Research Article

Isolation, Expression, and Promoter Analysis of GbWRKY2: A Novel Transcription Factor Gene from Ginkgo biloba

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WRKY transcription factor is involved in multiple life activities including plant growth and development as well as biotic and abiotic responses. We identified 28 WRKY genes from transcriptome data of Ginkgo biloba according to conserved WRKY domains and zinc finger structure and selected three WRKY genes, which are GbWRKY2, GbWRKY16, and GbWRKY21, for expression pattern analysis. GbWRKY2 was preferentially expressed in flowers and strongly induced by methyl jasmonate. Here, we cloned the full-length cDNA and genomic DNA of GbWRKY2. The full-length cDNA of GbWRKY2 was 1,713 bp containing a 1,014 bp open reading frame encoding a polypeptide of 337 amino acids. The GbWRKY2 genomic DNA had one intron and two exons. The deduced GbWRKY2 contained one WRKY domain and one zinc finger motif. GbWRKY2 was classified into Group II WRKYs. Southern blot analysis revealed that GbWRKY2 was a single copy gene in G. biloba. Many cis-acting elements related to hormone and stress responses were identified in the 1,363 bp-length 5'-flanking sequence of GbWRKY2, including W-box, ABRE-motif, MYBCOREs, and PYRIMIDINE-boxes, revealing the molecular mechanism of upregulated expression of GbWRKY2 by hormone and stress treatments. Further functional characterizations in transiently transformed tobacco leaves allowed us to identify the region that can be considered as the minimal promoter.

1. Introduction

Ginkgo biloba is the oldest relic plant among extant seed-bearing plants, usually referred to as a “living fossil” [1]. Experiencing million years of complicated climate, G. biloba not only shows strong adaptability but also exhibits minor changes in morphology. This phenomenon is possible because G. biloba can adapt to changing environments and tolerate harsh conditions [2]. Resistance genes encoding the enzymes in reactive oxygen-scavenging systems, including chloroplast copper/zinc-superoxide dismutase (GbCuZnSOD) [3], iron superoxide dismutase (GbFeSOD) [4], and manganese superoxide dismutase (GbMnSOD) [5], catalase (GbCAT1) [6], ascorbate peroxidases (GbAPX) [7], peroxidase (GbPOD1) [8], as well as dehydrin (GbDHN) [2], and GbASR [9] response to abscisic acid (ABA), stress, and ripening have been cloned from G. biloba. Studies on these genes help us to elucidate the molecular mechanism by which G. biloba tolerates severe conditions. Furthermore, stress conditions, such as drought, severe cold, harm, high temperature, and heavy metals, can stimulate accumulation and release of secondary metabolites of flavonoids and terpene lactones from G. biloba. Flavonoids and terpene lactones play an important role in improving self-protection, promoting competitive capacity, and coordinating interaction with the environment.

The WRKY family is among the ten largest families of transcription factor (TF) in higher plants and is found throughout the green lineage [10]. The defining feature of WRKY TFs is their DNA binding domain. This is called the WRKY domain containing the conserved WRKYGQK sequence at the N terminal, and as well as containing the WRKY signature it also has a typical zinc finger motif at
the C terminal. The zinc finger structure is either C₂H₂ (CX₄₋₅CX₂₋₅HX₂H) or C₂HC (CX₇₋₈CX₂₋₅HX₃C). Based on the number of the WRKY domains and the characteristic of a zinc finger motif, WRKY TFs can be divided into three groups: the first group contains two WRKY domains; the second group and the third group contain one WRKY domain each. The zinc finger motif of the second class is C₂H₂, which is the same as that of the first group; the zinc finger motif of the third group is C₂HC [11].

The WRKY domain binds to what is called W-box (TTGACC/T) in the promoters of target genes. This sequence is the minimal core element necessary for binding of a WRKY protein to DNA [12]. W-box is present in the promoter of many genes related to disease resistance, damage, growth, aging, and WRKY gene, which shows that the WRKY TF is closely related to biotic and abiotic stress responses [13]. Studies have successfully used the WRKY TF to improve the stress resistance of plants. For example, single or cosilence of NaWRKY3 and NaWRKY6 can promote the susceptibility of tobacco to herbivore damage by weakening the accumulation of volatile sesquiterpene and jasmonate [14]. The resistance of Arabidopsis thaliana to the fungal disease Botrytis is also improved by overexpressing AtWRKY3 and AtWRKY14 [15]. The tolerance of rice to high temperature and drought can be improved by overexpressing OsWRKY11 [16]. The expression level of MusaWRKY71 is improved after plants suffer from cold, drought, salt, ABA, H₂O₂, ethephon (ETH), salicylic acid (SA), and methyl jasmonate (MeJA) in Musa spp. [17]. The expression of HbWRKY1 in latex is induced by ETH and MeJA, while the expression of HbWRKY1 in the leaf is induced by drought and ABA from Hevea brasiliensis Müll. Arg. [18].

The WRKY TF can also participate in the control of the secondary metabolism of plants except in plant defense against exogenous stress. For example, Kato et al. [19] isolated and identified the GjWRKY1 TF that controls the biosynthesis of berberine from Coptis japonica. Ectopic expression of GjWRKY1 cDNA in C. japonica protoplasts clearly increased the level of transcripts of all berberine biosynthetic genes examined compared with control treatment, indicating that GjWRKY1 is a necessary positive regulator to control overall gene expression in berberine biosynthesis. Xu et al. [20] found that GbWRKY1 gene, which encodes a protein containing a single WRKY domain, could combine with W-box in the promoter region of the key gene encoding (+)-δ-cadinene synthase to metabolize terpene and promote sesquiterpene biosynthesis. Ma et al. [21] also isolated AaWRKY1 gene from glandular secretory trichomes of Artemisia annua in which artemisinin is synthesized and sequenced. Transient expression of AaWRKY1 cDNA in A. annua leaves clearly activated the expression of the majority of artemisinin biosynthetic genes, suggesting the involvement of the AaWRKY1 TF in the regulation of artemisinin biosynthesis. Recently, Li et al. [22] and Sun et al. [23] demonstrated that a TcWRKY1 gene and a MeJA inducible PqWRKY1 gene participated in regulation of the biosynthesis of taxol in Taxus chinensis and triterpene ginsenoside in Panax quinquefolius, respectively.

To date, the WRKY genes have been cloned from many species. A total of 5,936 WRKY genes are recorded in the database of plant TFs. These genes have also been reported in 83 species, such as algae, planus, needle-leaved plant, monocotyledons, and dicotyledons. However, no cloning and the WRKY gene in G. biloba has not been found. In this report, a total of 28 unigenes of WRKY transcription factor were identified using next-generation sequencing. Among these unigenes, a MeJA-inducible WRKY gene, named GbWRKY2, was cloned from G. biloba using the rapid amplification of cDNA ends (RACE) method. GbWRKY2 is preferentially expressed in flowers and induced by salinity stress and phytohormones such as SA, ETH, MeJA, and ABA but repressed by heat. Promoter analysis provided the molecular mechanism of upregulation of GbWRKY2 by phytohormones and abiotic stresses and allowed us to identify the region that can be considered as the minimal promoter. This work represents, to our knowledge, the first functional characterization of a G. biloba WRKY transcript factor.

