



Editorial

Protein networks – A driving force for discovery in plant science



Welcome to the 3rd special topics issue of *Current Plant Biology* on “Protein Networks”!

When reflecting on the tremendous sophistication of the structure and organization of living organisms, the proteome emerges as a major source of biological complexity. The number of proteins encoded by an organism is significantly augmented by the multiple activity states of individual protein molecules, imparted by post-translational modifications, splice variants, or multimerization states. Yet arguably the most critical characteristic of proteins is their propensity to establish specific interactions amongst themselves and with other biomolecules. Cellular networks, assembled *via* biochemically stable as well as transient interactions among proteins, are sufficiently robust yet dynamic to drive every physiological process in a living cell. Revealing the structure, parameters, and underlying dynamics of protein networks is a key topic in plant science.

With the central theme of protein networks as the anchor of this special issue, we have tried to capture proteins' centrality in the study of fundamental aspects of plant biology and plant interface with abiotic and biotic factors in the environment. The papers in this issue cover a broad range of protein functions including their role as information carriers in signal transduction pathways for plant growth, their activity in inter-species communication as components of host–pathogen networks, and as modulators in plant's response and adaptation to external variations in nutrient abundance.

The review by McCormack et al. (pp. 2–12) discusses the available methodologies for the experimental and analytical assembly of plant protein–protein interaction networks, alongside a comparative assessment of the state of network biology in plants relative to other model systems, and utilization of protein networks in uncovering principles governing host–pathogen communication.

In a similar vein, the review by Alexander and Cillia (pp. 13–24) comprehensively surveys the literature of plant–virus proteomics to examine proteome changes related to viral strategies in utilizing host pathways for sustaining the viral lifecycle, and identifies a set of biochemical pathways most likely to fall under viral control during infection.

Aspects of the higher-level organization and dynamics of protein networks are addressed in the paper by Jaiswal et al. (pp. 25–36). Spatial and temporal regulation of G-protein mediated signaling through the interactions established by the regulatory protein AtRGS1 are examined in a time-dependent manner under low- and high-energy conditions. Mechanistic details emerge from this study on the trafficking and signaling activity of AtRGS1 complexes.

The focus on protein functions in energy signaling for plant growth and acclimation to environmental stress continues in the paper by Nietzsche et al. (pp. 36–44). The authors focus on the signaling pathways mediated by SnRK1. In a quest to reveal the mechanisms of SnRK1 regulation and signaling specificity, Nietzsche et al. construct a protein–protein interaction network around the catalytic SnRK1 subunits AKIN10 and AKIN11. The aggregate network reveals thought-provoking functions of SnRK1 as a low-energy sensor and contributor to the major cellular pathways that adjust cellular metabolism according to the energy levels.

Nutrients act as strong determinants of the composition of plant proteomes. The review by Mai and Petra (pp. 45–56) makes a strong case for iron as a critical stimulus in plant nutrient-mediated signaling. Proteome changes in response to iron deficiency in multiple plants, both experimental model systems and crops, are summarized in a thorough model of iron homeostasis to uncover common patterns in plant response and possible avenues for agricultural applications.

Last but not least, the paper by Dale and Kato (pp. 57–64) tackles an important facet of protein networks – the necessity for quantitative measures of interactions that reflect the *in vivo* behavior of proteins. Dale and Kato utilize a well-known and widely used method for identification of protein interactions in live cells – the split-luciferase complementation assay – to investigate quantitative parameters and derive a mathematical model of protein–protein interactions. Although essential, studies such as this are scarce in plant science; if undertaken more widely they could help make molecular resolution of biochemical reactions in networks a reality.

We hope that the papers published in this issue illustrate current research efforts as well as novel directions of work in proteome networks. We also hope that the topics presented here will inspire reflections on current challenges in protein research and spark new trends in plant science. How do we approach the tremendous task of unraveling biological complexity of plants, what strategies and methodologies are best suited to explore their protein networks, and what aspects are most critical to study for maximum societal benefit?

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