



Short communication

Loss of the R2R3 MYB, AtMyb73, causes hyper-induction of the *SOS1* and *SOS3* genes in response to high salinity in *Arabidopsis*Jun Hyeok Kim^{a,b}, Nguyen Hoai Nguyen^a, Chan Young Jeong^a,
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ABSTRACT

Environmental stressors, including high salt, drought, and low or high temperatures, are often associated with significant losses in agricultural productivity. Plants have evolved a diverse array of signaling pathways to modulate their development in response to various environmental challenges. Here, we report the characterization of a member of the R2R3-MYB transcription factor family, AtMyb73. The expression of AtMyb73 was up-regulated by salt stress but not by other stresses. The maximum level of AtMyb73 expression occurred at 6 h of 300 mM NaCl treatment. Under salt stress, *atmyb73 ko* mutant plants exhibited higher survival rates compare to wild type (Col-0) plants. Using quantitative reverse transcription-polymerase chain reaction (qRT-PCR) analysis, we determined that the accumulation of salt overly sensitive (SOS) transcripts, *SOS1* and *SOS3*, was higher in *atmyb73 ko* and *atmyb73 eko* plants than in wild type plants in response to 300 mM NaCl treatment. These results indicate that AtMyb73 is a negative regulator of SOS induction in response to salt stress in *Arabidopsis thaliana*.

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Introduction

Abiotic stress is the primary cause of decreased agricultural production worldwide (Boyer, 1982; Mittler, 2006). High salinity is one of the most important environmental stresses, causing a significant loss of agricultural productivity. Therefore, it is important to understand the responses of plants to this major environmental stressor (Epstein et al., 1980). Salt-stress conditions produce an ion imbalance in plants, leading to metabolic imbalances. In addition, excess Na ions are toxic to plants. High-salt conditions can also lead to hyperosmotic stress (Ashraf and Akram, 2009). Plants have regulatory mechanisms that help them avoid the harmful effects of stress. In particular, cellular and metabolic reprogramming acts to adjust the signaling and regulatory pathways of plants in response to stress (Wu and Jinn, 2012).

MYB factors are a family of transcription factors that contain a conserved MYB DNA-binding domain. In contrast to animals,

plants contain an MYB-protein subfamily that is characterized by the presence of the R2R3-type MYB domain. In *Arabidopsis*, there are 125 known R2R3-MYB genes. R2R3-type MYB factors regulate many aspects of plant physiology including metabolism, stress mechanisms and growth (Stracke et al., 2001). In particular, MYB transcription factors function as positive or negative regulators of many pathways. For example, AtMyb96 serves as a molecular link that mediates ABA-auxin cross talk during the drought-stress response and during lateral root growth (Seo et al., 2009). AtMyb62 regulates phosphate starvation responses via changes in GA metabolism and signaling (Devaiah et al., 2009). Overexpression of AtMyb15 improves drought and salt tolerance in *Arabidopsis*, possibly by increasing the expression levels of the genes involved in ABA biosynthesis and signaling (Ding et al., 2009). Although more than 100 R2R3-MYBs have been identified in *Arabidopsis*, the functions of many MYB transcription factors remain largely unknown (Yanhui et al., 2006).

Here, we investigated the function of AtMyb73, a member of the R2R3-MYB transcription factor family. AtMyb73 is associated with the high rates of survival under salt-stress conditions. In this study, we investigated the expression profile of AtMyb73 under salt stress. We further examined the function of AtMyb73 during salt stress and compared survival rates of wild type and *atmyb73* knockout (KO) (*atmyb73 ko*) plants. qRT-PCR was adopted to examine transcript accumulation of SOS genes (*SOS1* and *SOS3*) between *atmyb73 ko* and wild type plants under salt-stress conditions. The

Abbreviations: ABA, abscisic acid; GA, gibberellin; GFP, green fluorescent protein; GUS, beta-glucuronidase; MYB, myeloblastosis; RT-PCR, reverse transcription-polymerase chain reaction; SOS, salt overly sensitive.

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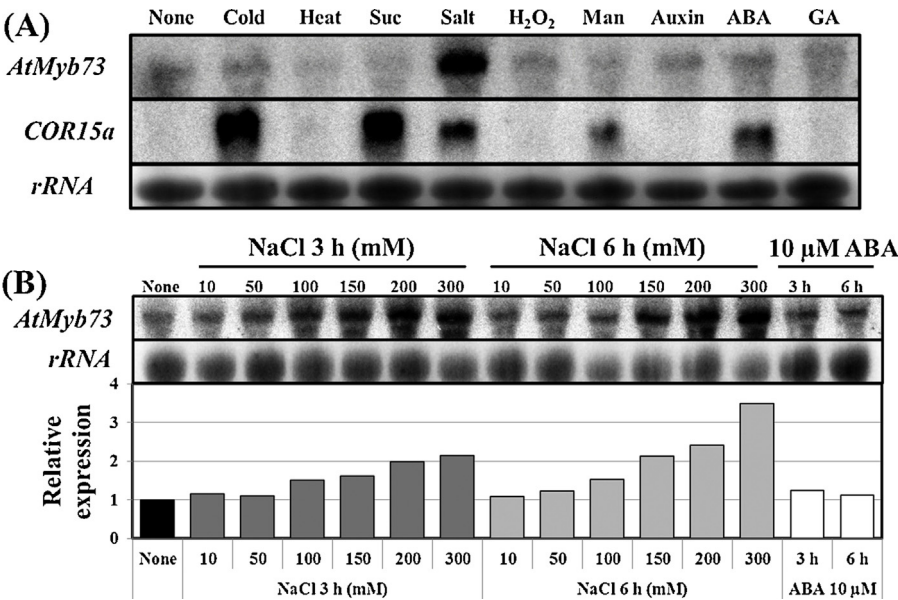


