

DNA RESEARCH **19**, 487–497, (2012)  
Advance Access publication on 2 November 2012

doi:10.1093/dnares/dss028

# Discovery of High-Confidence Single Nucleotide Polymorphisms from Large-Scale *De Novo* Analysis of Leaf Transcripts of *Aegilops tauschii*, A Wild Wheat Progenitor

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Edited by Masahiro Yano  
(Received 10 April 2012; accepted 4 October 2012)

## Abstract

**Construction of high-resolution genetic maps is important for genetic and genomic research, as well as for molecular breeding. Single nucleotide polymorphisms (SNPs) are the predominant class of genetic variation and can be used as molecular markers. *Aegilops tauschii*, the D-genome donor of common wheat, is considered a valuable genetic resource for wheat improvement. Our previous study implied that *Ae. tauschii* accessions can be genealogically divided into two major lineages. In this study, the transcriptome of two *Ae. tauschii* accessions from each lineage, lineage 1 (L1) and 2 (L2), was sequenced, yielding 9435 SNPs and 739 insertion/deletion polymorphisms (indels) after *de novo* assembly of the reads. Based on 36 contig sequences, 31 SNPs and six indels were validated on 20 diverse *Ae. tauschii* accessions. Because almost all of the SNP markers were polymorphic between L1 and L2, and the D-genome donor of common wheat is presumed to belong to L2, these markers are available for D-genome typing in crosses between common wheat varieties and L1-derived synthetic wheat. Due to the conserved synteny between wheat and barley chromosomes, the high-density expressed sequence tag barley map and the hypothetical gene order in barley can be applied to develop markers on target chromosomal regions in wheat.**

**Key words:** *Aegilops tauschii*; expression sequence tag; next generation sequencing; single nucleotide polymorphism; wheat

## 1. Introduction

Common wheat (*Triticum aestivum* L., genome constitution AABBDD) is an allohexaploid species that arose by natural hybridization between tetraploid wheat *Triticum turgidum* L. (AABB), including emmer

and durum wheats, and a diploid wild wheat relative *Aegilops tauschii* Coss. (DD).<sup>1,2</sup> *Ae. tauschii* is widely distributed in Eurasia and shows abundant genetic variation.<sup>3–11</sup> Population structure analyses revealed two major phylogenetic lineages and an HG17 minor lineage [haplogroup lineage (HGL) 17] in *Ae. tauschii*.<sup>12</sup> In turn, the major lineages 1 (L1) and 2 (L2) can be genealogically divided into six and three sublineages, respectively. It is supposed that the *Ae.*

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*tauschii* populations involved in the origin of common wheat are limited to a narrow distribution range, apparently restricted to L2, which has given rise to a founder effect in hexaploid wheat.<sup>12,13</sup> In fact, the D-genome of common wheat is less polymorphic than the A- and B-genomes.<sup>14–16</sup> Tetraploid wheat and *Ae. tauschii* can be crossed artificially to produce synthetic hexaploid wheat.<sup>17,18</sup> These synthetics can be used as intermediates to exploit the natural variation of *Ae. tauschii* in hexaploid wheat improvement.<sup>19</sup>

High-resolution genetic map construction is important for genetic and genomic research, as well as for molecular breeding.<sup>20</sup> In wheat, genetic maps are commonly constructed using simple sequence repeats (SSR) markers,<sup>21,22</sup> but the number of SSR markers reported in public databases such as the National BioResource Project (NBRP) KOMUGI website (<http://www.shigen.nig.ac.jp/wheat/komugi/strains/aboutNbrpMarker.jsp>) and GrainGene website (<http://wheat.pw.usda.gov/GG2/maps.shtml>) is not sufficient for high-resolution maps. Although SSR are the most popular marker system, the constructed map resolution remains low in plant species without a known genome sequence. An alternative marker system, single nucleotide polymorphism (SNP), has received considerable attention because it is the predominant class of genetic variation.<sup>23</sup> High-throughput SNP-typing systems can be developed for organisms with a reference genome or comprehensive expressed sequence tag (EST) database, e.g. barley.<sup>24</sup> But, in many plants having large and complex genomes and insufficient reference information, genome-wide SNP discovery is insufficient because of the presence of highly repetitive regions. In *Ae. tauschii*, an organism without a reference genome and composed of highly repetitive regions, annotation-based genome-wide SNP discovery has been developed to overcome these problems. In this strategy, Roche 454 shotgun reads with low genome coverage of one genotype were annotated, and then genomic and cDNA shotgun reads of another genotype were generated on SOLiD or Solexa platforms to identify putative SNPs. However, around 56% of the sequence length, characterized as a repetitive region, was excluded from the analysis.<sup>25</sup>

In the present study, RNA-seq, a next generation sequencing technology for transcripts, was used as a cost-effective, simpler means of SNP discovery than annotation. SNPs, insertion/deletion polymorphisms (indels), and SSRs were discovered from *de novo* assembly data from ESTs of two *Ae. tauschii* accessions, PI476874 (L1) and IG47182 (L2), that were mapped on an SSR linkage map using an F<sub>2</sub> population.<sup>26</sup> We show that SNP markers can be developed in a chromosomal region of interest using the low-coverage genome sequence of wheat chromosome 7D<sup>27</sup> or

barley GenomeZipper results obtained from a synteny model conserved among barley, *Brachypodium*, rice, and sorghum.<sup>28</sup>