2. Experimental Section

2.1. Plant Materials and Treatments. The 14-year-old grafts of G. biloba were grown in an orchard at Yangtze University, China. For tissue expression of GbWRKY2, GbWRKY16, and GbWRKY21, the roots, stems, leaves, and male and female flowers of G. biloba grafts were collected, immediately frozen in liquid nitrogen, and kept at −80°C prior to total RNA extraction. The cultured callus lines, initiated from mature zygotic embryos of G. biloba, were maintained on liquid MS basal medium supplementing with 1.5 mg/L naphthyleacetic acid (NAA) and 2 mg/L 6-benzyladenine (6-BA) on a rotary shaker at 100 rpm, in the light and at 25 ± 1°C. The suspension cultures were subcultured every 2 weeks and after four subcultures the differential was omitted. In the experiments for investigating induction by various elicitors, the callus lines were dipped into the appropriate treatment such as 100 μmol L⁻¹ MeJA, 100 μmol L⁻¹ ABA, 100 μmol L⁻¹ SA, 40 μmol L⁻¹ ETH, and 200 mmol L⁻¹ sodium chloride (NaCl), respectively, using ginkgo callus without any treatment as control. The cold and heat treatments were performed by placing the callus lines in a 4°C and 40°C growth room and the control in a 25°C growth room. The callus samples were harvested 0, 3, 6, 12, 24, 48, and 72 h after treatment and immediately frozen in liquid nitrogen, followed by storage at −80°C until use.

2.2. RNA and DNA Extraction. Total RNA was extracted from different tissues and all the treatments using CTAB method [42]. Genomic DNA was extracted from fresh leaves of G. biloba grafts following the CTAB method described by Xu et al. [43]. The RNA and DNA quality and quantity were determined by agarose gel electrophoresis and spectrophotometer analysis before use.

2.3. RNA-Seq Library Construction for Illumina Sequencing and Identification of WRKY Transcription Factor Gene from G. biloba Transcriptome. The extracted RNA was cleaned up using RNase-free DNasel (Dalian TaKaRa, China) and purified using oligo-dT-attached magnetic beads. The purified mRNAs were cleaved into small pieces (200–500 bp) by
Table 1: The primers used in this study.

| Primers       | Sequence (5′-3′) | Description                                      |
|---------------|------------------|--------------------------------------------------|
| WRKY2-FP      | CCCATAATCATCCTAAGCCTCTG | Forward primer for GbWRKY2 cDNA                  |
| WRKY2-3       | ATGGGACACTGTATCTTGAAGTTGAG | Reverse primer for GbWRKY2 cDNA                 |
| WRKY2-3N      | CAACCTTTGATGACAGCACCGACGCC | Forward primer for 5′-RACE, outer               |
| WRKY2-5N      | CGGTTAGGCAGAGGCTTGAAGTTA | Reverse primer for GbWRKY2 gDNA                 |
| WRKY2-G1      | ATGGGAGTTTGGTGCTGCT | Forward primer for 5′-RACE, nested               |
| WRKY2-G2      | TCAATGAAAAGAGGCTTCAAGG | Reverse primer for GbWRKY2 gDNA                 |
| WRKY2-SP1     | AACTGCAG | Reverse primer for 5′-promoter, outer            |
| WRKY2-SP2     | AACTGCAG | Reverse primer for 5′-promoter, nested           |
| WRKY2-U       | AACTGCAG | Gene forward primer for qRT-PCR                 |
| WRKY2-D       | AACTGCAG | Gene reverse primer for qRT-PCR                 |
| WRKY2-U       | AACTGCAG | Gene forward primer for promoter deletion        |
| WRKY2-D       | AACTGCAG | Gene reverse primer for promoter deletion        |
| WRKY2-U       | AACTGCAG | Gene forward primer for promoter deletion        |
| WRKY2-D       | AACTGCAG | Gene reverse primer for promoter deletion        |
| WRKY2-U       | AACTGCAG | Gene forward primer for promoter deletion        |
| WRKY2-D       | AACTGCAG | Gene reverse primer for promoter deletion        |
| WRKY2-U       | AACTGCAG | Gene forward primer for promoter deletion        |
| WRKY2-D       | AACTGCAG | Gene reverse primer for promoter deletion        |
| WRKY2-U       | AACTGCAG | Gene forward primer for promoter deletion        |
| WRKY2-D       | AACTGCAG | Gene reverse primer for promoter deletion        |
| WRKY2-U       | AACTGCAG | Gene forward primer for promoter deletion        |
| WRKY2-D       | AACTGCAG | Gene reverse primer for promoter deletion        |
| WRKY2-U       | AACTGCAG | Gene forward primer for promoter deletion        |
| WRKY2-D       | AACTGCAG | Gene reverse primer for promoter deletion        |
| WRKY2-U       | AACTGCAG | Gene forward primer for promoter deletion        |
| WRKY2-D       | AACTGCAG | Gene reverse primer for promoter deletion        |
| WRKY2-U       | AACTGCAG | Gene forward primer for promoter deletion        |
| WRKY2-D       | AACTGCAG | Gene reverse primer for promoter deletion        |

Super sonication. Cleaved mRNAs were used as templates to construct RNA-Seq library according to the manufacturer’s protocol. The constructed libraries were purified by the AMPure beads and recovered from the low melting agarose (2%) at the length of about 300 base-pair by the Qiagen Nucleic Acid purification kits (CA Qiagen, USA). Sequencing run was performed on Illumina HiSeq 2500 sequencer following the manufacturer’s protocols.

To obtain the complete G. biloba WRKY gene family, the male and female flowers of G. biloba transcriptome sequences were queried for 72 A. thaliana WRKY protein sequences using TBLASTN searching program. All of the collected G. biloba WRKY candidates were primarily analyzed using protein family database (Pfam) (http://pfam.xfam.org/) to confirm the presence of WRKY conserved domains on their protein structure.

