Thesis title : Determining the role of the MAPKKK17/18–ABI1 PP2C signalling module in regulating the cellular response to abscisic acid

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Abstract

Plant responses rely on complex signalling networks to adapt to abiotic stress while maintaining developmental flexibility. Abscisic acid is a key regulator of stress responses, and its interaction with mitogen-activated protein kinase signalling and proteasome-mediated regulation ensures both specificity and adaptability. This thesis investigated the functional roles of *Arabidopsis thaliana MAPKKK17*, *MAPKKK18*, *ABI1*, and E3 ubiquitin ligases *UPL4* and *UPL6*, using RNA sequencing, differential gene expression analyses, and phenotypic assays in mutant and overexpression lines. The results revealed distinct yet overlapping roles for *MAPKKK17* and *MAPKKK18* in mediating ABA responses. *MAPKKK17* preferentially may modulate RNA metabolism and post-transcriptional regulation during stress, whereas *MAPKKK18* has been linked to organ development and stomatal patterning, thereby linking ABA signalling to morphogenetic plasticity. Both kinases share transcriptional targets involved in ion transport, jasmonic acid signalling, and calcium-mediated stomatal regulation, revealing a dual-layered regulatory architecture. Transcriptional analyses further indicated that *ABI1* and *MAPKKK18* influence the expression of auxin-responsive gene families (SAUR, Aux/IAA, PIN), supporting a role for ABA-auxin antagonism through shared transcriptional modules. These findings shed light on how plants balance stress acclimation with growth by integrating hormonal pathways through common regulatory circuits. Based on observed transcriptional profiles, we next examined whether ABA-responsive regulation within the ABI1–MAPKKK18 signalling network also extends to the proteasomal layer, which plays a critical role in shaping (regulation and resetting) of signalling outputs. To examine transcriptional components involved in ubiquitin-mediated proteolysis within this circuit, we analysed the HECT-type E3 ligases UPL4 and UPL6. UPL4 exhibits a tissue-specific dual role: it acts as a positive regulator of ABA-dependent primary root elongation and as a negative regulator of stomatal development. UPL6 shows transcriptional and phenotypic patterns consistent with a role in ABA-dependent developmental regulation.

Together, these findings suggest a previously underexplored ABA-responsive regulatory framework where *MAPKKK17*/18, *ABI1*, and *UPL4*/6 converge. By integrating kinase cascades, phosphatase activity, and ubiquitin-mediated proteolysis, this work reveals an

additional layer of ABA–MAPK regulatory control, filling a key knowledge gap in how hormonal and proteolytic networks jointly fine-tune plant stress adaptation and development.