## 2. Materials and methods

### 2.1. Plant material, RNA extraction, and next generation sequencing

Twenty *Ae. tauschii* accessions from each sublineage were used (Table 1). Two *Ae. tauschii* accessions, PI476874 from the L1-2 sublineage and IG47182 from the L2-2 sublineage, were used for cDNA sequencing. Total RNA was isolated from leaves of 21-day-old seedlings using an RNeasy Plant Mini Kit (QIAGEN, Hilden, Germany). mRNA was isolated from 45 µg of RNA using an mRNA Purification Kit (Takara-Bio, Ohtsu, Japan). A 200 ng aliquot of mRNA was used to fragment the mRNA and synthesize cDNA from it using a cDNA Synthesis System (Roche Diagnostics, Mannheim, Germany). Approximately 10<sup>8</sup> adapter-ligated cDNA molecules from the samples were used for library preparation using a GS FLX Titanium Rapid Library Preparation Kit (Roche Diagnostics). The library was sequenced with a GS FLX Titanium Sequencing Kit on a GS FLX System (Roche Diagnostics) according to the manufacturer's instructions. Files containing raw sequence data were deposited in the sequence read archive of the DNA Data Bank of Japan (accession number: DRA000536).

### 2.2. Assembly, SNP and indel discovery, and SSR mining

All reads from both accessions were pooled and *de novo* assembled with the GS *de novo* assembler algorithm (Newbler) version 2.6 (Roche Diagnostics) to

**Table 1.** Lineage, sublineage, accession number, and origin of *Ae. tauschii* accessions used in this study

Lineage–sublineage <sup>12</sup>	Accession number (country)
L1–1	IG48508 (Turkmenistan), KU-2627 (Afghanistan)
L1–2	<u>PI476874</u> (Afghanistan), IG126387 (Turkmenistan)
L1–3	KU-2826 (Georgia), KU-2087 (Iran)
L1–4	IG131606 (Kyrgyzstan), IG48559 (Tajikistan)
L1–5	IG48747 (Armenia), KU-2144 (Iran)
L1–6	AT47 (China), AT76 (China)
L2–1	KU-2069 (Iran), KU-2811 (Armenia)
L2–2	<u>IG47182</u> (Azerbaijan), KU-2100 (Iran)
L2–3	KU-2159 (Iran), KU-2093 (Iran)
HGL17	AE454 (Georgia), AE929 (Georgia)

Underlining indicates the accessions used for RNA-seq.

generate reference contig sequences. During assembly, primer sequences and poly-A tails were trimmed from raw reads, and parameters of a minimum overlap length of 40 bp and minimum overlap identity of 90% were used. SNPs and indels were discovered by aligning all individual reads to the reference contig sequences using GS Reference Mapper version 2.6 (Roche Diagnostics). Only the accession-specific sequence variants (supported by at least two reads) were extracted as true polymorphisms from 'All' and 'HC' sequence differences produced by the GS Reference Mapper. SSR motifs within the reference contig sequences were identified by Sputnik software (<http://espressosoftware.com/sputnik/index.html>), and indels were searched for within these motifs to extract polymorphic SSRs.

### 2.3. Gene annotation and analysis of synonymous and non-synonymous mutations

The reference sequences were aligned with the National Center for Biotechnology Information (NCBI) non-redundant (nr) protein database and the *Brachypodium distachyon* (version 1.2, <ftp://ftpmips.helmholtz-muenchen.de/plants/brachypodium/v1.2>), rice (RAP-DB, <http://rapdb.dna.affrc.go.jp/>), and wheat TriFLDB protein databases (<http://trifldb.psc.riken.jp/index.pl>) using BlastX with an *E*-value cutoff of  $10^{-3}$ . Gene ontology (GO) terms were assigned using Blast2GO<sup>29</sup> and a locally installed database based on BlastX hits against the NCBI nr database.

To study whether the discovered SNPs and indels affect amino acid sequences, the longest open reading frames (ORFs) of the isotigs that include all the 1793 contigs with high confidence (HC) polymorphism were extracted using EMBOSS.<sup>30</sup> The isotigs without any BlastX result, described above, were excluded from analysis. Only the ORFs supported by the BlastX search were selected.

### 2.4. SNP and SSR validation

Validation of identified SNPs was performed through cleaved amplified polymorphic sequence (CAPS), derived CAPS (dCAPS), and high-resolution melting (HRM) methods. Gene-specific primer sequences, SNP locations, product length, and restriction enzymes are summarized in Supplementary Table S1. dCAPS primers were designed using the dCAPS Finder 2.0 program available on the website <http://helix.wustl.edu/dcaps/dcaps.html>.<sup>31</sup> The polymerase chain reaction (PCR) conditions for CAPS and dCAPS markers were 1 cycle of 94°C for 2 min and 40 cycles of 94°C for 30 s, 60°C (for CAPS) or 56°C (for dCAPS) for 30 s, and 68°C for 30 s. HRM analysis was performed using a LightCycler 480 Real-Time PCR System and LightCycler 480 HRM Master 2 × reagents

(Roche Diagnostics) according to our previous study.<sup>32</sup> For HRM analysis, all samples were spiked with 10–50% of PI476874 DNA to facilitate discrimination of the homozygous genotype. All PCR products were checked on a 1.5% agarose gel to ensure the presence of a single band.

SSR markers, depending on the indel length (see section 3.4), were amplified following the same conditions for CAPS markers or were analysed by HRM as described above. The polymorphic information content (PIC) was calculated using Excel Microsatellite toolkit add-in software.<sup>33</sup>

### 2.5. Comparison of HC SNPs and previously reported SNP dataset

For all of the 4337 HC SNPs, 100 bp sequences were extracted from 1748 contigs, positioning SNPs in the middle of the sequence. These sequences were BlastN searched against *Ae. tauschii* gene sequences with SNPs (*E*-value cutoff of 10 and gap extension penalty of 0) reported previously and published at <http://avena.pw.usda.gov/wheatD/agsnp.shtml>.<sup>25</sup>

### 2.6. Linkage map construction

A set of 104 F<sub>2</sub> individuals derived from a cross between PI476874 and IG47182 was used as the mapping population. A total of 19 cfd, 21 barc, 17 wmc, 20 gwm, 8 gdm, and 2 hbg SSR markers (<http://wheat.pw.usda.gov/GG2/index.shtml>, [http://nics.naro.affrc.go.jp/team/dna\\_marker/](http://nics.naro.affrc.go.jp/team/dna_marker/)) were assigned to each chromosome as anchor markers. A genetic map was constructed using MAPMAKER/EXP version 3.0b.<sup>34</sup> The genetic distances were calculated with the Kosambi function.<sup>35</sup>

### 2.7. In silico mapping of contigs with HC SNPs on virtual barley chromosomes

Shotgun barley genomic reads mapped on the virtual barley chromosomes were extracted from flow-sorted chromosome reads submitted by Mayer *et al.*<sup>28</sup> (accession number ERP000445). The tBlastX algorithm was used to align the 1793 contigs with extracted barley genomic reads and against a set of 5006 full-length cDNAs (accession numbers AK248134 to AK253139),<sup>36</sup> and a set of 23623 full-length cDNAs (accession numbers AK353559 to AK377172),<sup>37</sup> with an *E*-value cutoff of  $10^{-1}$ . The Blast search results obtained against *Brachypodium* and rice database were also used (see section 2.3).



### 3. Results and discussion

#### 3.1. Sequencing and assembly of *Ae. tauschii* ESTs

To see how many SNPs could be discovered in one RNA-seq experiment between two phylogenetically distinct *Ae. tauschii* accessions, PI476874 and IG47182 (respectively from L1 and L2) were selected. The sequencing of leaf cDNA libraries produced 669 383 and 700 124 reads corresponding, respectively, to 247 Mb and 254 Mb per accession after trimming. All reads from both accession-derived libraries were assembled using Newbler 2.6. Newbler assembled reads into a contig representing transcript regions, isotigs (sets of contigs representing a partial or entire transcript), and isogroups (sets of isotigs). During the assembly process, Newbler constructed multiple alignments of overlapping reads and divided them into consistent sequences, i.e. contigs. Alignments that cannot be divided are collected as isogroups, and branching structures between them are searched by traversal paths through connected branches, i.e. isotigs (isotigs and isogroups are Newbler-specific terms). Different isotigs within the same isogroup represent alternative splicing variants. Thus, an isogroup represents genes, isoforms, or gene families. In this study, sequences shorter than 100 bp were excluded from the following analyses. A total of 10 224 contigs were assembled into 9145 isotigs (including some contigs that were not combined into isotigs), with a total of 7753 isogroups obtained. The length of the majority of contigs and isotigs ranged between 500 and 1000 bp, with an average of 786 and 1021 bp, respectively (Table 2). However, among isotigs, a sequence length as long as 11 328 bp was found (isotig02315), which showed sequence similarity to a *Brachypodium distachyon* E3 ubiquitin-protein ligase UPL1-like protein (XP\_003575554.1, *E*-value = 0).

For functional gene annotation, isotigs were reassembled to remove redundancy and to obtain longer transcripts using CAP3 with default parameter settings (90% identity and overlap of 40 bp)<sup>38</sup>

according to Ewen-Campen *et al.*<sup>39</sup> Overall, 8895 assembled sequences were produced, and sequence similarity searches were conducted against the NCBI nr, rice, *Brachypodium*, and wheat protein databases using the BlastX algorithm. Of the query sequences, 90% had BlastX hits in the NCBI nr protein database. Similarly, 89 and 87% of the query sequences showed homology to annotated *Brachypodium* proteins and annotated rice proteins, respectively. On the other hand, 68% of the contig sequences had homology to wheat proteins, which might be due to the lower number of proteins deposited in the wheat database (8590 proteins) than the *Brachypodium* (31 029 proteins) and rice (40 353 proteins) databases.

To see whether the sequenced transcripts are functionally diverse or not, GO annotation was performed based on the BlastX hits against the NCBI nr database. In total, 7740 sequences were assigned to one or more GO annotations. Of the assigned GO terms, 13 260 were under the biological process domain, 10 280 under molecular function, and 9750 under cellular component (Fig. 1). A large functional diversity of genes was found in the transcriptomic data. Because the total RNA for the transcriptome analysis was extracted from leaves, a large proportion of the assignments fell into the plastids category of the cellular component subontology.

