.1	6.6	1.3	14.0	15.3	2.3	2.5	138
834	E4	1	DH95	674.1	35.4	1.1	630.0	32.3	73.5	15.6	1.5	18.8	10.4	7.2	1.6	14.0	15.6	2.2	2.5	138
835	E4	1	DH96	605.7	32.7	1.1	568.2	33.0	72.9	14.8	1.3	15.4	11.4	6.3	1.1	11.7	12.8	2.0	2.8	138
836	E4	1	DH97	672.5	36.9	1.2	580.8	31.6	79.0	14.7	1.6	18.7	9.2	6.3	1.1	13.4	14.5	2.3	2.7	139
837	E4	1	DH98	726.1	42.4	1.3	578.1	32.0	80.6	14.2	1.4	15.4	10.4	7.3	0.9	14.4	15.3	2.1	2.9	136
838	E4	1	DH99	671.3	39.2	1.1	601.0	29.5	77.2	16.2	1.5	19.2	10.9	6.6	0.6	13.8	14.4	2.2	2.8	141
839	E4	1	DH100	685.6	48.0	1.2	594.6	26.8	71.5	15.3	1.5	18.1	10.2	6.8	0.6	15.1	15.7	2.3	3.2	139
840	E4	1	DH101	696.2	44.8	1.1	634.7	27.7	79.2	13.7	1.4	15.3	9.7	7.2	0.5	14.8	15.3	2.1	3.0	138
841	E4	1	DH102	562.4	44.5	1.0	576.9	25.2	79.6	16.8	1.5	19.5	11.5	7.4	1.0	14.7	15.7	2.1	3.0	142
842	E4	1	DH103	535.9	33.4	0.9	623.9	27.8	77.8	15.8	1.7	21.1	9.3	6.9	2.2	13.7	15.9	2.3	2.4	142
843	E4	1	DH104	576.8	39.6	1.0	575.1	25.2	79.9	18.1	1.4	19.9	13.1	6.1	1.3	13.2	14.5	2.4	3.0	142
844	E4	1	DH105	687.7	39.6	1.0	665.7	28.2	77.2	16.0	1.4	17.3	11.7	5.8	1.4	13.3	14.7	2.6	3.0	140
845	E4	1	DH106	655.2	42.8	1.1	582.9	28.7	76.6	14.8	1.5	18.1	9.7	7.1	1.3	14.8	16.1	2.3	2.9	139
846	E4	1	DH107	612.6	36.0	1.0	609.6	28.2	75.7	13.0	1.3	13.1	10.2	6.5	0.8	12.8	13.6	2.1	2.8	139
847	E4	1	DH108	585.9	36.3	1.0	602.8	27.4	76.4	15.6	1.3	15.5	12.3	5.9	1.1	12.6	13.7	2.3	2.9	139
848	E4	1	DH109	.	38.0	1.1	.	26.8	72.1	15.5	1.4	17.6	10.7	7.0	1.2	14.1	15.3	2.2	2.7	139
849	E4	1	DH110	677.7	41.1	1.2	570.4	28.6	78.5	13.7	1.2	13.1	11.3	7.6	0.8	14.4	15.2	2.0	2.9	137
850	E4	1	DH111	583.4	43.8	1.1	529.4	27.0	79.0	16.1	1.4	17.6	11.7	7.2	1.1	14.1	15.2	2.1	3.1	139
851	E4	1	DH112	589.1	45.0	1.3	460.9	30.7	75.9	15.3	1.3	16.1	11.7	7.0	0.9	14.7	15.6	2.2	3.1	138
852	E4	1	DH113	692.1	33.2	0.9	752.3	32.8	80.2	13.5	1.4	15.1	9.6	5.9	1.6	12.9	14.5	2.5	2.5	139
853	E4	1	DH114	509.3	34.6	0.9	576.8	27.2	62.7	13.8	1.5	16.6	9.1	6.5	0.7	13.2	13.9	2.1	2.6	140
854	E4	1	DH115	576.7	36.8	1.1	537.4	29.0	74.1	13.1	1.3	13.0	10.5	6.7	1.4	13.6	15.0	2.2	2.6	139
855	E4	1	DH116	515.0	31.2	0.9	554.3	30.8	72.7	13.6	1.3	14.1	10.4	6.1	1.7	12.1	13.8	2.3	2.6	140
856	E4	1	DH117	495.7	33.0	1.0	505.8	30.3	64.8	13.1	1.4	14.3	9.6	6.5	0.9	12.8	13.7	2.1	2.6	138
857	E4	1	DH119	517.3	39.9	1.2	445.6	28.9	81.3	16.7	1.5	20.4	10.8	7.2	1.8	15.1	16.9	2.3	2.6	142
858	E4	1	DH120	581.5	35.1	1.0	589.2	30.4	70.1	14.9	1.3	15.9	11.0	6.0	1.1	12.8	13.9	2.3	2.7	141
859	E4	1	DH121	738.8	36.2	1.1	697.7	29.4	77.9	15.2	1.5	17.6	10.5	6.8	1.8	13.6	15.4	2.3	2.7	141
860	E4	1	DH122	672.2	39.3	1.0	674.4	26.6	84.7	15.2	1.4	16.6	11.0	6.4	1.7	14.1	15.8	2.5	2.8	142
861	E4	1	DH123	610.7	44.2	1.1	544.8	26.3	81.9	15.5	1.2	14.2	13.5	7.2	0.9	14.4	15.3	2.1	3.1	142
862	E4	1	DH124	677.6	37.1	1.0	646.6	28.0	72.4	16.3	1.4	18.0	11.8	7.6	1.2	14.2	15.4	2.0	2.6	141
863	E4	1	DH125	677.6	39.7	1.2	576.7	30.1	70.2	13.6	1.5	16.2	9.1	6.7	1.1	13.5	14.6	2.2	2.9	140
864	E4	1	DH126	637.4	41.3	1.1	601.8	27.4	72.4	15.2	1.6	18.6	9.8	7.4	1.1	15.4	16.5	2.2	2.7	142
865	E4	1	DH128	594.2	40.7	1.0	585.4	27.0	81.8	17.7	1.3	18.6	13.4	6.2	1.5	13.8	15.3	2.5	2.9	140
866	E4	1	DH129	593.2	40.9	1.2	510.5	29.3	79.5	13.9	1.4	15.1	10.3	6.6	1.5	13.3	14.8	2.3	3.1	140
867	E4	1	DH130	691.5	37.5	1.0	670.7	28.3	76.3	14.2	1.6	17.7	9.1	6.8	1.4	13.0	14.4	2.1	2.9	139
868	E4	1	DH131	574.1	36.0	1.1	515.3	32.8	80.1	17.1	1.7	22.5	10.3	7.3	2.5	14.3	16.8	2.3	2.5	142

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
869	E4	2	DH1	591.6	44.5	1.2	486.9	29.0	72.6	13.4	1.3	13.8	10.2	6.4	0.2	13.9	14.1	2.2	3.2	139
870	E4	2	DH3	584.3	41.6	1.2	491.4	27.5	77.0	15.7	1.5	18.9	10.4	6.2	0.6	13.6	14.2	2.3	3.1	141
871	E4	2	DH4	495.7	31.8	0.9	555.8	29.0	70.9	12.6	1.5	15.3	8.3	6.1	1.5	13.1	14.6	2.4	2.4	141
872	E4	2	DH5	541.2	42.7	1.2	442.0	27.3	71.5	13.8	1.5	16.9	9.0	7.5	0.7	14.2	14.9	2.0	3.0	141
873	E4	2	DH6	614.4	41.7	1.2	504.5	30.5	75.8	16.1	1.4	17.4	11.9	6.6	1.2	14.1	15.3	2.3	3.0	137
874	E4	2	DH7	575.8	35.3	0.9	616.5	28.6	72.6	15.8	1.6	20.4	9.8	6.5	2.7	14.3	17.0	2.6	2.5	143
875	E4	2	DH8	697.5	45.5	1.2	561.1	28.5	77.4	16.8	1.4	18.8	11.9	7.1	0.6	13.8	14.4	2.0	3.3	140
876	E4	2	DH9	557.6	44.4	1.4	403.2	30.6	75.0	13.9	1.5	16.2	9.5	7.2	1.5	15.8	17.3	2.4	2.8	142
877	E4	2	DH11	577.7	38.2	1.3	451.7	32.9	85.5	17.5	1.4	19.1	12.8	7.7	2.0	14.2	16.2	2.1	2.7	137
878	E4	2	DH12	379.3	39.4	1.1	355.8	27.4	52.7	12.4	1.6	15.6	7.9	6.1	0.6	13.7	14.3	2.4	2.9	142
879	E4	2	DH13	539.5	46.0	1.2	459.6	25.8	77.1	17.8	1.6	22.0	11.4	7.0	1.3	15.1	16.4	2.4	3.0	142
880	E4	2	DH14	703.3	40.9	1.3	555.5	30.2	78.0	15.2	1.5	17.9	10.3	7.3	1.3	15.3	16.6	2.3	2.7	140
881	E4	2	DH15	592.8	38.2	1.1	545.3	27.6	75.6	12.6	1.3	12.7	10.0	6.8	0.7	14.5	15.2	2.3	2.6	137
882	E4	2	DH16	580.0	52.4	1.5	398.1	28.7	74.2	15.4	1.5	17.7	10.5	7.4	0.4	16.0	16.4	2.2	3.3	137
883	E4	2	DH17	665.4	44.5	1.5	453.0	32.8	76.1	13.4	1.2	13.1	10.9	7.2	0.9	14.4	15.3	2.1	3.1	137
884	E4	2	DH18	553.9	48.1	1.4	406.0	28.7	74.0	18.1	1.9	26.8	9.7	7.7	0.6	16.1	16.7	2.2	3.0	142
885	E4	2	DH19	558.4	37.4	1.1	500.8	31.4	73.2	12.7	1.5	14.5	8.7	6.4	1.1	12.7	13.8	2.2	2.9	137
886	E4	2	DH20	607.5	48.6	1.3	464.1	26.7	74.7	15.5	1.6	19.6	9.7	7.1	1.0	15.5	16.5	2.3	3.1	142
