The development of molecular markers and sequencing techniques has been advanced tremendously in wheat. Biparental mapping of molecular markers is very valuable in the validation of genes and markers for their chromosomal locations, gene cloning, and QTL identification. Since the simple sequence repeat (SSR) markers were developed by Röder et al. (1995, 1998), many other types of molecular markers have been developed and used in genetic mapping and QTL identification. Several consensus maps in wheat have been developed, such as the integrated maps by Somers et al. (2004) and the International Triticeae Mapping Initiative (ITMI) maps by Song et al. (2005). Recently, genotyping-by-sequencing (GBS) techniques have integrated previous markers into the consensus map of synthetic W7984 (Syn) × OpataM85 (Op) double-haploid population (henceforth, SynOpDH) (Sorrells et al., 2011; Poland et al., 2012; Saintenac et al., 2013).

### ABSTRACT

Mapping single nucleotide polymorphisms (SNPs) in wheat (*Triticum aestivum* L.) can help to develop high throughput molecular markers for important traits. The 90K Infinium iSelect SNP array was used to screen three recombinant inbred line (RIL) populations derived from three crosses, CO 960293-2/'TAM 111' (CT), 'TAM 112'/TAM 111 (TT), and 'Halberd'/Len' (HL). The objective of this study was to compare and validate the chromosomal locations of mapped SNPs in wheat. A set of 152, 124, and 180 RILs were used in CT, TT, and HL. Among the 91,829 SNPs, 54,258 SNPs were called at least in one mapping population. A set of 5950, 4861, and 8376 SNPs were mapped onto chromosomes of CT, TT, and HL, respectively, with a total of 15,604 unique SNPs. Only 374 SNPs (2.4%) were commonly mapped across three populations, and 3025 SNPs (19.4%) were mapped across all combinations of two of the three populations. The number of uniquely mapped SNPs specific to each population was 3291 (21.1%) in CT, 2418 (15.5%) in TT, and 6224 (40.0%) in HL. With known chromosomal locations of the mapped 40K out of 90K array SNPs, linkage groups in all three mapping populations were assigned onto chromosomes. More than 76% of the mapped SNPs have consistent chromosomal locations with the previously mapped 40K SNPs. A set of 2190 (14.0%) unique newly mapped SNPs and 1316 (8.4%) SNPs mapped onto multiple chromosomes were presented. These chromosome maps are essential for the discoveries of genes and quantitative trait loci (QTL) of important traits in wheat.


**Abbreviations:** CT, CO 960293-2/'TAM 111'; DArT, diversity array technology; GBS, genotyping-by-sequencing; HL, ‘Halberd’/Len’; ITMI, International Triticeae Mapping Initiative; KASP, Kompetitive allele-specific polymerase chain reaction; LOD, logarithm of odds; QTL, quantitative trait loci; RIL, recombinant inbred line; SNP, single nucleotide polymorphism; SSR, simple sequence repeat; TT, ‘TAM 112’/‘TAM 111’.

**The development of molecular markers and sequencing techniques has been advanced tremendously in wheat. Biparental mapping of molecular markers is very valuable in the validation of genes and markers for their chromosomal locations, gene cloning, and QTL identification. Since the simple sequence repeat (SSR) markers were developed by Röder et al. (1995, 1998), many other types of molecular markers have been developed and used in genetic mapping and QTL identification. Several consensus maps in wheat have been developed, such as the integrated maps by Somers et al. (2004) and the International Triticeae Mapping Initiative (ITMI) maps by Song et al. (2005). Recently, genotyping-by-sequencing (GBS) techniques have integrated previous markers into the consensus map of synthetic W7984 (Syn) × OpataM85 (Op) double-haploid population (henceforth, SynOpDH) (Sorrells et al., 2011; Poland et al., 2012; Saintenac et al., 2013).**
Akhunov et al. (2009) validated the high throughput genotyping of SNP in bread wheat using Illumina (Illumina Inc.) GoldenGate assay. Cavanagh et al. (2013) reported a consensus map based on data from seven mapping populations. In their study, a total of 7160 SNPs were mapped with 332 SNPs localized onto two positions. A set of 3469 and 3425 SNPs were mapped onto the A and B genomes, respectively, while the D genome only had 620 SNPs (Cavanagh et al., 2013). Later, a set of 9K SNP iSelect assay, 1351 diversity array technology (DArT) markers (Akbari et al., 2006), 118 SSR, and more than 400,000 GBS markers were validated by Saintenac et al. (2013). They mapped 2740 gene-associated SNPs onto the reconstructed SynOpDH population that had 1468 SSR and DArT markers by Sorrells et al. (2011). Through a study on the D genome using a 10K Infinium iSelect SNP array, more than 7000 SNPs were mapped using an Agilops tauschii Cos. F2 population from AL8/78 × AS75 (Luo et al., 2013).

