



Nucleotide diversity and molecular evolution of the *WAG-2* gene in common wheat (*Triticum aestivum* L) and its relatives

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Abstract

In this work, we examined the genetic diversity and evolution of the *WAG-2* gene based on new *WAG-2* alleles isolated from wheat and its relatives. Only single nucleotide polymorphisms (SNP) and no insertions and deletions (indels) were found in exon sequences of *WAG-2* from different species. More SNPs and indels occurred in introns than in exons. For exons, exons+introns and introns, the nucleotide polymorphism π decreased from diploid and tetraploid genotypes to hexaploid genotypes. This finding indicated that the diversity of *WAG-2* in diploids was greater than in hexaploids because of the strong selection pressure on the latter. All dn/ds ratios were < 1.0 , indicating that *WAG-2* belongs to a conserved gene affected by negative selection. Thirty-nine of the 57 particular SNPs and eight of the 10 indels were detected in diploid species. The degree of divergence in intron length among *WAG-2* clones and phylogenetic tree topology suggested the existence of three homoeologs in the A, B or D genome of common wheat. Wheat *AG*-like genes were divided into *WAG-1* and *WAG-2* clades. The latter clade contained *WAG-2*, *OsMADS3* and *ZMM2* genes, indicating functional homoeology among them.

Key words: copy number variation, genetic diversity, molecular evolution, *Triticum*, *WAG-2*.

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Introduction

Common wheat (*Triticum aestivum*, $2n = 6x = 42$, AABBDD) is an allohexaploid formed by two processes of hybridization and successive chromosome doubling (Feuillet *et al.*, 2001; Huang *et al.*, 2002; Gu *et al.*, 2004; Petersen *et al.*, 2006). The initial hybridization was between *Triticum urartu* (the diploid ancestor of the A genome, $2n = 2x = 14$, AA) and *Aegilops speltoides* (the diploid ancestor of the B genome, $2n = 2x = 14$, SS). This process resulted in tetraploid wheat ($2n = 4x = 28$, AABB) that subsequently hybridized with *Aegilops tauschii* (the diploid ancestor of the D genome, $2n = 2x = DD$) to produce hexaploid common wheat.

The success of polyploid plants is often attributed to their genomic characteristics, including genomic stability, chromosomal rearrangement, genome size and differential gene expression (Soltics *et al.*, 2003). In addition, nucleotide diversity is always generated in the course of polyploidy. Nucleotide diversity in wheat reflects the rich history of human selection and migration combined with a

high level of recombination and out-breeding characteristic of this species. In the past decades, DNA markers such as RAPD, AFLP, and SSR have been extensively used for fingerprinting and exploring the genetic diversity and evolutionary relationships of wheat genetic resources. Although these molecular techniques are constantly being improved, in recent years several highly efficient and economic protocols have been introduced to differentiate closely related wheat species and their relatives.

Single nucleotide polymorphisms (SNP) are the most abundant type of variation in DNA sequences in all genomes studied to date (Brookes, 1999) and are considered last-generation molecular markers. SNPs are the most valuable molecular markers for research and application, including the detection of risk-associated alleles linked to human diseases, the study of evolutionary conservation among species, gene mapping and cloning, and crop breeding. The discovery of SNPs usually relies on re-sequencing alleles from different individuals or comparing the sequences to a reference sequence.

Wheat is the most important food crop in the world. The increase in the global human population and the very limited availability of suitable farmland make it essential to improve wheat yields. Wheat floral organs provide the ba-

sis for grain formation such that wheat yield and quality are directly influenced by floral organ development. Hence, understanding wheat floral development is important for improving wheat yield. Past research has been limited to the morphological description and physiology of flowering, whereas recent developments in molecular genetics have led to studies of flower development at a molecular level. Some MADS-box cDNA sequences, such as *WAP-1*, *WAP-2*, *WAP-3*, *WPI1*, *WPI2*, *WAG-1*, *WAG-2* and *TaMADS1*, have been identified (Murai *et al.*, 1998, 2002, 2003; Hama *et al.*, 2004; Zhao *et al.*, 2006; Mizumoto *et al.*, 2009; Shimada *et al.*, 2009). Ciaffi *et al.* (2005) described the cloning and expression analysis of eight MADS-box cDNA sequences, and Zhao *et al.* (2006b) reported the characterization and expression of 42 wheat MADS-box gene sequences. Shitsukawa *et al.* (2007) undertook a detailed structural, expression and functional analysis of the homoeologous sequences of two wheat *SEP*-like genes. Paolacci *et al.* (2007) cloned 45 full-length MIKC-type MADS-box cDNA sequences of common wheat and studied their expression and function.