887	E4	2	DH21	612.6	38.6	1.2	500.5	29.6	78.7	16.9	1.5	19.5	11.5	7.1	2.1	13.9	16.0	2.3	2.8	142
888	E4	2	DH22	621.2	46.8	1.4	457.5	30.3	86.8	15.0	1.5	18.0	9.9	7.3	1.3	15.9	17.2	2.3	2.9	142
889	E4	2	DH23	656.7	46.8	1.3	497.5	26.9	79.9	16.3	1.3	16.9	12.5	6.8	0.6	14.9	15.5	2.3	3.1	140
890	E4	2	DH24	679.4	44.0	1.2	558.2	27.2	79.5	13.2	1.5	16.1	8.6	6.7	0.5	14.2	14.7	2.2	3.1	139
891	E4	2	DH25	588.4	36.8	1.0	561.4	32.0	69.7	14.1	1.4	15.4	10.3	6.4	1.8	12.8	14.6	2.3	2.8	139
892	E4	2	DH26	578.6	40.7	1.1	518.0	27.7	77.0	17.1	1.5	20.0	11.6	7.0	1.4	14.7	16.1	2.3	2.8	140
893	E4	2	DH27	566.0	40.2	1.1	503.1	27.4	75.1	15.6	1.4	16.9	11.4	6.1	1.3	13.2	14.5	2.4	3.0	142
894	E4	2	DH28	680.7	42.2	1.3	523.2	29.7	81.4	13.9	1.3	15.0	10.4	6.5	1.1	13.6	14.7	2.3	3.1	140
895	E4	2	DH29	626.3	35.5	1.0	599.9	29.2	69.0	15.2	1.4	16.3	11.2	7.0	1.2	13.2	14.4	2.1	2.7	140
896	E4	2	DH30	704.1	38.0	1.3	556.6	31.2	78.0	17.4	1.4	19.9	12.1	6.9	0.9	15.2	16.1	2.3	2.5	140
897	E4	2	DH31	495.4	43.4	1.1	434.2	28.3	74.9	15.0	1.5	18.2	9.8	7.3	1.4	14.4	15.8	2.2	3.0	142
898	E4	2	DH32	520.6	37.4	0.9	564.0	23.5	78.2	12.5	1.4	13.5	9.2	6.4	1.2	14.4	15.6	2.4	2.6	143
899	E4	2	DH33	573.3	45.5	1.1	509.6	26.8	85.2	16.3	1.6	20.9	10.1	6.8	1.5	15.8	17.3	2.5	2.9	145
900	E4	2	DH34	667.0	47.8	1.3	522.3	28.3	83.8	13.3	1.3	13.5	10.4	7.3	0.9	15.9	16.8	2.3	2.9	139
901	E4	2	DH35	552.5	36.8	1.1	482.1	31.2	72.6	14.0	1.5	16.2	9.6	6.9	0.8	13.6	14.4	2.1	2.7	138
902	E4	2	DH36	652.8	39.9	1.2	558.4	30.3	75.1	15.7	1.6	20.0	9.8	7.5	1.0	14.8	15.8	2.1	2.7	141
903	E4	2	DH37	550.2	44.7	1.2	478.0	29.4	78.7	15.4	1.2	15.0	12.6	6.8	1.1	14.4	15.5	2.3	3.1	140
904	E4	2	DH38	622.8	43.2	1.3	488.4	28.9	73.2	15.9	1.4	17.4	11.5	7.5	0.7	16.3	17.0	2.3	2.6	138
905	E4	2	DH39	611.7	38.3	1.2	511.4	29.7	71.1	12.8	1.2	12.3	10.7	5.5	0.9	12.7	13.6	2.5	3.0	139
906	E4	2	DH40	524.8	35.3	1.0	504.1	29.7	81.8	16.4	1.5	19.2	11.0	7.1	0.8	14.0	14.8	2.1	2.5	142
907	E4	2	DH41	720.2	41.3	1.1	631.8	28.9	83.1	16.0	1.5	19.6	10.4	7.2	1.1	14.6	15.7	2.2	2.8	142
908	E4	2	DH42	602.7	38.6	1.1	537.7	28.7	78.3	16.2	1.4	17.7	11.7	6.5	1.1	13.9	15.0	2.3	2.8	140
909	E4	2	DH43	649.7	31.9	0.9	686.8	29.9	72.7	14.6	1.3	15.1	11.2	5.8	1.6	11.8	13.4	2.3	2.7	139
910	E4	2	DH44	751.4	35.2	1.2	641.7	31.8	86.8	17.1	1.4	19.5	11.8	7.2	1.3	13.3	14.6	2.0	2.6	142
911	E4	2	DH45	593.1	30.0	1.0	578.0	35.2	75.3	12.8	1.3	13.4	9.7	6.3	1.7	12.1	13.8	2.2	2.5	139
912	E4	2	DH46	528.6	37.2	1.1	501.5	29.5	80.7	17.0	1.5	19.8	11.6	7.3	1.6	13.8	15.4	2.1	2.7	141
913	E4	2	DH47	690.0	43.2	1.2	558.3	29.5	79.4	12.8	1.4	13.8	9.4	6.9	0.9	14.7	15.6	2.3	2.9	141
914	E4	2	DH49	585.8	40.3	1.1	524.5	31.1	80.4	15.2	1.3	16.2	11.4	6.7	1.4	13.8	15.2	2.3	2.9	141
915	E4	2	DH50	578.8	31.9	1.0	603.5	29.3	81.9	12.9	1.4	13.8	9.5	6.1	1.3	12.7	14.0	2.3	2.5	140
916	E4	2	DH51	564.7	43.4	1.0	575.7	27.9	78.9	15.9	1.5	18.3	10.9	6.9	2.4	14.9	17.3	2.5	2.9	142
917	E4	2	DH52	720.3	38.2	0.9	759.0	25.2	67.7	13.8	1.3	13.7	10.9	6.3	0.8	13.7	14.5	2.3	2.8	139
918	E4	2	DH53	534.4	41.2	1.1	469.6	29.6	65.0	13.4	1.4	14.5	10.0	6.7	0.7	14.8	15.5	2.3	2.8	141
919	E4	2	DH54	570.0	35.8	1.1	501.8	31.2	72.8	16.8	1.4	19.2	11.7	7.1	1.7	13.3	15.0	2.1	2.7	139
920	E4	2	DH55	596.8	43.4	1.2	495.7	27.7	78.4	12.9	1.3	13.6	9.8	6.5	0.9	14.7	15.6	2.4	3.0	139
921	E4	2	DH56	632.9	40.3	1.3	494.9	30.2	76.6	14.1	1.4	16.3	9.8	6.6	1.2	13.4	14.6	2.2	3.0	140
922	E4	2	DH57	551.5	38.6	1.1	486.8	28.5	74.1	12.8	1.4	14.2	9.2	6.0	0.7	13.9	14.6	2.4	2.8	139
923	E4	2	DH58	632.5	41.0	1.1	570.4	28.5	77.6	15.9	1.4	18.2	11.1	6.7	1.4	13.3	14.7	2.2	3.1	139
924	E4	2	DH59	757.5	38.0	1.1	678.7	29.3	71.8	13.9	1.3	14.6	10.5	6.4	1.4	14.0	15.4	2.4	2.7	139
925	E4	2	DH60	607.4	43.3	1.3	458.0	30.6	70.4	16.2	1.5	19.2	11.1	6.9	1.0	13.5	14.5	2.1	3.2	140
926	E4	2	DH61	605.5	38.4	1.1	560.1	28.1	75.8	15.6	1.5	18.8	10.2	7.3	1.2	14.6	15.8	2.2	2.6	142
927	E4	2	DH62	514.4	40.6	1.2	440.4	28.9	64.5	14.6	1.3	14.8	11.5	6.0	0.2	12.5	12.7	2.1	3.2	138
928	E4	2	DH63	539.9	52.6	1.5	351.9	29.2	78.3	15.5	1.4	17.0	11.3	8.5	0.8	16.2	17.0	2.0	3.2	139
929	E4	2	DH64	764.0	42.2	1.4	563.8	33.8	85.8	17.3	1.5	20.8	11.4	7.4	1.1	14.5	15.6	2.1	2.9	138
930	E4	2	DH65	587.2	55.8	1.5	389.7	27.2	74.8	16.8	1.3	17.9	12.6	8.3	0.7	17.0	17.7	2.1	3.3	138

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
931	E4	2	DH66	600.6	41.2	1.2	494.7	32.6	76.2	16.5	1.6	21.4	10.1	7.6	1.9	15.4	17.3	2.3	2.7	143
932	E4	2	DH67	586.4	35.7	1.1	544.0	31.7	68.7	13.0	1.2	12.5	10.7	6.3	0.9	13.6	14.5	2.3	2.6	138
933	E4	2	DH68	389.7	36.4	0.9	435.9	25.0	72.8	16.5	1.5	20.1	10.8	6.6	0.8	14.0	14.8	2.2	2.6	139
934	E4	2	DH69	585.2	43.2	1.2	484.4	29.7	64.9	14.2	1.4	15.2	10.5	6.6	0.9	14.3	15.2	2.3	3.0	140
935	E4	2	DH70	582.2	34.7	1.1	548.8	30.2	77.9	15.4	1.4	16.9	11.2	6.8	1.8	14.4	16.2	2.4	2.4	142
936	E4	2	DH71	531.8	36.0	1.1	479.1	30.7	72.6	14.9	1.4	16.9	10.5	6.6	0.9	12.9	13.8	2.1	2.7	142
937	E4	2	DH72	578.4	41.6	1.1	515.1	27.0	77.1	15.5	1.5	19.1	10.0	7.2	1.2	15.6	16.8	2.3	2.7	142
938	E4	2	DH73	637.7	43.9	1.3	508.2	27.3	78.9	13.7	1.5	16.2	9.2	7.2	1.1	15.4	16.5	2.3	2.8	141
939	E4	2	DH75	725.4	41.6	1.3	551.2	33.2	81.8	15.3	1.4	17.1	10.9	7.5	1.2	14.9	16.1	2.2	2.8	137