Using the available public expressed sequence tag and next-generation sequences of new complementary DNA libraries, Allen et al. (2011) identified new SNPs and converted to Kompetitive allele–specific polymerase chain reaction (KASP). They mapped 480 SNPs onto a mapping population derived from ‘Avalon’ × ‘Cadenza’.

The continuous progress in high throughput genomic technologies has resulted in numerous sequencing platforms for wheat. More and more wheat genome sequences have been developed, and SNPs have been identified (Wilkinson et al., 2012; http://www.cerealsdb.uk.net/cerealgenomics/CerealsDB/indexNEW.php, accessed 20 Nov. 2014). The recent wheat 90K SNP iSelect assay developed by Illumina is a very useful genetic resource for tagging agronomically important traits. Wang et al. (2014) mapped 40,267 (hereafter, 40K) SNPs out of the 91,829 (90K) SNPs and constructed consensus maps using eight biparental mapping populations. Here we present the three diverse genetic mapping populations screened with 90K iSelect SNP array to validate the chromosomal locations for those mapped SNPs. Newly mapped SNPs beyond those mapped 40K SNPs were presented. The applications of saturated SNP wheat maps were also discussed.

**MATERIALS AND METHODS**

**Plant Materials**
A set of 124 F1 derived RILs were developed from TAM 112/TAM 111 (TT). TAM 111 (PI 631352, TAM 107/TX78V3630/Centurk 78/3/TX87V1233) and TAM 112 (PI643143, [TAM 200/TA2640]/[TAM 105*/4/Amigo*4*/Largol]) are two hard red winter wheat cultivars widely adapted in the Southern Great Plains of the United States (Lazar et al., 2004; Rudd et al., 2014). Both of them were reported to have drought tolerance but with different mechanisms (Xue et al., 2014; Reddy et al., 2014). TAM 112 has the 1AL.1RS rye translocation, wheat curl mite resistance, and Gb3 for greenbug resistance gene (Dhakal, 2014; Liu et al., 2014; Rudd et al., 2014; Reddy et al., 2013). The germplasm line CO 960293-2 (PI 615160, PI 222668/TAM 107//((Novi Sad 14//Novi Sad 603//Newton/3//Probrand 835, CO850034) has Wsm2 gene resistant to wheat streak mosaic virus (Haley et al., 2002; Lu et al., 2011, 2012). A set of 152 randomly selected RILs out of 217 F7 RILs derived from the cross CO960293-2/TAM 111 (CT) was genotyped. The third population with 180 RILs was developed from Halberd/Len (HL). Halberd (Scimitar/KenyaC6042//Bobin/3/Insignia49) is an Australian spring cultivar, developed at Roseworthy Agricultural College in 1969 (Paull et al., 1998). It has durable rust resistance, drought tolerance, and ability to maintain carbohydrate accumulation during moisture stress. Hard red spring cultivar Len (ND499/3/Justin/RL4205/Wisc261), was developed by North Dakota State University in 1979 (http://www.ag.ndsu.nodak.edu/aginfo/seedstock/varieties/VE-HRSW.htm, accessed 1 Dec. 2014). It is moderately drought and heat susceptible.

