

## Identification and Characterization of Protein Interacting with the *Phytophthora*-Induced NAC1 Transcription Factor

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Once a plant is infected with a pathogen numerous defense-related genes are expressed in the cells therefore tight regulation of their transcription is important for defense against pathogen. Colinge and Boller found when potatoes are exposed to late blight, *Phytophthora infestans*, the *NAC1* (NAM1, ATAF1/2 and CUC2) gene, encoding a defense-related transcription factor, becomes highly expressed. However, we recently found that the NAC1 protein is unstable in plant cells due to the ubiquitin-proteasome-mediated degradation, suggesting the NAC1 transcription factor is fine-tuned at both the transcriptional and post-translational levels. To further characterize the regulation of NAC1 transcription factor, we performed a yeast two-hybrid screening using the NAC1<sub>1-260</sub> as bait and identified several NAC1-interacting proteins. After verification by DNA sequencing, the possible function of #5 protein caught our attention and we selected it for further investigation. The #5 protein was predicted to have a ZZ motif and might play a role in ubiquitination. We co-expressed the #5 protein with NAC1 in *Nicotiana benthamiana* leaves and found that the #5 protein promotes the degradation of NAC1 and, in doing so, degrades itself. These results suggest that the #5 protein plays an important role in the regulation of NAC1.

### References

Collinge, M., & Boller, T. (2001). Differential induction of two potato genes, *Stprx2* and *StNAC*, in response to infection by *Phytophthora infestans* and to wounding. *Plant Molecular Biology*, 46, 521-529