940	E4	2	DH76	531.9	38.2	1.1	493.0	29.0	68.4	14.0	1.4	15.5	10.0	6.4	0.8	13.1	13.9	2.2	2.9	140
941	E4	2	DH77	599.9	40.6	1.3	478.8	31.8	72.3	14.2	1.2	13.0	12.2	7.9	1.3	15.8	17.1	2.2	2.6	140
942	E4	2	DH78	736.2	44.9	1.3	572.1	31.7	73.1	16.0	1.3	16.1	12.6	7.3	1.1	15.1	16.2	2.2	3.0	137
943	E4	2	DH79	643.6	39.1	1.1	563.6	30.7	79.4	14.2	1.3	14.7	10.8	6.5	2.0	12.8	14.8	2.3	3.0	137
944	E4	2	DH80	660.4	45.3	1.4	484.5	29.6	77.9	15.2	1.3	16.2	11.4	6.7	0.8	14.1	14.9	2.2	3.2	139
945	E4	2	DH81	525.3	39.9	1.2	444.4	30.4	72.2	14.6	1.6	18.4	9.5	6.8	0.5	14.9	15.4	2.3	2.7	140
946	E4	2	DH82	567.5	40.6	1.2	490.1	29.0	74.2	13.7	1.4	14.8	10.0	6.9	0.9	14.2	15.1	2.2	2.8	138
947	E4	2	DH83	615.3	27.2	0.9	681.4	33.5	77.7	13.8	1.2	13.3	11.3	5.5	2.7	10.5	13.2	2.4	2.6	141
948	E4	2	DH84	617.8	38.8	1.3	488.8	31.5	75.9	12.9	1.2	11.9	11.1	7.2	0.9	13.4	14.3	2.0	2.9	136
949	E4	2	DH85	662.2	40.1	1.2	560.7	28.9	66.6	17.7	1.5	21.2	11.8	6.5	0.7	13.6	14.3	2.2	2.9	140
950	E4	2	DH86	647.5	41.5	1.1	582.8	30.3	81.4	13.9	1.3	14.1	10.9	6.1	0.9	13.8	14.7	2.4	3.0	140
951	E4	2	DH87	581.6	40.3	1.1	512.8	29.0	71.0	13.4	1.3	13.9	10.3	6.2	0.7	13.1	13.8	2.2	3.1	139
952	E4	2	DH89	588.1	33.1	1.0	578.8	31.8	78.6	13.1	1.3	14.0	9.7	6.0	1.4	12.6	14.0	2.3	2.6	141
953	E4	2	DH90	488.7	43.9	1.3	364.5	29.4	71.0	13.6	1.2	12.7	11.7	7.5	1.3	15.8	17.1	2.3	2.7	137
954	E4	2	DH91	671.3	39.2	1.1	588.3	29.8	84.0	14.3	1.3	15.2	10.7	6.4	1.2	14.1	15.3	2.4	2.8	139
955	E4	2	DH92	518.8	31.4	0.9	560.9	27.7	66.6	13.4	1.3	13.6	10.5	6.0	1.7	12.0	13.7	2.3	2.6	140
956	E4	2	DH93	559.0	49.5	1.3	423.2	26.8	69.1	14.3	1.3	14.8	11.0	7.4	0.7	15.6	16.3	2.2	3.2	139
957	E4	2	DH94	662.9	38.9	1.1	579.4	29.8	79.9	13.3	1.3	13.3	10.6	6.9	1.1	15.1	16.2	2.3	2.6	139
958	E4	2	DH95	587.8	32.8	1.0	579.7	32.6	71.4	12.3	1.3	12.8	9.6	6.5	1.5	12.4	13.9	2.2	2.6	139
959	E4	2	DH96	719.5	35.4	1.2	601.1	33.0	77.2	14.6	1.4	16.0	10.6	6.5	1.5	12.5	14.0	2.2	2.8	136
960	E4	2	DH97	604.5	45.7	1.4	436.2	31.0	77.3	14.8	1.6	18.8	9.2	7.1	0.1	15.6	15.7	2.2	2.9	139
961	E4	2	DH98	566.3	32.4	1.1	518.6	33.0	67.9	13.8	1.3	13.9	10.9	6.4	1.3	12.2	13.5	2.1	2.7	137
962	E4	2	DH99	672.8	40.4	1.2	570.1	28.8	71.9	13.7	1.5	15.8	9.4	6.6	0.4	13.7	14.1	2.2	2.9	141
963	E4	2	DH100	475.9	45.9	1.3	378.3	26.8	65.9	11.4	1.2	11.2	9.3	7.1	1.0	15.2	16.2	2.3	3.0	138
964	E4	2	DH101	559.2	39.9	1.1	508.8	27.3	71.5	12.4	1.3	13.2	9.2	6.6	0.6	13.2	13.8	2.1	3.0	138
965	E4	2	DH102	510.9	42.8	1.1	454.1	26.8	74.0	14.8	1.4	16.3	10.7	7.1	1.3	13.7	15.0	2.1	3.1	142
966	E4	2	DH103	560.1	37.0	1.1	518.1	28.8	75.1	16.5	1.6	21.4	10.1	7.0	1.6	13.9	15.6	2.2	2.6	142
967	E4	2	DH104	691.0	45.5	1.2	583.1	27.4	83.9	16.2	1.4	18.2	11.4	6.9	1.3	15.0	16.3	2.4	3.0	142
968	E4	2	DH105	649.9	45.6	1.2	553.6	26.6	76.1	16.6	1.5	19.7	11.1	6.2	1.2	14.5	15.7	2.5	3.1	140
969	E4	2	DH106	561.9	47.3	1.3	428.9	27.8	74.3	13.7	1.6	17.4	8.6	6.9	0.8	14.6	15.4	2.2	3.2	140
970	E4	2	DH107	679.5	38.3	1.1	594.4	27.0	78.7	14.5	1.4	16.2	10.3	7.0	0.8	13.8	14.6	2.1	2.8	139
971	E4	2	DH108	725.8	42.6	1.3	572.9	28.4	85.2	14.3	1.2	13.9	11.7	7.0	1.4	15.0	16.4	2.3	2.8	137
972	E4	2	DH109	479.3	41.9	1.1	453.9	26.2	72.0	15.9	1.5	19.0	10.5	7.7	1.2	14.9	16.1	2.1	2.8	141
973	E4	2	DH110	638.3	43.3	1.3	481.7	29.7	77.4	14.9	1.2	14.0	12.9	7.4	0.8	14.6	15.4	2.1	3.0	137
974	E4	2	DH111	584.5	38.9	1.1	526.1	30.0	79.5	15.4	1.3	16.2	11.5	6.9	1.5	13.3	14.8	2.1	2.9	139
975	E4	2	DH112	566.3	38.7	1.1	497.2	30.2	73.5	12.1	1.3	12.9	9.0	6.6	1.5	13.6	15.1	2.3	2.8	139
976	E4	2	DH113	575.7	33.2	1.0	555.7	31.8	72.9	11.9	1.2	11.3	10.0	5.7	1.5	12.4	13.9	2.4	2.7	139
977	E4	2	DH114	526.9	40.5	1.2	447.7	27.2	63.2	13.1	1.5	15.1	9.1	7.2	0.6	14.3	14.9	2.1	2.8	140
978	E4	2	DH115	534.1	36.4	1.1	484.2	29.4	73.0	14.6	1.3	14.8	11.4	6.8	1.4	13.8	15.2	2.2	2.6	138
979	E4	2	DH116	657.9	33.1	1.0	650.7	32.1	78.7	12.6	1.3	13.1	9.7	6.3	1.7	12.7	14.4	2.3	2.6	139
980	E4	2	DH117	483.4	38.8	1.2	393.0	30.4	59.9	16.0	1.4	17.7	11.4	7.1	0.5	13.4	13.9	2.0	2.9	139
981	E4	2	DH119	589.3	49.1	1.5	390.3	29.1	86.8	18.7	1.7	25.8	10.7	7.7	0.6	16.0	16.6	2.2	3.1	141
982	E4	2	DH120	655.7	36.2	1.1	614.0	29.8	58.9	14.4	1.3	15.0	11.0	6.2	1.0	12.9	13.9	2.2	2.8	139
983	E4	2	DH121	614.8	38.2	1.1	548.4	29.3	71.8	15.0	1.5	17.3	10.3	6.9	1.3	13.8	15.1	2.2	2.8	141
984	E4	2	DH122	578.0	40.9	1.1	547.4	25.7	82.8	14.6	1.4	16.1	10.5	6.6	1.2	14.9	16.1	2.4	2.7	142
985	E4	2	DH123	541.9	41.6	1.1	506.5	26.3	80.5	14.9	1.3	15.3	11.7	7.1	1.3	14.3	15.6	2.2	2.9	140
986	E4	2	DH124	674.8	42.8	1.2	549.9	28.0	77.5	16.0	1.4	18.0	11.3	7.7	1.3	14.6	15.9	2.1	2.9	143
987	E4	2	DH125	628.6	35.5	1.0	656.1	29.8	69.7	12.9	1.4	14.7	9.0	5.9	1.3	12.6	13.9	2.4	2.8	139
988	E4	2	DH126	647.9	44.9	1.2	533.2	28.2	71.8	15.2	1.6	19.0	9.6	7.8	0.6	16.2	16.8	2.2	2.8	142
989	E4	2	DH128	574.6	46.0	1.2	480.0	25.4	71.6	16.5	1.5	19.3	11.3	6.4	1.4	14.0	15.4	2.4	3.3	142
990	E4	2	DH129	684.4	44.0	1.3	535.1	30.1	83.8	14.5	1.3	15.4	10.8	6.9	1.5	14.0	15.5	2.2	3.1	138
991	E4	2	DH130	575.3	42.5	1.2	480.2	27.2	73.1	14.5	1.5	17.1	9.7	7.3	0.9	14.5	15.4	2.1	2.9	140
992	E4	2	DH131	480.2	41.5	1.3	383.9	31.9	72.5	16.3	1.5	19.6	10.8	7.6	1.7	15.1	16.8	2.2	2.7	142

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