**DNA Extraction and Marker Analyses**

Five to ten leaves of 10–d-old seedlings were collected from individual lines of each population. DNA was extracted following the Cetyl trimethylammonium bromide (CTAB) protocol with minor modifications (Liu et al., 2013). One microliter of extracted DNA was run on 1% agarose gel (Ameresco) along with standard lambda DNA to estimate the quality and concentration. The DNA samples were diluted to 20 ng µL\(^{-1}\) and a 50 µL of diluted DNA per sample was used for genotyping at USDA–ARS Genotyping Lab in Fargo, ND. The Infinium 90K SNP iSelect platform was used for genotyping using BeadStation and iScan according to the manufacturer’s protocol from Illumina.

**Single Nucleotide Polymorphism Calling and Linkage Map Construction**

The output files from the hybridization were analyzed using GenomeStudio v2011.1 (Illumina Inc.). Four replicates of the parental DNA for each mapping population were included in the DNA plates for hybridization. First, all SNP genotypes were called among a total of 480 lines including parents from all three populations to eliminate monomorphic SNPs and SNPs with low quality across the three mapping populations. The SNPs that showed polymorphism to at least one population were retained. Second, clusters of each polymorphic SNP were adjusted based on the parental SNP calling scores. Clusters of each SNP in individual population were confirmed with manual curation and six types of polymorphism were grouped (Table 1). Only those SNPs validated from at least three out of four duplicated sets of parents for each population were retained for further analyses. The output SNP calling scores were converted to linkage mapping scores by assigning the scores of female parents as “A” and those of male parents as “B” for each individual population regardless of their polymorphic type. “Not called (NC)” was assigned as missing data. In addition, SNPs with more than 20% missing data and the A/B ratios outside of the range of 0.25 to 4.0 were excluded for genetic map construction.

Linkage maps were constructed using JoinMap 4.0 (Van Ooijen, 2006) based on the regression mapping algorithm and an independence logarithm of odds (LOD) scores ranged from 3.0 to 30. Genetic distance of Kosambi function (Kosambi, 1944) was used. The LOD threshold values for each linkage

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group were based on the maximum number of SNPs that can be grouped, but no marker intervals were larger than 35 cM. If a linkage group had SNPs from two subgroups of different chromosomes compared with the maps from Wang et al. (2014), the linkage group was further broken down to have a unique chromosomal location for each linkage group.

RESULTS

Types of Polymorphic Single Nucleotide Polymorphisms

Based on the types of clustering on genotyping plots, six groups of SNPs were identified in the dataset (Table 1). Type I and type II SNPs had three clearly distinguishable clusters including two parental homozygous genotypes (AA and BB) and heterozygote (AB), while only two clusters (AA or BB and AB) were classified for the other four types. The number of SNPs ranged from 856 to 2001 for each type across three populations. On average, about 300 (3.7%) commonly mapped SNPs were consistently grouped into the same polymorphic type across all three mapping populations while 675 (8.4%) commonly mapped SNPs were grouped into different polymorphic types. In total, there were only 12.1% commonly mapped SNPs across the three populations. A set of 8819, 6936, and 8440 polymorphic SNPs from all six types were used to construct genetic maps of CT, TT, and HL mapping populations, respectively (Table 1, 2).

Single Nucleotide Polymorphisms Mapped in Three Populations

A total of 5950, 4861, and 8376 SNPs were located onto chromosomes of CT, TT, and HL mapping populations covering 1608, 4252, and 4828 cM of chromosome genetic length, respectively (Table 2; Fig. 1). The identical SNPs with 100% similarity of genotyping scores were excluded for genetic map construction. The chromosomal locations of those identical SNPs were determined based on their cosegregated SNPs from the same population or themselves from another mapped population (Supplemental Data S1, S2). About 30% SNPs used to construct the genetic maps cosegregated in CT and TT, but only 0.1% cosegregated in HL. The average centimorgan per SNP was 0.27, 0.87, and 0.58 for CT, TT, and HL, respectively. Since 40K out of 90K SNPs were mapped onto chromosomes (Wang et al., 2014), comparing the SNP chromosomal locations of the mapped 40K SNPs with the three mapping populations in this study, more than 76% mapped SNPs across CT, TT, and HL were consistent with those mapped in the 40K SNPs for their chromosomal locations (Table 2). A set of 3.1 to 8.4% mapped SNPs had chromosomal locations differing from those mapped 40K SNPs. These SNPs across the three populations in our study had multiple chromosomal locations combined from various populations (Table 2; Supplemental Data S3, S4). There were about 12.5 to
15.2% SNPs mapped uniquely onto chromosomes and beyond the mapped 40K SNPs from Wang et al. (2014) (Table 2; Supplemental Data S5).

