Proteins post-translational modifications: implications for signal transduction in the plant immune system

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Abstract

Plants are dynamic living systems wherein external and internal signals are integrated to sustain growth in a continuously changing environment. The perception of pathogen signals by the plant cell triggers specific molecular responses, which propagate within the plant and modify its physiology and rate of growth in a signal-specific manner. Arguably, a significant portion of the plant’s reaction and adjustment mechanisms to biotic stress takes place at the level of signal transduction. In our research, we use experimental and analytical tools that permit us to capture essential information on plant signalome composition, topology, regulation, and dynamics. In my presentation, I will focus on current lab projects that exemplify the roles of two types of post-translational modifications, protein phosphorylation, and reversible oxidation, in signal transduction pathways activated in response to pathogen infection.

In the first project, we adapted an integrative network approach to identify kinase-mediated pathways in the basal immune response of Solanaceae and understand how pathogen effectors may disrupt the flow of information through the cell. We propose that the topology of immune signal networks is determined by the ability of the plant to activate compensatory pathways in response to the effectors’ disruptive actions. Conversely, we show that pathogens increase their virulence by disrupting signaling at the membrane-located end of the signaling network, and by recruiting cytosolic kinases.

The second project will explore the emerging role of reversible oxidation states of proteins in the effector-triggered immunity (ETI). Shifts in the cellular redox potential in the early stages of the ETI lead to oxidation of cysteine residues in proteins. The composition of the plant redoxome and its contribution to defense remain largely unknown. We characterized the ETI redoxomes of wild-type Arabidopsis and top1top2 mutant using mass spectrometry. Col-0 and top1top2 redoxomes differ in the identity of oxidized cysteines, and the amplitude of fluctuations in protein oxidation. Our results argue for TOPs determining role in maintaining the proper level and dynamics of proteome oxidation during ETI.

Publications:
