

Assessing and integrating the various levels of complexity in plant-microbe interactions

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Plant immunity is a highly dynamic process and hence requires dynamic models to encapsulate the events of recognition and response between host plant and the inflicting pathogen [1, 2]. The pathogen attack interferes with cellular organization at multiple levels and this demands integrated systems biology approaches to resolve the underlying interactions [3, 4, 5]. Establishing the concerted, multi-level plant immune response from genome, transcriptome, and interactome data, we transformed the zigzag model of plant immunity into an integrated semi-quantitative dynamic model of the *Arabidopsis* interaction with *Pst* DC3000 [2,3]. Comparing the effect of elicitors, effectors and coronatine toxin as pathogenic cues we quantified their impact on the host immune system. We extended the concept of the zigzag model by considering the host cellular interactome, network modules and hub proteins, topological and functional parameters [1]. We show new changes in pathogen virulence affect cellular interactome dynamics and network behavior. The integrative adaptation of *Pst* DC3000 to *Arabidopsis* is furthermore analyzed by a targeted metabolic model. Pathogen infection causes the induction of salicylic acid and jasmonate pathway enzymes with concomitant mild repression in the activity of photosynthetic enzymes [5, 6]. Visualization and characterization of the overlap between signaling and protein-protein interaction networks recognizes new signaling sectors with immune functions in the cellular interactome around proteins of

jasmonate, auxin and gibberellin signaling pathways [7,8]. Likewise, the intersection between metabolic and PPI networks reveals regulatory functions for metabolic enzymes such as photosystem subunit D-1 and D-2, plastidial pyruvate kinase, and peroxisomal citrate synthase. A multi-level network biology model of *Arabidopsis* infection with *Pst* DC3000 integrates signaling cascades, protein-protein interaction networks and metabolic modeling to analyze plant immune responses taking different pathogen virulence strategies into account.

References

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