

Complete inventory of Soybean NAC transcription Factors: The relationship between sequence and function

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We performed an inventory of soybean NAC transcription factors, in which 101 NAC-domain containing proteins were annotated into 15 different subgroups, showing a clear relationship between structure and function. The six previously described *GmNAC* proteins (*GmNAC1* to *GmNAC6*) were located in the nucleus and a transactivation assay in yeast confirmed that *GmNAC2*, *GmNAC3*, *GmNAC4* and *GmNAC5* function as transactivators. We also analyzed the expression of the six *NAC* genes in response to a variety of stress conditions. *GmNAC2*, *GmNAC3* and *GmNAC4* were strongly induced by osmotic stress. *GmNAC3* and *GmNAC4* were also induced by ABA, JA and salinity but differed in their response to cold. Consistent with an involvement in cell death programs, the transient expression of *GmNAC1*, *GmNAC5* and *GmNAC6* in tobacco leaves resulted in cell death and enhanced expression of senescence markers. Our results indicate that the described soybean *NACs* consist of functionally non-redundant transcription factors involved in response to different abiotic stresses and in cell death events in soybean.

Keywords : NAC genes, Stress expression pattern, Soybean, plant specific transactors

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