2.4. Expression Analysis by Quantitative Real-Time PCR.
Quantitative real-time PCR (qRT-PCR) was performed according to the instructions provided for the Applied Biosystems 7500 Real-Time PCR system (Foster City, CA, USA) and the SYBR Premix Ex Taq II (Dalian TaKaRa, China). The RNA samples were reversely transcribed using the PrimeScript RT-PCR kit (Dalian TaKaRa, China). Expression levels of WRKY genes in G. biloba were normalized using the glyceraldehyde-3-phosphate dehydrogenase (GbGAPDH, GenBank accession number L26924) as an internal reference gene. Based on the screened transcripts, three annotated WRKY transcripts (T2_Unigene_BMK.10348 named GbWRKY2, T1_Unigene_BMK.13300 named GbWRKY16, and T1_Unigene_BMK.18545 named GbWRKY21) were selected for expression analysis. Primers were designed using the Sequence Detection System software and shown in Table 1. qRT-PCR was performed with 20 μL reaction consisting of 2x SYBR Premix Ex Taq 10 μL, 0.4 μL each primer and 50x ROX Reference Dye I, and 100 ng cDNA as the template. The thermal cycler conditions recommended by the manufacturer were used with first stage at 95°C for 30 s, and the second stage (40 cycles) at 95°C for 5 s followed by 60°C for 34 s, and the third stage at 95°C for 15 s followed by 60°C for 1 min and 95°C for 15 s. The amplification of the target genes was monitored every cycle by SYBR green fluorescence. The Ct (threshold
cycle), defined as the real-time PCR cycle at which a statistically significant increase of reporter fluorescence was first detected, was used as a measure for the starting copy numbers of the target gene. Three replicates of each experiment were performed, and data were analysed by the Livak method [44] and expressed as normalized relative expression level ($2^{-\Delta\Delta CT}$) of the respective genes in various samples. In each case, three technical replicates were performed for each of at least three independent biological replicates.

2.5. Cloning of the Full-Length cDNA and Genomic DNA of GbWRKY2. Two specific primers WRKY2-SP and WRKY2-SP (Table 1) were designed and synthesized (Shanghai Sangon, China) based on the transcripome data to obtain the internal fragment. One step RT-PCR was carried out and a fragment of 689 bp was obtained by using one step RT-PCR kit (Dalian TaKaRa, China) under the following condition: 50°C for 30 min and 94°C for 3 min, followed by 35 cycles of amplification (94°C for 1 min, 54°C for 1 min, and 72°C for 1 min), and then followed by extension for 10 min at 72°C. The PCR product was purified and cloned into pMD18-T vector (Dalian TaKaRa, China) followed by sequencing. Subsequent BLAST results confirmed that amplified product was partial fragment of WRKY2 gene.

Based on the sequence of the internal fragment of GbWRKY2 gene, the specific primers WRKY2-3WRKY2-5 and the nested primer WRKY2-3N/WRKY2-5N (Table 1) were designed to amplify the 3' and 5' end of the GbWRKY2 gene using the SMART RACE cDNA Amplification kit (Clontech, USA). The 3'-RACE-PCR and 5'-RACE-PCR were performed according to the manufacturer's instructions. The PCR products were purified and cloned into pMD18-T vector for sequencing. After comparing and aligning the sequence of 3'-RACE, 5'-RACE, and the internal region products, the full-length cDNA sequence of GbWRKY2 was obtained and verified through PCR amplification using 3'-Ready cDNA as the template and a pair of primers WRKY2-G1 and WRKY2-G2 (Table 1) under the following conditions: 94°C for 3 min, followed by 35 cycles of amplification (94°C for 20 s, 56°C for 30 s, and 72°C for 2 min). After sequencing, the full-length cDNA of GbWRKY2 was subsequently analyzed for molecular characterization. Two gene-specific primers, WRKY2-G1 and WRKY2-G2, designed based on the cDNA sequence were used to amplify the genomic sequence of GbWRKY2.

2.6. Amplification of the Promoter Region of GbWRKY2. Ginkgo genome walker libraries were constructed using the Genome Walker Universal Kit User (Clontech, USA). To clone the promoter region of GbWRKY2, two round PCR were performed using gene-specific primers (WRKY2-SP1 and WRKY2-SP2) that were designed according to the sequence of GbWRKY2 cDNA and the adapter primers (AP1 and AP2) provided by the kit. Their sequences were shown in Table 1. After the nested PCR was carried out, amplified fragments were cloned and then sequenced. The sequences that extended upstream of the cDNA of GbWRKY2 were isolated as the 5'-upstream region of GbWRKY2 gene and used for further analysis.

2.7. Promoter Deletion-GUS Constructs and Agrobacterium-Mediated Transient Expression Assay. For construction of the GbWRKY2 promoter-driven GUS fusion genes, the GbWRKY2 promoter fragment-covering regions were amplified by PCR. Forward primers (Table 1) were designed to correspond to the −1363, −1018, −721, −668, −521, −288, −137, and −48 of GbWRKY2 promoter and reverse primers, WRKY2P-anti and WRKY2-5UTR-R, were complementary to the 3'-end sequence of GbWRKY2 promoter and 5'-UTR region, respectively. In addition, a supplementary fragment was amplified using primers WRKY2-1363 and WRKY2P-anti lacking the 5'-UTR region of GbWRKY2. Each fragment was digested with PstI/BamHI and subcloned into PstI/BamHI-digested pBI21 to generate seven promoter deletion derivatives. The promoterless construct (pBI21) was used as negative control. All constructs were verified by sequence analysis. Each promoter-GUS fusion construct was introduced into A. tumefaciens LBA4404 via electroporation. Agrobacterium-mediated transient expression assays were performed according to the method of An et al. [45]. Agrobacterium-mediated transient expression was conducted on fully expanded tobacco leaves, and the intercellular spaces of the intact leaves were infiltrated with the bacterial suspension. After agroinfiltration, tobacco plants were maintained in a moist chamber at 24°C for 48 h. The GUS activity was examined in the tobacco leaves coinfilitrated with Agrobacterium strains harboring different GbWRKY2 promoter-GUS fusion constructs.

2.8. GUS Activity Assay. The seedlings of tobacco transformant were ground in liquid nitrogen. The crude proteins were extracted with 50 mM phosphate buffer, pH 7.0, containing 10 mM β-mercaptoethanol, 10 mM EDTA, and 0.1% Triton X-100. Homogenates were cleared by centrifugation, and the supernatants were assayed by Bradford assay for total protein (DU700, Beckman, Germany). GUS activity was measured as described by Jefferson et al. [46].

2.9. Southern Blot Analysis. Aliquots of DNA (30 μg/sample) were digested overnight at 37°C with BamHI and PstI, respectively, which does not cut within the probe region, fractionated by 0.85% agarose gel electrophoresis and transferred to a Hybond-N+ nylon membrane (Amersham Pharmacia, UK). The 283-bp probe was generated by PCR using genomic sequence of GbWRKY2 including intron as template with primers FWR2PIN and RWR2PIN (Table 1). Probe labeling (biotin), hybridization, and signal detection were performed using Gene Images random prime labeling module and CDP-Star detection module following the manufacturer's instructions (Amersham Pharmacia, UK). The film was washed under stringent conditions (60°C) and signals were visualized by exposure to Fuji X-ray film at room temperature for 1.5 h.

