

Research Article

Transcriptome of Homoeologous Genes Deduced from the Full-Length cDNA Clones of Common Wheat, *Triticum aestivum* L

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Abstract

Allopolyploidization is an important event in plants, since it enhances heterosis and wide environmental adaptations. Common wheat, *Triticum aestivum* (AABBDD), arose through hybridization between *T. turgidum* (AABB) and *Aegilops tauschii* (DD) and subsequent whole genome duplication. To identify homoeologous genes expressed from the three distinct genomes of common wheat, we comprehensively surveyed available Expressed Sequence Tags (ESTs), based on the proofed 26,241 full-length cDNA data. In total, 76,568 homoeologous genes were classified. These homoeologous genes were grouped into the 36,389 gene clusters, and assigned to each chromosome and/or chromosome arm of common wheat. Transcript specific homoeologous genes could be identified. In addition to protein coding genes, non-coding genes were located on

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chromosomes and/or chromosome arms. About half of the homoeologous genes acted as single copy genes, showing diploidization of these genes. Preferential gene expression from the B genome was found not only in single copy genes, but also in genes with multiple copies. Wheat specific genes were mostly in single copies, and expressed more from the B genome than the other genomes. GO classification showed that expressed genes have typical functions that characterize hexaploid wheat. This reference set of expressed genes in common wheat should be an indispensable genome resource.

Keywords: Allohexaploid; Full-length cDNAs; Homoeologous transcriptome; Subgenome fractionation; Wheat

Introduction

Widespread occurrence of polyploidization (whole genome duplication) in plants provides evidence that it has advantages in development, adaptation and diversification [1-3]. Allopolyploidy resulting from interspecific or intergeneric hybridization and multiplication of more than two sets of genomes provides evolutionary advantages through speciation and environmental adaptation of higher plants, including many important crops [2,4-6]. At certain times, whole genome duplication has led to paleopolyploidy, showing structural genetic diploidization and subgenome fractionation (selective loss and retention of protein coding genes and non-coding RNA genes) leading to balance at the steady state of intergenomic orchestration [7-9]. These processes leading to allopolyploidization should bring about a broad range of genetic and epigenetic responses such as chromosome deletions, rearrangements, transpositions and epigenetic modifications [4,10-20].

Common wheat, *Triticum aestivum* ($2n = 6x = 42$, genome formula AABBDD), formed through two additive allopolyploidizations. About 0.5 million years ago, the first allopolyploidization occurred by hybridization between the wild relatives *Aegilops speltoides* ($2n = 2x = 14$, SS÷BB) and *T. urartu* ($2n = 2x = 14$, AA). Common wheat was spontaneously produced about 10,000 years ago from the second allopolyploidization between the early-cultivated allotetraploid *T. turgidum ssp. dicoccum* ($2n = 4x = 28$, AABB) and wild goat grass, *Ae. tauschii ssp. strangulata* ($2n = 2x = 14$, DD) followed by chromosome doubling of unreduced gametes [21-24]. Common wheat has been widely cultivated across the world, since it reveals more features of heterosis, such as growth vigor, environmental adaptability, and disease resistance than tetraploids [25]. Since there was a time lag between the two allopolyploidization events of common wheat, it should provide a model system to study genetic interactions among three genomes.

Orchestration of allopolyploid genomes after whole genome duplication leads to genome fractionation (unequal gene loss) as well as neo- and subfunctionalization of duplicated genes due to alternative nucleotide substitution rates. In addition to the biased fractionation of polyploid genomes, genes located on dominant genome regions have a tendency toward higher expression [26-28]. Actually, genomic

asymmetry due to the non-random retention of controlling genes favoring one genome over others is manifested in allopolyploid wheat by the control of various genetic traits and syntenic genes [8,29]. Whole genome shotgun sequencing of Chinese Spring wheat showed that allohexaploid wheat lost 10,000 to 16,000 genes during the course of allohexaploidization [30]. Furthermore, reported accelerated alteration of homoeologous genes, such as nucleotide mutations and alternative splicing [31]. These structural changes of the common wheat genome are likely to occur during allotetraploidization, mainly because of the duration of the allopolyploid [32,33]. However, precise genome-wide data are required to show which homoeologous genes are expressed among the three genomes of common wheat for better understanding of gene regulation in allopolyploid. Hence, the present study is aimed to clarify transcriptome of homoeologous genes in common wheat, based on the full-length cDNA clones.

Here, we took advantage of the Full-Length (FL) cDNA sequence data of common wheat to complete reference set of its expressed homoeologous genes. We used all Expressed Sequence Tags (ESTs) of common wheat that had been cloned from cDNAs containing a poly(A)⁺ tail, and sequenced from both ends of the inserts. The full-length cDNAs which Cover The Coding Sequences (CDSs) or non-coding RNAs were proofed from these ESTs, including the CAP-trapped cDNAs, were classified into homoeologous genes expressed from the A, B and D genomes, and these homoeologous genes were grouped into gene clusters corresponding to those of the diploid [34]. Chromosome locations of these homoeologous genes were determined to show the subgenome fractionation of expressed genes [35].

Results

Completion of Full-Length (FL) cDNA data of common wheat

In addition to the two rounds of complete sequencing of CAP-trapped cDNA clones in common wheat, we further screened and determined the sequences of 4,886 Full-Length (FL) cDNAs [34]. In total, 21,693 FL cDNA sequences are now available. Size distribution of the 21,693 FL cDNAs is shown in figure S1A. The mean size of the wheat transcripts (1839±900bp) was longer than barley (1641±842bp), *Brachypodium* (1603±951bp) and rice (1542±924bp) transcripts in the public databases of cereal FL cDNAs. The data suggest that CAP-trapped cDNAs captured the complete Open Reading Frames (ORFs) of common wheat. Gene Ontology (GO) Slim annotations of wheat FL cDNAs were compared to those of other cereals as shown in figure S1B. GO Slim patterns were similar among cereal FL cDNAs, suggesting that wheat FL cDNAs were selected similar to the cereal transcriptomes. Predicted ORFs of the 21,693 wheat FL cDNAs were searched against the Poaceae (barley, *Brachypodium*, rice and sorghum) peptide and other data sets in the Pfam and UniProt databases, suggesting that 1,538 ORFs (7.0%) were transcripts having least homology with grass genes (wheat specifically expressed genes).

