染色体活性化および細胞内局在のアブラナプターゼATL31のDefenseおよびCarbon/Nitrogen応答

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Plants are affected by abiotic and biotic stresses, with species preservation requiring them to perceive and develop optimal responses to environmental conditions. Transcriptional induction of stress-related genes and the appropriate intracellular delivering of proteins are required for plant adaptation. In this doctoral dissertation, I investigated the molecular mechanism of transcriptional activation and intracellular localization of an *Arabidopsis* ubiquitin ligase ATL31 which plays a critical role in plant defense responses to pathogen attack and carbon/nitrogen (C/N)-nutrient responses during post-germinative growth.

1. **The Arabidopsis ubiquitin ligase ATL31 is transcriptionally controlled by WRKY33 transcription factor in response to pathogen attack.**

   Transcriptional induction of stress-related genes involves the appropriate temporal and spatial binding of transcription factors to DNA sequences present in promoter regions of target genes. On the base of ATL31 research background, which *ATL31* gene expression is strongly induced in response to pathogen-associated molecular patterns (PAMPs) and pathogen infection, and which *ATL31* expression was found to highly correlate with the expression of the transcription factors WRKY33 and WRKY53. Since WRKY33 was reported to play essential role in plant defense, I further investigated detailed transcriptional regulation of *ATL31* by WRKY33 in response to pathogen attack. The results showed that WRKY33 positively regulates *ATL31* expression in *Arabidopsis* cells via specific W-box cis-acting element in the *ATL31* promoter. In addition, analyses of responses to bacterial and fungal PAMPs, flg22 and chitin, as well
as to *Pseudomonas* bacteria in plants overexpressing *WRKY33* and those with the *wrky33-1* mutant provided genetic evidence suggesting that WRKY33 plays a positive role in plant disease resistance by promoting *ATL31* expression. Taken together, these findings indicated that WRKY33 acts as a transcription factor of *ATL31* and positively regulates its expression during activation of plant defense responses.

2. **The ubiquitin ligase ATL31 regulates C/N-nutrient response through its association with a TGN-localized SNARE protein.**

   After the appropriate transcription and translation process, proteins are accurately sorted to a specific cellular localization through its intracellular trafficking between compartments. These trafficking pathways are involved in different cellular functions and response to environmental stresses. The *trans*-Golgi network (TGN) is an important endomembrane organelle in plant cells where the endocytic and secretory pathways are merged. In this study, co-immunoprecipitation coupled to mass spectrometry analysis was established to identify the detailed function of ATL31 using *Arabidopsis* cultured cells expressing *ATL31*. The TGN-localized SNARE SYNTAXIN OF PLANTS43 (SYP43) was identified as a novel ATL31 interacting protein. Coimmunoprecipitation and split-Ub Y2H assays demonstrated the ATL31 interact with SYP43 in vivo. Moreover, microscope analysis showed that ATL31 is localized on the TGN compartment and its localization is severely affected in *syp42 syp43* mutant. Interestingly, *syp42 syp43* mutant showed hypersensitive phenotype to C/N-nutrient stress condition similar to *atl31* mutant. These results proposed an important role of the TGN-localized SNARE in ATL31 intracellular transport pathways in response to abiotic stress.