2.10. Bioinformatic Analysis and Molecular Evolution Analyses. The obtained sequences were analyzed using bioinformatic tools at websites (http://www.ncbi.nlm.nih.gov and http://www.expasy.org/). The software vector NTI Suite 10 was used for sequence multialignment. The isolated 5'-upstream sequence was analyzed for the putative cis-acting
Table 2: The WRKY transcription factors in G. biloba.

| Sequence ID*       | Male flower RPKM | Female flower RPKM | CDs (bp) | Annotation to the Arabidopsis WRKYs |
|--------------------|------------------|--------------------|----------|-------------------------------------|
| T1_Uniongene_BMK.14363 | 10.97            | 13.00              | 2583     | WRKY2                              |
| CL1186Contig1      | 21.20            | 5.54               | 1977     | WRKY4                              |
| T1_Uniongene_BMK.20451 | 15.23            | 38.68              | 2019     | WRKY3                              |
| CL8351Contig1      | 7.37             | 10.07              | 2037     | WRKY4                              |
| CL197Contig1       | 7.25             | 14.22              | 2325     | WRKY20                             |
| CL6861Contig1      | 50.14            | 3.48               | 2121     | WRKY31                             |
| T1_Uniongene_BMK.5610 | 1.92             | 0.00               | 783      | WRKY61                             |
| CL6024Contig1      | 3.55             | 2.24               | 1338     | WRKY57                             |
| CL10281Contig1     | 12.46            | 3.65               | 744      | WRKY28                             |
| T1_Uniongene_BMK.13300 | 23.85            | 18.55              | 1068     | WRKY21                             |
| CL7935Contig1      | 68.18            | 44.85              | 1206     | WRKY11                             |
| T1_Uniongene_BMK.24659 | 7.59             | 0.45               | 1281     | WRKY42                             |
| CL10826Contig1     | 2.54             | 1.29               | 1374     | WRKY14                             |
| T1_Uniongene_BMK.18545 | 25.53            | 3.26               | 642      | WRKY16                             |
| T1_Uniongene_BMK.20037 | 15.38            | 39.75              | 1440     | WRKY4                              |
| CL7199Contig1      | 11.59            | 6.68               | 1086     | WRKY21                             |
| T1_Uniongene_BMK.7872 | 3.06             | 1.19               | 900      | WRKY31                             |
| T1_Uniongene_BMK.15740 | 11.05            | 13.52              | 1806     | WRKY2                              |
| CL2657Contig1      | 2.31             | 23.10              | 804      | WRKY71                             |
| CL3411Contig1      | 5.22             | 1.97               | 1527     | WRKY48                             |
| T1_Uniongene_BMK.8142 | 21.95            | 18.36              | 1068     | WRKY21                             |
| CLI1312Contig1     | 32.03            | 14.08              | 1101     | WRKY7                              |
| T1_Uniongene_BMK.4532 | 0.08             | 1.46               | 258      | WRKY12                             |
| T1_Uniongene_BMK.10348 | 10.05            | 2.10               | 808      | WRKY2                              |
| T1_Uniongene_BMK.10347 | 18.22            | 4.04               | 915      | WRKY2                              |
| CL1517Contig1      | 22.31            | 6.87               | 1080     | WRKY21                             |
| T1_Uniongene_BMK.9572 | 0.13             | 2.84               | 1404     | WRKY49                             |
| CL4085Contig1      | 1.76             | 0.69               | 378      | WRKY23                             |

*The candidate gene is indicated in bold.

regulatory elements using the PLACE (http://www.dna.affrc.go.jp/PLACE/) and the Signal Scan Program PlantCARE (http://bioinformatics.psb.ugent.be/webtools/plantcare/html/) database. Phylogenetic tree analysis of GbWRKY2 and known WRKYs from other plant species retrieved from GenBank were aligned with CLUSTALW. Subsequently, a phylogenetic tree was constructed by neighbor-joining (NJ) method. The reliability of the tree was measured by bootstrap analysis with 1000 replicates.

3. Results

3.1. WRKY Candidate Genes Were Identified in G. biloba Transcriptome. Transcriptomes of male and female flowers from G. biloba were sequenced using Illumina RNA-seq technology, yielding 20 and 19 million transcript reads, respectively. Using the PFAM protein family database with the WRKY domain (PF03106), we identified a total of 28 WRKY transcription factors (Table 2). There were differences in the lengths of proposed sequences of 28 WRKY genes, ranging from 258 bp to 2325 bp. These differences may have been due largely to assembly error in partial chromosomal regions and require further confirmation. Gene expression level was estimated using RPKM (reads per kilobase per million mapped reads) value. Among these 28 WRKY transcripts, 20 WRKY genes were identified to be highly expressed in male flowers and the others were highly expressed in female flowers. Subsequently, we selected GbWRKY2, GbWRKY16, and GbWRKY21 for expression analysis.

3.2. Expression Analysis in Different Tissues. The expression profile of GbWRKY2, GbWRKY16, and GbWRKY21 was assessed by qRT-PCR in leaves, roots, stems, and male and female flowers of 14-year-old graft ginkgo trees (Figure 1). The results showed that all of three genes transcripts could be detected in all tissues, but at different expression levels. The highest expression level of GbWRKY2 was observed in flowers and significantly higher than in the leaves and roots. The lowest expression level of GbWRKY2 was observed in stems and was significantly lower (P < 0.05) in other tissues. In contrast, the expression level of GbWRKY16 was very low in flowers, and the expression level of GbWRKY21 was
significantly higher in leaves, stems, and female flowers than in roots and male flowers.

3.3. Effect of Abiotic Stresses on the Expression of Three WRKY Genes. To determine the function of \textit{GbWRKY2}, \textit{GbWRKY16}, and \textit{GbWRKY21} in ginkgo callus treated with NaCl, cold, and heat. As shown in Figure 2(a), \textit{GbWRKY2} and \textit{GbWRKY16} transcript levels were enhanced by NaCl, showing a 1.9-fold and 2.8-fold, respectively, compared with the control at 3 hpt (hours after treatment). Afterwards, the transcript levels of these two genes were decreased sharply after 6 hpt. \textit{GbWRKY21} transcript level was increased slightly and then decreased along with the treatment. \textit{GbWRKY2} transcript levels were also somewhat enhanced by low temperature (4°C) at 12 hpt (Figure 2(b)) but were decreased slightly along with the treatment time under high temperature (40°C) stress (Figure 2(c)). The relative expressions of \textit{WRKY16} and \textit{GbWRKY21} were significantly decreased under both low and high temperature treatments (Figure 2(c)).

