

## The role of AtTZF gene family in mRNA turnover

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mRNA turnover represents an important regulatory step of post-transcriptional regulation of gene expression. Gene expression levels are determined by both transcriptional and decay rates. Thus, identifying the mechanism by which *trans*-acting protein factors and *cis*-regulatory motifs involved in mRNA degradation work is crucial to understanding gene regulation dynamics. In humans, mRNA half-life is largely controlled through an AU-rich element (ARE) mediated degradation (AMD) pathway in which, TTP, an RNA-binding Tandem Zinc Finger protein (TZF), acts as a key recognition and recruiting factor for RNA degradation machineries. This process, though intensively studied in animals, has not yet been characterized in Plants. Preliminary evidence gathered in our laboratory suggested a potential orthologous role of *Arabidopsis thaliana* TZF gene family (*AtTZF*) to that of animal TTP. Analysis of *AtTZF* gene and its homologs revealed novel sub-cellular localization patterns and protein sequence regions that are strikingly similar to that of animal TTP. This observation lead us hypothesize the existence of a plant-orthologous AMD pathway with *AtTZF* as the RNA-binding factor. The objective of our study is to characterize this putative AMD pathway in plants and identify its main components through the following experiments:

- 1) Identifying components of AtTZF-dependent RNA processing complex and determining the dynamics of their subcellular localization.
- 2) Functional analyses of AtTZF RNA processing complex by reverse genetic analyses.
- 3) Determining RNA-binding capacity and global identification of targets of AtTZF by RNA immunoprecipitation couple GeneChip analyses (RIP-chip).

### References:

Lai WS, Carballo E, Thorn JM, Kennington EA, and Blackshear PJ (2000). Interactions of CCCH Zinc Finger Proteins with mRNA. J Biol Chem June 9;275(23):17827-17837