Grand challenge: viewing transporter function in a pointillist landscape

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Membrane transport proteins play vital roles in plant development, signaling, environmental interactions, and biosynthesis. Transporter activity has been traditionally studied either at the level of whole plant physiology or in single cells and artificial systems. The tools available for these studies have expanded dramatically over the past decade. Genomic, transcriptomic, proteomic, metabolomic, and associomic/interactomic methodologies (Lalonde et al., 2010) have produced large datasets that can be probed with bioinformatic tools to visualize transport networks within whole plants, organs, and tissues. Large collections of characterized mutants and mapped natural variation collections provide tools for rapid turnaround of forward genetic screens and reverse genetic assessment of gene function. Improved systems for heterologous expression of plant membrane proteins and an expanding set of defined pharmacological inhibitors provide the capability to rapidly evaluate the function of transporters in relative isolation and to identify proteins that regulate their activity. Live imaging of functional fluorescently tagged proteins has revolutionized plant cell biology and accelerated the understanding of membrane protein trafficking mechanisms (see Gilroy, 2011). Finally, improved crystallization and structural resolution technologies have increased the number of membrane protein structures available for threading of plant amino acid sequences to create testable models for experimental design. Frontiers in Plant Traffic and Transport is expected to serve as a forum for research utilizing all of these approaches and to function as a specialized journal for the portrayal and synopses within whole plants, organs, and tissues. 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which exhibit polar and apolar distributions on the plasma membrane as well as endomembrane internalizations depending on cell type, developmental stage, membrane domain composition, cell wall interactions, transcriptional activity, and environmental inputs (reviewed in Grunewald and Friml, 2010; Feraru et al., 2011). With so many regulatory factors involved, assays of transport activity from heterologous single cell expression systems, especially those lacking a cell wall, are unlikely to reflect the full complexity of transport activity and regulation observed in an intact cell (Zazímalová et al., 2010).

4. Pharmacological agents that are used to inhibit transport activities are generally somewhat shabby toxins used by other plants, fungi, animals, or antischocial chemists to cause harm to competitors. However, qualified use of an inhibitor in a high profile biological assay often results its repackaging as a highly specific antagonist. These characterizations usually are as credible as the mythological “surgical bombing strikes” reported in military press briefings. Inevitably, the exciting discovery of a pharmacological transport inhibitor is followed by reports of activity with other targets. For example, wortmannin, a fungal toxin, inhibits phosphoinositide-3-kinase signaling at the plasma membrane (Templeton and Moorhead, 2005), clathrin-mediated endocytosis (Van Damme et al., 2011), and trafficking to the vacuole (daSilva et al., 2005), yet is often described as “specific.”

5. There are still only a very small number of solved structures for plant transport proteins. This is a direct result of the difficulty encountered in producing high resolution X-ray crystal structures of membrane proteins. Linked to this difficulty is the financial reality that funding agencies have historically preferentially supported efforts to solve bacterial and mammalian protein structures. Although it is hoped that this bias will change as new technologies for solving structures with smaller crystals take hold, current efforts to thread plant amino acid sequences onto existing crystal structures is still more like ordering a mail order suit than visiting a custom tailor.

The necessity of improving our understanding of plant transport function in the face of these challenges is greater than ever. Growing demands on food supplies, water availability, and energy resources place a premium on technologies that will increase and improve the quality of plant food, fiber, and biomass production. Improvement efforts will only be successful if the tools and approaches required to map molecular data into whole plant physiology are developed and refined rapidly over the course of the next decade. Elucidation of plant transport processes must be a central component of these efforts, as membrane transport proteins are the workhorses that mobilize the nutrients, metabolites, signaling molecules, and structural components required for plant productivity. Arguably, the development of sensor technologies that allow monitoring of small molecule movements in intact tissues (Chaudhuri et al., 2011) is the highest priority for the field. The inherent limitations of non-invasive sensors that perturb the cellular environment must be overcome by technologies that maximize signal to noise ratios and minimize response times. We expect that Frontiers in Plant Traffic and Transport will be the premier specialty journal for publication of applications of this type of sensor research and modeling approaches that will reveal paradigms as elegant as Seurat’s Sunday afternoon figures at le Grand Jatte.

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