993	E5	1	DH1	439.4	36.8	0.9	490.9	25.5	.	.	.	.	.	6.6	1.6	14.6	16.2	2.4	2.5	113
994	E5	1	DH3	593.4	37.9	1.0	584.0	29.0	.	.	.	.	.	6.9	2.8	14.9	17.7	2.6	2.5	119
995	E5	1	DH4	454.2	38.0	0.9	532.3	28.0	.	.	.	.	.	7.4	3.1	16.0	19.1	2.6	2.3	117
996	E5	1	DH5	601.4	33.7	0.8	737.9	24.5	.	.	.	.	.	7.4	3.5	14.2	17.7	2.4	2.4	116
997	E5	1	DH6	508.2	42.3	1.1	462.0	27.9	.	.	.	.	.	7.3	2.2	16.2	18.4	2.5	2.6	110
998	E5	1	DH7	459.0	41.9	1.1	426.1	25.3	.	.	.	.	.	6.9	3.3	16.6	19.9	2.9	2.5	123
999	E5	1	DH8	439.9	50.7	1.3	338.1	27.2	.	.	.	.	.	7.9	1.9	16.8	18.7	2.4	3.0	115
1000	E5	1	DH9	404.7	57.0	1.5	274.9	24.8	.	.	.	.	.	8.3	2.3	19.8	22.1	2.7	2.9	119
1001	E5	1	DH11	598.9	39.8	1.4	440.0	33.2	.	.	.	.	.	8.6	2.7	15.7	18.4	2.1	2.5	114
1002	E5	1	DH12	288.8	43.3	1.0	285.7	21.7	.	.	.	.	.	7.3	1.9	16.3	18.2	2.5	2.7	115
1003	E5	1	DH13	582.9	50.7	1.3	455.4	24.5	.	.	.	.	.	8.2	2.3	19.2	21.5	2.6	2.6	116
1004	E5	1	DH14	639.1	38.1	1.2	515.4	31.7	.	.	.	.	.	7.4	2.9	15.9	18.8	2.5	2.4	116
1005	E5	1	DH15	604.2	40.9	1.1	542.4	27.8	.	.	.	.	.	7.5	1.8	15.4	17.2	2.3	2.6	111
1006	E5	1	DH16	537.1	37.5	1.0	541.5	27.8	.	.	.	.	.	7.1	2.6	14.3	16.9	2.4	2.6	111
1007	E5	1	DH17	486.5	37.9	1.2	421.5	30.8	.	.	.	.	.	7.4	2.8	14.4	17.2	2.3	2.6	112
1008	E5	1	DH18	525.9	47.1	1.2	443.0	27.5	.	.	.	.	.	8.0	2.8	17.5	20.3	2.5	2.7	123
1009	E5	1	DH19	634.5	36.5	1.1	582.7	29.7	.	.	.	.	.	6.8	2.8	14.1	16.9	2.5	2.6	113
1010	E5	1	DH20	545.9	51.0	1.2	437.1	25.0	.	.	.	.	.	7.3	2.4	17.1	19.5	2.7	3.0	119
1011	E5	1	DH21	664.7	40.3	1.2	554.4	31.2	.	.	.	.	.	7.5	3.7	15.1	18.8	2.5	2.6	118
1012	E5	1	DH22	597.5	46.7	1.2	516.4	26.3	.	.	.	.	.	8.2	2.3	18.2	20.5	2.5	2.6	116
1013	E5	1	DH23	517.6	47.0	1.2	433.1	24.8	.	.	.	.	.	7.0	1.8	15.6	17.4	2.5	3.0	111
1014	E5	1	DH24	622.5	40.1	1.1	560.8	28.8	.	.	.	.	.	6.9	2.5	14.3	16.8	2.4	2.8	111
1015	E5	1	DH25	558.5	40.1	1.0	535.5	25.0	.	.	.	.	.	7.5	2.5	15.7	18.2	2.4	2.5	112
1016	E5	1	DH26	461.1	47.0	1.1	408.0	22.2	.	.	.	.	.	7.6	2.1	16.3	18.4	2.4	2.9	115
1017	E5	1	DH27	542.5	40.9	1.1	482.6	29.0	.	.	.	.	.	6.3	3.3	14.2	17.5	2.8	2.9	120
1018	E5	1	DH28	461.1	40.6	1.1	428.1	30.7	.	.	.	.	.	6.9	3.0	14.7	17.7	2.6	2.7	117
1019	E5	1	DH29	442.9	41.8	1.1	419.4	25.3	.	.	.	.	.	7.9	2.4	17.0	19.4	2.5	2.5	117
1020	E5	1	DH30	324.8	40.2	1.1	298.2	26.8	.	.	.	.	.	7.7	2.4	16.6	19.0	2.5	2.4	116
1021	E5	1	DH31	493.6	46.6	1.1	460.4	24.8	.	.	.	.	.	8.4	1.9	17.0	18.9	2.3	2.7	116
1022	E5	1	DH32	559.0	42.0	0.9	592.8	23.0	.	.	.	.	.	7.6	2.4	17.9	20.3	2.7	2.3	123
1023	E5	1	DH33	599.8	59.3	1.2	496.9	24.3	.	.	.	.	.	7.9	1.9	20.2	22.1	2.8	2.9	123
1024	E5	1	DH34	688.2	45.9	1.3	515.1	29.6	.	.	.	.	.	7.7	1.8	16.2	18.0	2.3	2.8	110
1025	E5	1	DH35	548.0	35.7	1.1	517.5	30.3	.	.	.	.	.	7.4	2.8	15.0	17.8	2.4	2.4	115
1026	E5	1	DH36	525.9	40.2	1.1	466.2	26.4	.	.	.	.	.	8.2	2.7	16.7	19.4	2.4	2.4	117
1027	E5	1	DH37	464.2	44.1	1.1	437.5	24.2	.	.	.	.	.	7.8	2.5	17.1	19.6	2.5	2.6	117
1028	E5	1	DH38	492.9	41.1	1.0	508.7	23.8	.	.	.	.	.	7.6	2.2	16.2	18.4	2.4	2.5	110
1029	E5	1	DH39	596.8	42.5	1.2	493.2	25.3	.	.	.	.	.	6.2	2.0	16.4	18.4	3.0	2.6	116
1030	E5	1	DH40	368.8	39.6	0.9	391.1	25.6	.	.	.	.	.	8.1	2.5	17.2	19.7	2.4	2.3	118
1031	E5	1	DH41	648.9	37.7	1.0	659.4	25.9	.	.	.	.	.	7.0	2.9	14.6	17.5	2.5	2.6	118
1032	E5	1	DH42	554.6	46.3	1.2	450.9	26.7	.	.	.	.	.	7.7	2.4	17.7	20.1	2.6	2.6	117
1033	E5	1	DH43	381.2	47.8	1.2	314.7	23.1	.	.	.	.	.	7.4	2.2	16.5	18.7	2.5	2.9	116
1034	E5	1	DH44	574.9	47.0	1.4	396.8	29.0	.	.	.	.	.	8.5	2.2	17.2	19.4	2.3	2.7	121
1035	E5	1	DH45	504.1	40.4	1.3	386.3	34.5	.	.	.	.	.	7.9	2.1	16.8	18.9	2.4	2.4	115
1036	E5	1	DH46	506.4	46.4	1.1	448.2	23.7	.	.	.	.	.	8.7	3.3	17.9	21.2	2.4	2.6	119
1037	E5	1	DH47	482.3	37.9	1.0	503.4	24.5	.	.	.	.	.	7.1	3.5	14.6	18.1	2.5	2.6	119
1038	E5	1	DH49	457.2	52.4	1.4	337.4	27.1	.	.	.	.	.	8.0	2.2	16.6	18.8	2.4	3.1	120
1039	E5	1	DH50	512.9	36.1	1.0	498.9	28.1	.	.	.	.	.	7.2	2.8	15.7	18.5	2.6	2.3	117
1040	E5	1	DH51	535.3	46.4	1.1	492.4	24.0	.	.	.	.	.	7.9	3.3	16.7	20.0	2.5	2.8	120
1041	E5	1	DH52	702.4	39.4	1.0	706.0	26.5	.	.	.	.	.	7.1	1.9	15.3	17.2	2.4	2.6	114
1042	E5	1	DH53	612.7	37.2	1.1	568.9	27.8	.	.	.	.	.	6.7	2.2	15.8	18.0	2.7	2.4	116
1043	E5	1	DH54	612.7	47.9	1.6	392.7	32.9	.	.	.	.	.	8.3	1.9	15.7	17.6	2.1	3.0	110
1044	E5	1	DH55	573.7	43.4	1.2	484.1	27.8	.	.	.	.	.	7.2	2.2	15.9	18.1	2.5	2.7	116
1045	E5	1	DH56	643.6	37.4	1.2	554.8	29.4	.	.	.	.	.	6.9	2.2	14.2	16.4	2.4	2.6	114
1046	E5	1	DH57	402.5	36.1	0.9	467.5	22.8	.	.	.	.	.	6.7	2.4	15.8	18.2	2.7	2.4	115
1047	E5	1	DH58	584.9	37.9	1.1	554.9	28.4	.	.	.	.	.	6.8	2.3	13.7	16.0	2.4	2.8	114
1048	E5	1	DH59	581.6	39.1	1.0	592.9	24.4	.	.	.	.	.	6.5	1.7	14.1	15.8	2.4	2.7	109
1049	E5	1	DH60	568.4	48.2	1.4	406.6	27.9	.	.	.	.	.	8.0	2.2	15.9	18.1	2.3	3.0	110
1050	E5	1	DH61	595.6	42.1	1.2	503.1	27.0	.	.	.	.	.	7.4	2.2	15.8	18.0	2.4	2.7	120
1051	E5	1	DH62	228.7	41.4	0.7	308.6	18.3	.	.	.	.	.	7.0	1.6	15.3	16.9	2.4	2.7	115
1052	E5	1	DH63	547.1	54.9	1.5	361.9	28.1	.	.	.	.	.	8.6	1.6	17.2	18.8	2.2	3.2	110
1053	E5	1	DH64	590.2	38.7	1.2	504.8	33.1	.	.	.	.	.	7.9	2.0	15.8	17.8	2.3	2.4	112
1054	E5	1	DH65	428.8	50.4	1.2	369.7	24.0	.	.	.	.	.	8.6	1.9	18.7	20.6	2.4	2.7	110

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