Furthermore, the cDNA clones of common wheat having certain gaps in the inserts and homology with cereal genes, rather than the 21,693 FL cDNA clones, were selected from the EST contigs. The nucleotide sequences of the resultant 4,548 cDNA clones harboring the complete CDS were determined. Finally, the 26,241 FL cDNA clones of common wheat were complete.

Construction of expressed homoeologous genes set from the cDNA clones of common wheat

To construct reference set of transcriptome expressed from three kinds of genome in allohexaploid wheat, we exhaustively surveyed the sequenced cDNA clones from various developing stages grown in normal and abiotic as well as biotic stressed conditions including the full-length cDNAs [34]. The samples included 45 tissues for the cDNA clones, and 17 for the full-length cDNAs. All the sequence data of the cDNA clones including 1,285,673 ESTs in the NCBI database and 107,353 one-path sequences of the CAP-trapped cDNA clones from both ends were utilized to establish standard transcripts in common wheat. A flowchart to categorize these standard transcripts is shown in figure 1. In total, 1,420,092 sequences were initiated for assembly to homoeologous genes (6x level) and gene clusters (2x level). After a high confidence check of the transcript groups, 76,568 expressed homoeologous genes were obtained. These homoeologous genes were classified into gene clusters corresponding to the gene numbers in common wheat. The resultant 36,389 wheat gene clusters were used to search for counterparts in the grass gene database. Of 36,389 wheat gene clusters, 24,748 showed homology to grass genes. The remaining 11,641 gene clusters with lower homology to the grass genes were checked for protein coding ability. Finally, 7,677 wheat specific protein coding gene clusters (8,711 homoeologous genes) were obtained (Figure 1). Consequently, 32,425 protein coding gene clusters (72,604 homoeologous genes) were obtained (Table 1). GO Slim annotation of these transcripts suggests that the components of the classification were similar to those of other grass plants (Figure 2), suggesting that these common wheat transcripts should cover almost all expressed genes. GO patterns between homoeologous genes (6x) and gene clusters (2x) were similar, suggesting that the overall gene functions of homoeologous genes were not specific.

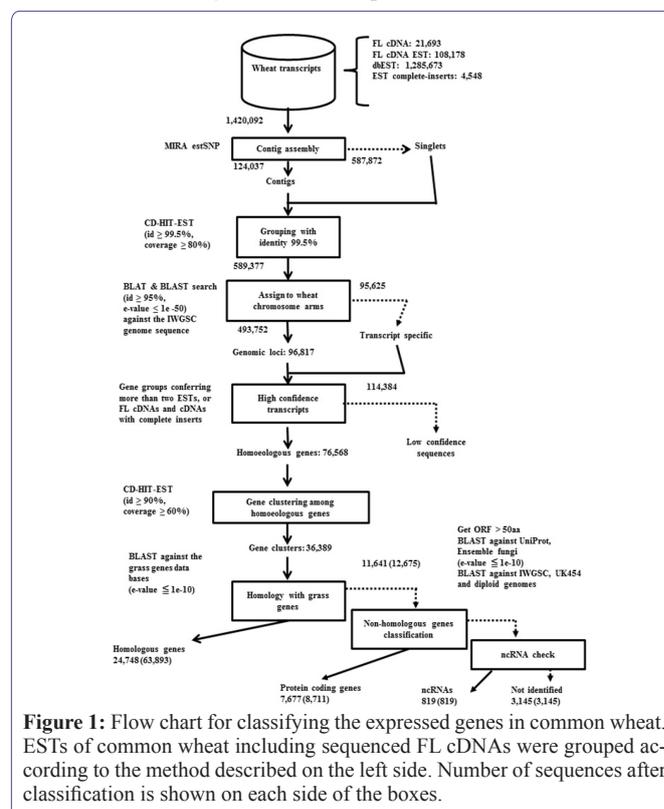


Figure 1: Flow chart for classifying the expressed genes in common wheat. ESTs of common wheat including sequenced FL cDNAs were grouped according to the method described on the left side. Number of sequences after classification is shown on each side of the boxes.

	Protein coding genes			Non-coding genes			
	Homology with the grass genes	Wheat specific gene	Subtotal	miRNA*	ncRNA**	Not identified	Subtotal
Assigned to the IWGSC genome sequence	22,792	7,477	30,269	204	12	927	1,143
	(61,452)	(8,497)	(69,949)				
Not assigned to the IWGSC genome sequence	1,956	200	2,156	585	18	2,218	2,821
	(2,441)	(214)	(2,655)				
Total	24,748	7,677	32,425	789	30	3,145	3,964
	(63,893)	(8,711)	(72,604)				

Table 1: Classification of transcripts expressed from common wheat.

*: microRNAs were searched against psRNATarget: A Plant Small RNA target analysis server (<http://plantgrn.noble.org/psRNATarget/>).

** : Non-coding RNAs were searched against NONCODE (<http://www.noncode.org/download.php>).

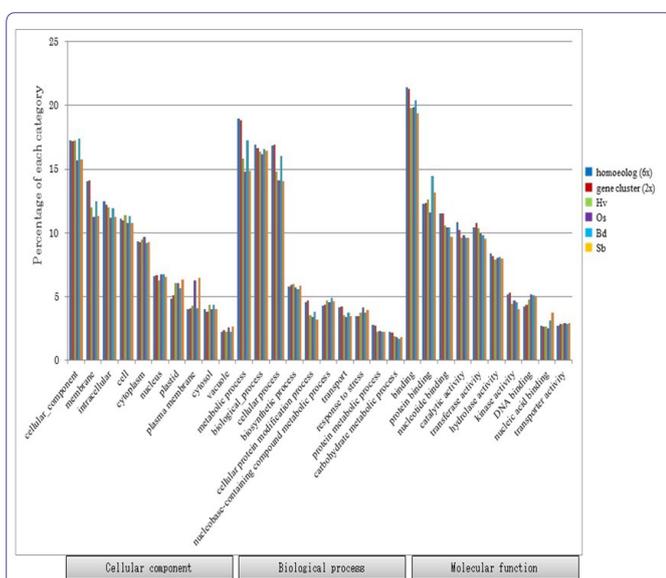


Figure 2: Gene Ontology (GO Slim) analysis of expressed genes in common wheat.