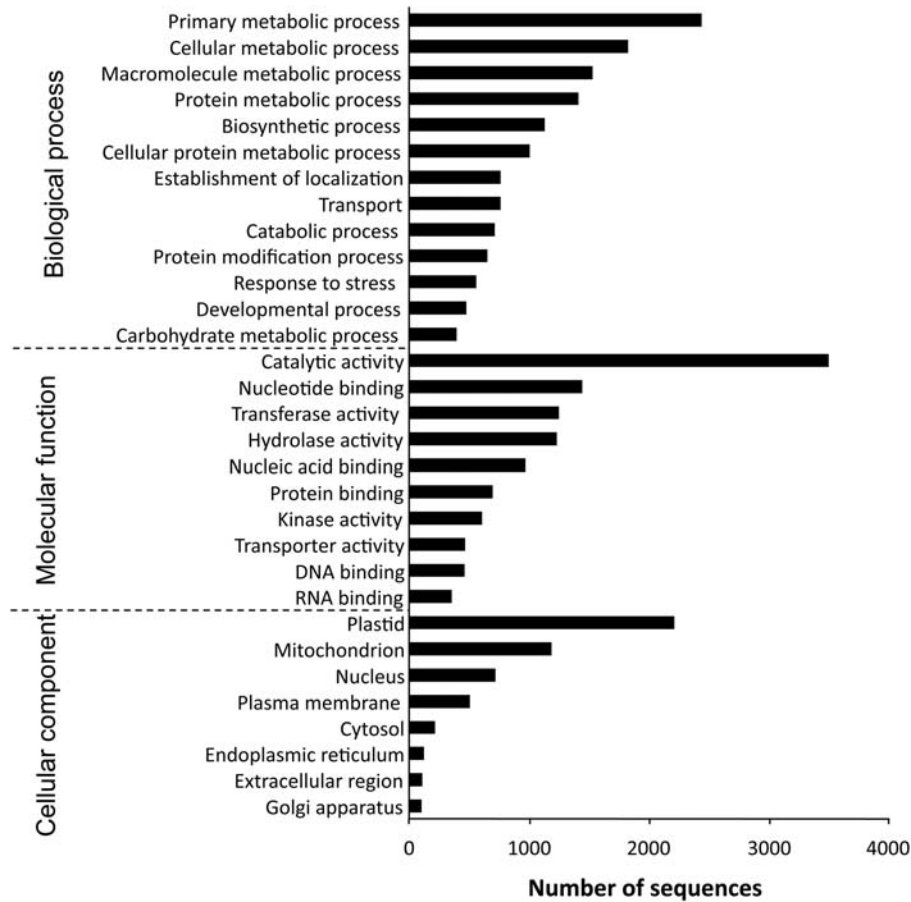
#### 3.2. SNP and indel discovery

Polymorphic sites were discovered using GS Reference Mapper to align individual reads from both accessions against the reference contig sequences. Among the 10 351 total polymorphic sites, 9435 were SNPs and 739 were indels (Table 3). Furthermore, according to the read depth ( $\geq 3$  non-duplicate reads) and quality ( $QV \geq 20$ ), 4578 polymorphic sites were classified as HC polymorphisms, including 4337 SNPs (in 1748 contigs), 198 indels (in 153 contigs), and 44 variants with two or more nucleotide changes. The HC SNPs data are available online as Supplemental data (Supplemental Data1.fna). HC SNP frequency was one SNP per 1854 bp, and when considering all the discovered SNPs the frequency, it was 852 bp per SNP (Table 3).

To study how many HC SNPs are also present in the polymorphism dataset reported by You *et al.*,<sup>25</sup> a BlastN search was performed using as query 4337 100-bp sequences, in which each of the HC SNPs were positioned in the middle. Hits were obtained for all the 4337 sequences with an *E*-value cutoff of 10, of which 546 SNPs were common to our dataset (Supplementary Tables S2 and S3). With an *E*-value cutoff of  $10^{-5}$ , 1943 hits were obtained, but the number of common SNPs between the two datasets did not differ greatly (538 SNPs). These results

**Table 2.** Contig and isotig sequence length distribution

Sequence length (bp)	Number of contig	Number of isotig
100–500	3300	1162
501–1000	4350	4612
1001–1500	1622	1934
1501–2000	594	828
2001–2500	199	305
>2500	159	304
Total	10 224	9145
Average length (bp)	786	1021



**Figure 1.** GO classification of assembled sequences. The results are summarized into three main subontologies: biological process, molecular function, and cellular component. Based on BlastX results against the NCBI nr protein database, 7740 sequences were assigned to one or more GO annotations.

**Table 3.** Polymorphisms detected between two *Ae. tauschii* accessions

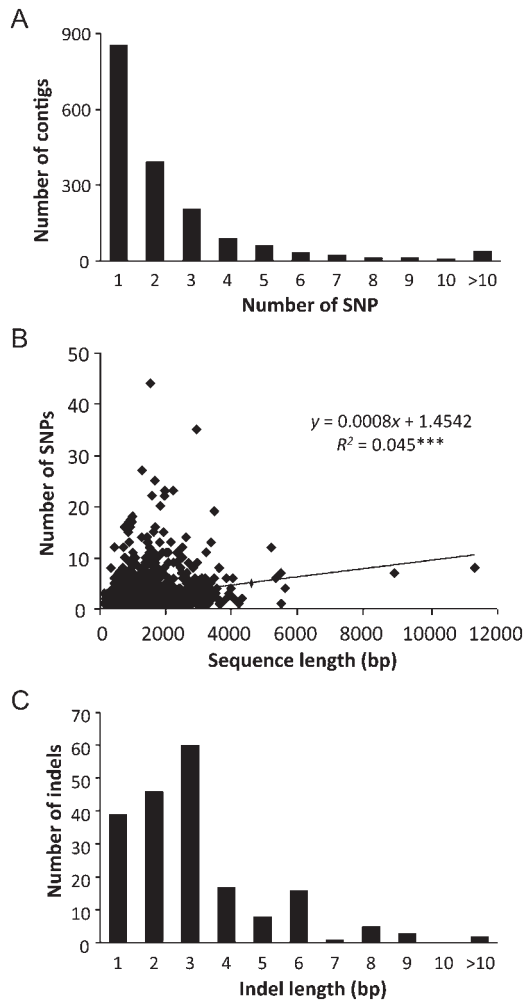
	Number of polymorphic sites	
	Total polymorphic sites	HC polymorphic sites
Total	10 351 (3578 contigs)	4578 (1793 contigs)
SNPs	9435 (3444 contigs)	4337 (1748 contigs)
Indel	739 (539 contigs)	198 (153 contigs)
Involving two or more nucleotides	112 (100 contigs)	44 (42 contigs)
Average bp per polymorphic site <sup>a</sup>	777	1756
Average bp per SNP <sup>a</sup>	852	1854