WAG-2, a class C MADS-box gene, has been isolated from the wheat expressed sequence tag (EST) database (Ogihara *et al.*, 2003). Compared to other MADS-box genes, few studies have compared the sequences and investigated the evolutionary dynamics of *WAG-2*. In this study, we partially cloned the *WAG-2* gene from wheat and its relatives and used the data (1) to analyze the sequence characteristics and investigate the inter-specific variability of the *WAG-2* gene, and (2) to examine the relationship between the *WAG-2* gene in common wheat and related species and other AG-like genes from different species.

Materials and Methods

Plant materials and DNA isolation

One accession each of *Triticum monococcum* ($2n = 2x = 14$, A^mA^m), *T. urartu*, ($2n = 2x = 14$, A^uA^u) and

A. tauschii ($2n = 2x = 14$, DD), two accessions of *A. speltoides* ($2n = 2x = 14$, SS), four accessions of tetraploid wheat ($2n = 2x = 28$, AABB) and two accessions of *T. aestivum* ($2n = 6x = 42$, AABBDD) were used (Table 1). All seeds were provided by Dr. Dengcai Liu of Sichuan Agriculture University, Yaan, Sichuan, China. Genomic DNA was extracted from fresh leaves by the modified CTAB procedure (Doyle and Doyle, 1987).

PCR amplification and sequencing

The gene sequence data of *WAG-2* (AB465688) were obtained from NCBI (<http://www.ncbi.nlm.nih.gov>). Specific primers used for partial amplification of the *WAG-2* gene were designed with Primer Premier 5.0 (Clarke and Gorley 2001). The forward primer was *WAG-2F* (5'-CATTGAGAGGTACAAAAAGGCC-3') and the reverse primer was *WAG-2R* (5'-CCGTATGATTCCAGAAACTTCC-3'). Figure 1 schematically shows the partial sequence of the *WAG-2* gene and the location of the primers. Using the primers *WAG-2F* and *WAG-2R*, the region from exon II to exon VII of the *WAG-2* gene was amplified in different species. PCR amplification was done in a thermocycler (My-Cycler; Bio-Rad, San Diego, CA, USA) in a volume of 50 μ L containing approximately 100 ng of template DNA, 100 μ M each of dNTP, 1.5 mM Mg²⁺, 1 U of *Taq* DNA polymerase, 0.4 μ M of each primer and 1 x PCR buffer. The PCR cycling included pre-denaturation at 94 °C for 5 min followed by 35 cycles of 94 °C for 1 min, 60 °C for 1 min and 72 °C for 2 min, and a final extension at 72 °C for 5 min. The amplified products were visualized by gel electrophoresis in 1% agarose gels and then documented with a Gel Doc 2000TM system (Bio-Rad). The target DNA bands were recovered and purified from the gels using Qiaquick Gel extraction kits (QIAGEN, Shanghai, China). The purified PCR products were cloned in the p^{MD}19T vector according to the manufacturers instructions (Takata, Dalian, China). Transformants were plated on LB agar containing ampicillin. Clones with inserts were identified us-

Table 1 - Plant materials of *Triticum* and *Aegilops* accessions used in this study.

Material accession or variety	Species	Genome	Gene Bank accession no.
PI 428181	<i>T. urartu</i>	A ^u	JF330195
AS262	<i>T. monococcum</i>	A ^m	JF330184
PI486262	<i>A. speltoides</i>	S	JF330185
PI487231	<i>A. speltoides</i>	S	JF330196
AS75	<i>A. tauschii</i>	D	JF330187
D48	<i>T. dicoccoides</i>	AB	JF330190
D49	<i>T. dicoccoides</i>	AB	JF330191-JF330192
AS2255	<i>T. turgidum subsp. durum</i>	AB	JF330186
Landon	<i>T. turgidum ssp durum cv.</i>	AB	JF330193-JF330194
Chinese Spring	<i>T. aestivum</i>	ABD	JF330188-JF330189
Wheat mutant TP	<i>T. aestivum</i>	ABD	JF330197-JF330198

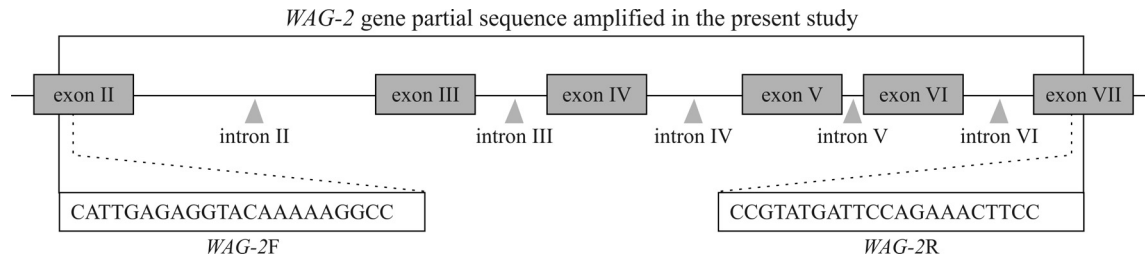


Figure 1 - Schematic drawing of the *WAG-2* gene partial sequence showing the amplified region and location of primers used in this study.

ing blue/white colony selection. Positive clones were then screened and sequenced by Taihe Biotechnology Co. Ltd. (Beijing, China). In total, 56 clones of 11 accessions belonging to eight species were sequenced using the universal M13 forward and reverse primers. The partial nucleotide sequences of 15 *WAG-2* gene haplotypes were submitted to GenBank at NCBI. The GenBank accession number of each nucleotide sequence is listed in Table 1.

