



Mini Review

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# Analysis of *SOS1* Promoter in Various Plant Species for WRKY Transcription Activation



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## Abstract

WRKY transcription factors play a critical role in plant stress response to salinity tolerance. *SOS1* promoter alignment was analyzed for WRKY binding domain for Arabidopsis, Cochlearia, Tomato, Rice, Salicornia and Wheat using multialin. The analysis using Plant CARE showed Arabidopsis and tomato have one, Wheat and two Salicornia species have two, Rice has four and Cochlearia has exceptional six WRKY binding domains present in their *SOS1* promoter. We hypothesize that WRKY transcription factor play an important role in response to abiotic stress and needs further investigation for their possible function in salt stress tolerance.

**Keywords:** *SOS1*, WRKY, Transcription, Salt stress

## Mini Review

Salinity is a major constraint to food production as the percentage of agricultural land that is affected by high salinity is continuously increasing throughout the world [1]. The extent of the problem is illustrated by the fact that one-third of the global arable land or half of the irrigated arable land is significantly affected by salinization [2]. Seed germination, seedling growth and vigor, vegetative growth, flowering and fruit set are adversely affected by salinity in many crops [3]. The tolerance to soil salinity varies greatly among plant species [4]. Among cereals, rice is highly salt-sensitive whereas barley is relatively salt-tolerant. Variation in salt tolerance is more pronounced in the dicotyledonous crops, wild plant species such as salt bush (*Atriplex halimus*, *A. vesicaria*) and several members of the Chenopodeaceae (*Suaeda* sp., *Salicornia* sp.) can grow at salinity levels far higher than that of seawater [2,4].

The *SOS*-signaling pathway mainly involved in salt tolerance in plants, consists of three main components including *SOS1*, *SOS2* and *SOS3*. *AtSOS3* encodes a  $Ca^{2+}$ -binding protein, which is sensitive to cytosolic  $Ca^{2+}$  level [5]. One of the consequences of salt stress is an increase in the cytoplasmic  $Ca^{2+}$  concentration. This increase in  $Ca^{2+}$  is sensed by *SOS3*, and it activates *SOS2*, which is a Ser/Thr protein kinase [6]. This *SOS2-SOS3* complex ultimately phosphorylates and activates *NHX1* and other transporters involved in vacuolar  $Na^+$  transport along with *SOS1* [7]. *SOS1* is an electro-neutral  $Na^+/H^+$  exchanger that is specific

for  $Na^+$ . GUS expression under *AtSOS1* promoter exhibited a high promoter activity in root epidermal cells (particularly at root tip), and in stellar cells throughout the plant [8]. *Atsos1* mutants are extremely salt-sensitive and have combined defects in  $Na^+$  extrusion and long-distance transport of  $Na^+$  from root to shoot [5,7]. Moreover, *AtSOS1* mRNA is more abundant in roots than in shoots [8]. Thus, the suggested roles of *SOS1* are:

- to pump  $Na^+$  back into the soil solution
- to decrease  $Na^+$  delivery to the shoot under salt exposure by its retrieval from xylem [9]. Similar functions for *SOS1* has been proposed for Poplar, *Thellungiella salsuginea*, wheat and rice [10-13].

The interaction between transcription factors and cis-acting regulatory sequences in plant promoters is the key step involved in the altered regulation of gene expression under stress conditions [14]. It has been shown that differential gene expression contributes to the salt tolerance that are strongly and rapidly induced in response to abiotic stress [15]. WRKY transcription factors (TFs) have shown to bind to conserved DNA motifs in the promoter region involved in abiotic salt stress. In Arabidopsis, 72 members of WRKY family have been described [16]. Characteristic for these factors is their conserved WRKY DNA-binding domain (W-box) in the promoter region of targeted genes. WRKY transcription factors regulate transcript levels of these

targeted genes upon binding to the W-box (TTGAC/CT) promoter element [15]. These TFs are defined by a conserved DNA binding domain of ~60 amino acids containing the nearly invariant stretch

WRKYGQK followed by a unique zinc-finger pattern of Cys and His residues. WRKYs are sub-divided into three groups in Arabidopsis model plant based on WRKY domains [17].