<sup>a</sup>Calculated by dividing the total number of (HC) polymorphic sites or SNPs by the total length of contigs (8 039 509 bp).

indicate that the majority of HC SNPs (around 3800) are only present in our dataset. Because the genome of *Ae. tauschii* is composed of large repetitive

regions, only 44% of the total genomic read length has been available for SNP discovery.<sup>25</sup> Our results indicate that SNP discovery by RNA-seq is cost-effective in organisms with complex genomes, as reported in maize.<sup>40</sup>

Although most contigs with HC polymorphisms contained one or two HC SNPs, 41 contigs had a large number of SNPs, ranging from 11 to 44 (Fig. 2A). The number of SNPs per contig was not completely dependent on sequence length, indicated by the low coefficient of determination ( $R^2 = 0.05$ ) (Fig. 2B). To study whether these nucleotide variations affect amino acid sequences, the longest ORFs from isotigs that include contigs with HC polymorphisms were extracted. The longest ORFs supported by BlastX search were found in 1538 out of the 2214 isotigs. Synonymous and non-synonymous mutations were analysed on contig sequences. In about 1100 out of the 1379 selected contigs, nucleotide variations were found mainly within the ORF, whereas the number of SNPs was similar between the ORF and untranslated region (UTR) in around 80 contigs (Supplementary Table S4). Although the number of



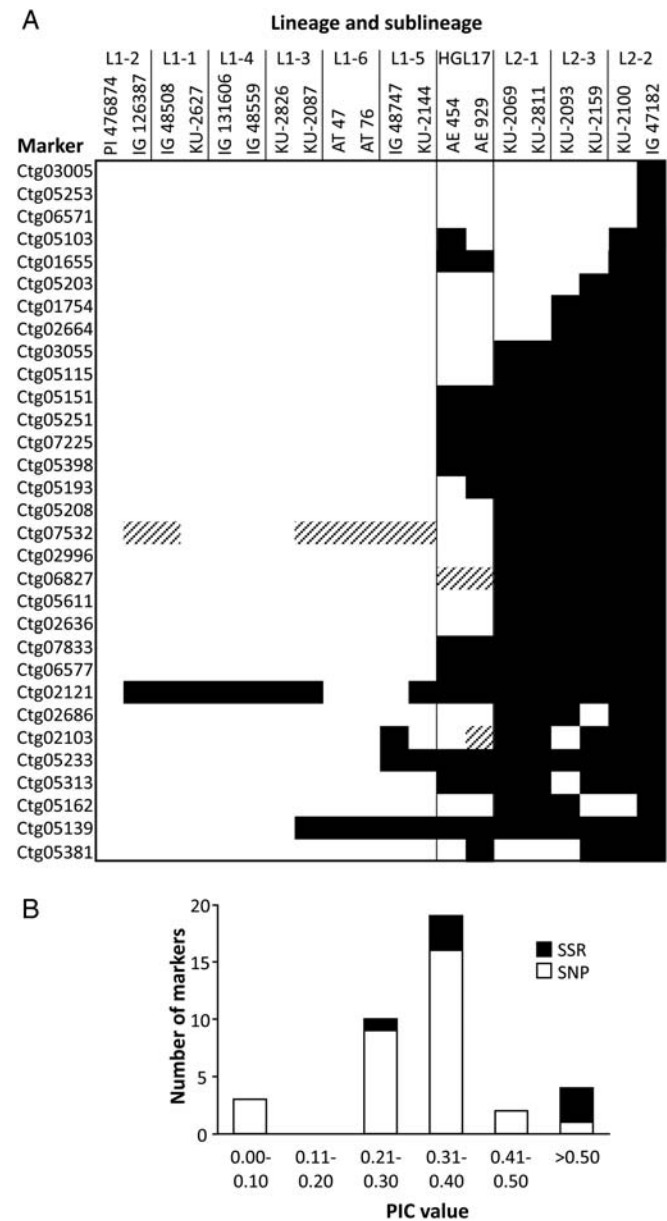
**Figure 2.** Detection of SNPs and indels in the contigs. (A) Frequency distribution of HC SNPs per contig ( $n = 1748$  contigs). (B) Relationship between the number of SNPs per contig and the contig length; data are from 1748 contigs containing SNPs. Significant correlation is indicated by asterisks ( $^{***}P < 0.001$ ). (C) Frequency distribution of HC indel length in base pairs per contig in a total of 153 contigs.

SNPs was higher in ORFs than in UTRs, synonymous mutations predominated in most cases. Non-synonymous mutations outnumbered synonymous ones in 370 contigs. Nonsense mutations were observed in four contigs. However, we cannot discharge the possibility that the reads of paralogous genes are included in these highly polymorphic contigs.

The predominant length of indels was 3 bp, followed by 2, and 1 bp (Fig. 2C). The longest indel mutation was 11 bp in contig04102 and contig05280. Indels were found in 90 out of the 1379 analysed contigs (Supplementary Table S4), of which 45 contigs included indel mutations within ORF, and frame-shift mutations occurred in 16 contigs. These results indicate that, despite the high number of polymorphic sites, the effect on protein sequence is not necessarily high.

