Wheat NF-YA10 functions independently in salinity and drought stress

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The transcription factor NUCLEAR FACTOR Y (NF-Y) plays an essential role in many developmental and stress-responsive processes in plants. NF-Y composed of 3 subunits, NF-YA, NF-YB, and NF-YC, targets the CCAAT box, a common cis-element in eukaryotic promoters. We recently identified a gene TaNF-YA10–1 from the wheat salinity tolerant cultivar SR3 and found that recombinant TaNF-YA10–1 could successfully bind to the CCAAT motif in vitro. We also showed that the constitutive expression of TaNF-YA10–1 in Arabidopsis thaliana significantly increased the plant's sensitivity to salinity. Here, we further demonstrated that TaNF-YA10–1-overexpressing plants conferred drought tolerance as judged from the relative root length and whole-plant growth under drought stress. These results suggest that TaNF-YA10–1 functions independently in salinity and drought stress. Our findings are helpful in understanding the distinct roles of NF-YA in plant stress responses.

Keywords: drought stress, NF-Y transcription factor, salinity stress, SR3, wheat

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medium containing a gradient concentration of mannitol. As shown in Figure 1, the root length of TaNF-YA10–1 overexpression lines was longer than the wild type and vector control transgenic line when exposure to 300 or 350 mM mannitol. Assay of whole-plant drought tolerance confirmed that the seedlings of TaNF-YA10–1 overexpression line were more tolerant of the drought stress (Fig. 2). These interesting observations suggest that TaNF-YA10–1 is involved in different signaling pathways in response to different abiotic stresses.

In transgenic A. thaliana constitutively expressing TaNF-YA10–1, the ABA dependent pathway genes AtRAB18, AtRD29B and AtABI5, as well as the ABA-independent pathway genes AtCBF1 and AtCBF3, were all down-regulated when plants were exposed to salinity stress.\(^\text{15}\) The NF-Y transcription factors have mainly been considered as activators of transcription; however, recent evidence suggests their involvement in gene repression.\(^\text{17,18}\) Thus, TaNF-YA10–1 might function as repressor of transcription under salt stress conditions. It is suggested that NF-YAs could act as transcriptional activators of a subset of genes that contain the CCAAT-box and as repressors of genes whose promoters lack the CCAAT-box.\(^\text{18}\) However, clear CCAAT motif enrichment was detected in the promoters of AtCBF1, AtCBF3 and AtRAB18. Transcriptional activation or repression using protoplasts or yeast one-hybrid system will be required to provide direct evidences. Here, we further demonstrated that TaNF-YA10–1-overexpressing plants conferred drought tolerance, suggesting that TaNF-YA10–1 functions independently in salinity and drought stress. Transcriptional behavior of stress responsive genes in TaNF-YA10–1 overexpression lines under osmotic stress conditions remains to be elucidated.

The expansion of NF-Y families in plants, combined with their heterotrimeric nature, means that many possible NF-Y complexes can form. This leads to the formation of a flexible, combinatorial system of transcription factors that may allow subtle adjustments to many different environmental conditions.\(^\text{19}\) These different functions of TaNF-YA10–1 might be explained by the diverse combination of NF-YA with other NF-YB/NF-YC factors, which thus affected different regulating pathways. We propose that there exists dual transcriptional control of TaNF-YA10–1 through the interaction with different NF-YB/NF-YC heterodimers via its role in activating target drought-responsive genes or repressing target salt-responsive genes. Alternatively, other proteins associating with TaNF-YA10–1 subunit of NF-Y complexes may be different in
the presence of salinity and drought stresses. Further study on protein-protein interactions will be needed to elucidate the inner mechanisms.

Disclosure of Potential Conflicts of Interest

No potential conflict of interest was disclosed.

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