Gene ontology of homoeologs (■) and gene clusters (■) were compared to those of barley (■), rice (■), Brachypodium (■) and Sorghum (■). Subcategories are shown underneath the grouped GO terms.

Furthermore, 819 non-coding RNAs were found, including 789 microRNA precursors and 30 non-coding RNAs. Finally, 3,145 transcripts remained to be identified (Figure 1). All this gene information is available in research data.

Homology of wheat and grass transcripts

As mentioned above, out of 32,425 protein coding gene clusters, 24,748 clusters (76.3%) showed homology with those of grass plants (Figure 1). Among the 24,748 gene clusters, 21,588 (87.2%) were commonly found in grass genes (Figure 3). The remaining 3,160 genes revealed homology with at least one species of grass. On the other hand, 7,677 gene clusters (8,711 homoeologs) had the least homology so far with those of other grass plants, revealing specific genes of common wheat. The gene ontology of this genesis shown in figure 4. Higher proportions of wheat specific genes were observed in the “nucleus” cellular component category, “protein metabolic process” in the biological process category, and “hydrolase activity” and “nuclear acid binding” in the molecular function category.

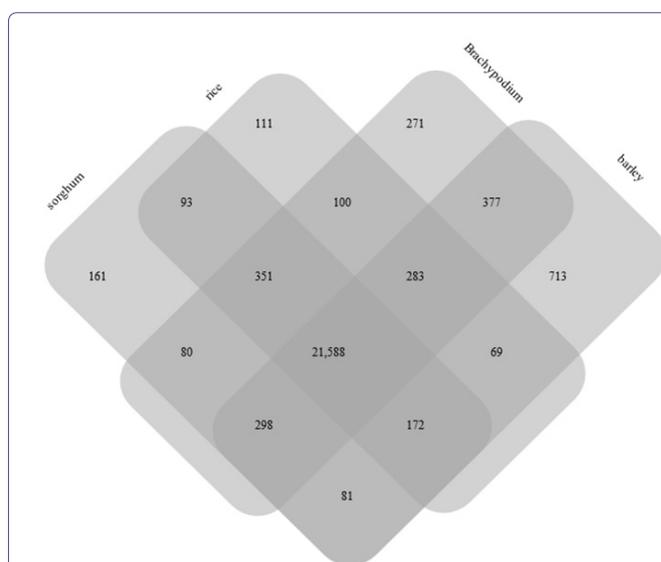


Figure 3: Number of wheat gene clusters homologous to grass genes.

The numbers of genes having homology to other grass genes are presented in the overlapping areas. In total, 24,748 wheat genes have homology to grass genes.

Chromosome assignment of the expressed homoeologous genes

Chromosome assignments of the 76,568 homoeologous genes (Figure 1) were examined. Out of 76,568 homoeologous genes, 71,092 (92.8%) were assigned to each chromosome and/or chromosome arm of Chinese Spring wheat [35]. Of these, 69,949 homoeologous genes were estimated to encode proteins, of which 61,452 had homology with grass genes (Table 1). In addition to the protein coding genes, 1,143 non-coding genes were obtained, including 204 microRNA precursors (<http://plantgrn.noble.org/psRNATarget/>) and 12 non-coding RNAs (<http://www.noncode.org/download.php>). Furthermore, 2,655 protein coding genes, 585 microRNAs and 18 non-coding RNAs were predicted in the wheat genome, although their chromosome locations could not be determined using the IWGSC sequence [35]. Consequently, 74,350 transcripts from the three homoeologous genomes of common wheat were identified (Table 1).

The chromosome assignments of 71,092 homoeologous genes are shown in figure 5A and B. Chromosome 3B harbored the most genes (4,399), while 6D contained the least (2,296). The average number

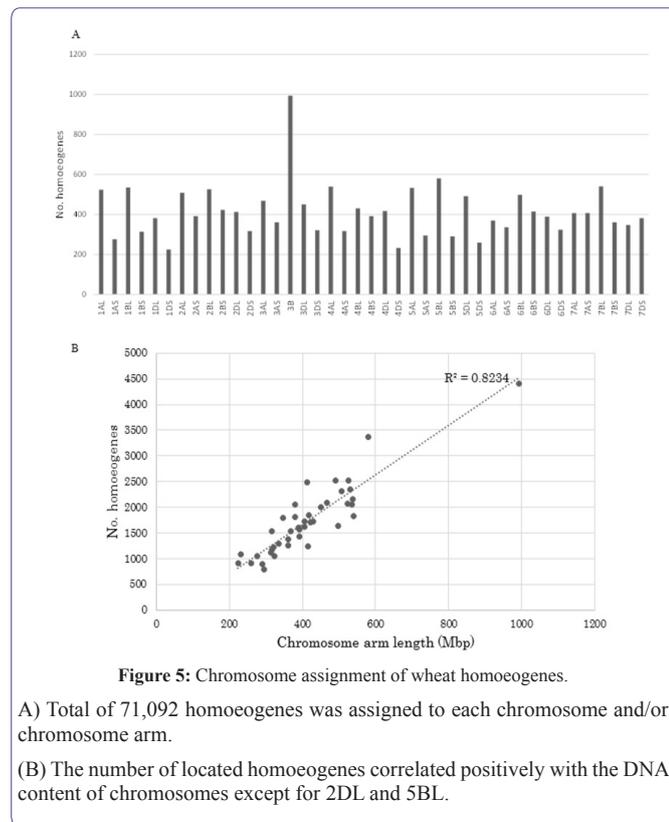


Figure 5: Chromosome assignment of wheat homoeogenes.