Nucleotide diversity estimate

Fifteen partial *WAG-2* gene sequences were verified and corrected. The complementary strands were assembled using DNAMAN 5.2.2 software (Lynnon Biosoft Company). To confirm whether the sequences were *WAG-2* homologs, the coding regions were compared with *WAG-2* gene sequences available in GenBank using BLAST searches (Altschul *et al.*, 1990). Nucleotide sequence alignments were done using ClustalW (Thompson *et al.*, 1994) and then optimized using SeaView version 4.1 (Galtier *et al.*, 1996). The alignments were refined manually using the GeneDoc program (Nicholas and Nicholas, 1997) in order to maximize the positional homology. To reduce the possible effect of PCR artifacts, unique substitutions in single clones were ignored. Several sequences were represented by a single original sequence in alignments.

Exon+intron, exon, and intron sequences from diploid, tetraploid and hexaploid species were used to estimate nucleotide diversity based on the calculation of π as described by Tajima (1989). The value of π quantifies the mean percentage of nucleotide difference among all pairwise comparisons for a set of sequences. The π values of non-synonymous (dn) or synonymous (ds) differences and the mean dn/ds ratios were also estimated (Nielsen and Yang, 1998). These parameters were calculated using DnaSP 4.10.9 (Rozas *et al.*, 2003).

Phylogenetic analysis

The 15 partial *WAG-2* gene sequences were also used to construct phylogenetic trees. Neighbor-joining and maximum likelihood trees were generated with MEGA software version 5.0 (Saitou and Nei, 1987; Tamura *et al.*, 2007) with 1000 bootstrap replicates. Gaps were treated as missing values.

Alignment of the corresponding amino acid sequences of the 15 *WAG-2* genes, along with other MADS-box genes included in the *AG* group from several species, was done using ClustalW (Thompson *et al.*, 1994). Phylogenetic trees of the MADS-box genes were then constructed using the neighbor-joining and maximum likelihood methods. The amino acid sequences of MADS-box genes from *Arabidopsis* (*AG*: X53579), *Antirrhinum* (*PLE*: S53900), maize (*ZAG1*: L18924, *ZMM2*: L81162), barley (*HvAG1*: AF486648, *HvAG2*: AF486649), rice (*OsMADS3*: L37528, *OsMADS58*: FJ750942) and wheat (*WAG-1*: AB084577; *WAG-2*: AB465688; *WM29A*: AM502898; *WM29B*: AM502899; *TaAGL39*: DQ512355) were obtained from NCBI.

Results

Characteristics of the partial *WAG-2* gene sequences and genomic structure

Partial sequences of the *WAG-2* gene were amplified and sequenced from different species using the primers *WAG-2F* and *WAG-2R*. The sequences were deposited in GenBank under accession numbers JF330184 to JF330198. BLAST searches, which explored the coding region of each sequence, confirmed the cloned sequences to be homologs of the *WAG-2* orthologs found in GenBank. Sequence comparisons showed that the 15 partial sequences of the species studied had similar structures, including six exons and five introns (Figure 1). The exon+intron lengths ranged from 1824 to 1899 bp among species. The total length of the six exons studied was 425 bp. The five introns fulfilled the *GT-AG* rule, but they varied markedly in length and sequence composition. The length of intron II was 938–964 bp, which was longer than the other four introns. The lengths of intron III were 98, 95 and 94 bp for genomes AA, BB and DD, respectively. For AABB tetraploids (*T. dicoccoides* and *T. turgidum ssp durum cv.*) and the AABBDD hexaploid (*T. aestivum*) the length of intron III was 98 and 95 bp, respectively. Introns IV, V and VI also showed marked variations in length. The lengths of intron IV were 151, 193 or 206, and 231 bp for the AA, SS and DD genome diploids, respectively; two of these lengths (151 and 193 bp) were also observed for intron IV in AABB tetraploids (*T. dicoccoides* and *T. turgidum ssp durum cv.*) and the AABBDD hexaploid (*T. aestivum*), respectively.

Intron V had three lengths, *i.e.*, 102, 100, and 92 bp, as did intron VI, *i.e.*, 106, 102 and 72 bp (Table 2).

Inter-specific variation in the partial sequences of the *WAG-2* gene

Table 3 summarizes the *WAG-2* sequence variation identified in this study. The nucleotide variation in exons was generally less than in introns because of strong constraints.

