Graduate School Event

Thesis Defense: Evolution of auxin transport and MIZ1-mediated developmental responses during plant adaptation to terrestrial environments

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The successful colonization of terrestrial environments by plants required the evolution of developmental and signalling mechanisms that enabled adaptation to increasingly heterogeneous environments. Among these innovations, environmental sensing and directional transport of the plant hormone auxin have played central roles in shaping plant morphology and adaptation to external cues. However, the evolutionary origins of these regulatory systems remain incompletely understood. This thesis investigates two fundamental evolutionary questions: when auxin transport mediated by PIN auxin transporters emerged during plant evolution and how MIZ1 proteins acquired their role in root hydrotropism.The first part of the thesis examines the evolution of PIN-FORMED (PIN) auxin transporters using chlorophyte algae and other early-diverging eukaryotic lineages. Physiological analyses demonstrated that chlorophyte algae exhibit concentration-dependent responses to exogenous auxin and possess both passive and energy-dependent auxin transport systems, indicating that fundamental aspects of auxin biology predate the emergence of land plants. Phylogenetic, structural, and functional analyses revealed that PIN homologs are broadly distributed across diverse eukaryotic lineages and retain the characteristic PIN protein fold and predicted auxin-binding residues. However, heterologous expression assays in Xenopus laevis oocytes, tobacco BY-2 cells, and Arabidopsis thaliana demonstrated that these ancestral PIN homologs lack the directional auxin export activity characteristic of canonical land plant PIN proteins. Instead, they predominantly localize to the endoplasmic reticulum and display limited or no auxin transport activity, suggesting that ancestral PIN proteins primarily functioned in intracellular auxin homeostasis before being recruited for polar auxin transport during land plant evolution.The second part of the thesis investigates the evolutionary diversification of MIZ1 proteins, key regulators of root hydrotropism in Arabidopsis thaliana. Phylogenetic analyses showed that MIZ1 proteins are conserved throughout land plants but absent from green algae, indicating that the protein family originated early during terrestrialization. Although MIZ1 homologs from Marchantia polymorpha, Physcomitrium patens, Selaginella moellendorffii, and Amborella trichopoda displayed highly conserved predicted structures and endoplasmic reticulum localization, none were able to complement the hydrotropic or cytokinin-response defects of the Arabidopsis miz1 mutant. Functional characterization of Marchantia revealed that

MpMIZ1a regulates thallus development, cytokinin-dependent growth responses, expression of cytokinin biosynthetic genes, and normal sporophyte development, indicating an ancestral role in cytokinin homeostasis and developmental regulation rather than hydrotropism. Furthermore, protein docking predicted an interaction between MpMIZ1a and its native cytokinin receptor MpCHK, which was supported experimentally by bimolecular fluorescence complementation (BiFC). BiFC revealed interactions between the cognate protein pairs MpMIZ1a–MpCHK and AtMIZ1–AtAHK4, whereas little or no interaction was detected for the reciprocal cross-species combinations MpMIZ1a–AtAHK4 and AtMIZ1–MpCHK. This species-specific interaction compatibility provides a potential mechanistic explanation for the inability of MpMIZ1a to functionally complement the Arabidopsis miz1 mutant. Together, the findings presented in this thesis demonstrate that both auxin transport and MIZ1 protein function evolved through the progressive modification and recruitment of ancestral molecular components. The results support a model in which early PIN proteins primarily regulated intracellular auxin homeostasis before evolving into specialized plasma membrane auxin exporters, while MIZ1 proteins originated as endoplasmic reticulum-associated regulators of cytokinin-dependent development and were subsequently recruited into the hydrotropic signalling pathway of seed plants. By integrating comparative genomics, structural biology, molecular genetics, live-cell imaging, and physiological analyses across diverse evolutionary lineages, this work provides new insights into the molecular innovations that contributed to the successful colonization of terrestrial environments and the evolution of developmental plasticity in land plants.

Monday, October 19, 2026 10:00am - 11:00am

Central Bldg / O1 / Mondi 2a (I01.O1.008)

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