A) Total of 71,092 homoeogenes was assigned to each chromosome and/or chromosome arm.

(B) The number of located homoeogenes correlated positively with the DNA content of chromosomes except for 2DL and 5BL.

Expression of 7,477 wheat specific homoeologous genes from three distinct genomes was characterized. About 90% of these were transcribed as single genes from one of the three genomes (Table 1). However, 5% of homoeologous genes were not expressed in one of the three, and only 0.4% was expressed from all three genomes, suggesting a characteristic contribution of wheat specific genes. Preferential expression of the wheat specific genes by the B genome was found (Table 1).

Functional estimation of homoeologous genes classified by their expression profiles

In order to estimate functions of the homoeologous genes characterized by their copy number and genome assignment, their gene ontology was examined by the agri GO tools [39]. Out of 30,269 expressed gene clusters, 13,703 single copy genes expressed by only one genome, 3,951 single copy genes simultaneously expressed by all three genomes, and 717 (626 + 91) multigenes expressed by all three genomes (Table 2) were analyzed. Typical gene functions for each gene category of copy numbers were shown (Figures S3(A-C)-S6 and Table 1): single copy genes expressed from only one genome tended to contain significantly more genes in the categories related to signal transduction and gene regulation, such as phosphorylation (protein kinase), components of nucleotides (ATP synthase) and proteins (e.g., tryptophan synthase), and defense response (Gutathione S-transferase; Figure S3(A-C)). On the other hand, single copy genes transcribed from all three genomes were specifically concerned with metabolic processes (e.g., starch synthase; Figure S4), showing that these genes control basic metabolism. As for multigenes expressed

from all three genomes, stress-response genes (salt-responsive genes) were notable, in addition to those involved with basic metabolic processes (Figure S5).

Discussion

Reference set of transcripts is indispensable clues for gene prediction. Hence, we have completely surveyed expressed genes from various wheat tissues of common wheat grown under ordinary conditions and in biotic- and abiotic-stressed conditions, including CAP-trapped cDNAs (FL cDNAs;) [34]. Although collections of FL cDNAs are recognized as significant genetic resources, full-set surveys of FL cDNAs expressed from each genome of common wheat (allohexaploid: AABBDD) are not readily available. Therefore, we completed the sequencing of an additional 4,886 CAP-trapped FL cDNAs, so that 21,693 sequences for Chinese Spring wheat are now available. In addition to these CAP-trapped FL cDNAs, the inserts of 4,548 independent cDNA clones which cover the protein coding regions had been determined. Finally, the nucleotide sequences of the 26,241 FL-cDNA clones are available. This number is equivalent to those of Arabidopsis annotated from the genome (TAIR 10 <https://www.arabidopsis.org/>), suggesting that almost all expressed wheat genes containing poly-(A)⁺ tail can be captured with the cDNA clones (Figure S1) [40-43]. This is indispensable genome resource to predict the expressed genes in wheat.

Based on these wheat FL cDNAs, all of the available wheat ESTs, including one-path sequences of CAP-trapped wheat cDNAs, were clustered. Finally, 76,568 homoeologously expressed genes (homoeologous genes) were identified (Figure 1). These classified expressed genes were clone-based and relatively abundant. The homoeologous genes were grouped to estimate the gene members of common wheat, designated as 36,389 gene clusters (Figure 1), of which 32,425 were protein coding genes (Table 1). This estimated gene number is equivalent to the gene number predicted from the genome sequences of diploid tetraploid, and hexaploid wheats [30,35,44-46]. Overall GO analysis of these homoeologous genes exhibited GO terms that were similar to grouped gene clusters of diploids and other cereal genes (Figure 2), suggesting that the list here of cDNA clones could survey almost all expressed genes in common wheat.

The A and B genomes of common wheat have a long history of co-existence, ca. 0.5 million years, before pollination with *Ae. tauschii* (DD) and genome-wide duplication about 10,000 years ago, giving rise to the allohexaploid [22,23,47]. Accumulation of genomics data in cereals enables characterization of the features of expression of the allohexaploid wheat genes located on the three distinct genomes [48-50]. Thus, orchestration of expressed homoeologous genes in natural hexaploid wheat at a steady level should be clarified. In this study, the number of expressed homoeologous genes in each gene cluster was estimated. About half of expressed genes in common wheat were expressed only from one of three genomes. While, a quarter of expressed genes used two genomes, and remaining a quarter were expressed from all three genomes (Table 2). On the other hand, almost all (ca. 95 %) wheat specific genes were transcribed from one genome (Research Data SF1A), suggesting characteristic feature of wheat specific genes. Preferential gene expression from the B genome was found for both single copy genes and multigenes families (Table 2 and Research Data SF1B). This expression preference was also found in wheat specific genes (Table 1). Furthermore, significantly fewer wheat specific homoeologous genes were expressed as single copy

genes by the D genome, while the number of wheat specific single copy genes assigned to the A and B genomes were not significantly different (Table 2 and Research Data SF1A and SF1B). These lines of evidence suggest both more negative regulation of the D genome for wheat specific genes and maternal effects on expression of homoeologous genes [33,51]. The observation that certain chromosome arms most of which were of the B genome, harbored more expressed homoeologous genes than expected (Figure 5 and Figure S2) suggests that gene regulation system (s) might operate on specific chromosome regions. Preferential transcription of genes from one progenitor genome has been reported in cotton, Arabidopsis and maize as well as in wheat [17,26,52-55].