In four haplotypes from two accessions of the hexaploid, 288 SNPs and 68 indels were identified from 7228 bp sequences (average of 1 SNP/25 bp and 1 indel/106 bp). A total of 288 SNPs were shared by 146 loci of the *WAG-2* sequences cloned. Only eight SNPs (polymorphic rate of 1 SNP/213 bp) were detected in the exon region (Table 3). Seven SNPs (87.5% of total) were in exon IV. The intron region contained 280 SNPs (1 SNP/20 bp). All 68 indels were detected in the intron region. Forty indels were found in intron II and were involved in 18 sites (1 indel site/53 bp). Two indels located in intron III belonged to one site (1 indel site/96 bp). In intron IV, there were 24 indels shared by eight sites (1 indel site/21 bp). Finally, two indels in intron V were shared by one site (1 indel site/96 bp). The indel mutation of a single nucleotide in intron VI was detected only at one site; indel mutations at the other seven sites were mainly large fragment aberrations involving at

least two nucleotides (Figure S1). The high polymorphic rates of SNPs and large fragment aberrations meant that exon IV and intron IV were two hotspots for the *WAG-2* gene in hexaploid genotypes.

496 SNPs and 113 indels were identified from 10,964 bp sequences in the six haplotypes from four tetraploid accessions, which yielded an average of 1 SNP/22 bp and 1 indel/97 bp, respectively (Table 3). Among the 33 SNPs in the exon region, 18 SNPs (54.5%) were in exon VII. 463 SNPs were detected in the intron region (1 SNP/18 bp). The intron region had 113 indels associated with 31 sites; intron IV had 35 indels with a higher frequency (1 indel site /21 bp) than the others. Consequently, highly polymorphic SNP was detected in exon VII. Intron IV also had a high frequency of indels (Figure S1).

389 SNPs and 80 indels were identified in 9,236 bp sequences in five haplotypes from the five diploid accessions (1 SNP /24 bp and 1 indel /115 bp, respectively) (Table 3). The highest frequency of SNPs occurred in exon VII, which had 64.4% (18 out of 28) SNPs. The indel frequency in intron IV (1 indel site/24 bp) was higher than in the other four introns. Apparently, exon VII and intron IV are two mutation hotspots for the *WAG-2* gene in diploid genotypes.

Table 3 shows the nucleotide polymorphism π for synonymous differences, non-synonymous differences and

Table 2 - Characteristics of the *WAG-2* partial sequences among different species (length of each feature given in bp).

Species	Exon II (partial)	Intron II	Exon III	Intron III	Exon IV	Intron IV	Exon V	Intron V	Exon VI	Intron VI	Exon VII (partial)	Exon+Intron
<i>T. monococcum</i>	70	945	62	98	103	151	42	102	42	110	106	1831
<i>T. urartu</i>	70	938	62	98	103	151	42	102	42	110	106	1824
<i>A. speltoides</i>	70	951/964	62	95	103	193/206	42	92	42	72	106	1828/1854
<i>A. tauschii</i>	70	951	62	94	103	231	42	92	42	106	106	1899
<i>T. turgidum subsp. durum</i>	70	944	62	98	103	151	42	102	42	110	106	1830
<i>T. dicoccoides</i>	70	938/951	62	98/95	103	151/193	42	102/92	42	110/72	106	1824/1828
<i>T. turgidum ssp durum cv.</i>	70	940/951	62	98/95	103	151/193	42	102/92	42	110/72	106	1826/1828
<i>T. aestivum</i>	70	940/951	62	98/95	103	151/193	42	100/92	42	72	106	1786/1828

Table 3 - SNPs and indels of the *WAG-2* partial sequences identified in all accessions and comparison of genetic diversity.

Accession	Region	Size	SNP	Frequency of SNP	Indel	Frequency of indels	Tajima's π	π of synonymous difference	π of non-synonymous difference	<i>dn/ds</i>
Hexaploid	Exon+Intron	7228	288	1/25	68	1/106	0.43813			
	Exon	1700	8	1/213	0	0	0.01137	0.04245	0.00301	0.071
	Intron	5528	280	1/20	68	1/81	0.45649			
Tetraploid	Exon+Intron	10964	496	1/22	113	1/97	0.50969			
	Exon	2550	33	1/77	0	0	0.01788	0.05422	0.00803	0.148
	Intron	8414	463	1/18	113	1/74	0.38506			
Diploid	Exon+Intron	9236	389	1/24	80	1/115	0.62555			
	Exon	2125	28	1/75	0	0	0.01812	0.06048	0.00663	0.102
	Intron	7111	361	1/19	80	1/88	0.34996			

mean dn/ds in exons+introns, exons and introns. The nucleotide polymorphism π was lowest in hexaploids and highest in diploids. The values of π for synonymous differences were lowest in hexaploids (0.04245) and highest in diploids (0.06048). The values of π for non-synonymous differences were 0.00301, 0.00803 and 0.00663. The mean dn/ds for all coding regions was < 1 .