3.4. Effect of Hormones on the Expression of Three WRKY Genes. Phytohormones, such as SA, MeJA, ABA, and ETH, serve as important signaling molecules and play crucial roles in controlling the expression of downstream defense genes and physiological reactions against biotic and abiotic stresses. To assess the possible involvement of three \textit{WRKY} genes in signaling pathways utilized by these hormones, the transcript level of \textit{GbWRKY2}, \textit{GbWRKY16}, and \textit{GbWRKY21} in ginkgo callus was determined by qRT-PCR treated with ABA, SA, ETH, and MeJA. All the transcript levels of the \textit{GbWRKY2}, \textit{GbWRKY16}, and \textit{GbWRKY21} were significantly ($P < 0.05$)
Figure 3: Relative expression levels of *GbWRKY2*, *GbWRKY16*, and *GbWRKY21* with ABA (a), SA (b), ETH (c), and MeJA (d) treatments. Relative expressions of *GbWRKY2*, *GbWRKY16*, and *GbWRKY21* at various hours after treatment under ABA, SA, ETH, and MeJA treatments with *GbGAPDH* gene as internal reference gene. Each sample was individually assayed in triplicate. Values shown represent the mean reading from three treated samples and the error bars indicated the standard errors of the mean.

increasingly treated with ABA compared with the control. The strongest response of *GbWRKY2* (5.1-fold compared with the control), *GbWRKY16* (2.9-fold compared with the control), and *GbWRKY21* (1.8-fold compared with the control) to ABA treatment was observed at 12, 6, and 24 hpt, respectively (Figure 3(a)).

In regard to SA, *GbWRKY2* transcript level was increased between 3 and 24 hpt (Figure 3(b)). The highest levels of *GbWRKY2* transcript level (3.9-fold compared with the control) were reached at 6 hpt. *GbWRKY16* transcript level was sustainably upregulated during SA treatment and the highest level of *GbWRKY16* (2.5-fold compared with the control) was reached at 12 hpt. In contrast, *GbWRKY21* transcript level was firstly decreased after treatment and increased between 12 and 24 hpt, treated with SA compared with the control. The strongest response to SA (4.2-fold compared with the control) was observed at 24 hpt.

Figure 3(c) showed that the transcript levels of *GbWRKY2* and *GbWRKY16* were decreased sharply before 12 hpt but enhanced rapidly and reached the peak, nearly 3.5-fold and 5.6-fold compared with the control, respectively, under ETH treatment. *GbWRKY21* transcript level was continuously upregulated until 12 hpt reaching a 6.5-fold compared with the control and then was decreased.

For MeJA treatment, *GbWRKY2* transcript level was significantly (*P* < 0.05) induced between 0 and 3 hpt, after which they decreased to the similar level to the control (Figure 3(d)). In contrast to GbWRKY2, no significant effect of MeJA was observed in *GbWRKY16* transcript level, while *GbWRKY21* transcript level was significantly (*P* < 0.05) decreased by MeJA.

3.5. Cloning of *GbWRKY2* and Its Sequence Analysis. The WRKY genes have previously been determined to respond to MeJA and are involved in many life processes, including stress resistance [47], secondary metabolism [23], and plant defense [48]. The exploration of the function of MeJA-inducible WRKY genes in *G. biloba* would be beneficial for discovering genes involved in stress resistance and in secondary metabolite biosynthesis in *G. biloba*. Since qRT-PCR analysis
indicated that GbWRKY2 might be involved in the signal transduction of MeJA in stress resistance of ginkgo. We cloned the full-length cDNA, genomic DNA, and promoter region of GbWRKY2 to further study the function of GbWRKY2 in stress defense.

The full-length cDNA of GbWRKY2 (GenBank accession number KP987204) was 1,713 bp and contained a 1,014 bp open reading frame encoding a 337 amino acid proteins. One possible polyadenylation signal (AATAA) was found at 194 bp position downstream from the stop codon (Figure 4). A pair
of specific primers was designed to synthesize cDNA between the start codon and the terminator codon of GbWRKY2. The genomic sequence of GbWRKY2 (GenBank accession number KP987205) with a length of 1,137 bp was amplified and exhibited 100% identity of the coding region of the full-length cDNA sequence. The genomic sequence of GbWRKY2 contained one intron with a length of 123 bp. This intron was smaller than that of Arabidopsis (241 bp) and rice (868 bp). The putative splicing site obeyed the GT/AG rule [11] (Figure 4). Compared with the identities of the nucleotides of other plants in NCBI, the identities of GbWRKY2 with the nucleotide sequence of the WRKY gene from Picea glauca, P. sitchensis, Amborella trichopoda, Medicago truncatula, and Morus notabilis were 83%, 82%, 81%, 81%, and 83%, respectively.

3.6. Southern Blot Analysis. To investigate the genomic organization of GbWRKY2, we carried out a Southern blot analysis by digesting genomic DNA of G. biloba with BamHI and PstI, followed by hybridization with a 283 bp probe generated by PCR using the genomic sequence of GbWRKY2 as template. As shown in Figure 5, only one hybridized band was detected in each lane, indicating that GbWRKY2 was a single copy gene in G. biloba.

3.7. Analysis of GbWRKY2 Protein. The GbWRKY2 was predicted to encode a protein of 337 amino acid residues. The relative molecular mass and theoretical isoelectric point (pI) of the predicted protein were 36.25 kDa and 6.16, respectively. BLASTP analysis in NCBI revealed that the deduced GbWRKY2 amino acid showed high identity to known WRKY TFs from other plants (Figure 6). The analysis of the deduced amino acid revealed that GbWRKY2 contained one conserved WRKY domain and a zinc finger motif of C2H2 (Figure 6), suggesting GbWRKY2 is a member of the WRKY II family [10, 11]. Like other members of WRKY II family, the conserved domain zinc finger motif for binding Zn2+ ion required for protein function presents at similar positions in GbWRKY2. In addition, sequence analysis using WoLF PSORT (http://www.genscript.com/psort/wolf_psort.html) indicated that the predicted GbWRKY2 protein contains a putative nuclear localization signal (78KRRKK30). All the observed conservations of these domains and motifs in all aligned sequences, especially in G. biloba, suggested the function of the GbWRKY2 protein.

To investigate the evolutionary relationships among GbWRKY2 and other WRKY TF proteins, the phylogenetic tree was constructed using neighbor-joining method (Figure 7). The results showed a total of 19 WRKY proteins divided into three classes. Among these proteins, MnWRKY2, NtWRKY4, GsWRKY2, and AtWRKY2 belonged to class I; AtWRKY53, AtWRKY70, and CrWRKY1 belonged to class III. GbWRKY2, HbWRKY1, CjWRKY1, TwWRKY, and GaWRKY1, as well as PsWTKY1, clustered in Group II. Furthermore, GbWRKY2 and PsWRKY of gymnosperms clustered in the same branch, implying that these two WRKY TFs may exhibit a close genetic relationship and display similar protein function.