GO analysis revealed that single copy genes of common wheat play characteristic roles distinct from other categories of genes such as signal transduction and stress responses (Figure S3). In addition to the GO categories of single copy genes found in common among the three genomes, single copy genes of the B genome fell into further categories (Figure S3B). Categories of the genes expressed from two of the three genomes, and those expressed from each of the three genomes were concerned with basic metabolism (Figure S4). Moreover, multigenes expressed from all three genomes, among which genes of the B genome exhibited preferential expression, showed characteristic functional categories such as stress responses in addition to metabolic processes (Figure S5). These data suggest functional partitioning of respective homoeologous genes. Genetic alterations and epigenetic regulation are known to play roles in gene expression of polyploids [56]. Although substantial DNA loss especially from the A and B genomes, has been reported in common wheat, genetic alterations alone of allohexaploid wheat are unable to explain the observed expression profiles of homoeologous genes: the number of expressed homoeologous genes was similar for the A and D genomes, while more were found in homoeologous genes from the B genome (Tables 1 and 2) [8,12,30,57,58]. This suggests that the epigenetic regulation operating on the genes in each genome is substantial [59-62]. In fact, silencing of homoeologs through altered DNA methylation and repression of counterpart homoeologous genes with miRNAs and siRNAs plays important roles in control of expression of target genes [51,63,64].

Materials and Methods

Final collection of CAP-trapped cDNA sequences

A full-length cDNA library was constructed with the CAP-trapper method from pooled RNAs derived from 17 samples of common wheat (*Triticum aestivum* L. cv. Chinese Spring) tissues, in which those formed during the wheat life cycle, and those subjected to abiotic stresses such as heat shock, salt-stress and dehydration, were included [34]. After the second round of screening of non-redundant full-length cDNA clones, 55,968 cDNA clones were subtracted from the library. These clones were sequenced from both ends of the inserts and assembled according to the one-path method previously reported [34]. Selected cDNA clones underwent six runs on a next-generation sequencer (Roche 454 FLX+), and sequenced fragments were assembled with Trinity r2013-02025 software [65]. Vector sequences (GenBank: X52331) were cut from the assembled fragments. Contaminating sequences of *Escherichia coli* (GenBank: U00096) and fungi (Ensemble Fungi cDNA, release 17) were removed from the assembled sequences. Insert DNA sizes of the clones were checked by agarose gel electrophoresis after digestion of the cDNA clones with SfiI and/or BamHI. Sequences of ambiguous clones were determined with the Sanger method (Applied Biosystems 3500 instruction manual).

Another source of cDNA clones having the full CDS

Homoeologous cDNA clones to the full-length cDNA clones described above and homologous clones to the genes of *Brachypodium* (mips v1/2), barley (mips 23 Mar 2012), rice (IRGSP 1.0) and sorghum (mips v1.4) that covered the CDS were selected from the 45 cDNA libraries constructed by tissues from various developing stages grown in normal and abiotic as well as biotic stressed conditions [66]. DNA sequences of the selected clones were determined using the 454 FLX+ sequencer and/or the Sanger method.

Expressed genomes	No. expressed genes						Total
	1	2	3	4-6	7-12	>13	
A	4199	349	43	13	1	0	4605
B	5236	410	85	35	2	0	5768
D	4268	290	49	6	0	0	4613
Subtotal	13703	1049	177	54	3	0	14986 (49.5)
A + B	-	1506	488	236	29	1	2260
A + D	-	1482	508	248	21	0	2259
B + D	-	1515	503	236	18	0	2272
Subtotal	-	4503	1499	720	68	1	6791 (22.4)
A+B+D	-	-	3951	3824	626	91	8492 (28.1)
Total	13703 (45.3)	5552 (18.3)	5627 (18.6)	4598 (15.2)	697 (2.3)	92 (0.3)	30269

Table 2: No. of gene clusters differentially expressed by the three genomes of common wheat.

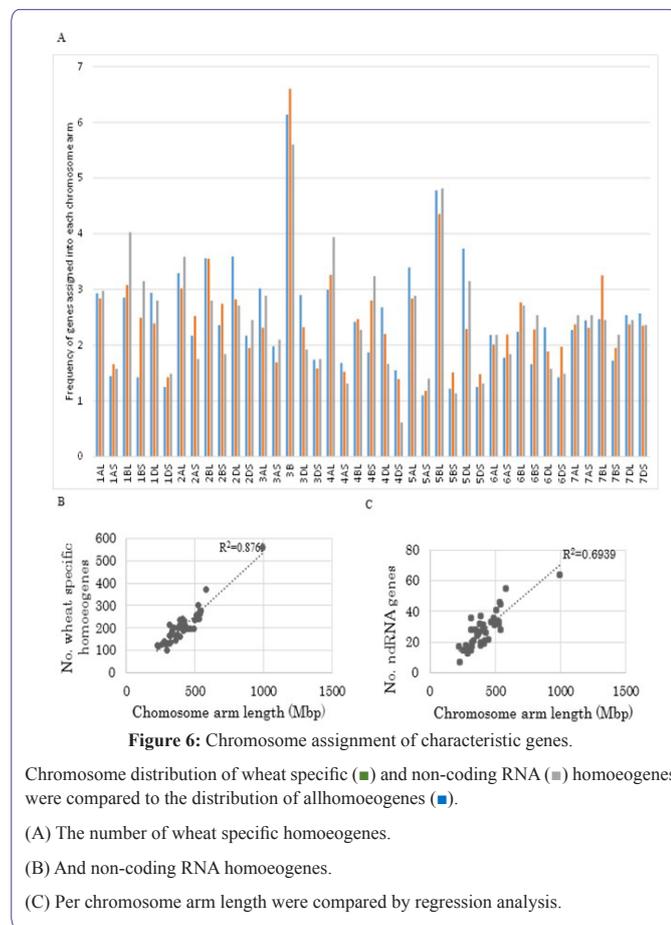


Figure 6: Chromosome assignment of characteristic genes.

Chromosome distribution of wheat specific (■) and non-coding RNA (▨) homoeogenes were compared to the distribution of all homoeogenes (■).

(A) The number of wheat specific homoeogenes.

(B) And non-coding RNA homoeogenes.

(C) Per chromosome arm length were compared by regression analysis.