Point mutations involve transitions between purines (A and G) or pyrimidines (C and T), but may also involve transversions or changes between purines and pyrimidines. Table 4 shows the types of base substitutions in SNPs in different species. The exon+intron Ti/Tv ratio was 0.84:1, 0.88:1 and 0.96:1 for hexaploid, tetraploid and diploid genotypes, respectively. In exons, the main point mutations involved transitions, with Ti/Tv ratios of 3, 5.6 and 4.6. The ratio of $A \leftrightarrow G$ vs. $C \leftrightarrow T$ mutations was approximately 1 in hexaploid genotypes. In contrast, in tetraploid and diploid genotypes the main transition was $A \leftrightarrow G$, with the ratio of $A \leftrightarrow G$ vs. $C \leftrightarrow T$ transitions being 2.1 and 1.3, respectively. In introns, the ratio of $A \leftrightarrow G$ vs. $C \leftrightarrow T$ transitions was 0.95 for hexaploid genotypes. The difference between tetraploid and diploid genotypes was that their ratios of $A \leftrightarrow G$ vs. $C \leftrightarrow T$ transitions were 1.14 and 1.07, respectively.

Based on the different species studied, 57 particular SNP mutations were identified, with seven (12.3%), 11 (19.3%) and 39 (68.4%) in hexaploid, tetraploid and diploid genotypes, respectively. Of the 39 SNPs, six SNPs were found in species of genome AA whereas 13 belonged to species of genome BB. Twenty SNPs were specific in species of genome DD. A common feature of these findings was that the main type of base substitution involved transitions among species. In exons, only transitions were detected among the species, and in introns the main substitutions in particular SNPs were also transitions. Seven SNPs from hexaploid genotypes were all transitions. Seven out of 11 SNPs were transitions from tetraploid genotypes. Diploid genotypes also had 24 SNPs, of which 66.7% were transitions. In addition, several specific SNPs shared by four sites were detected in groups A, B and D genomes.

Phylogenetic analyses of the partial sequences

The first series of phylogenetic analyses, which was done using the 15 *WAG-2* gene sequences and the MEGA

program, resulted in two phylogenetic trees generated by different algorithms. The topologies of the two phylogenetic trees were very similar to each other. A neighbor-joining tree (Figure 2) indicated that the *WAG-2* genes formed three major clades (I, II and III). Clade I, referred to as the A genome group of *WAG-2* (although it may include the B genome), contained seven sequences from the AA diploid (*T. monococcum*, *T. urartu*), AABB tetraploid (*T. turgidum*, *T. dicoccoides*) and AABBDD hexaploid (*T. aestivum*) genomes. This clade was called *WAG-2A* because all of the species belonging to the clade contained the A genome. This clade also contained seven sequences with identical lengths in introns III (98 bp), IV (151 bp) and V (102 bp and 100 bp in *T. aestivum*). These seven sequences showed high sequence identity with 81 SNPs. Only 19 SNPs were shared by 12 sites in exons. Clade II, referred to as *WAG-2B*, contained seven sequences from the BB diploid (*A. speltoides*), AABB tetraploid (*T. turgidum*, *T. dicoccoides*) and AABBDD hexaploid (*T. aestivum*) genomes. In this clade, the lengths of introns III, IV and V in the seven sequences were 95, 193 and 92 bp, respectively. High sequence identities were also detected in the seven sequences with 45 SNPs, in which only two SNPs were shared by two sites in the exons. Lastly, clade III, re-

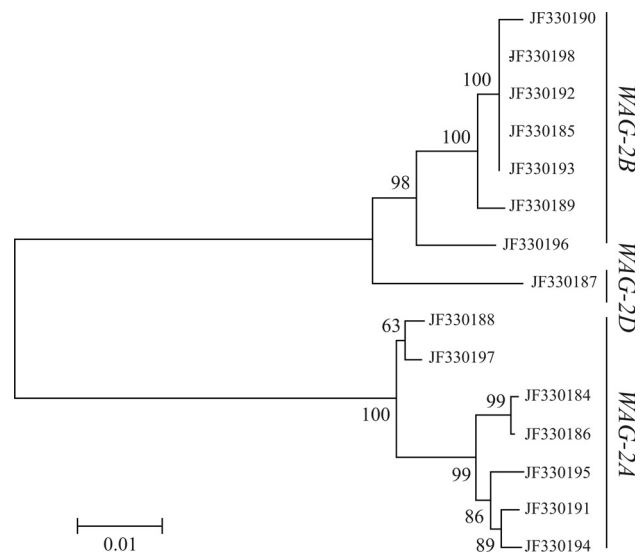


Figure 2 - Neighbor-joining phylogenetic tree. The GenBank accession numbers (JF330184 to JF330198) for the cloned *WAG-2* sequences are shown in Table 1. Bootstrap values are shown as percentages for 1000 replicates.