The distributions of mapped SNPs across all the chromosomes showed that chromosomes 1A, 2B, 5B, 6B, 7A, and 7B had relatively higher number of SNPs while chromosome 4D and 5D had much fewer SNPs in all the three populations (Fig. 1). In addition, chromosomes 5A and 6A in TT, and 4A and 6A in HL also had more SNPs mapped. On each chromosome, there was correspondence between the number of SNPs tagged and the genetic distance covered (Fig. 1).

Comparisons of Chromosomal Locations of Mapped Single Nucleotide Polymorphisms across the Three Populations and the 40K Single Nucleotide Polymorphism Map

Among those uniquely mapped 15,604 SNPs across CT, TT, and HL populations, 12,298 (78.8%) SNPs have the same chromosomal locations as the mapped 40K SNPs from Wang et al. (2014) in at least one of the three populations (Table 2; Fig. 2A). A set of 336 SNPs had the same chromosomal locations across all three populations and the 40K genetic map. A unique set of 2530 (1034, 650, and 846 for CT, TT, and HL populations, respectively) SNPs had consistent chromosomal locations between the mapped 40K and two of the three populations while 9432 (2495, 1692, and 5245 for CT, TT, and HL populations, respectively) unique SNPs were located onto the same chromosome between the 40K SNPs and one of the three populations (Fig. 2A). Since there is one common parent, TAM 111, between CT and TT, more commonly mapped SNPs between CT and TT were observed (Fig. 2A, 2B).

Single Nucleotide Polymorphisms Mapped onto Multiple Chromosomes

Among the mapped 40K SNPs, there were 1405 SNPs mapped onto more than one chromosome (Wang et al., 2014; Supplemental Data S3). Similarly, there were SNPs mapped onto different chromosomes across the three populations from this study. A set of 473 SNPs were part of the 1405 SNPs with their multiple chromosomal locations in agreement with the 40K SNPs (Fig. 3A; Supplemental Data S3). Only four out of the 473 SNPs were commonly mapped across three populations and the 40K SNPs, while 89 (35 + 14 + 40) SNPs were commonly mapped across two of the three populations and 380 (176 + 55 + 149) SNPs were uniquely mapped onto
The major reason for some SNPs being mapped onto multiple chromosomal locations is that some array SNP oligonucleotide probes can hybridize to the target locus and their homoeologues or paralogues (Wang et al., 2014).

**Newly Mapped Single Nucleotide Polymorphisms with Unique Chromosomal Location**

A total of 2190 SNPs were newly mapped. Among them, only 30 SNPs were commonly mapped across three populations while 355 (160 + 78 + 117) SNPs were commonly mapped across two of the three populations and 1775 (521 + 455 + 799) SNPs were mapped onto individual populations (Table 2; Fig. 2B, 3C; Supplemental Data S5). This also included the 30 SNPs mapped onto multiple chromosomes from two of the three populations (Fig. 3C).

