



Transcription factors WRKY11 and WRKY17 are involved in abiotic stress responses in *Arabidopsis*



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ABSTRACT

Plant WRKY transcription factors play a vital role in abiotic stress tolerance and regulation of plant defense responses. This study examined *AtWRKY11* and *AtWRKY17* expression under ABA, salt, and osmotic stress at different developmental stages in *Arabidopsis*. We used reverse transcriptase PCR, quantitative real-time PCR, and promoter:GUS lines to analyze expression. Both genes were upregulated in response to abiotic stress. Next, we applied the same stressors to seedlings of T-DNA insertion *wrky11* and *17* knock-out mutants (single and double). Under stress, the mutants exhibited slower germination and compromised root growth compared with the wild type. In most cases, double-mutant seedlings were more affected than single mutants. These results suggest that *wrky11* and *wrky17* are not strictly limited to plant defense responses but are also involved in conferring stress tolerance.

1. Introduction

WRKY transcription factors (TFs) are members of the WRKY-GCM1 superfamily of zinc finger TFs (Babu et al., 2006), currently found only in plants (Ulker and Somssich, 2004). These proteins have a characteristic N-terminal WRKYGQK motif with slight modifications and a C-terminal zinc-finger-like motif. The motifs are vital to WRKY TFs binding with W-boxes (TTGACT/C; cis-acting elements) (Ciolkowski et al., 2008). *Arabidopsis* has 74 WRKY genes divided into three groups, each with subgroups based on WRKY domains and inferred phylogeny (Eulgem et al., 2000).

Abiotic stress limits crop productivity and influences gene expression (Xiong et al., 2002; Yamaguchi-Shinozaki and Shinozaki, 2006; Hirayama and Shinozaki, 2010); common stressors include salinity, drought, osmotic stress, heat, and cold. Stress can increase abscisic acid (ABA) biosynthesis and accumulation, as part of plant defense responses (Koornneef et al., 1998). The multiple morphological,

physiological, biochemical, and molecular strategies that plants have evolved to cope with stress are under genetic modulation (Joshi et al., 2016). Notably, WRKY TFs are crucial in regulating plant reactions to biotic and abiotic stress (Rushton et al., 2010; Phukan et al., 2016). Currently, we still do not fully understand how the numerous WRKY TFs function under diverse environmental stressors (Ulker and Somssich, 2004; Chen et al., 2012), despite research on multiple plant species (Gadjev et al., 2006; Miller et al., 2008; Pnueli et al., 2002; Zhou et al., 2016; Jiang and Deyholos, 2006, 2009; Jiang and Deyholos, 2009). These studies have shown us, however, that WRKYs form interconnecting networks to regulate multiple stress responses synchronously (Banerjee and Roychoudhury, 2015). Additionally, examples from rice, *Arabidopsis*, tobacco, ginseng, and sunflowers have shown that a single WRKY TF can mediate multiple abiotic stress responses. For example, salt-inducible WRKY25 and WRKY33 influenced salt stress response in *Arabidopsis* (Jiang and Deyholos, 2009). Similarly, *GhWRKY41/SpWRKY1* in transgenic tobacco improved drought and

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