Table 4 - Base type substitutions in SNPs.

Accession	G \leftrightarrow T	A \leftrightarrow C	A \leftrightarrow G	C \leftrightarrow G	A \leftrightarrow T	C \leftrightarrow T	Ts/Tv*
Hexaploid	24	41	62	32	54	65	0.84:1
Tetraploid	44	69	128	51	100	104	0.88:1
Diploid	31	52	100	43	72	92	0.96:1

*Ts: transitions, Tv: transversions.

ferred to as *WAG-2D*, contained only one sequence from the DD diploid genome (*A. tauschii*).

To examine the relationships among wheat *AG*-like genes, the 15 *WAG-2* genes and other *AG* group genes were analyzed phylogenetically. The neighbor-joining and maximum likelihood trees were reconstructed using amino acid sequences. The neighbor-joining tree is shown in Figure 3. Both phylogenetic trees were very similar to each other and differed only in the positions of *ZAG1* (L18924) and *OsMADS58* (FJ750942). The neighbor-joining tree indicated that the *AG* group was classified in dicot and monocot clades. Monocot genes were subdivided into *WAG-1* and *WAG-2* clades. The *WAG-1* clade consisted of barley *HvAG2*, rice *OsMADS58* and maize *ZAG1*, while the *WAG-2* clade consisted of barley *HvAG1*, rice *OsMADS3* and maize *ZMM2*. The *WAG-2* clade was divided into three subclades: *OsMADS3* and *ZMM2* were included in subclade 1, *WAG-2* (JF330184, AB465688), *WM29A* and *TaAGL39* were clustered in subclade 2, and the other

WAG-2 genes that were amplified in this study, along with *WM29B* and *HvAG1*, were clustered in subclade 3.

Discussion

Nucleotide diversity of *WAG-2* in different species

Most protein-coding nuclear genes of plants have exons and introns. Exons, which are usually under strong selection pressure that eliminates deleterious mutations, have a relatively slow rate of nucleotide substitution whereas, unlike chloroplast genes, the introns of nuclear genes have a higher rate of nucleotide substitution (Gaut, 1998). As shown here, all exons of the *WAG-2* gene shared high sequence similarities. Only SNPs were found in the exons of different species; there were no indels. Compared with exons, the introns showed greater inter-specific polymorphism. In all species, there were more SNPs in introns than in exons because of the stronger selection pressure in the latter compared to the former.

The frequencies of SNPs and indels were analyzed in hexaploid, tetraploid and diploid species. In exons+introns, the frequency of SNPs among hexaploids (1 SNP/25 bp), tetraploids (1 SNP/22 bp) and diploids (1 SNP/24 bp) was similar. Likewise, there were no marked differences in the frequency of indels among hexaploids (1 indel/106 bp), tetraploids (1 indel /97 bp) and diploids (1 indel /117 bp). SNPs are the most abundant form of variation in all genomes studied to date. Plant SNPs in genomic regions are at least as abundant as in humans. Preliminary estimates range from 1 SNP/60 bp in outbreeding maize (Ching *et al.*, 2002) to 1 SNP/300 bp for inbreeding rice and *Arabidopsis* (Schmid *et al.*, 2003). Some plant species also display a large number of indels (Bhatramakki *et al.*, 2002; Rafalski, 2002). In the present study, the frequencies of SNPs and indels among different species were higher than those reported in most other plants. This may reflect the fact that the exon+intron region investigated here corresponded to the most polymorphic region of *WAG-2* genome DNA. This conclusion agrees with the detection of hotspot regions, such as exon IV in hexaploid species and exon VII in tetraploid and diploid species (high rate of SNP variation), and intron IV, which had a high indel mutation rate in different species.

Strong selection pressure is important in decreasing the nucleotide diversity of some plant species. Most studies on the effect of selection pressure on nucleotide diversity have focused on domesticated crops and on comparing the diversity between wild relatives and cultivars. During the selection of advantageous phenotypes, some crops appear to pass through bottlenecks that substantially reduce diversity (Doebley, 1992). In contrast, many grass domesticates have undergone moderate decreases in diversity compared with their wild relatives (Buckler *et al.*, 2001). In the present study, the nucleotide diversity of the *WAG-2* gene during the evolution of common wheat was estimated by