When the number of newly mapped SNPs across populations and chromosomes were compared with the individual population (Fig. 3A). Among those SNPs with chromosomal locations differing from the 40K SNPs and not part of the 1405 SNPs, their proposed chromosomal locations combined all the chromosomes from the 40K SNPs and any of the mapped chromosomal locations from this study forming a new set of 844 SNPs (Table 2; Fig. 3B; Supplemental Data S4). Seven of the 844 SNPs combined the chromosomal locations from the mapped 40K SNPs and one of the three populations, and six of them were consistent with each other for the combined chromosomal locations (Supplemental Data S4). Among the 111 (65 + 23 + 23) SNPs combining chromosomal locations of the 40K SNPs and any two mapping populations, 106 SNPs had consistent multiple chromosomal locations (Fig. 3B; Supplemental Data S4). The rest of 726 (275 + 271 + 180) SNPs had chromosomal locations combined the 40K SNPs and the mapped locations from one of the three populations (Fig. 3B; Supplemental Data S4).
total number of mapped SNPs, they showed a similar trend (Fig. 1, 4). The number of SNPs mapped onto D genome was much lower than those mapped onto A and B genomes (11.2 vs. 44.8 and 44.0%). Chromosome 5D did not have any newly mapped SNPs in TT. Among the newly mapped SNPs, CT still had six and HL had eight SNPs without determined chromosomal locations. Therefore, these newly mapped SNPs could help to determine chromosomal locations of linkage groups constructed in other populations.

Cosegregated Single Nucleotide Polymorphisms in CO 960293-2/TAM 111 and TAM 112/TAM 111

There were more than 2000 SNPs cosegregated to other markers in CT and TT (Table 2; Supplemental Data S1, S2). In CT, each one of the 1113 mapped SNPs cosegregated with at least one of 2606 SNPs. They were localized either on the same chromosomes as their corresponding cosegregated SNPs in CT or were mapped onto chromosomes through genetic mapping of populations other than CT. Among the 1113 SNPs, 981 (88.1%) SNPs had consistent chromosomal locations across CT, TT, HL and the 40K SNPs when compared with their corresponding cosegregated SNPs. There were 107 SNPs showing consistent chromosomal locations when multiple chromosomal locations of a SNP across populations were considered. Only 25 out of 1113 SNPs showed different chromosomal locations with their respective cosegregated SNPs, but 22 out of 25 were mapped onto homoeologous chromosomes (Supplemental Data S1). We also observed that one SNP was mapped onto 7A and 4A across populations, indicating that there might be a translocation between these two chromosomes, which is in agreement with the previous study (Wang et al., 2014).

In TT, a total of 2074 SNPs cosegregated with 742 mapped SNPs. A set of 684 out of 742 (92.2%) SNPs had consistent chromosomal locations with their respective cosegregated SNPs (Supplemental Data S2). The additional 27 SNPs showed consistent chromosomal locations when multiple chromosomal locations of a SNP were considered. Among 31 SNPs with chromosomal locations differing from their corresponding cosegregated SNPs, 24 SNPs were mapped onto homoeologous groups. One SNP, on chromosome 7A and 4A, may indicate a translocation same as what we found in CT. When the 2606 SNPs from CT and 2074 SNPs from TT were compared, the same set of 499 SNPs were found (data not shown). These results showed that the chromosomal locations of these identical SNPs can be determined by either taking the chromosome locations of their corresponding cosegregated SNPs in the same population or their own chromosomal locations if they were mapped in other two mapping populations from this study or consensus maps from Wang et al. (2014) (Supplemental Data S1, S2).

Mapped Single Nucleotide Polymorphisms from Various Sources

From the 91,829 array SNPs, a unique set of 15,604 SNPs were mapped onto chromosomes of at least one of the three mapping populations (Table 3). This included the 15,360 SNPs mapped uniquely in at least one of the three mapping populations and 98 SNPs from CT, plus 146 SNPs from TT mapped based on their corresponding cosegregated SNPs (Supplemental Data S1, S2). Based on the wheat germplasm and their countries of origin used to develop SNPs, 11 groups were classified (Table 3). For all SNPs mapped across the three populations, 2714 SNPs from the confirmed 9K SNP array (Cavanagh et al., 2013) in Group
5 had the highest number and percentage over the total 91,829 SNPs (38.5%) and over the total mapped SNPs from this study (17.4%) (Table 3). Group 4 (USA, Jagger) and Group 6 (UK) SNPs were the top two groups with the highest number (1019, 1011; 717, 947) and percentage (17.1, 17.0; 14.8, 19.5%) across groups for CT and TT while Group 5 (USA-9K) had the highest number (1676) and percentage (20%) for HL. Overall, Group 5, 6, and 11 had much higher proportion of SNPs mapped across three mapping populations compared with their proportion in 90K SNPs (13.7 to 20 vs. 7.7%; 12.2 to 19.5 vs. 8.5%; 4.5 to 4.8 vs. 2.5%). However, Group 8 from durum (T. turgidum subsp. durum) and Group 9 from A. tauschii had lower percentage of SNPs mapped across the three populations compared with their percentages in 90K SNP (6.2 to 6.4 vs. 9.7%; 1.3 to 1.4 vs. 5.4%), which addressed the low polymorphism of SNPs in D genome (Poland et al., 2012; Wang et al., 2014).

