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Genome-wide analysis of the WRKY gene family in physic nut (Jatropha curcas L.)



Wangdan Xiong ^{a,b}, Xueqin Xu ^{a,b}, Lin Zhang ^{a,b}, Pingzhi Wu ^a, Yaping Chen ^a, Meiru Li ^a, Huawu Jiang ^a, Guojiang Wu ^{a,*}

a Key Laboratory of Plant Resources Conservation and Sustainable Utilization, South China Botanical Garden, Chinese Academy of Sciences, Guangzhou 510650, PR China

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ABSTRACT

The WRKY proteins, which contain highly conserved WRKYGQK amino acid sequences and zinc-finger-like motifs, constitute a large family of transcription factors in plants. They participate in diverse physiological and developmental processes. WRKY genes have been identified and characterized in a number of plant species. We identified a total of 58 WRKY genes (JcWRKY) in the genome of the physic nut (Jatropha curcas L.). On the basis of their conserved WRKY domain sequences, all of the JcWRKY proteins could be assigned to one of the previously defined groups, I-III. Phylogenetic analysis of JcWRKY genes with Arabidopsis and rice WRKY genes, and separately with castor bean WRKY genes, revealed no evidence of recent gene duplication in JcWRKY gene family. Analysis of transcript abundance of JcWRKY gene products were tested in different tissues under normal growth condition. In addition, 47 WRKY genes responded to at least one abiotic stress (drought, salinity, phosphate starvation and nitrogen starvation) in individual tissues (leaf, root and/or shoot cortex). Our study provides a useful reference data set as the basis for cloning and functional analysis of physic nut WRKY genes.

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1. Introduction

The WRKY transcription factors contain one or two WRKYGQK sequence domains followed by a zinc finger motif, which can bind to the W box of target genes, thus regulating their expression (Eulgem et al., 2000; Sun et al., 2003). The first WRKY gene to be identified, SPF1, which was found in sweet potato, was considered to play a potential negative role in the regulation of sucrose induced genes (Ishiguro and Nakamura, 1994). Since then, increasing numbers of WRKY genes have been recognized in plants. In the Arabidopsis genome, 72 WRKY genes have been predicted and they can be divided into three groups on the basis of the WRKY domain sequence (Eulgem et al., 2000). There are 109 WRKY genes in rice (Oryza sativa L.) (Ross et al., 2007), 57 in cucumber (Cucumis sativus var. sativus L.) (Ling et al., 2011), and 105 in poplar (Populus trichocarpa) (He et al., 2012).

WRKYs play important roles in development and stress responses. Firstly, WRKYs have been proved to be involved in the processes of lateral root formation (Devaiah et al., 2007; Zhang et al., 2008), seed

E-mail address: wugj@scbg.ac.cn (G. Wu).

development (Gonzalez et al., 2009; Luo et al., 2005) and leaf senescence (Besseau et al., 2012). Additionally, members of the WRKY protein are central to the innate immune systems of plants, such as the pathogen associated molecular pattern (PAMP) and effector-triggered immunity (ETI) based defense pathways and systemic resistance (Eulgem and Somssich, 2007). In *Arabidopsis* and rice, many *WRKY* genes have been shown to participate in responses to various abiotic stresses, such as threshold temperatures, cold, salinity, drought and low inorganic phosphate (Chen et al., 2009; Jiang and Deyholos, 2009; Li et al., 2011; Qiu and Yu, 2008; Wu et al., 2009).

The physic nut (Jatropha curcas L.) is a small perennial tree or large shrub, which belongs to the Euphorbiaceae family. Physic nut is a drought-resistant, non-food oilseed plant that could meet many of the requirements for commercial biodiesel production. It is welladapted to semiarid and barren soil environments that are not suitable for cultivation of most crops (Makkar et al., 1997). Following the recent sequencing of the physic nut genome and the development of expressed sequence tag (EST) libraries by our group and others (Natarajan and Parani, 2011; Sato et al., 2011), it is now a useful model for studying the members of different families of transcription factor genes and their evolution. In this study, we searched the genome sequences in order to identify the WRKY genes in physic nut (IcWRKY). Subsequently, we characterized the motifs and exon–intron organization of these genes and subjected them to phylogenetic analysis. Finally, we analyzed the expression of the JcWRKY genes under normal growth conditions and under various abiotic stresses.

^b University of Chinese Academy of Sciences, Beijing 100049, PR China

Abbreviations: ERK, extracellular signal-regulated protein; EST, expression sequence tag; ETI, effector-triggered immunity; LRR, leucine-rich repeat; MAP, mitogen-activated protein; NBS, nucleotide binding site; NJ, Neighbor-joining; PAMP, pathogen associated molecular pattern; PCR, polymerase chain reaction; RT-PCR, reverse transcriptase polymerase chain reaction; TPM, transcripts per million; UTR, untranslated region; WD, WRKY domain.

* Corresponding author at: Xingke Road 723, Tianhe District, Guangzhou 510650, PR China. Tel.: +86 20 37252703.

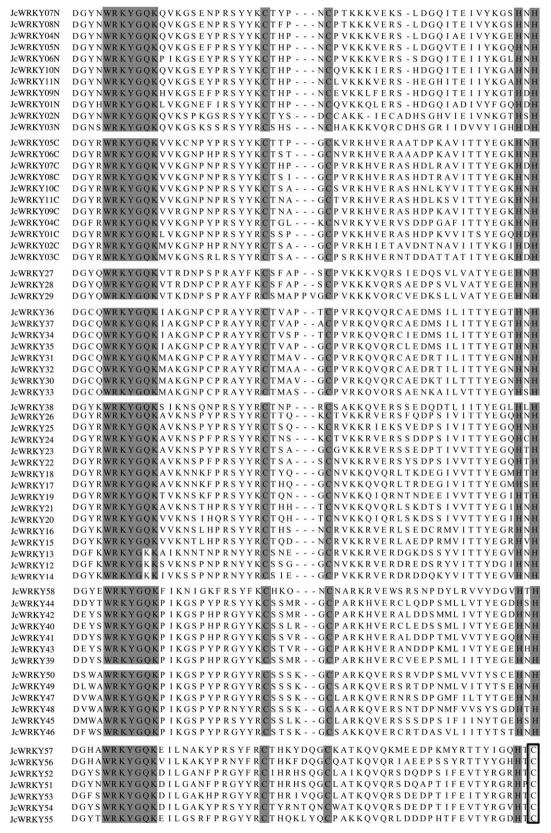


Fig. 1. WRKY domains in proteins of the WRKY superfamily in physic nut. Conserved amino acid residues are shown in gray.

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