Fig. 1. Expression of *AtMyb73* in stress treatment plants. (A) Ten-d-old wild type plants exposed to 6 h treatments of cold (4 °C), heat (37 °C), 8% sucrose, 200 mM NaCl, 10 mM H₂O₂, 200 mM mannitol, 10 μM indole-3 acetic acid (IAA), 10 μM ABA, and 10 μM GA were collected for total RNA extraction using the aurintricarboxylic (ATA) method. (B) Ten-d-old wild type plants exposed to 10, 50, 200, 250, and 300 mM NaCl and 10 μM ABA for 3 and 6 h were collected for total RNA extraction using the ATA method. Total RNA was used as a loading control. The cDNAs of *AtMyb73* and *COR15a* were used as probes.

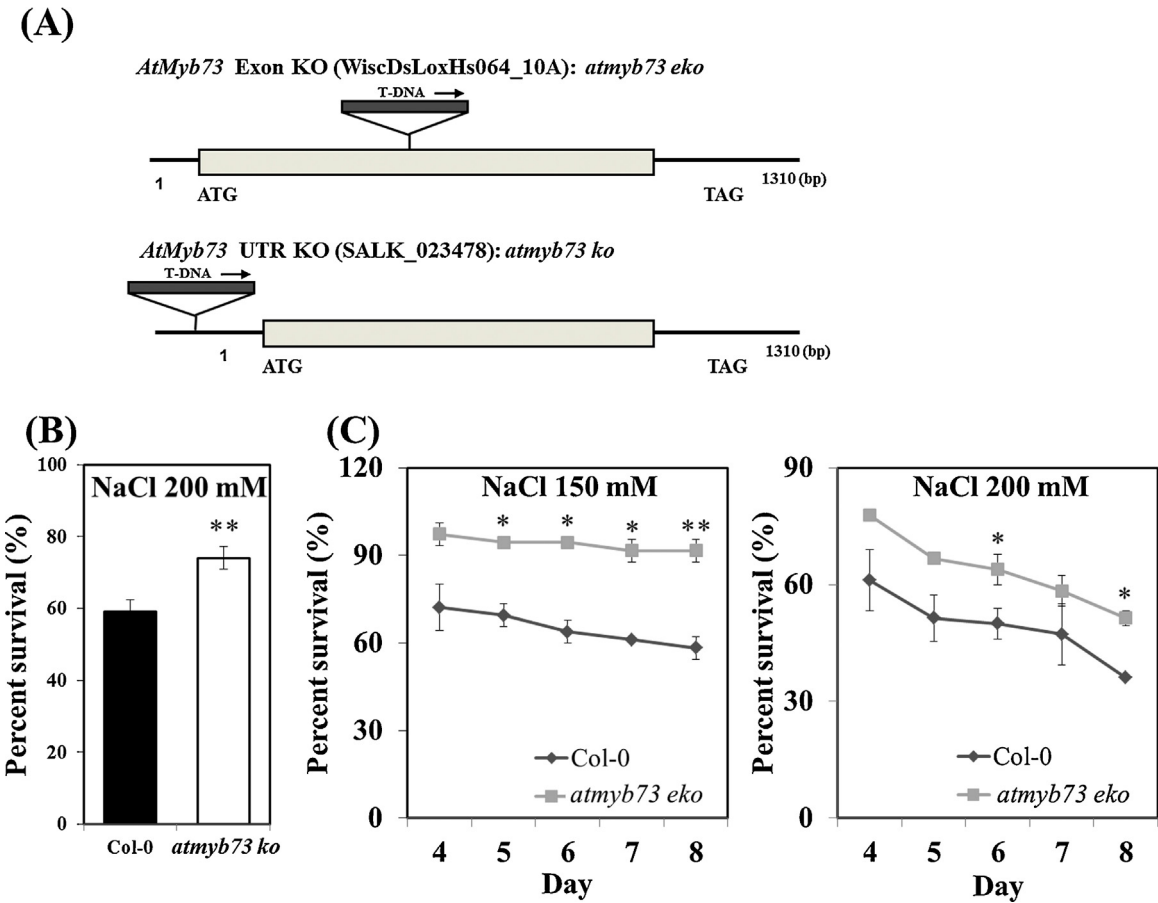


Fig. 2. Survival of *Arabidopsis* wild type and *atmyb73* seedlings on medium supplemented with NaCl. (A) Genomic structure of *AtMyb73* showing T-DNA insertions. (B) Four-d-old wild type and *atmyb73* seedlings grown on MS medium were transferred to test medium containing 200 mM NaCl. Data were obtained 5 days after transfer. (C) Four-d-old wild type and *atmyb73 eko* seedlings grown on MS medium were transferred to test medium containing 150 or 200 mM NaCl. Data were obtained 5 days after transfer. Error bars = s.d.; * indicates a statistical difference between the means of wild type and mutant plants (**P* < 0.05, ***P* < 0.01).

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