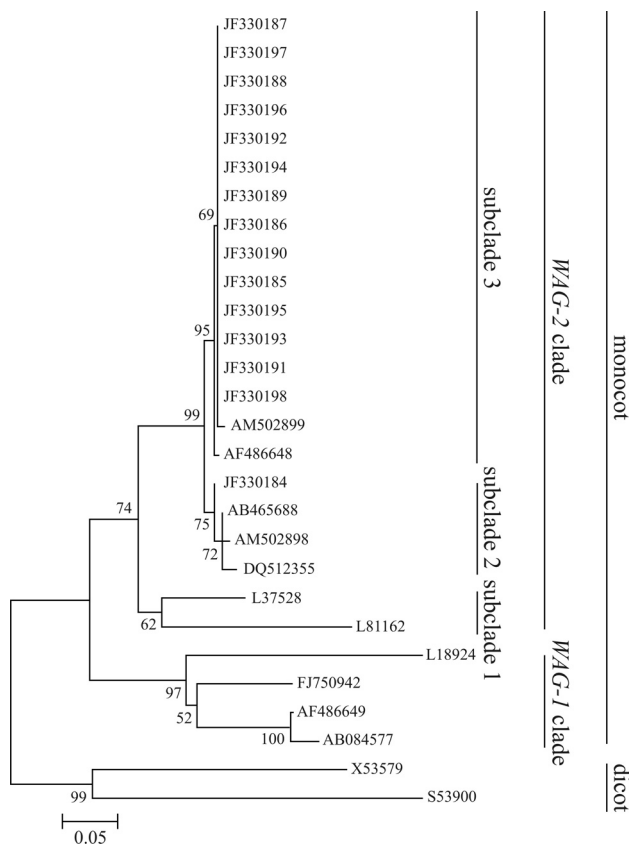


Figure 3 - Neighbor-joining phylogenetic tree of *AG* group MADS-box genes. Predicted amino acid sequences of the partial coding region were obtained from the NCBI: X53579 (*AG*) from *Arabidopsis*, (S53900) *PLE* from *Antirrhinum*, (L18924) *ZAG1* and L81162 (*ZMM2*) from maize, L37528 (*OsMADS3*) and FJ750942 (*OsMADS58*) from rice, AF465688 (*HvAG1*) and AF486649 (*HvAG2*) from barley, AB084577 (*WAG-1*), AB465688 (*WAG-2*), AM502898 (*WM29A*), AM502898 (*WM29B*) and DQ (*TaAGL39*) from wheat. The GenBank accession numbers (JF330184 to JF330198) for the cloned *WAG-2* sequences are shown in Table 1. Bootstrap values are shown as percentages for 1000 replicates.

calculating π using the method employed by Tajima (1989). For exons, π was 0.01812, 0.01788 and 0.01137, indicating that polymorphism was 1 SNP/55 bp, 1 SNP/56 bp and 1 SNP/88 bp between two homoeologous chromosomes in diploid, tetraploid and hexaploid species, respectively. For the exon+intron and intron regions, there was a common trend in that nucleotide polymorphism π decreased from diploid and tetraploid to hexaploid genotypes. These results indicate that the nucleotide diversity of the *WAG-2* gene in hexaploid species was lower than in diploid species. Hexaploid species probably suffered from long, strong artificial selection pressure that reduced nucleotide diversity.

The dn/ds ratio represents the selection effect and its direction. A dn/ds ratio < 1.0 indicates negative selection and a conserved gene, whereas a dn/ds ratio > 1.0 indicates positive selection and a gene susceptible to rapid evolutionary change. All of the dn/ds ratios calculated here were < 1.0, indicating that *WAG-2* is a conserved gene affected by negative selection (Nielsen, 2005). Furthermore, the dn/ds ratio was lowest among hexaploids and highest among diploids. This result implies that the *WAG-2* gene experienced rapid changes in its genome during the evolution of common wheat. The selection pressure was weak among diploid and tetraploid species, whereas natural and artificial selection pressure were stronger among hexaploid species.

Transitions generally occur more frequently than transversions such that the rate of transitions in DNA sequences differs from that of transversions. In mammalian nuclear DNA, transition mutations are approximately twice as frequent as transversions (Gojobori *et al.*, 1982; Li *et al.*, 1984; Cargill *et al.*, 1999; Lindblad-Toh *et al.*, 2000; Rosenberg *et al.*, 2003). In contrast to the moderate transition bias observed in mammalian nuclear DNA, transitions are approximately 15 times as frequent as transversions in human mitochondrial DNA (Brown *et al.*, 1982; Tamura and Nei, 1993). Transition bias also occurs in plant nuclear DNA. Transitions are about twice as frequent as transversions in rice (Hayashi *et al.*, 2004) and maize (Batley *et al.*, 2003). As shown here, the Ts/Tv ratio of the *WAG-2* gene partial sequences was nearly 1:1. The characteristics of transition bias suggest that the transition frequency was probably higher in other regions of the *WAG-2* genome DNA. These regions may not have been detected and should be studied in future research based on the overall *WAG-2* genome DNA. There was also a gradual decrease in the Ts/Tv ratio of the *WAG-2* gene partial sequences, from diploid and tetraploid to hexaploid species, especially in the exon region. Additional investigations on how transitions and transversions occur in the *WAG-2* gene of hexaploid wheat should improve our understanding of the molecular evolution of this gene. The A ↔ G to C ↔ T ratio was larger in tetraploid and diploid genotypes (> 1) than in hexaploid genotypes (approximately 1 or < 1). This finding implies a higher level of methylation in hexaploid geno-

types than in tetraploid or diploid species since most cytosines in CpG can be methylated and changed into thymine through deamination.