**Figure 1:** Arabidopsis thaliana (*A. thaliana*), Cochlearia x hollandica (*C. hollandica*), Oryza sativa (*O. sativa*), Salicornia brachiata (*S. brachiata*), Salicornia dolichostachya (*S. dolichostachya*), Solanum lycopersicum (*S. lycopersicum*) and Triticum aestivum (*T. aestivum*) showing WRKY binding domain (TGAC) in SOS1 through their promoter alignment (multalin.toulouse.inra.fr/multalin/). Alignment shows six WRKY binding site in *C. hollandica*, four in *O. sativa*, two in *T. aestivum*, *S. brachiata*, *S. dolichostachya* and one in *A. thaliana* and *S. lycopersicum* respectively.

Three WRKY genes namely AtWRKY18, AtWRKY40 and AtWRKY60 showed to form a complex networking during salt and osmotic stress where AtWRKY40 antagonized the putative functions of AtWRKY18 and AtWRKY60 [18]. Thus, these WRKY TFs form a highly interacting regulatory network that modulates gene expression by acting as either transcription activator or repressor during stress response. Similarly ZmWRKY33 and TaWRKY71 over expression in Arabidopsis were shown to be induced by salt stress [19-20]. Tomato plants containing 35S::SIWRKY3 showed

reduced oxidative stress and proline contents with the expressions of SOS1 and SOS2 significantly induced in the transgenic plants [21]. Overexpression of GhWRKY34 also promoted expression of SOS1 and SOS2 in transgenic plants through activating the SOS pathway with enhanced activity of Na<sup>+</sup>/H<sup>+</sup> antiporter SOS1 [22]. As WRKYs are clearly involved in the abiotic stress tolerance, WRKY specific DNA binding domains in SOS1 promoter of various plant species that could be involved in salt tolerance were analyzed. The promoter region of the SOS1 from different

plants species for WRKYs binding domain; W-box were align using for *Arabidopsis thaliana* (*A. thaliana*), *Cochlearia x hollandica* (*C. hollandica*), *Oryza sativa* (*O. sativa*), *Salicornia brachiata* (*S. brachiata*), *Salicornia dolichostachya* (*S. dolichostachya*), *Solanum lycopersicum* (*S. lycopersicum*) and *Triticum aestivum* (*T. aestivum*) (Figure 1). WRKY cis-acting elements were found presents in the promoter regions of SOS1 using PlantCARE database. We found that *O. sativa* contains four W-box cis-elements and *T. aestivum* has two W-box cis-elements in their promoter region. *A. thaliana* and *S. lycopersicum* has one each W-box whereas *S. brachiata* and *S. dolichostachya* have two W-box cis elements in their promoter region. We speculate that as compared to wheat, rice is a more salt sensitive crop and therefore it has more W-box cis elements in the promoter of SOS1 to cope with salt stress. Salt tolerant plants as *S. brachiata* and *S. dolichostachya* have two W-box in SOS1 promoter. Considering these halophytes have small genome as compared to *T. aestivum* and *O. sativa*, we predict that the two WRKY TFs would significantly contribute to plant high salinity stress response by maintaining Na<sup>+</sup>/K<sup>+</sup> ion potential and activating salt stress responsive genes [14-15]. WRKYs 25 and WRKY33 were characterized using *sos1-1*, *sos2-1* and *sos3-1* mutants and their result suggested that the NaCl-induced expression of WRKY25 and WRKY33 is independent of SOS-signaling pathway [23]. It seems interesting as most of the salt stress responses in plants, involve typical SOS pathway. These results indicate that WRKY25/33 may have different downstream target gene to play their role in salt stress. The exceptional six cis-element WRKY motifs found in *C. hollandica* needs to be explored for their role in salinity tolerance. The transcriptional network of WRKY proteins forms an intricate signaling complex that plays an important role in plant response to cope with salt stress by excluding excessive Na<sup>+</sup> and maintaining ion homeostasis. Since many members of the WRKY family act as important node of convergence for abiotic stress during transcriptional reprogramming, understanding the complex mechanism of WRKY TFs will pave way for improved agriculture production for important crop plants in salt tolerance.

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