3.8. Analysis of 5′-Flanking Sequence of GbWRKY2. Based on the DNA sequence of GbWRKY2 gene, the nested primer is designed, and the 5′-flanking sequence (KP987205) with 1,363 bp of GbWRKY2 was isolated by genome walking method. Taking into account the result of 5′-RACE PCR, we concluded the initiation site of GbWRKY2 transcription at −97 bp in the upstream of ATG (Figure 1S in the Supplementary Material available online at http://dx.doi.org/10.1155/2015/607185). The promoter region of GbWRKY2 possessed a typically high A + T content of 58.0%, which was commonly found in other plant promoters. The promoter region of GbWRKY2 was then submitted to PLACE and PlantCARE databases for the analysis of putative cis-element. The result showed that the TATA box was located at −26 bp in the upstream of the transcription initiation site. Another conserved eukaryotic cis-element, the CAAT box, was also found at 232, 787, and 824 bp (Figure 1S), consistent with typical characteristics of the plant promoter. Other stress-related cis-elements were also observed in the promoter region of GbWRKY2 (Table 3). For example, one low temperature response (CRTDREHVCBF2) [30], two drought stress response and aging response (ACGTATERD1) [27], and four disease defense (BIHD1OS) [28] cis-elements were found. Motifs related to light regulation, including three GT1 [49] and one IBOX [36], were also detected. Furthermore, cis-acting elements related to hormones were also predicted (Figure 1S). For example, we found one core motif for binding DBPBF TF, three GT1 motifs, seven ARRIAT TF binding sites, and four PYRIDINIDE-boxes that participate in the signal response of ABA, salicylic acid, cytokinin, and gibberellin [26, 32, 39, 49], respectively, in the promoter region of GbWRKY2. Two ABA response cis-elements were also found at 10 and 585 bp position [24, 25]. Moreover, some TF binding sites were also detected. For example, five Dof TF binding sites were found in the promoter region of GbWRKY2, and these motifs participate in the signal response of auxin [50],
jasmonic acid, or ethylene [51] in other plants. In addition, we found ten E-boxes, five MYB-boxes, nine MYC-boxes, and one W-box in *GbWRKY2* promoter, which is conservative binding motif of bHLH [33], MYB [38], MYC [37], and WRKY [12] TFs, respectively. Interestingly, the presence of a putative W-box binding site within the *GbWRKY2* promoter might indicate that this ginkgo gene can be subjected to autoregulation or can be modulated by other WRKY members [52, 53]. Prediction results showed that the regulatory cis-elements of *GbWRKY2* promoter were related to stress-induced response, indicating that the promoter may play an important role in response to external environmental stress and biological defense process.

3.9. Deletion Analysis of the *GbWRKY2* Promoter in Tobacco Leaf Tissues. To gain insight into the functional role of
Table 3: Putative cis-acting regulatory elements identified in the promoter of *GbWRKY2* using PLACE (http://www.dna.affrc.go.jp/PLACE/) and the Signal Scan Program PlantCARE (http://bioinformatics.psb.ugent.be/webtools/plantcare/html/) database.

| Name of cis-element | Position | Signal sequence | Function | References |
|---------------------|----------|----------------|----------|------------|
| ABRELATERD1         | 585      | ACGTG          | ABA-responsive elements | [24] |
| ABRERATCAL          | 10       | MACGYGB        | Ca\(^{2+}\)-responsive and ABA upregulated genes | [25] |
| ARRIAT              | 629, 634, 564, 90, 751, 883 | NGATT       | ARRI binding element involved in cytokinin signaling | [26] |
| ACGTATERD1          | 262, 585 | ACGT           | Involved in upregulation by dehydration stress and dark-induced senescence | [27] |
| BIHDIOS             | 595, 772, 863, 1307 | TGTCA       | BELL recognition site involved in disease resistance responses | [28] |
| CAATBOXI            | 232, 787, 824 | CAAT         | Common cis-acting element in promoter and enhancer regions | [29] |
| CRTDREHVCBF2        | 18       | GTCGAC         | Low-temperature responsive | [30] |
| DOFCOREZM           | 354, 621, 687, 1258, 1301 | AAAG        | Dof1 and Dof2 binding element involved in carbon metabolism | [31] |
| DPBFSCOREDCDC3      | 1089     | ACACNNG        | DPBF-1 binding core sequence involved in ABA signaling | [32] |
| EBOXBNNAPA          | 86, 232, 318, 714, 729, 775, 1090, 1246, 1280, 1350 | CANNTG    | cis-element binding BHLH factor is dispensable for light responsiveness | [33] |
| GATABOX             | 124, 222, 290, 640, 681, 1253, 1276 | GATA      | Common cis-acting element in promoter | [34] |
| GTICONSENSUS        | 475, 803, 928 | GRWA AW | Consensus GT-1 binding site in many light-regulated genes and influence the level of SA-inducible gene expression | [35] |
| IBOX                | 124      | GATAAG         | Conserved sequence upstream of light-regulated genes | [36] |
| MYB2CONSENSUSAT     | 318, 1246, 1280, 591 | YAACKG     | MYB recognition site involved in dehydration responsiveness | [37] |
| MYCCONSENSUSAT      | 86, 232, 318, 714, 729, 775, 1090, 1246, 1280 | CANNTG   | MYC recognition site involved in dehydration responsiveness and cold responsiveness | [38] |
| PYRIMIDINE-box      | 214, 840, 869, 890 | CTTTTT     | Gibberellin-response cis-element | [39] |
| ROOTMOTIFTAPOXI     | 178, 223, 546, 641, 722 | ATATT     | Root specific expression | [40] |
| WBOXATNPRI          | 887      | TTGACY         | WRKY binding site, involved in many physiological processes | [10] |

the *GbWRKY2* promoter region, series deletions were sequential of the cis-elements and fusion of the remaining promoter to the GUS reporter gene was constructed. A promoterless construct (pBI121) was used as a negative control (Figure 8). Sequential 5’-deletions of the promoter were performed by PCR, and the responsiveness of the deleted versions of the *GbWRKY2* promoter was analyzed by transient assays in tobacco leaves. As shown in Figure 8, the GUS activity of the maximum-length containing 5’-UTR of *GbWRKY2* (construct −1363) was 358.36 nM 4-methylumbelliferone (MU) mg\(^{-1}\) protein min\(^{-1}\), although the GUS activity (352.19 nM 4-mg\(^{-1}\) protein min\(^{-1}\)) of 5’-UTR deletion of full-length promoter (−1363Δ) was slightly less than that of construct −1363 but did not reach significant level (P > 0.05), suggesting that 5’-UTR had no effect on the transcript level of *GbWRKY2* promoter under our experimental condition. The highest level of GUS activity was observed in transgenic tobacco leaves harboring the −1018 promoter construct and significantly higher (P < 0.05) than that of the full-length promoter (construct −1363), implying that negative cis-elements may be present in the promoter region between −1363 and −1018. By contrast, deletion of the *GbWRKY2* promoter from −1018 to −668 caused a significant (P < 0.05) reduction of the promoter expression. Successive deletion from −668 to −521 had no additional significant effect on GUS activity while further deletion to −228 containing a W-box causes a significant (P < 0.05) decrease of GUS activity. Likewise, both further deletions from −228 to −137 and from −137 to −48 led to 39.3% and 16.7% decrease of promoter expression, respectively. Finally, both the constructs containing
5′-UTR and negative constructs present a quasicomplete disappearance of GUS activity, suggesting 5′-UTR region had no contribution to GbWRKY2 expression.