57 specific SNP mutations were identified, of which 39 belonged to diploid species. Eight of 10 indels were also detected in diploid species. These SNPs and indels can be used as specific molecular markers. Those specific SNPs and indels in diploid species may persist for longer than in tetraploid or hexaploid species and have a long evolutionary history, which could explain why the number of specific SNPs and indel mutations decreases with the increase of ploidy. There is also the possibility that the specific SNPs and indel mutations may occur later than common variants. As suggested by population genetics theory, in contrast to common variants, rare variants are more likely to be recently derived and therefore more likely to be population-specific (Stephens *et al.*, 2001).

Copy number of the *WAG-2* gene

The partial sequences of the *WAG-2* gene cloned from different species were assigned to three genomes: AA, BB and DD. The *WAG-2* gene of common wheat (*T. aestivum* L.) can also be copied to A, B and D genomes. The degree of divergence in the length of introns among *WAG-2* clones suggests conclusively that more than one copy of *WAG-2* is present in hexaploid or tetraploid species (Table 2). In the A or B genome group of *WAG-2*, sequences with high identities were clustered in *WAG-2A*, *WAG-2B* and *WAG-2D*. A previous study by Paolacci *et al.* (2007) revealed the possibility of three homoeologs in the A, B or D genome of common wheat. Most nuclear genes are considered members of multi-gene families (Vision *et al.*, 2000; Martin and Burg, 2002). The differences between two products within a taxon could be attributed to differences in the introns alone, as indicated elsewhere (Grob *et al.*, 2004). This finding proves that the number of copies of *WAG-2* is an important consideration for future work. Functional diversification of the three homoeologs should also be examined in subsequent research.

Phylogenetic relationships among AG-like genes

The two phylogenetic trees using different algorithms had very similar topologies, thus confirming the validity of the phylogenetic analysis. Most MADS-box genes are organized into distinct gene groups that share similar functions in regulating plant development (Purugganan *et al.*, 1995; Theissen *et al.*, 1996). Wheat AG-like genes were grouped into *WAG-1* and *WAG-2* clades (Figure 3), indicating that wheat AG orthologs were duplicated in monocot wheat species and showed functional differentiation. *WAG-1*, *ZAG1*, *OsMADS58* and *HvAG2* were clustered into one subgroup, suggesting similar functions among them. A loss of functional analysis indicates that maize *ZAG1* determines the floral meristem (Mena *et al.*, 1996). Mutant and transgenic studies indicate that *OsMADS58* has

an important role in determining floral meristem and in regulating carpel morphogenesis (Yamaguchi *et al.*, 2006). Wheat *WAG-1* transcripts preferentially accumulate in developing spikes during the late stages, suggesting that *WAG-1* is involved in the development of floral organs (Meguro *et al.*, 2003).

WAG-2 genes, together with *OsMADS3* and *ZMM2*, were clustered in the *WAG-2* clade (Figure 3), indicating functional homoeology among them. *OsMADS3* plays a more predominant role in inhibiting lodicule development and in specifying stamen identity (Kang *et al.*, 1995). *ZMM2* participates in regulating the formation of stamens and carpels (Mena *et al.*, 1996). *WAG-2* has been isolated from a wheat EST database (Ogihara *et al.*, 2003), however its function remains unknown. *WAG-2* transcripts have been preferentially detected in the central region of pistils but not in developing stamens during floral organ development (Mizumoto *et al.*, 2009). Future work should examine the functional role of *WAG-2* in the development of the floral organ in wheat. Apart from the *WAG-2* gene (JF330184), other *WAG-2* genes (JF330185-JF330198) clustered with *WM29B* (AM502899) and *HvAG1* (AF486648) in a single subgroup, probably because of their functional similarity and the high similarity in their amino acid sequences. Likewise, the *WAG-2* gene (JF330184, AB465688), *WM29A* (AM502898) and *TaAGL39* were clustered in a single subgroup, probably also because of the similarities in their amino acid sequences and functions. The *WAG-2* clade clearly contains several different wheat genes clustered into two subgroups in diploid, tetraploid and hexaploid species. Further study will show whether this sequence diversity involves different functions.

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Supplementary Material

The following supplementary material is available for this article:

Figure S1 - Alignment of the intron IV sequence of the *WAG-2* gene from different species.

This material is available as part of the online article at <http://www.scielo.br/gmb>.

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