Construction of the reference set of expressed genes in common wheat

A flowchart of the assembly of the expressed homoeologous genes in common wheat is shown in figure 1. A set of publically available 1,285,673 ESTs in common wheat was obtained from dbEST (NCBI 13 Aug 2013). In total, 1,420,092 partially or fully sequenced data of cDNAs in common wheat including full-length cDNAs, one-path sequences of CAP-trapped cDNAs, cDNAs harboring CDS, and the dbEST EST set were assembled with the MIRA EST SNP pipeline step 2 assembler (version 4.0rc3). Contigs and singlets identified by the MIRA program were clustered with CD-HIT ver. 4.6.1 software (identity $\geq 99.5\%$, coverage $\geq 80\%$). The resultant clusters were assigned to the common wheat genome using the survey sequence of Chinese Spring wheat [35] from BLAT (Src35) and BLAST searches (e-value $\leq 1e-50$, identity $\geq 95\%$ and total alignment length ≥ 200). Expressed clusters were considered distinct when other mapped clusters were 2 kbp apart from the identified clusters. Furthermore, clusters (high confidence inserts) were only verified either when they contained more than two EST members, full-length cDNAs or full CDSs. The resultant homoeogenes were grouped using the CD-HIT program (identity $\geq 90\%$, coverage $\geq 60\%$) to construct gene clusters to estimate the number of gene members at the diploid level. Counterparts of these expressed genes were searched with the blastx and blastn algorithms (e-value $\leq 1e-10$) against the grass gene databases: *Brachypodium* (mips v1.2, RBFLDB 2013), barley (mips 23Mar 2012), rice (IRGSP 1.0) and *sorghum* (mips v1.4). The only gene

clusters homologous to grass genes that were selected were those having more than 50 amino acids, homology identified by blastx (e-value $\leq 1e-10$) to sequences in the UniProt and Ensemble Fungi databases, by blastn to predicted genes deduced from shotgun sequencing of Chinese Spring wheat (UK454_OrthAssembly mips UK454), the wild diploid ancestor of the A genome (*T. urartu* final_120813.gff.cds) and the D genome (*Ae. tauschii* final_43150.gff.cds GigaDB 13-03-07), and a chromosome sorted genomic assembly of Chinese Spring wheat (IWGSC MIPS_feb2013).

ORF prediction and gene ontology annotation

Candidate ORFs of the expressed homoeogenes and/or gene clusters were predicted using getorf in jemboss package version 1.5 [67]. The blastp searches were carried out against amino acid sequences in the rice, *Brachypodium*, barley, *sorghum* and UniProt databases (e-value $\leq 1e-10$). Protein motifs were searched for in the Pfam database using InterProScan version 5.2-45.0 software [68]. Gene Ontology (GO) IDs were assigned by Pfam id lookup in the Gramene ontology database (Ensemble data set). GO annotation of barley, *Brachypodium*, rice and *sorghum* were obtained from Gramene (GO_ensembl). GO terms were summarized into GO Slim categories using the GO Slim Viewer tool (AgBase) with the plant definition table (agri GO) [39,69]. microRNAs and non-coding RNAs were respectively searched against psRNATarget: A Plant Small RNA Target Analysis Server (<http://plantgrn.noble.org/psRNATarget/>) and NONCODE (<http://www.noncode.org/download.php>).

Data access

Nomenclatures of homoeogenes and their gene clusters, and their annotations are presented in Data File S1 and <https://rcshige3.nig.ac.jp/wheat/komugi/genes/est/>. Sequenced cDNA data were deposited in the BioProject accessions Nos. PRJDB4671 and PRJDB4672 of DDBJ, Japan.