1055	E5	1	DH66	382.9	47.7	1.2	321.8	24.4	.	.	.	.	.	8.1	3.1	18.4	21.5	2.6	2.6	121
1056	E5	1	DH67	492.9	41.1	1.1	467.2	27.9	.	.	.	.	.	7.2	1.9	15.8	17.7	2.5	2.6	114
1057	E5	1	DH68	322.2	39.9	0.9	340.2	24.3	.	.	.	.	.	7.6	2.0	15.6	17.6	2.3	2.5	115
1058	E5	1	DH69	468.5	47.4	1.0	463.0	22.6	.	.	.	.	.	7.1	1.5	15.8	17.3	2.5	3.0	113
1059	E5	1	DH70	554.6	47.3	1.3	411.7	27.5	.	.	.	.	.	7.7	2.8	17.3	20.1	2.6	2.7	120
1060	E5	1	DH71	529.4	50.5	1.3	400.4	27.8	.	.	.	.	.	8.5	2.1	17.8	19.9	2.3	2.8	119
1061	E5	1	DH72	491.2	48.9	1.2	401.0	25.0	.	.	.	.	.	8.1	2.7	17.4	20.1	2.5	2.8	118
1062	E5	1	DH73	514.6	48.7	1.2	426.3	24.2	.	.	.	.	.	7.8	2.4	16.9	19.3	2.5	2.9	118
1063	E5	1	DH75	730.8	43.6	1.3	543.8	31.7	.	.	.	.	.	7.8	1.6	15.7	17.3	2.2	2.8	110
1064	E5	1	DH76	621.8	40.7	1.2	500.2	29.2	.	.	.	.	.	7.0	2.1	15.6	17.7	2.5	2.6	117
1065	E5	1	DH77	632.3	39.3	1.2	513.2	30.6	.	.	.	.	.	8.6	2.8	17.2	20.0	2.3	2.3	114
1066	E5	1	DH78	602.8	48.5	1.4	422.7	29.5	.	.	.	.	.	8.1	1.5	17.2	18.7	2.3	2.8	113
1067	E5	1	DH79	583.5	40.7	1.2	468.7	29.6	.	.	.	.	.	7.5	2.8	15.7	18.5	2.5	2.6	115
1068	E5	1	DH80	559.8	45.9	1.3	423.8	28.2	.	.	.	.	.	7.3	2.1	17.5	19.6	2.7	2.6	116
1069	E5	1	DH81	404.2	39.7	1.0	387.5	27.0	.	.	.	.	.	7.4	1.8	17.3	19.1	2.6	2.3	115
1070	E5	1	DH82	559.8	39.3	1.0	573.0	26.0	.	.	.	.	.	7.4	2.3	15.0	17.3	2.4	2.6	109
1071	E5	1	DH83	678.2	35.0	1.2	560.5	33.8	.	.	.	.	.	7.1	3.9	14.1	18.0	2.6	2.4	116
1072	E5	1	DH84	688.7	39.8	1.3	547.0	31.0	.	.	.	.	.	7.7	1.8	15.2	17.0	2.2	2.6	109
1073	E5	1	DH85	606.0	40.9	1.2	501.2	30.2	.	.	.	.	.	7.3	2.6	15.6	18.2	2.5	2.6	115
1074	E5	1	DH86	587.6	41.5	1.2	508.8	29.2	.	.	.	.	.	6.7	2.0	15.4	17.4	2.6	2.7	114
1075	E5	1	DH87	485.9	51.4	1.3	380.5	25.5	.	.	.	.	.	7.3	0.9	16.9	17.8	2.4	3.0	109
1076	E5	1	DH89	529.4	35.5	1.1	495.9	31.7	.	.	.	.	.	7.0	2.9	15.1	18.0	2.6	2.5	116
1077	E5	1	DH90	481.7	38.7	1.2	414.6	29.7	.	.	.	.	.	7.5	3.0	15.7	18.7	2.5	2.4	108
1078	E5	1	DH91	428.3	41.9	1.2	349.6	29.7	.	.	.	.	.	7.2	2.7	15.7	18.4	2.6	2.8	115
1079	E5	1	DH92	508.2	40.0	1.1	468.8	28.9	.	.	.	.	.	7.5	1.9	15.6	17.5	2.3	2.6	115
1080	E5	1	DH93	454.7	53.4	1.3	350.9	22.6	.	.	.	.	.	8.2	1.3	18.0	19.3	2.3	3.0	110
1081	E5	1	DH94	563.2	40.3	1.2	485.9	28.9	.	.	.	.	.	7.6	2.6	16.2	18.8	2.5	2.5	117
1082	E5	1	DH95	527.1	37.7	0.9	593.6	24.5	.	.	.	.	.	7.7	2.3	15.0	17.3	2.2	2.5	108
1083	E5	1	DH96	837.8	40.1	1.5	572.7	35.2	.	.	.	.	.	7.2	2.2	14.1	16.3	2.3	2.8	111
1084	E5	1	DH97	581.0	46.8	1.4	410.3	31.8	.	.	.	.	.	7.9	1.5	17.7	19.2	2.4	2.6	114
1085	E5	1	DH98	545.9	50.2	1.4	389.9	28.0	.	.	.	.	.	8.2	1.4	15.5	16.9	2.1	3.2	107
1086	E5	1	DH99	501.6	47.7	1.2	427.3	26.5	.	.	.	.	.	7.3	1.9	17.4	19.3	2.6	2.7	120
1087	E5	1	DH100	534.1	48.0	1.1	472.6	25.4	.	.	.	.	.	7.5	3.0	17.2	20.2	2.7	2.8	114
1088	E5	1	DH101	550.6	48.8	1.3	421.2	27.3	.	.	.	.	.	7.9	1.9	16.4	18.3	2.3	3.0	114
1089	E5	1	DH102	661.6	54.3	1.3	516.5	24.4	.	.	.	.	.	8.7	2.6	19.0	21.6	2.5	2.8	121
1090	E5	1	DH103	584.0	42.5	1.3	456.2	28.7	.	.	.	.	.	7.8	2.4	16.4	18.8	2.4	2.6	123
1091	E5	1	DH104	753.5	48.8	1.2	613.1	25.8	.	.	.	.	.	7.1	2.8	17.7	20.5	2.9	2.7	120
1092	E5	1	DH105	721.1	40.3	1.1	652.5	27.7	.	.	.	.	.	6.7	3.0	15.3	18.3	2.7	2.6	116
1093	E5	1	DH106	575.0	38.7	1.1	525.6	28.8	.	.	.	.	.	7.8	2.8	15.9	18.7	2.4	2.4	116
1094	E5	1	DH107	537.5	36.9	1.1	506.1	27.9	.	.	.	.	.	7.4	2.5	14.5	17.0	2.3	2.5	113
1095	E5	1	DH108	473.7	36.2	1.0	483.4	28.4	.	.	.	.	.	6.7	3.0	15.3	18.3	2.7	2.4	116
1096	E5	1	DH109	502.9	40.2	1.1	455.1	27.8	.	.	.	.	.	8.2	2.9	16.5	19.4	2.4	2.4	117
1097	E5	1	DH110	432.1	46.1	1.3	331.9	29.7	.	.	.	.	.	8.8	2.0	17.9	19.9	2.3	2.6	113
1098	E5	1	DH111	444.7	48.8	1.4	328.7	28.3	.	.	.	.	.	8.8	2.2	17.8	20.0	2.3	2.7	114
1099	E5	1	DH112	373.7	40.3	1.1	328.1	27.7	.	.	.	.	.	7.2	3.2	15.8	19.0	2.7	2.5	117
1100	E5	1	DH113	545.3	39.7	1.2	442.9	29.4	.	.	.	.	.	6.7	2.3	14.5	16.8	2.5	2.7	115
1101	E5	1	DH114	552.5	43.6	1.2	453.2	26.2	.	.	.	.	.	8.1	1.5	16.7	18.2	2.3	2.6	115
1102	E5	1	DH115	494.7	39.9	1.1	447.3	29.4	.	.	.	.	.	7.5	2.3	15.6	17.9	2.4	2.5	115
1103	E5	1	DH116	663.2	34.7	1.1	615.2	31.5	.	.	.	.	.	7.0	2.8	13.7	16.5	2.3	2.5	114
1104	E5	1	DH117	535.3	40.4	1.1	484.2	26.3	.	.	.	.	.	7.9	1.2	15.7	16.9	2.2	2.6	113
1105	E5	1	DH119	651.1	46.2	1.4	481.9	31.9	.	.	.	.	.	8.8	2.3	17.6	19.9	2.3	2.6	115
1106	E5	1	DH120	620.3	38.7	1.0	605.8	27.3	.	.	.	.	.	6.6	3.2	15.1	18.3	2.8	2.6	119
1107	E5	1	DH121	527.5	38.2	1.1	475.3	28.3	.	.	.	.	.	7.2	4.2	15.0	19.2	2.7	2.5	120
1108	E5	1	DH122	535.0	48.5	1.1	472.6	23.1	.	.	.	.	.	7.4	1.9	17.1	19.0	2.6	2.9	120
1109	E5	1	DH123	609.8	39.5	1.1	565.7	25.5	.	.	.	.	.	7.3	2.6	15.5	18.1	2.5	2.5	117
1110	E5	1	DH124	679.2	46.1	1.2	552.2	25.4	.	.	.	.	.	8.2	2.7	16.7	19.4	2.4	2.8	119
1111	E5	1	DH125	774.4	36.4	1.2	670.5	31.2	.	.	.	.	.	7.0	2.9	14.8	17.7	2.5	2.5	116
1112	E5	1	DH126	729.7	45.4	1.2	597.6	25.1	.	.	.	.	.	8.2	2.0	18.0	20.0	2.5	2.5	119
1113	E5	1	DH128	504.7	43.9	1.1	476.1	23.8	.	.	.	.	.	7.2	3.0	17.3	20.3	2.8	2.6	119
1114	E5	1	DH129	651.8	41.0	1.3	503.3	30.2	.	.	.	.	.	7.5	3.0	15.8	18.8	2.5	2.6	115
1115	E5	1	DH130	596.5	37.4	1.0	588.3	26.8	.	.	.	.	.	7.9	2.6	15.4	18.0	2.3	2.5	115
1116	E5	1	DH131	508.2	42.6	1.2	409.5	29.3	.	.	.	.	.	8.1	3.4	17.4	20.8	2.6	2.4	121

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