Comparisons of mapped SNPs in three genomes within each group showed that the number of SNPs mapped onto A and B genomes was much higher than those mapped onto D genome (Fig. 5). Since SNPs in Group 9 were from A. tauschii line AL8/78, the majority of them were mapped onto the D genome as expected, 64.0 to 72.9% in three populations. Similarly, the majority of those SNPs from durum wheat in Group 8 were mapped onto the A and B genome ranging from 95.4 to 98.2% across the three populations. This scenario is consistent with the 40K SNPs mapped through the analyses of eight biparental mapping populations using 90K SNP array (Wang et al., 2014). The three biparental mapping populations including BT-Schomburgk × AUS33384, Young × AUS33414, and W7984 × Opata M85 (ITMI) had similar trends for Group 8 and Group 9. However, in the other five of the eight mapping populations, the number of SNPs from A. tauschii mapped onto genomes A, B, and D was very low and about the same number (Data not shown). Wang et al. (2014) also found that the proportion of SNPs mapped were 35% on A, 50% on B, and only 15% on D. Similarly, the percentages of SNPs mapped onto the

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### Table 3. Groups of single nucleotide polymorphisms (SNPs) based on original sources of SNP development and comparisons of mapped SNPs in each population across groups.

<table>
<thead>
<tr>
<th>Groups of SNPs</th>
<th>SNP from cultivars</th>
<th>SNP from singletons</th>
<th>SNP from EST or singletons</th>
<th>Total SNPs</th>
</tr>
</thead>
<tbody>
<tr>
<td>A. tauschii</td>
<td>1204</td>
<td>1019</td>
<td>929</td>
<td>3162</td>
</tr>
<tr>
<td>Young</td>
<td>1019</td>
<td>911</td>
<td>929</td>
<td>2862</td>
</tr>
<tr>
<td>W7984 × Opata M85 (ITMI)</td>
<td>929</td>
<td>911</td>
<td>929</td>
<td>2862</td>
</tr>
<tr>
<td>T. turgidum subsp. durum</td>
<td>929</td>
<td>911</td>
<td>929</td>
<td>2862</td>
</tr>
</tbody>
</table>

*CALCULATED BASED ON SNPS MAPPED IN THE THREE POPULATIONS OVER 90K SNPS WITHIN EACH GROUP.*

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### Table 4. Mapped SNPs in each population across the three mapping populations.

<table>
<thead>
<tr>
<th>Groups of SNPs</th>
<th>SNP in CT</th>
<th>SNP in TT</th>
<th>SNP in HL</th>
</tr>
</thead>
<tbody>
<tr>
<td>A. tauschii</td>
<td>1204</td>
<td>1019</td>
<td>929</td>
</tr>
<tr>
<td>Young</td>
<td>1019</td>
<td>911</td>
<td>929</td>
</tr>
<tr>
<td>W7984 × Opata M85 (ITMI)</td>
<td>929</td>
<td>911</td>
<td>929</td>
</tr>
<tr>
<td>T. turgidum subsp. durum</td>
<td>929</td>
<td>911</td>
<td>929</td>
</tr>
</tbody>
</table>

*PERCENTAGE OF SNPS MAPPED FOR EACH GROUP OVER THE TOTAL MAPPED SNPS IN THE SAME POPULATION.*

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### Table 5. Mapped SNPs in each population across the three mapping populations.