4. Discussion

Given the important roles that WRKY transcription factors play in response to various stresses, the traditional gene-by-gene research was not a high-efficiency method to study the plant that had no genome sequence. High throughput sequencing data have been used for functional gene mining in other plant species, three GbWRKYs were found to be expressed in all tissues we used, but at different expression levels in different tissues. These data suggested that GbWRKY2 might respond to various environment stimulus. Functional gene mining in plants has been greatly enhanced using individual promoters [55]. Thus, we isolated a 1,363 bp-length promoter of GbWRKY2 (Figure 1S). Bioinformatics analysis showed that multiple cis-acting elements including fundamental and special elements associated with abiotic stresses and hormone regulations were found in the GbWRKY2 promoter (Table 3), indicating that GbWRKY2 gene might respond to various environment stimulus. Furthermore, a series of 5′ end deletion fragments of this promoter were detected using transient expression assays, which demonstrated that the activity of a truncated promoter from position −1 to −48 bp retained the ability to initiate the expression of GUS in transgenic tobacco leaves. This region is enough to keep the basic function of GbWRKY2 promoter. Bioinformatics analysis showed a TATA box was located in the region between −1 and −48 bp. Together taken into the results of bioinformatics and deletion analysis, we conclude that the region of −1 to −48 bp is the equal of core promoter and positions of TATA box correspond to the typical core promoter model [56]. Moreover, our experiments showed that deletion of the promoter regions between positions −1018 and −668 or between positions −288 and −137 caused very significant (P < 0.01) reductions in promoter activity suggesting that these regions likely contain potential transcription-enhancing cis-acting elements. Sequence analysis discussed above indicates that both regions contain three and two DoF TF binding sites, respectively, which might be important for the hormonal responsiveness of GbWRKY2 promoter.

4.1. GbWRKY2 Is a Group II WRKY Transcription Factor. A ginkgo gene (GbWRKY2) encoding a protein with sequence homology to members of the WRKY family has been characterized. This newly characterized gene is the first WRKY factor described in G. biloba and presents structural hallmarks that allow us to classify it within Group II of WRKY TFs [11]. The phylogenetic analysis also clearly showed that GbWRKY2 belong to Group II WRKY family. Numerous members of plant WRKY genes belong to Group II family and play roles in transcriptional reprogramming associated with resistance to various stresses [11]. A predicted nuclear localization signal (NLS) (Figure 4) strongly suggests that GbWRKY2 protein is translocated into the nucleus to control gene expression. These data suggested that GbWRKY2 might play an important role in defense response of ginkgo to biotic and abiotic stresses.

4.2. Multiple cis-acting Elements Response to Stress and Hormone in the Promoter Region of GbWRKY2. Stress-inducible gene expression is transcriptionally regulated by a change in the level and/or activity of sequence-specific DNA-binding transcription factors bound to specific cis-acting elements of promoter regions [54]. These regulatory factors are involved in the activation, suppression, and modulation of various signaling pathways in plant cells on biotic and abiotic stresses. Many plant promoters have therefore been identified and isolated, and genetic engineering in plants has been greatly enhanced using individual promoters [55]. Thus, we isolated a 1,363 bp-length promoter of GbWRKY2 (Figure 1S). Bioinformatics analysis showed that multiple cis-acting elements including fundamental and special elements associated with abiotic stresses and hormone regulations were found in the GbWRKY2 promoter (Table 3), indicating that GbWRKY2 gene might respond to various environment stimulus. Furthermore, a series of 5′ end deletion fragments of this promoter were detected using transient expression assays, which demonstrated that the activity of a truncated promoter from position −1 to −48 bp retained the ability to initiate the expression of GUS in transgenic tobacco leaves. This region is enough to keep the basic function of GbWRKY2 promoter. Bioinformatics analysis showed a TATA box was located in the region between −1 and −48 bp. Together taken into the results of bioinformatics and deletion analysis, we conclude that the region of −1 to −48 bp is the equal of core promoter and positions of TATA box correspond to the typical core promoter model [56]. Moreover, our experiments showed that deletion of the promoter regions between positions −1018 and −668 or between positions −288 and −137 caused very significant (P < 0.01) reductions in promoter activity suggesting that these regions likely contain potential transcription-enhancing cis-acting elements. Sequence analysis discussed above indicates that both regions contain three and two DoF TF binding sites, respectively, which might be important for the hormonal responsiveness of GbWRKY2 promoter.

4.3. GbWRKY2 Might Participate in the Development of Ginkgo Inflorescence. Similar to expression patterns observed in other plant species, three GbWRKYs were found to be expressed in all tissues we used, but at different expression
levels. Moreover, the transcription of GbWRKY2 was observed abundant in flowers. In contrast, expression levels of GbWRKY16 were very low in flowers. And the expression levels of GbWRKY21 were significantly higher in leaves, stems, and female flowers than in roots and male flowers. The result may indicate that GbWRKY2, GbWRKY16, and GbWRKY21 played different roles involved in regulating plant developmental and physiological processes. The highest expression level of GbWRKY2 is in flowers while the lowest expression level of in stems, consistent with the spatial expression profile of ChWRKY2 from Corylus heterophylla [57]. Given highest transcript level of GbWRKY2 in flowers, it can be speculated that GbWRKY2 might play an important role in tolerance to low temperature in inflorescence, which developed in cold early spring. Thus, we deduced that GbWKY2 likely exhibited similar function of ChWRKY2 TF to participate in the developmental process of ginkgo inflorescence.

4.4. GbWRKYs Might Play Role in Stress-Related Signal Pathways. Salinity is an important abiotic stress factor, usually affecting plant growth, development, survival, and crop productivity. Thus, understanding the complex mechanism of salinity tolerance is important for agriculture production. Interestingly, several WRKY proteins were shown to be involved in plant salinity stress response. For example, the expression of CmWRKY17 was induced by salinity in Chrysanthemum morifolium and overexpression of CmWRKY17 in Chrysanthemum and Arabidopsis increased the sensitivity to salinity stress [58]. The transcripts of two closely related WRKY TFs (AtWRKY25 and AtWRKY33) from Arabidopsis were increased by NaCl treatment and both the Atwrky33 null mutants and Atwrky25Atwrky33 double mutants showed moderately increased NaCl sensitivity [59].