Acknowledgement

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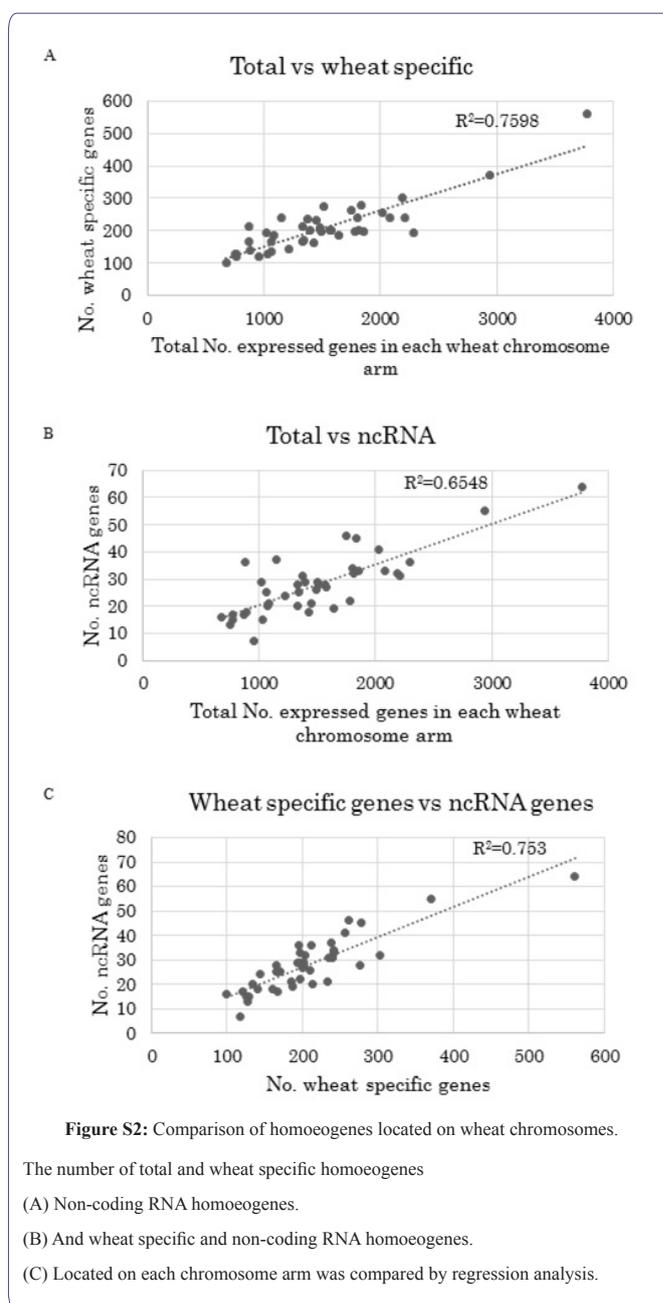
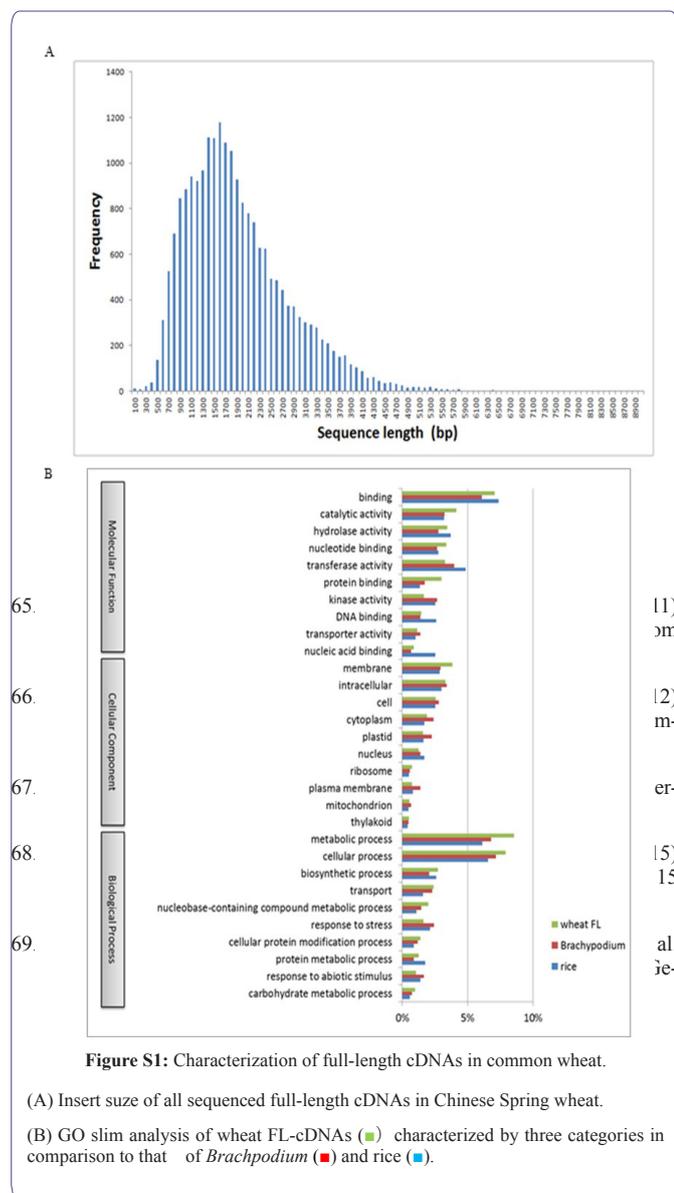
Author Contributions

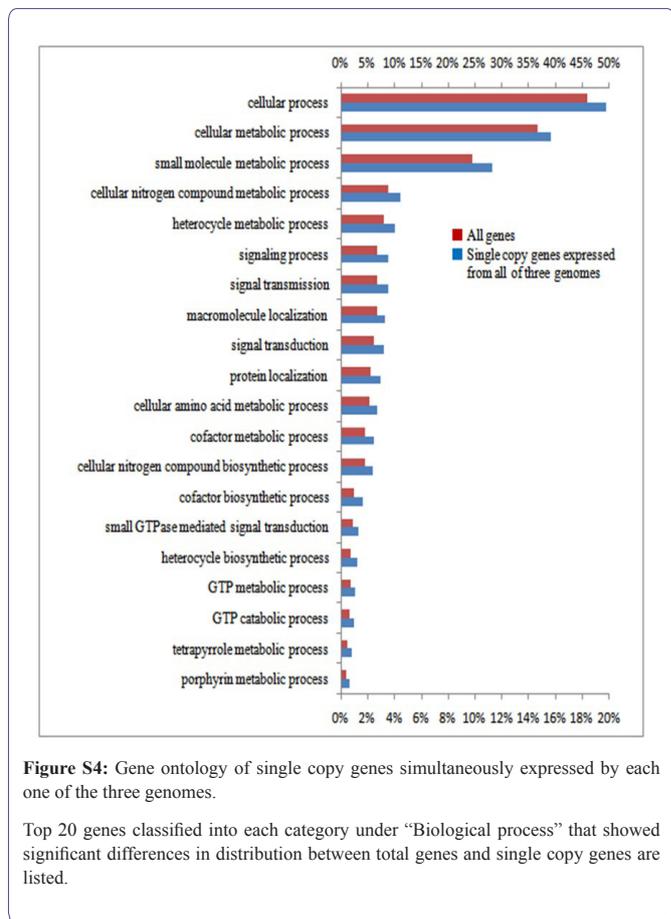
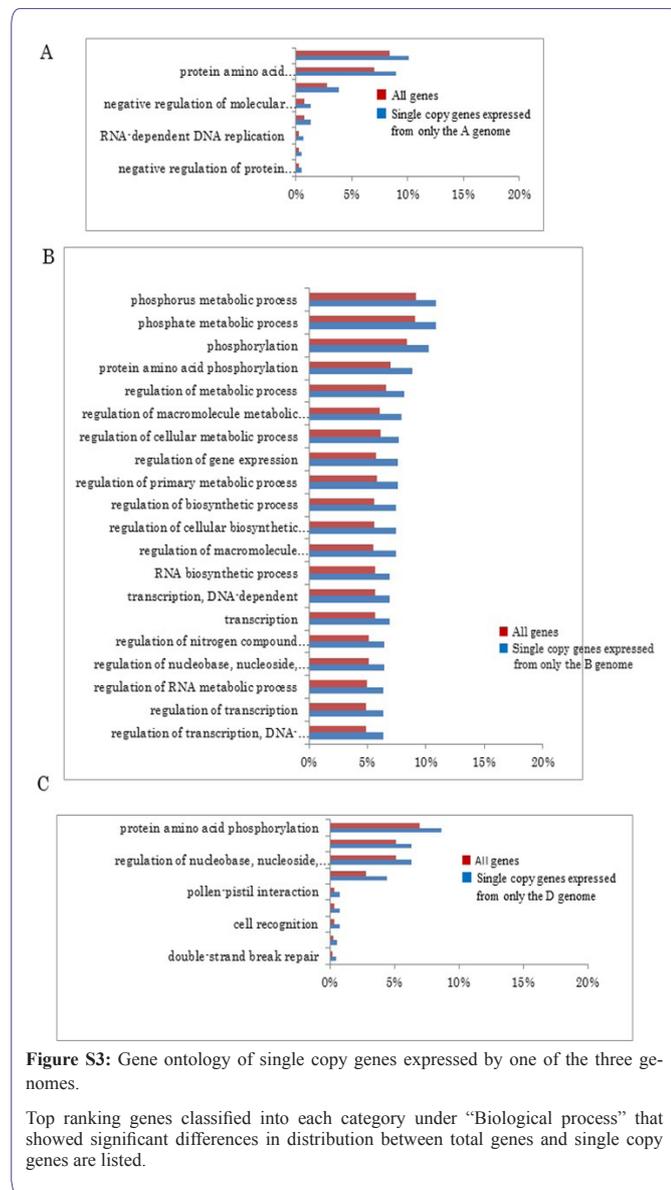
KM collected cDNA clones, designed images, carried out computational analyses and participated in manuscript writing. KK designed images and performed DNA sequencing of cDNA clones. YK performed computational analyses and developed DATA base. KM contributed to construct full-length cDNA libraries, sequence the full-length cDNA clones, and construct full-length cDNA data base of common wheat. HT, MT NS, JK developed new sequencing strategy of cDNA clones, carried out sequencing and computational analyses. YN and KN contributed in computational data analyses and construction of data base of wheat transcriptome. YO and JK designed the research, and wrote manuscript. All authors read and approve the final manuscript.