<table>
<thead>
<tr>
<th>Groups of SNPs</th>
<th>SNP in CT</th>
<th>SNP in TT</th>
<th>SNP in HL</th>
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<td>911</td>
<td>929</td>
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<tr>
<td>T. turgidum subsp. durum</td>
<td>929</td>
<td>911</td>
<td>929</td>
</tr>
</tbody>
</table>

*PERCENTAGE OF SNPS MAPPED FOR EACH GROUP OVER THE TOTAL MAPPED SNPS IN THE SAME POPULATION.*

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### Table 6. Mapped SNPs in each population across the three mapping populations.

<table>
<thead>
<tr>
<th>Groups of SNPs</th>
<th>SNP in CT</th>
<th>SNP in TT</th>
<th>SNP in HL</th>
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<tr>
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<td>Young</td>
<td>1019</td>
<td>911</td>
<td>929</td>
</tr>
<tr>
<td>W7984 × Opata M85 (ITMI)</td>
<td>929</td>
<td>911</td>
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<tr>
<td>T. turgidum subsp. durum</td>
<td>929</td>
<td>911</td>
<td>929</td>
</tr>
</tbody>
</table>

*PERCENTAGE OF SNPS MAPPED FOR EACH GROUP OVER THE TOTAL MAPPED SNPS IN THE SAME POPULATION.*
three populations in this study were 38% on A, 50% on B and 12% on D genome.

**DISCUSSION**

The eight mapping populations in Wang et al. (2014) have the parental lines from Australia and Europe. The current study has five out of six parental lines from the United States. The SNP similarity and the number of mapped SNPs across all three mapping populations reflected the diversity of the parental lines. Population TT has two parents from the same breeding program of Texas A&M AgriLife Research, so it has the lowest number of SNPs mapped. Population CT has two parents from two US wheat breeding programs, while HL has two parents from two countries, so that it had relatively higher number of SNPs mapped (Table 2). The diversity of parents in HL and the larger number of RILs partly explained why HL has a very low percentage of identical SNPs (Table 2). The comparisons of chromosomal locations of SNPs mapped in this study and in Wang et al. (2014) showed that the 90K SNP can be used to construct saturated chromosome maps for genes and QTL discovery for the US wheat.

Genetic maps from multiple populations screened using the same set of 90K SNPs can be used to compare tightly linked markers across traits and populations so that the major genes and QTL for agronomically important traits can be validated.

The applications of these chromosome maps to tag various genes and QTL in each of the three populations will be very promising. For HL population, QTL for wax content under drought, heat, and normal growth were mapped (D. Hays, unpublished data, 2015). For CT, Wsm2 and QTL for yield and yield components were mapped. For TT, Gb3 and wheat curl mite resistance gene were mapped and KASP SNPs have been developed from these array SNPs for marker-assisted breeding (S.Y. Liu, unpublished data, 2015).

**CONCLUSIONS**

This study validated that the wheat 90K Infinium iSelect SNPs had a high quality and was very suitable for high throughput genotyping of biparental mapping populations. Three biparental mapping populations had 15,604 unique SNPs mapped onto all of the 21 chromosomes. The SNP chromosomal locations were validated using three biparental populations compared with those 40K SNPs mapped based on eight biparental populations. More than 76.4% SNPs have consistent and unique chromosomal locations. There were only ~12% commonly mapped SNPs across the three mapping populations. A set of 2190 SNPs from this study were uniquely mapped beyond those mapped 40K SNPs. Kompetitive Allele Specific PCR SNPs for three resistance genes, Wsm2, Gb3, and wheat curl mite resistance, have been developed.

**Acknowledgments**

The authors thank the technical help from Peihua Yan and Jay Martin at Amarillo and Padmavathi Sengodon at College Station from Texas A&M AgriLife Research. We thank Charlie Johnson, Director of Genomics and Bioinformatics Center, Texas A&M Agrilife Research at College Station provided us access to the GenomeStudio v2011.1 from Illumina Inc. We appreciated the review and discussion with Shichen Wang from Kansas State University. The funding sources are Monsanto Beachell-Borlaug International Scholarship, Texas Wheat Producer Board, and Texas A&M AgriLife Research.