1117	E5	2	DH1	433.6	37.4	0.9	458.3	24.3	.	.	.	.	.	6.7	1.8	14.1	15.9	2.4	2.6	113
1118	E5	2	DH3	596.5	36.2	1.1	565.4	28.3	.	.	.	.	.	6.6	2.9	13.9	16.8	2.5	2.6	120
1119	E5	2	DH4	505.9	37.2	1.1	479.0	27.8	.	.	.	.	.	7.3	2.7	16.1	18.8	2.6	2.3	117
1120	E5	2	DH5	678.2	40.0	1.1	593.8	27.2	.	.	.	.	.	8.0	2.4	15.1	17.5	2.2	2.6	117
1121	E5	2	DH6	727.2	42.6	1.2	585.9	29.2	.	.	.	.	.	7.2	1.9	15.9	17.8	2.5	2.7	109
1122	E5	2	DH7	637.6	45.6	1.2	547.3	25.2	.	.	.	.	.	6.9	3.2	16.7	19.9	2.9	2.7	123
1123	E5	2	DH8	606.0	47.5	1.3	451.5	27.8	.	.	.	.	.	7.9	2.2	16.1	18.3	2.3	2.9	116
1124	E5	2	DH9	451.0	42.7	1.1	408.5	24.4	.	.	.	.	.	7.6	3.9	16.9	20.8	2.8	2.5	120
1125	E5	2	DH11	608.1	38.7	1.3	458.9	34.5	.	.	.	.	.	8.3	2.6	15.4	18.0	2.2	2.5	114
1126	E5	2	DH12	314.5	40.9	1.1	292.8	21.9	.	.	.	.	.	7.3	2.5	16.6	19.1	2.6	2.5	115
1127	E5	2	DH13	620.3	46.5	1.3	480.1	25.1	.	.	.	.	.	7.8	3.4	18.0	21.4	2.7	2.6	116
1128	E5	2	DH14	668.4	39.3	1.3	509.9	33.8	.	.	.	.	.	7.8	3.6	16.1	19.7	2.5	2.4	117
1129	E5	2	DH15	660.2	37.7	1.1	603.5	27.7	.	.	.	.	.	7.5	2.0	15.1	17.1	2.3	2.5	112
1130	E5	2	DH16	713.0	40.7	1.2	604.2	29.3	.	.	.	.	.	7.0	1.8	15.2	17.0	2.4	2.7	112
1131	E5	2	DH17	657.9	42.2	1.4	467.9	32.2	.	.	.	.	.	8.0	2.0	16.1	18.1	2.3	2.6	112
1132	E5	2	DH18	538.1	48.0	1.3	401.6	27.3	.	.	.	.	.	8.4	2.2	18.2	20.4	2.4	2.6	123
1133	E5	2	DH19	605.3	37.4	1.1	533.7	31.1	.	.	.	.	.	6.9	2.2	14.3	16.5	2.4	2.6	114
1134	E5	2	DH20	541.8	43.7	1.2	470.8	26.2	.	.	.	.	.	7.0	3.2	16.2	19.4	2.8	2.7	119
1135	E5	2	DH21	538.1	33.4	1.1	511.5	30.8	.	.	.	.	.	7.1	4.0	14.1	18.1	2.5	2.4	118
1136	E5	2	DH22	469.0	46.4	1.3	361.0	28.7	.	.	.	.	.	7.8	2.9	17.5	20.4	2.6	2.6	117
1137	E5	2	DH23	484.8	44.6	1.2	415.4	26.0	.	.	.	.	.	6.9	2.0	15.1	17.1	2.5	3.0	112
1138	E5	2	DH24	635.4	39.4	1.2	545.8	28.8	.	.	.	.	.	7.1	2.1	15.0	17.1	2.4	2.6	112
1139	E5	2	DH25	607.7	42.8	1.2	504.3	25.5	.	.	.	.	.	7.8	3.2	16.3	19.5	2.5	2.6	112
1140	E5	2	DH26	531.6	40.2	1.0	520.6	23.7	.	.	.	.	.	7.1	2.6	15.2	17.8	2.5	2.6	115
1141	E5	2	DH27	791.0	41.9	1.2	642.6	27.4	.	.	.	.	.	6.5	3.1	14.6	17.7	2.7	2.9	119
1142	E5	2	DH28	658.7	38.9	1.2	542.6	30.4	.	.	.	.	.	6.8	2.8	15.0	17.8	2.6	2.6	117
1143	E5	2	DH29	595.6	39.3	1.2	515.3	25.1	.	.	.	.	.	7.7	3.5	15.9	19.4	2.5	2.5	117
1144	E5	2	DH30	460.6	34.4	1.1	433.3	30.2	.	.	.	.	.	7.3	3.2	15.9	19.1	2.6	2.2	116
1145	E5	2	DH31	542.1	40.4	1.1	511.4	26.2	.	.	.	.	.	7.7	2.6	15.6	18.2	2.3	2.6	116
1146	E5	2	DH32	550.7	38.8	0.9	622.3	23.6	.	.	.	.	.	7.1	2.5	16.4	18.9	2.7	2.4	123
1147	E5	2	DH33	617.5	56.5	1.3	489.7	22.2	.	.	.	.	.	7.8	2.3	20.1	22.4	2.9	2.8	123
1148	E5	2	DH34	705.3	54.0	1.6	445.5	30.0	.	.	.	.	.	8.3	1.4	17.5	18.9	2.3	3.1	110
1149	E5	2	DH35	576.3	34.3	1.1	543.6	30.6	.	.	.	.	.	7.6	3.0	14.9	17.9	2.4	2.3	115
1150	E5	2	DH36	657.2	42.5	1.2	566.1	27.3	.	.	.	.	.	8.6	2.9	16.9	19.8	2.3	2.5	117
1151	E5	2	DH37	580.8	45.2	1.2	500.3	26.5	.	.	.	.	.	8.0	2.7	17.1	19.8	2.5	2.6	116
1152	E5	2	DH38	519.8	43.9	1.1	473.9	23.2	.	.	.	.	.	7.9	1.9	16.4	18.3	2.3	2.7	109
1153	E5	2	DH39	578.9	40.3	1.3	457.7	29.3	.	.	.	.	.	6.3	2.1	16.5	18.6	3.0	2.4	116
1154	E5	2	DH40	421.5	36.8	1.0	404.6	28.1	.	.	.	.	.	8.2	2.0	17.1	19.1	2.3	2.2	117
1155	E5	2	DH41	542.7	37.7	1.1	504.4	29.7	.	.	.	.	.	7.1	2.6	14.5	17.1	2.4	2.6	118
1156	E5	2	DH42	459.0	45.9	1.3	364.0	26.8	.	.	.	.	.	7.3	2.3	17.8	20.1	2.8	2.6	116
1157	E5	2	DH43	443.1	40.3	1.2	380.4	27.4	.	.	.	.	.	7.0	2.8	15.2	18.0	2.6	2.6	116
1158	E5	2	DH44	621.9	43.0	1.4	453.0	31.4	.	.	.	.	.	8.1	2.9	15.4	18.3	2.3	2.8	120
1159	E5	2	DH45	586.9	36.8	1.4	431.2	35.5	.	.	.	.	.	8.1	2.8	16.6	19.4	2.4	2.2	115
1160	E5	2	DH46	545.5	46.3	1.1	476.0	26.8	.	.	.	.	.	8.6	3.6	16.8	20.4	2.4	2.8	120
1161	E5	2	DH47	598.2	37.6	1.0	589.9	23.9	.	.	.	.	.	7.2	3.7	14.6	18.3	2.5	2.6	119
1162	E5	2	DH49	622.5	47.4	1.3	472.7	28.5	.	.	.	.	.	7.9	3.0	16.4	19.4	2.5	2.9	120
1163	E5	2	DH50	618.9	33.7	1.0	596.2	31.4	.	.	.	.	.	7.2	3.5	14.8	18.3	2.5	2.3	116
1164	E5	2	DH51	548.6	45.1	1.0	538.9	23.7	.	.	.	.	.	7.6	3.4	15.9	19.3	2.6	2.8	119
1165	E5	2	DH52	585.6	37.2	1.0	600.0	25.4	.	.	.	.	.	7.1	2.2	15.4	17.6	2.5	2.4	114
1166	E5	2	DH53	555.8	39.5	1.1	507.6	28.1	.	.	.	.	.	7.2	2.7	15.6	18.3	2.6	2.5	116
1167	E5	2	DH54	619.4	47.0	1.5	409.1	30.4	.	.	.	.	.	7.9	2.0	15.2	17.2	2.2	3.1	110
1168	E5	2	DH55	630.1	37.7	1.1	582.4	27.8	.	.	.	.	.	7.0	2.5	15.3	17.8	2.5	2.5	115
1169	E5	2	DH56	699.2	36.2	1.1	608.5	31.0	.	.	.	.	.	6.9	2.4	14.2	16.6	2.4	2.5	113
1170	E5	2	DH57	426.4	42.1	1.0	412.4	21.1	.	.	.	.	.	7.1	2.0	16.4	18.4	2.6	2.6	114
1171	E5	2	DH58	617.9	37.9	1.1	541.1	29.8	.	.	.	.	.	6.9	2.7	13.7	16.4	2.4	2.8	114
1172	E5	2	DH59	654.9	45.4	1.2	560.2	27.0	.	.	.	.	.	7.0	0.9	15.8	16.7	2.4	2.9	109
1173	E5	2	DH60	568.4	51.0	1.5	375.7	27.1	.	.	.	.	.	8.0	1.8	16.4	18.2	2.3	3.1	110
1174	E5	2	DH61	567.0	41.6	1.2	485.8	28.2	.	.	.	.	.	7.6	2.0	15.4	17.4	2.3	2.7	119
1175	E5	2	DH62	272.2	40.2	0.9	307.5	20.0	.	.	.	.	.	7.3	1.8	15.6	17.4	2.4	2.6	114
1176	E5	2	DH63	382.9	49.6	1.3	285.5	27.2	.	.	.	.	.	8.2	1.8	16.1	17.9	2.2	3.1	110
1177	E5	2	DH64	519.4	40.1	1.2	434.6	30.6	.	.	.	.	.	7.8	1.7	15.6	17.3	2.2	2.6	113
1178	E5	2	DH65	440.4	49.2	1.2	364.6	23.5	.	.	.	.	.	8.4	1.7	18.5	20.2	2.4	2.7	110

Table E.1 Continued.