Poplar species increase expressions of transcription factors to deal with salt environments. Salinity increased heat-shock transcription factor (HSF) transcription in Poplar species [60]. Similarly, the first evidence pointing towards a role for GbWRKY2 and GbWRKY16 in defense comes from the data showing that the GbWRKY2 and GbWRKY16 transcript is dramatically upregulated in ginkgo in response to NaCl. Further study on suppression/overexpression of GbWRKY2 and GbWRKY16 was required for unveiling the molecular mechanism of GbWRKY2 and GbWRKY16 gene participation in ginkgo tolerance to salt.

Temperature that exceeds an organism’s optimal tolerance range is considered as an important abiotic stress factor. Tremendous work has been done in the past two decades to reveal the complex molecular mechanism in plants’ responses to extreme temperature and there is increasing evidence that WRKY proteins are involved in responses to both heat and cold stresses. For example, a WRKY TF in Nicotiana tabacum responds to a combination of drought and heat stress [61]. Another example is that transgenic Arabidopsis plants overexpressing GmWRKY21 exhibited increased tolerance to cold stress when compared with wild-type plants [62]. In our studies, the expression levels of GbWRKY2, GbWRKY16, and GbWRKY21 were all repressed by heat stress. The expression level of GbWRKY2 was upregulated by cold stress and there was no significant effect of cold stress on GbWRKY16 transcript levels. In contrast, the expression level of GbWRKY21 was downregulated by cold stress. We also reported for the first time an increase of GbWRKY2 transcript level by cold but decrease by heat, consistent with the observation of

![Figure 8: Deletion analysis of the GbWRKY2 promoter-driven GUS activity. Schematic diagram of the constructs used for GUS activity assays in leaves of transgenic tobacco plants is shown at left. Dash line pinpoints the deletion of the 5’-UTR region for the construct −1363Δ. Quantitative analyses of GUS activity of transgenic plants driven by deletion constructs of the GbWRKY2 promoter are shown at right. Error bars represent standard deviation (SD). Data are mean ± SD from triplicate experiments. Values with different letters show significant differences at P = 0.05 according to the Fisher’s least significant difference (LSD) test.](image-url)
cold responsive cis-elements (CRTDRE/HVCF and MYC recognition site) (Table 3). Although low-temperature related WRKYs were isolated in several species [62–64]. The mechanism of how WRKYs respond to cold signals and regulated the expression downstream genes is still largely unknown. Further work is needed to elucidate the function of these important genes in low-temperature related signal pathways.

ABA is an important signal molecule related to abiotic stress. Previous studies have demonstrated that WRKY proteins may act as activator in ABA signaling [65]. It was reported that the expression of LtrWRKY21 in Larrea tridentata was shown to function as an activator to control ABA-regulated expression of genes [66]. Recently, Sun et al. also [67] reported that 13 numbers of WRKY family in O. sativa were upregulated by ABA, indicating that these OsWRKY genes may play an important role in the response to abiotic stress, particularly as a key regulatory factor in ABA signaling pathway. MYBCORE, DPBF, and ABRE are known to involve in ABA and drought responses. Some MYBCORE, DPBF, and ABRE motifs were detected in the GbWRKY2 promoter by bioinformatic analysis (Figure 1S). The upregulated expression of GbWRKY2, GbWRKY16, and GbWRKY21 in ginkgo callus by ABA gave the direct evidence, suggesting that these WRKY genes probably function as key components during ABA signaling. Our results also showed that all three GbWRKYs were upregulated by ABA, indicating that these GbWRKY genes may participate in ABA signaling pathway responding to abiotic stress.

The upregulation of GbWRKY2 by SA is expected because three cis-elements (GT1 motifs) associated with SA were identified in the GbWRKY2 promoter region. Interestingly, GbWRKY2 also responds with a strong induction to a wide range of molecules such as MeJA and ETH, which constitute key signaling elements modulating defense responses to pathogens. This suggests that GbWRKY2 is a common component in the signaling pathways mediated by these hormones. Numerous studies report the induction of WRKY gene expression in response to SA and MeJA [13, 68, 69], but few analyses report the effect of other signal molecules such as ETH [38, 70]. Pathways involving MeJA and ET are considered to be mainly effective against necrotrophic pathogens, insects, and wounding, whereas those involving SA are more effective against biotrophs [71]. Thus, little attack of pathogens and insects in ginkgo may be due to the fact that WRKY protein, such as GbWRKY2, played important roles in defense responses by mediating SA, MeJA, and ETH signaling.

Taken together, GbWRKY2, GbWRKY16, and GbWRKY21 were activated by more than one type of stress condition. GbWRKY2 was observed to be upregulated in response to many different sources of stress, including salinity, ABA, SA, ETH, and MeJA treatment. GbWRKY16 was observed to be upregulated in response to salinity, ABA, SA, and ETH treatment. GbWRKY21 was observed to be upregulated in response to ABA, SA, and ETH treatment. GbWRKYS were upregulated in response to more than two types of stress which supported the occurrence of cross-talk between signal transduction pathways in response to different stress conditions in plants. Moreover, GbWRKYS displayed complex expression patterns in response to the stress. For example, GbWRKY2 and GbWRKY16 were upregulated at 3hpt in response to salinity treatment and then downregulated quickly, demonstrating that GbWRKYs could be quickly and instantaneously responded to the stress. GbWRKY16 was not disturbed by the cold and MeJA treatment. GbWRKY16 was sustainably upregulated during the whole SA treatment. All of these showed that GbWRKYS played complicated and essential roles in defense in response to the stress.

5. Conclusion

This study presents the isolation and expression profile of the novel WRKY transcription factor gene GbWRKY2, which encodes a protein of 337 amino acid residues. The protein domain and phylogenetic analysis also showed that GbWRKY2 belong to Group II WRKY family. Bioinformatics analysis showed that multiple cis-acting elements including fundamental and special elements associated with abiotic stresses and hormone regulations were found in the GbWRKY2 promoter. Expression pattern analysis suggested that GbWRKY2 might play an important role in tolerance to salt and cold stresses and defense responses by mediating ABA, SA, MeJA, and ETH signaling. Studies on downstream function genes regulated by WRKY TF and mutual regulation between WRKY TFs in G. biloba have not been reported. On the basis of response abiotic adversity of GbWRKY2, we establish the binary overexpression vector of this gene. Studies on the genetic transformation of this gene in the callus of G. biloba are underway. This study will provide a basis to further reveal that the upregulated gene expression can strengthen the ability of plants to resist abiotic stress and identify some targeted genes regulated by WRKY TF in G. biloba. The present work on cloning and characterization of GbWRKY2 provided new clues for future studies on Ginkgo response to various stresses, such as salinity, drought, cold, and disease.

Conflict of Interests

The authors declare no conflict of interests.

Authors’ Contribution

Yong-Ling Liao cloned and characterized GbWRKY2 gene and wrote the paper. Yong-Bao Shen screened the candidate transcripts of WRKY unigenes from transcriptome data. Wei-Wei Zhang and Jie Chang analyzed the qRT-PCR. Shui-Yuan Cheng performed the promoter analysis. Feng Xu designed the study and wrote the paper.

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