### 3.3. SNP validation

To validate the detected SNPs, 33 polymorphic contigs were randomly selected. Of the 33 contigs, 30 contained HC SNPs and the remaining 3 contained lower confidence (LC) SNPs. The validation was performed by genotyping 20 diverse *Ae. tauschii*



**Figure 3.** Validation of identified polymorphisms in the contigs. (A) Summary of genotyping results of the 31 polymorphic SNP markers in the 20 *Ae. tauschii* accessions. Genotypes of the two accessions used in transcriptome sequencing, PI476874 and IG47182, are shown in the first and last columns, respectively. White, black, and shaded regions indicate the PI476874, IG47182, and other alleles, respectively. (B) Frequency distribution of PIC values of SNP markers (open bars) and SSR markers (black bars) among the 20 *Ae. tauschii* accessions. A total of 31 SNP and 6 SSR markers were used.



accessions, chosen based on the intraspecific diversification patterns of *Ae. tauschii*.<sup>12</sup> The selected accessions consisted of two accessions from each of the nine *Ae. tauschii* sublineages (six of L1 and three of L2) and HGL17, excluding any admixtures (Fig. 3A).

First, all 33 contigs were searched for restriction enzyme recognition sites, with at least 14 SNPs found and converted into CAPS markers. All 14 CAPS markers were polymorphic among the examined accessions (Supplementary Fig. S1A). An alternative to a CAPS marker is a dCAPS marker that consists of the introduction of one or more mismatches into the primer, creating a restriction site dependent on the presence or absence of the SNP.<sup>41</sup> Five of the SNPs that were not converted into CAPS markers were used to develop dCAPS markers by introducing one or two mismatches in the primer sequence. Two dCAPS markers could not be used for genotyping because unexpected bands were amplified by PCR, and a dCAPS marker for contig05220 was unavailable due to the generation of digestion-resistant PCR products in some accessions (Supplementary Fig. S1B). In dCAPS markers, a single mismatch at position 1, 2, or 3 from the 3' end of the primer is preferred to avoid digestion-resistant products.<sup>42</sup> However, in some cases, a mismatch at position 1 or 2 may also lead to undigested products, if the polymerase has proofreading exonuclease activity.<sup>43</sup> The digestion-resistant products were generated for unknown reasons because in the dCAPS analysis of the contig05220 marker, a single mismatch was introduced at position 1 and amplification was performed using a *Taq* DNA polymerase lacking proofreading activity. The remaining two dCAPS markers were successfully used in genotyping (Supplementary Fig. S1C).

SNP genotyping based on HRM analysis has also been reported in hexaploid wheat and *Ae. tauschii*.<sup>32</sup> Primers for HRM analysis were designed for the remaining 17 contigs (including the three contigs that failed in the dCAPS analysis) to obtain PCR products of ~100 bp. Only two of the 17 HRM primer sets failed in polymorphism detection, although both amplified genomic regions contained HC SNPs between PI476874 and IG47182. HRM analysis is useful as an alternative to SNP-typing because it is cost-effective when the restriction enzyme in CAPS/dCAPS markers is expensive. Another advantage of HRM is the possibility of detecting more than two alleles (Supplementary Fig. S2), which is not possible with CAPS/dCAPS. In addition, the relatively short length of the PCR products required for HRM analyses increases the probability that primer pairs are located within a single exon because more than half of the exons in plant genomes are less than 145–156 bp (Supplementary Table S5). Our results indicate that almost all of these SNPs can be converted to

PCR-based molecular markers, at least in diploid wheat species.

To evaluate the allelic diversity within the *Ae. tauschii* population, PIC values were calculated for each validated SNP marker. PIC values ranged from 0.091 to 0.591 (average, 0.313) in the 20 *Ae. tauschii* accessions (Fig. 3B). Among the 31 markers, three showed IG47182-specific SNP alleles, and 15 clearly distinguished the L1 accessions from L2 (Fig. 3A). Because many of the validated SNPs were polymorphic between L1 and L2 accessions, the markers developed using information about these SNPs can be used in genotyping of mapping populations obtained from interlineage crosses (L1 × L2). Moreover, considering that the subspecies *strangulata* is a possible major D-genome donor and the evolutionary birthplace of hexaploid common wheat, the D-genome donor has been thought to belong to L2,<sup>12</sup> indicating that these markers might be useful for genotyping the progeny of common wheat cultivars crossed with L1-derived hexaploid wheat synthetics. Further studies are needed to confirm this hypothesis. The HGL17 accessions, considered one of the ancestral lineages of *Ae. tauschii*, are not included in either L1 or L2, but rather are located genealogically between these two lineages.<sup>12</sup> Consistently, the genotype patterns of the two HGL17 accessions analysed (AE454 and AE929) were intermediates between L1 and L2 accessions.

### 3.4. EST-SSR mining and validation

Among all 10 224 contigs, a total of 2778 SSR motifs were found in 2072 contigs and were composed mainly of trinucleotide motifs (Table 4). Indel polymorphisms between PI476874 and IG47182 were searched as polymorphic SSRs in the 2778 motifs. In total, 54 polymorphic SSRs were found in 50 contigs, with 20 of them HC SSRs. Based on these data, 18 EST-SSR markers, including 14 HC and 4 LC polymorphic SSRs, were developed for validation in the 20 *Ae. tauschii* accessions. Seven EST-SSR markers generated multiple bands or amplified products with a length much longer than expected

**Table 4.** SSR motifs found in 10 224 contigs

	Number of motifs
Total motifs	2778 (2072 contigs)
Dinucleotide motifs	201
Trinucleotide motifs	1896
Tetranucleotide motifs	380
Pentanucleotide motifs	301
Polymorphic SSRs	54 (50 contigs)
HC polymorphic SSRs	20 (19 contigs)

(probably due to the presence of introns) and were excluded from further analyses. Four out of the eight EST-SSR markers with more than a 4-bp difference were able to distinguish genotypes of samples in 13% non-denaturing polyacrylamide gels. HRM analysis was conducted for the other EST-SSR markers, including indels with less than a 5-bp difference, and this detected polymorphisms in only two of the seven EST-SSR markers. PIC values of these six markers ranged from 0.305 to 0.686, with an average of 0.424 (Fig. 3B). The number of alleles in the EST-SSR markers ranged from two to six (average, 3.0), which was higher when compared with that in SNP markers with two to three alleles (average, 2.1). This difference might reflect the higher average PIC value of the EST-SSR markers.