No.	Env.	Rep.	Name	GYLD	GPS	GWPS	SPSM	TGW	PHT	FLL	FLW	FLA	FLS	SL	SSN	FSN	TSN	SC	GSP	HD
1179	E5	2	DH66	451.0	46.5	1.3	334.4	26.9	.	.	.	.	.	8.0	3.5	17.9	21.4	2.7	2.6	121
1180	E5	2	DH67	540.0	41.6	1.2	447.0	29.9	.	.	.	.	.	7.5	2.0	16.2	18.2	2.4	2.6	114
1181	E5	2	DH68	495.9	39.3	1.0	479.6	24.1	.	.	.	.	.	7.8	2.5	15.7	18.2	2.3	2.5	116
1182	E5	2	DH69	652.6	53.3	1.4	480.2	24.3	.	.	.	.	.	7.3	0.9	16.5	17.4	2.4	3.2	113
1183	E5	2	DH70	708.5	49.4	1.5	468.6	26.9	.	.	.	.	.	8.1	2.3	18.3	20.6	2.6	2.7	119
1184	E5	2	DH71	620.8	47.9	1.3	477.9	23.3	.	.	.	.	.	8.2	2.4	17.2	19.6	2.4	2.8	119
1185	E5	2	DH72	485.3	43.4	1.2	420.9	25.1	.	.	.	.	.	7.5	2.9	16.3	19.2	2.6	2.6	118
1186	E5	2	DH73	523.5	44.7	1.2	429.8	25.0	.	.	.	.	.	7.4	2.6	16.4	19.0	2.6	2.7	118
1187	E5	2	DH75	735.1	37.4	1.2	601.1	30.8	.	.	.	.	.	7.2	2.2	14.6	16.8	2.3	2.6	110
1188	E5	2	DH76	629.2	35.5	1.1	592.5	28.6	.	.	.	.	.	6.9	2.6	14.6	17.2	2.5	2.4	116
1189	E5	2	DH77	623.9	38.7	1.2	499.6	27.7	.	.	.	.	.	8.3	2.7	16.8	19.5	2.3	2.3	114
1190	E5	2	DH78	717.5	43.1	1.3	561.8	29.3	.	.	.	.	.	8.0	2.2	16.3	18.5	2.3	2.6	111
1191	E5	2	DH79	635.4	45.3	1.4	461.7	29.5	.	.	.	.	.	7.7	2.0	16.3	18.3	2.4	2.8	115
1192	E5	2	DH80	549.9	45.6	1.3	425.3	27.5	.	.	.	.	.	7.3	1.4	16.8	18.2	2.5	2.7	116
1193	E5	2	DH81	399.8	38.1	1.1	362.5	27.5	.	.	.	.	.	7.5	1.8	16.6	18.4	2.5	2.3	114
1194	E5	2	DH82	507.6	39.0	1.0	487.2	24.8	.	.	.	.	.	7.5	1.4	15.5	16.9	2.3	2.5	108
1195	E5	2	DH83	500.6	36.6	1.3	396.0	33.5	.	.	.	.	.	7.2	3.6	14.2	17.8	2.5	2.6	116
1196	E5	2	DH84	532.8	32.2	1.0	511.8	32.4	.	.	.	.	.	7.1	2.6	13.7	16.3	2.3	2.3	108
1197	E5	2	DH85	528.8	39.7	1.2	435.6	30.1	.	.	.	.	.	7.5	2.3	15.8	18.1	2.4	2.5	115
1198	E5	2	DH86	571.1	44.6	1.4	415.3	29.5	.	.	.	.	.	6.9	1.3	15.8	17.1	2.5	2.8	114
1199	E5	2	DH87	491.8	41.5	1.2	412.5	26.2	.	.	.	.	.	7.3	1.7	15.8	17.5	2.4	2.6	108
1200	E5	2	DH89	586.2	37.0	1.2	484.9	32.4	.	.	.	.	.	7.2	2.5	14.9	17.4	2.4	2.5	115
1201	E5	2	DH90	645.1	46.9	1.5	443.1	28.6	.	.	.	.	.	7.9	2.3	16.0	18.3	2.3	2.9	108
1202	E5	2	DH91	561.1	41.6	1.2	472.3	28.3	.	.	.	.	.	7.3	2.4	15.5	17.9	2.4	2.7	115
1203	E5	2	DH92	614.1	41.6	1.2	520.4	29.0	.	.	.	.	.	7.5	1.5	15.3	16.8	2.3	2.7	114
1204	E5	2	DH93	502.9	49.8	1.4	361.8	23.1	.	.	.	.	.	8.1	1.9	17.3	19.2	2.4	2.9	109
1205	E5	2	DH94	521.1	32.9	1.0	521.6	29.7	.	.	.	.	.	7.1	3.5	15.8	19.3	2.7	2.1	117
1206	E5	2	DH95	545.9	33.7	1.0	559.9	27.0	.	.	.	.	.	7.2	2.4	14.1	16.5	2.3	2.4	108
1207	E5	2	DH96	729.9	37.3	1.3	557.6	34.3	.	.	.	.	.	7.1	2.1	13.8	15.9	2.2	2.7	112
1208	E5	2	DH97	581.0	41.0	1.2	472.3	31.8	.	.	.	.	.	7.4	2.1	16.0	18.1	2.4	2.6	114
1209	E5	2	DH98	551.8	46.1	1.3	424.8	25.8	.	.	.	.	.	8.1	1.3	15.6	16.9	2.1	3.0	107
1210	E5	2	DH99	597.0	42.6	1.1	538.8	25.9	.	.	.	.	.	7.4	2.0	16.1	18.1	2.4	2.6	120
1211	E5	2	DH100	567.8	55.2	1.4	407.6	22.6	.	.	.	.	.	7.7	1.8	17.6	19.4	2.5	3.1	113
1212	E5	2	DH101	553.3	53.1	1.4	403.5	27.2	.	.	.	.	.	8.2	1.3	17.5	18.8	2.3	3.0	113
1213	E5	2	DH102	556.6	48.0	1.2	470.5	23.8	.	.	.	.	.	8.3	2.9	17.9	20.8	2.5	2.7	121
1214	E5	2	DH103	487.3	36.1	1.1	441.0	30.4	.	.	.	.	.	7.6	3.3	15.2	18.5	2.4	2.4	123
1215	E5	2	DH104	538.1	47.8	1.4	398.0	26.0	.	.	.	.	.	7.2	2.6	17.8	20.4	2.9	2.7	120
1216	E5	2	DH105	527.5	36.7	1.1	465.6	28.2	.	.	.	.	.	6.6	3.3	14.5	17.8	2.7	2.5	116
1217	E5	2	DH106	465.9	47.0	1.2	377.4	28.3	.	.	.	.	.	8.3	2.2	17.6	19.8	2.4	2.7	116
1218	E5	2	DH107	535.0	38.7	1.2	446.2	28.6	.	.	.	.	.	7.2	1.9	14.3	16.2	2.3	2.7	113
1219	E5	2	DH108	519.8	37.1	1.1	484.5	28.4	.	.	.	.	.	7.0	2.4	15.9	18.3	2.6	2.3	116
1220	E5	2	DH109	526.9	41.3	1.1	477.7	23.4	.	.	.	.	.	8.0	2.7	16.1	18.8	2.4	2.6	116
1221	E5	2	DH110	573.0	47.3	1.5	389.0	29.2	.	.	.	.	.	9.2	2.0	18.2	20.2	2.2	2.6	113
1222	E5	2	DH111	611.2	50.5	1.5	400.0	27.1	.	.	.	.	.	9.1	1.6	18.4	20.0	2.2	2.7	115
1223	E5	2	DH112	480.1	37.7	1.1	447.0	29.4	.	.	.	.	.	7.3	3.1	15.8	18.9	2.6	2.4	116
1224	E5	2	DH113	555.2	41.0	1.3	440.6	29.6	.	.	.	.	.	6.9	2.4	15.2	17.6	2.6	2.7	115
1225	E5	2	DH114	571.7	39.7	1.1	516.5	26.5	.	.	.	.	.	7.9	2.2	15.9	18.1	2.3	2.5	115
1226	E5	2	DH115	507.6	32.0	1.0	510.7	30.6	.	.	.	.	.	7.2	2.6	14.8	17.4	2.4	2.2	115
1227	E5	2	DH116	656.4	34.8	1.1	592.4	29.8	.	.	.	.	.	7.1	2.5	14.0	16.5	2.3	2.5	114
1228	E5	2	DH117	548.0	39.8	1.1	497.3	25.6	.	.	.	.	.	7.5	1.1	15.2	16.3	2.2	2.6	112
1229	E5	2	DH119	639.1	40.4	1.2	516.7	30.6	.	.	.	.	.	8.5	3.1	16.4	19.5	2.3	2.5	115
1230	E5	2	DH120	727.2	37.1	1.1	682.8	24.8	.	.	.	.	.	6.7	2.8	14.9	17.7	2.6	2.5	117
1231	E5	2	DH121	560.5	45.6	1.3	431.8	26.9	.	.	.	.	.	7.9	3.9	16.9	20.8	2.6	2.7	119
1232	E5	2	DH122	494.8	54.0	1.3	390.2	23.3	.	.	.	.	.	7.5	2.2	18.0	20.2	2.7	3.0	121
1233	E5	2	DH123	520.4	42.7	1.2	428.4	26.6	.	.	.	.	.	7.3	2.2	16.0	18.2	2.5	2.7	117
1234	E5	2	DH124	573.0	43.1	1.2	461.0	26.0	.	.	.	.	.	8.0	2.8	16.0	18.8	2.4	2.7	119
1235	E5	2	DH125	597.5	37.8	1.2	489.0	32.2	.	.	.	.	.	7.2	2.7	15.2	17.9	2.5	2.5	115
1236	E5	2	DH126	520.0	39.4	1.1	476.2	26.9	.	.	.	.	.	7.6	3.3	16.3	19.6	2.6	2.4	118
1237	E5	2	DH128	487.0	47.6	1.3	376.4	24.9	.	.	.	.	.	7.2	2.6	17.6	20.2	2.8	2.7	119
1238	E5	2	DH129	606.3	44.4	1.4	422.2	31.4	.	.	.	.	.	7.6	2.2	16.0	18.2	2.4	2.8	115
1239	E5	2	DH130	630.1	42.9	1.3	470.2	27.9	.	.	.	.	.	7.9	2.3	15.7	18.0	2.3	2.7	116
1240	E5	2	DH131	503.5	41.8	1.3	394.3	28.8	.	.	.	.	.	8.0	3.6	17.1	20.7	2.6	2.4	121

Table E.2 Average phenotypic data for yield contributing traits evaluated at greenhouse 2012 and 2013. Three replications in 2012 and four in 2013. Missing data is indicated by dot.