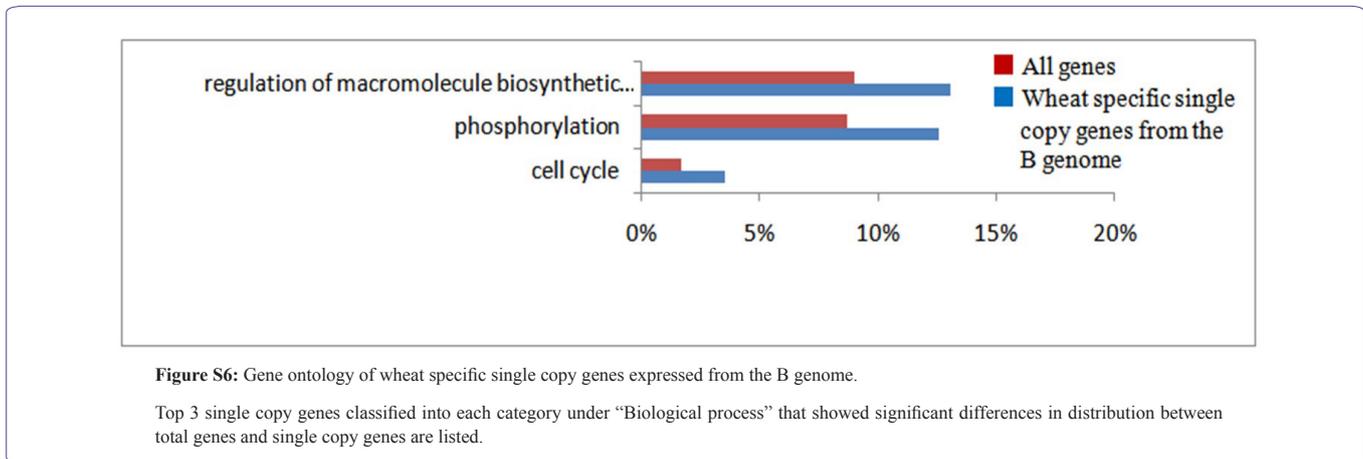
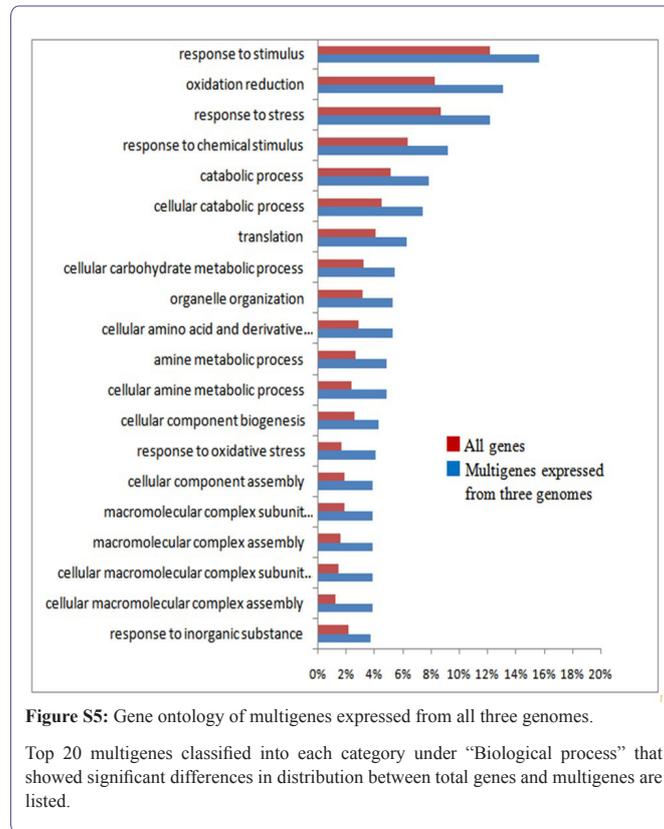
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