


# Three stress-responsive NAC transcription factors from *Populus euphratica* differentially regulate salt and drought tolerance in transgenic plants

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Stress-responsive *NAM*, *Arabidopsis* transcription activation factor 1/2 (*ATAF1/2*) and *CUC2* (*SNAC*) genes are being used to alter stress tolerance in *Arabidopsis* or grasses through genetic engineering. However, limited reports are available about the functional characteristics of *SNAC* in trees. In this study, three putative NAC proteins were identified from *Populus euphratica*. *PeNAC034* and *PeNAC045* were classified into the ATAF subgroup and *PeNAC036* into the ANAC072 subgroup. These three *SNAC* transcription factors were localized in the nucleus and contained the transcription activation domain in their C-terminal. Under drought and salt stresses, *PeNAC036* was strongly induced in the whole plant, but *PeNAC034* was significantly suppressed in the roots and stems, and *PeNAC045* was inhibited in the roots. *PeNAC036* overexpression in *Arabidopsis* wild-type (WT) (*OEPeNAC036*) and *PeNAC036* complementation in mutant *anac072* (*anac072/PeNAC036*) lines increased tolerance to salt and drought, whereas *PeNAC034* overexpression in WT (*OEPeNAC034*) and *PeNAC034* complementation in mutant *ataf1* (*ataf1/PeNAC034*) lines enhanced salt and drought sensitivity. After drought and salt treatments, the expression levels of *COR47*, *RD29B*, *ERD11*, *RD22* and *DREB2A* were upregulated in *OEPeNAC036* and *anac072/PeNAC036* lines, but were downregulated in *OEPeNAC034* and *ataf1/PeNAC034* plants. Compared with WT and Vector lines, *PeNAC045* overexpression in poplar WT (*OEPeNAC045*) led to a significant decrease in the net photosynthesis rate, stomatal conductance and transpiration rate under salinity and drought conditions. These results suggest that *P. euphratica* can adapt to the environment of high salinity and drought, which may be related to the differential expression patterns of *SNAC* genes.

## Introduction

Plant growth and productivity are affected by environmental stresses, such as drought and high salinity. To deal with these stresses, plants have evolved adaptive

molecular mechanisms, including the expression of a number of genes that alter plant morphology, and physiological and metabolic processes. During these processes, stress-response genes and downstream machinery are regulated via signal transduction pathways (Shinozaki

**Abbreviations** – Ade, adenine; CUC2, cup-shaped cotyledon; GFP, green fluorescent protein; His, histidine; NAC, NAM-ATAF-CUC; NAM, no apical meristem; ORF, open reading frame; qRT-PCR, quantitative reverse transcriptase PCR; RSMC, relative soil moisture content; SD, synthetic dropout; *SNAC*, stress-responsive NAC; TFs, transcription factors; Trp, tryptophan; WT, wild-type.