Name	Greenhouse 2012					Greenhouse 2013				
	PHT	FLL	FLW	FLA	FLS	PHT	FLL	FLW	FLA	FLS
DH1	73.7	23.6	1.7	32.5	13.6	78	24.1	2	37.7	12.2
DH3	76.1	27	2.1	45.8	12.6	80.2	27.3	2.6	56.1	10.5
DH4	64.9	20.7	1.9	31.5	10.8	65.8	24.7	2.2	43.5	11.1
DH5	68.9	22.5	1.9	33.2	12	75.9	26.4	2.2	45.9	12.1
DH6	79	22.5	1.9	34.2	11.7	78.6	23.7	2	38.3	11.6
DH7	66.1	17	1.9	25.3	9	71.3	28.7	2.4	53.3	12.2
DH8	72.4	18.4	1.7	24.9	10.9	78.3	28.5	2.1	46.6	13.8
DH9	72.9	17.2	2	27.8	8.5	73.9	27.7	2.5	55.4	11
DH11	91.9	21.5	1.8	31.1	11.7	86.8	29.8	2.1	50.3	14
DH12	51.9	18.8	2.1	30.5	9.2	54.8	21.6	2.2	37.2	10
DH13	65.9	18	1.8	25.3	10.1	72	27.1	2	43.1	13.5
DH14	61.8	19.1	1.9	27.9	10.3	71.9	25.9	2.3	46.5	11.4
DH15	63.7	20	1.6	25.2	12.5	70.1	24	1.7	33.4	13.7
DH16	66.9	20.2	1.7	27.3	12	76.1	27	2.1	45.7	12.6
DH17	68.7	26.6	1.6	32.6	17.5	81.7	28.5	2	45.2	14.2
DH18	73.6	16.9	2	26.1	8.6	71.8	30.5	2.6	62.4	11.8
DH19	79.9	15.6	1.9	23.7	8.3	78.4	28	2.3	51.4	12
DH20	70.8	18.1	1.8	26.4	9.9	73.5	29.3	2.5	59	11.5
DH21	81.3	18.6	1.8	26.1	10.5	82.8	28.9	2.4	54.4	12.1
DH22	82.3	15.1	1.6	19.3	9.4	83.4	23.4	1.9	37	11.8
DH23	76.6	21.6	1.6	26.3	13.9	78.9	27.8	2	42.8	14.3
DH24	65.2	20.3	1.9	30.6	10.7	60.5	22.3	2	36.4	11
DH25	73.4	21.5	1.6	26.6	14.5	72.6	25.6	1.9	39.5	13.2
DH26	63.3	14.9	1.5	18.3	9.6	66.2	21.9	1.8	32	12.1
DH27	78.5	15.5	1.5	18.3	10.5	79	30.3	2.4	58.4	12.4
DH28	81.5	19.7	1.6	24.1	12.7	81.4	23.7	1.8	34.2	13.1
DH29	68.7	23	2.1	37.4	11.2	69.8	25.8	2.2	45.3	11.6
DH30	74.6	25.1	1.8	35.2	14.2	78.8	26.6	2.1	44.2	12.9
DH31	74.6	19.1	2.3	34.7	8.3	76.8	23.3	2.2	40.7	10.5
DH32	68.3	15.6	1.8	21.7	8.9	70.8	25.2	2.2	43.8	11.6
DH33	79.7	20.6	1.9	30.9	11	78.6	29.7	2.4	55.8	12.5
DH34	79	17	1.9	25.5	8.9	74.7	26.5	1.9	40.5	13.8
DH35	79.5	14.5	2	22.9	7.3	74.8	20.9	2.1	34.3	10.1
DH36	75	21.1	2	34.1	10.4	76.7	27.2	2.5	53.8	10.9
DH37	77	21.2	2	33.5	10.6	76.9	27.8	1.9	40.2	15.4
DH38	66	20.6	1.5	24.5	13.7	77.1	24.7	1.9	38	12.9
DH39	76.4	13.6	1.5	16.4	8.9	74.8	22.4	1.9	33.6	11.8
DH40	78.5	13.7	1.6	17	8.7	84.2	22.2	1.8	32.8	12.1
DH41	79.2	17.4	1.6	21.9	11.1	84.5	26.4	2	41.8	13.3
DH42	72.3	18.4	1.5	21.8	12.3	77.1	26.2	2.1	42.6	12.7
DH43	77.5	14.3	1.6	18.3	8.9	79	26.7	2	42.9	13.2
DH44	84.4	19.3	1.8	26.5	11	92	28.3	2.5	56.1	11.5
DH45	68.8	18.2	1.7	24.6	10.7	77.6	24.2	2.2	41.5	11.1
DH46	77.6	21.7	1.9	32.9	11.3	79.6	30.9	2.3	56.4	13.4
DH47	74	21	1.7	29	12.1	76.8	23.8	2.2	41.5	10.8
DH49	79.4	26.2	2	41.4	13.2	77.9	29.1	2.2	50.3	13.9
DH50	75	26.1	1.9	39.6	13.6	81.4	24.5	2.1	40.6	11.7
DH51	71.1	28.7	2	45.1	14.5	74.8	24.2	2	40	11.8
DH52	62.5	27.2	1.4	30.2	19.4	70.7	25.4	1.8	35.3	14.5
DH53	57.3	18.9	2	29.5	9.6	59.8	24.9	2.2	42.9	11.5
DH54	67.7	28.3	2.2	48.3	13.2	78.4	29.8	2.4	55.5	12.7
DH55	67.6	22.1	1.7	29.8	12.9	75	23.1	1.9	35.2	12.2
DH56	62.8	26	2	40.3	13.3	70.8	22.4	2	35.6	11.2
DH57	75.3	21	1.9	30.8	11.3	69.4	24	2.1	40.2	11.3
DH58	78.6	25.4	2	39	13	83.7	25.9	2	41.3	12.8
DH59	71.1	21.8	1.5	26.6	14.1	80.5	26.4	1.9	39.9	13.9
DH60	78.9	20.5	2.1	34.1	9.7	76.6	31.9	2.3	57.4	14
DH61	70.4	16.7	1.8	23.8	9.3	72.9	27	2.1	44.3	13
DH62	78.1	21.3	1.8	30.2	11.8	75.6	28.9	2.1	48.7	13.6
DH63	73.1	25.9	2.2	44.4	11.9	77.1	28.2	2.3	50.7	12.5
DH64	79.9	21.3	1.8	30.6	11.8	85.6	23.7	1.9	36.6	12.2
DH65	66.7	14.8	1.4	16.9	10.3	75.3	27.9	1.9	42.3	14.6

Table E.2 Continued.

Name	Greenhouse 2012					Greenhouse 2013				
	PHT	FLL	FLW	FLA	FLS	PHT	FLL	FLW	FLA	FLS
DH66	71.6	16.6	2	26.2	8.3	79.4	30.3	2.8	67.9	10.8
DH67	69.4	25.4	1.8	36.1	14.1	73.3	26.3	1.8	38	14.5
DH68	69.3	21.4	2.1	34.7	10.4	73.4	24	2.4	45.3	10.1
DH69	67.7	20.4	1.6	26.3	12.6	78.3	26.8	2	41.1	13.7
DH70	76.7	16.9	1.8	24	9.4	80.2	24.9	2.1	41.8	11.8
DH71	64.7	19.8	2	31.3	9.9	67.6	26.1	2.5	51.8	10.5
DH72	67.7	22.1	1.8	31	12.5	71	23.1	1.9	34.7	12.2
DH73	68.7	18.4	1.8	26.2	10.2	72.6	27	2.1	44.7	12.9
DH75	77.1	18	1.3	17.6	14.6	85.2	26.7	1.8	38.4	14.7
DH76	69.2	21	1.8	29.9	11.7	70.7	24.4	2	38.4	12.6
DH77	75.6	22.3	1.6	27.6	14.3	76.7	31.3	1.8	45.6	17
DH78	82.2	15.3	1.6	20.1	9.5	80.3	28.4	2	45.6	14.1
DH79	79.1	20.5	1.7	27.5	12	82	26.3	2	41.2	13.3
DH80	77.6	19.3	1.7	25.9	11.3	75.8	27.6	1.9	42.2	14.3
DH81	66.5	11.8	1.6	14.9	7.4	70	27	2.3	48.8	11.9
DH82	72.2	20.5	1.8	28.7	11.6	78.8	27	2.1	45.1	12.8
DH83	85.9	19.3	2	30.5	9.7	88.4	24.3	1.8	35.4	13.3
DH84	72.5	17.4	1.6	22.4	10.7	77.4	25	1.9	36.6	13.5
DH85	67.3	17.1	2.1	27.9	8.3	71.5	26	2.2	44.7	12
DH86	72.2	22.8	1.7	30.1	13.6	79.5	24.2	1.8	34.5	13.5
DH87	75.9	21.5	1.6	27.8	13.3	83.2	28.4	1.9	42.7	15
DH89	.	.	.	.	.	79.3	23.2	2.1	39.2	10.9
DH90	68.1	27.1	2.1	45	12.9	73.2	27.4	2.2	47.9	12.4
DH91	74	13.8	1.4	15.3	9.9	78.8	27.1	1.9	40.3	14.4
DH92	75.7	22.6	1.8	31.7	12.8	76.1	26.9	1.9	40.2	14.2
DH93	72.5	18.5	1.7	25.2	10.9	67.2	26.1	1.8	37.5	14.4
DH94	72.1	19	1.7	25.5	11.2	81.2	21.3	1.9	32.6	11.1
DH95	86.3	21.5	1.6	27.2	13.4	74.2	22	1.8	32.4	12
DH96	82	17.2	1.5	20.4	11.5	80	27.8	2	45	13.6
DH97	76.5	18.7	2.1	31	8.9	78.1	23.8	2.1	40.4	11.1
DH98	72.6	21.3	2.1	35.3	10.1	72.7	27.2	2.1	44.1	13.4
DH99	77.6	14	1.7	18.8	8.2	74.8	29.1	2.7	61.9	10.8
DH100	64.7	23	1.8	32.6	12.8	66.6	26.2	2	41.2	13.2
DH101	67.9	22.4	1.8	32.3	12.3	80.3	26.3	2.1	44.6	12.2
DH102	78	16.6	1.8	23.6	9.2	79.7	29.6	2.2	52.2	13.3
DH103	71.9	28.3	2.3	50.4	12.6	74.7	28.3	2.6	59	10.8
DH104	78.2	25.2	1.9	37.8	13.3	83	28	2.2	49	12.6
DH105	67.7	28	1.9	40.9	15.2	75.8	28.9	1.9	32.9	11.4
DH106	72.1	17.8	1.9	26.7	9.4	71.3	24.7	2.2	42.3	11.4
DH107	71.1	19.3	1.7	25.7	11.5	76.4	24.4	2	39.2	12
DH108	79.2	11	1.6	14.1	6.8	77.1	27.3	2	42.4	13.8
DH109	69.9	16	1.8	22.8	8.9	68.8	26.6	2	41.1	13.6
DH110	80.1	21.4	1.7	28.3	12.8	81.3	26.5	2	41.4	13.4
DH111	77.8	26.8	1.8	37.1	15.4	82.9	29.1	2.1	47.6	14.1
DH112	81	13.2	1.6	16.4	8.4	74.4	23.7	1.9	36.5	12.2
DH113	82.4	12.6	1.8	17.3	7.2	83.2	24.8	2.1	40.6	12
DH114	62.9	18.8	1.9	28.2	9.9	68.7	27.1	2.2	47.5	12.2
DH115	76.6	12.1	1.6	15.6	7.5	74.9	24	1.9	36.4	12.6
DH116	83.4	18.8	1.9	27.5	10.2	83.6	22.4	2.1	36.5	10.9
DH117	72	22	2.1	36.1	10.6	77.6	25.5	2.3	46	11.2
DH119	76.7	22.4	1.9	34	11.7	78.4	25.3	2.1	43	11.9
DH120	77.6	15.2	1.6	19.4	9.5	76.7	26.6	2	42.1	13.4
DH121	72.9	20.7	1.8	29.9	11.4	72.3	28.2	2.4	53.6	11.8
DH122	79.6	20.4	1.4	22.2	15.5	81.2	27.6	1.9	41.3	14.6
DH123	77.6	17.6	1.4	18.9	13	76.7	21.6	1.3	22.7	16.4
DH124	76.7	20.2	1.9	29.9	10.7	73.4	27.6	2.3	51.2	11.8
DH125	67.8	19.2	1.9	29.2	10.1	71.7	22.6	2	35.1	11.6
DH126	61.6	25.6	1.7	34.9	15.3	74.8	28.9	2.4	53.9	12.3
DH128	70.3	21.4	1.6	28.2	13.1	75.8	29.7	2.3	55.4	12.9
DH129	69.1	27.9	1.7	38.1	16.1	80	24.3	1.9	36.3	12.9
DH130	69.2	22.5	2	35.6	11.3	71.7	25.8	2.1	42.8	12.3
DH131	73.5	17.9	2	28.3	9	77.3	29.2	2.6	60.2	11.2

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