### 3.5. Genetic map construction

We developed 37 polymorphic markers, including 31 SNPs and 6 EST-SSRs. To study the proportion of these markers that can be assigned to a genetic map, genotypes of 104 F<sub>2</sub> individuals obtained from a cross between PI476874 and IG47182 were determined. All these markers were successfully mapped onto a linkage map constructed using 87 publicly available SSR markers.<sup>26,32</sup> The total map length was 1282.1 cM, with an average interval of 9.5 cM between markers. In total, 12 markers were distorted on chromosome 1D, 24 markers on chromosome 2D, 6 markers on chromosome 4D, and 10 markers on chromosome 5D. Segregation ratios of the newly mapped markers are presented in Supplementary Table S6. The distribution of the 37 marker positions ranged from 1 on chromosome 1D to 12 on chromosome 5D (Supplementary Fig. S3). Two markers, one SNP marker and an SSR marker, were derived from different sites of contig06827, and both mapped to the same location.

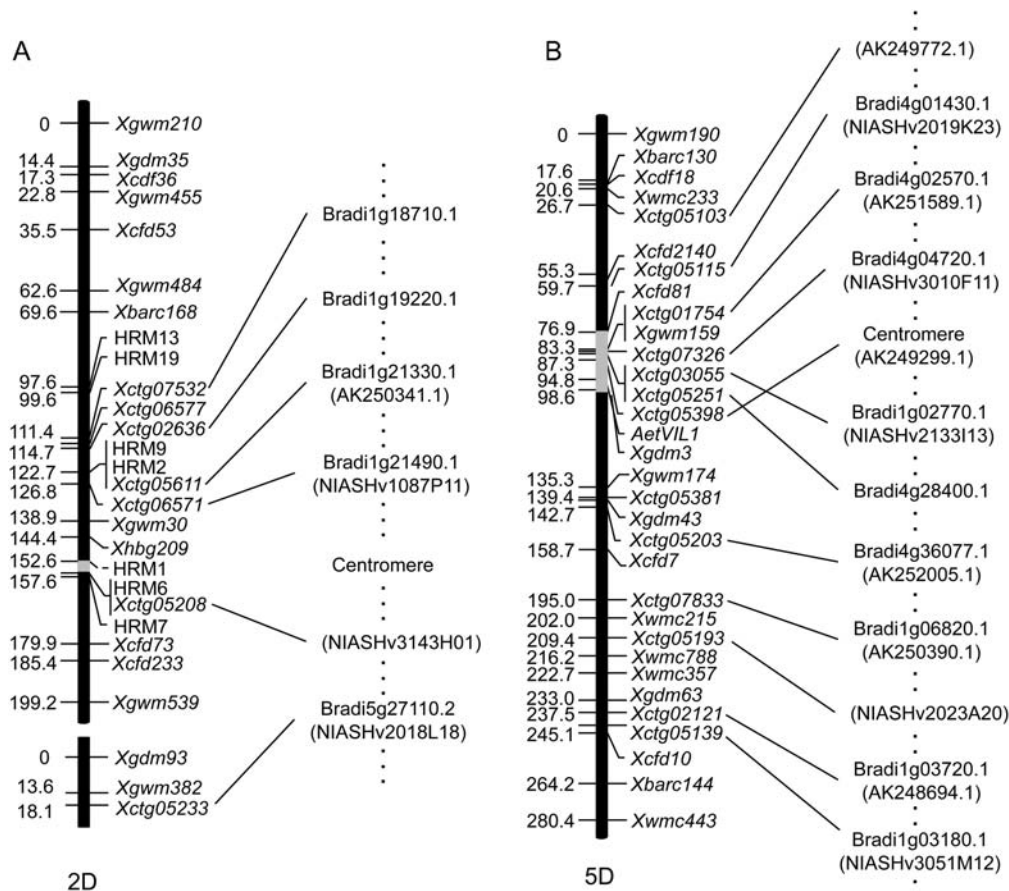
We performed a BlastN search of the 36 mapped contigs against the deletion-mapped ESTs of common wheat,<sup>44</sup> obtaining 17 matches (Supplementary Table S7). Of the 17 contigs, 14 (82%) were located on the same homoeologous group chromosomes as the deletion-mapped ESTs. Recently, a genome survey sequence of common wheat chromosome 7D was published.<sup>27</sup> To compare the order of the six contigs that mapped to chromosome 7D of *Ae. tauschii*, a BlastN search was performed against the 7D Synthetic Build v2.0.<sup>27</sup> Four contigs were assigned to the short arm and two to the long arm of chromosome 7D, as expected based on the *Ae. tauschii* genetic map (Supplementary Table S8). The contig order in the survey sequence data was similar to that in the 7D linkage map, although the position of contig02996 differed slightly.

In barley, a hypothetical gene order has been proposed for each of the seven chromosomes based on conserved synteny among barley, *Brachypodium*, rice, and sorghum.<sup>28</sup> Due to the conserved synteny between wheat and barley,<sup>45</sup> the contigs with HC SNPs were mapped on the virtual barley chromosomes, aligning with the shotgun barley genomic sequences.<sup>28</sup> A total of 1450 contigs (*E*-value cutoff of 10<sup>-20</sup>) were mapped with a distribution of around 200 contigs per chromosome (Table 5). The order of contigs on the genetic map of chromosomes 2D and 5D was also compared, respectively, with the virtual barley chromosomes 2H and 5H. These two chromosomes were selected because the number of mapped contigs was higher than that for the remaining chromosomes. Of the seven contigs that mapped to chromosome 2D, one failed to be assigned to any barley chromosomes, four were assigned to chromosome 2H, and two to other chromosomes (Supplementary Table S9). To confirm this result, tBlastX search was performed against 5006 and 23 614 barley full-length cDNAs,<sup>36,37</sup> and BlastX search was performed against *Brachypodium* and rice protein database. Based on these Blast hits, six out of the seven contigs were located on chromosome 2H (Supplementary Table S9), indicating that some homologous genes on the chromosome other than 2H were hit in the former analysis. Contig06577 failed to be assigned to any barley chromosome. The contig order on chromosome 2D of *Ae. tauschii* corresponded to the gene order on chromosome 2H of barley (Fig. 4A). Similarly, 12 out of 13 contigs of *Ae. tauschii* chromosome 5D were assigned to chromosome 5H of barley based on tBlastX hits against barley shotgun genomic reads (Supplementary Table S10). Contig05381 was assigned to chromosome 2H, and this result was confirmed by performing a Blast search against barley cDNA and *Brachypodium* and rice protein sequences (Supplementary Table S10). The contigs on chromosome 5D of *Ae. tauschii*, except for contig05398, showed an order identical to

**Table 5.** Number of contigs with HC SNPs mapped on the virtual barley chromosome

Chromosome number	<i>E</i> -value cutoff		
	<0.1	<10 <sup>-5</sup>	<10 <sup>-20</sup>
1H	229	209	197
2H	247	235	219
3H	234	214	205
4H	203	187	182
5H	275	254	241
6H	211	199	192
7H	259	234	214
Total	1658	1532	1450





**Figure 4.** Synteny between chromosomes 2D and 5D of *Ae. tauschii* and 2H and 5H of barley. Based on tBlastX hits against barley full-length cDNA and *Brachypodium* protein database, the contig orders on chromosomes 2D (A) and 5D (B) were compared with those on the barley virtual chromosome in the genome zipper. The clone names and accession numbers of barley cDNAs are indicated in parentheses.

that on barley chromosome 5H, whereas contig05398 was located in a slightly different region (Fig. 4B). Previously, ~14% of barley genes could not be assigned to virtual chromosomes by the GenomeZipper approach.<sup>28</sup> Therefore, contig06577 that failed to be assigned to the virtual barley chromosomes might correspond to the unassigned 14% of barley genes. Indeed, this contig showed sequence similarity with *Brachypodium* and rice genes Bradi1g19250 and Os07g0656700 that are probably located on the short arm of chromosome 2H, according to the synteny with barley (Supplementary Table S9). Furthermore, contig05381 (mapped on chromosome 5DL but assigned to barley 2HS) also showed sequence similarity with Bradi4g34390 and Os09g0502200 that probably map to chromosome 5HL of barley (Supplementary Table S10). The chromosomal locations of the remaining mapped contigs were similarly confirmed (Supplementary Table S11). These results suggest that the contigs should be assigned to virtual barley chromosomes not only by alignment with the shotgun genomic reads, but also by alignment with *Brachypodium* and

rice protein sequences. The chromosomal locations of unassigned contigs might be searched based on the synteny among barley, *Brachypodium*, and rice. Our results indicate that information on hypothetical gene order in barley may be useful for the development of molecular markers in target chromosomal regions of wheat.

### 3.6. Conclusion

Marker development in targeted chromosomal regions is important for map-based gene cloning and for molecular breeding in wheat and other crops. In this study, transcriptomes of two *Ae. tauschii* accessions belonging to different major lineages were compared, yielding 4578 HC-polymorphic sites from 1793 contigs. Thirty-one SNPs were validated in the 20 diverse *Ae. tauschii* accessions through conversion into CAPS, dCAPS, and HRM markers. Development of CAPS markers is dependent on the availability of appropriate restriction enzymes and their cost. In some dCAPS markers, generation of digestion-resistant PCR products interferes with precise genotyping.

In this study, we showed that HRM analysis is available for SNP typing. The SNP markers developed in this study could be applied to construct an F<sub>2</sub> map between L1 and L2 accessions of *Ae. tauschii*, and probably between the D genomes of common wheat and L1-derived synthetic wheat. One next generation sequencing experiment on transcriptomes of parental accessions leading to *de novo*-generated SNP markers was able to identify the chromosomal location of more than 1700 genes in the wheat D genome. RNA-seq is a more cost-effective method for SNP discovery than the annotation-based one in organisms with large and complex genomes. In addition, due to the conserved synteny between wheat and barley chromosomes, the barley high-density EST map and linear gene order can be applied to develop markers on the target chromosomal regions of wheat. Accompanied by further progress on the wheat genome project coordinated by the International Wheat Genome Sequencing Consortium (<http://www.wheatgenome.org/>), more information about genomic sequence data of each chromosome will become available for wheat marker development.

**Acknowledgements:** The authors would like to thank Ms Yuka Motoi at Okayama University for technical assistance.

**Supplementary data:** Supplementary Data are available at [www.dnaresearch.oxfordjournals.org](http://www.dnaresearch.oxfordjournals.org).

## Funding

This work was supported by grants from the Ministry of Education, Culture, Sports, Science, and Technology (MEXT) of Japan (Grant-in-Aid for Scientific Research (B) No. 21380005 and Grant-in-Aid for Challenging Exploratory Research No. 23658010) to S.T., and by MEXT as part of a Joint Research Program implemented at the Institute of Plant Science and Resources, Okayama University in Japan.

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