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Biotic interactions From molecular networks to inter-organismal communities

Editorial overview

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Current Opinion in Plant Biology 2005, 8:343–345

Available online 3rd June 2005

1369-5266/\$ – see front matter

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DOI 10.1016/j.pbi.2005.05.011

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For many years, research on molecular plant–microbe interactions has been dominated by experimental approaches that enabled the identification of single molecular components dictating infection phenotypes. Clearly, genetics and mutational analysis had a leading role during this phase, and the rewards of these endeavors can sometimes be nothing short of spectacular. For example, long-lasting efforts of several laboratories have now unraveled a range of plant components that are required for the function of symbiotic relationships with *Rhizobia* bacteria and mycorrhiza fungi. On the other hand, molecular genetics is sometimes criticized for a reductionist simplification of biological traits. In reality, one has witnessed in recent years an opposite trend that integrates genetically defined components into biochemical pathways, cell biology, and physiological contexts. An example of this is recent advances that directly link physiological alterations in cellular redox status during systemic acquired resistance with the activity of key regulatory proteins that were identified some time ago using molecular genetic approaches. Likewise, small molecules and proteins that were originally shown to serve critical functions in plant immunity (e.g. nitric oxide and respiratory burst oxidase homologs), are now known to have been re-used several times in the context of other biological processes. The re-utilization of the same module in different regulatory networks might serve as a widespread design principle in the evolution of biological traits.

Despite this trend towards integrative approaches in several research fields of molecular plant–microbe interactions, there are still many fascinating phenomena of biotic interactions in nature that deserve future attention by molecule-driven scientists. This is beautifully illustrated by the formation of plant ‘domatia’ that accommodate mutualist arthropods such as predaceous or fungivorous mites or the complex communities of grasses and fungal endophytes. The links that connect fundamental molecular and cellular networks to dynamic processes at the population level are still poorly understood. How these presumed links drive the evolution of plant–microbe communities remains an important future challenge.

The symbiotic interaction of legumes and rhizobial bacteria leads to the formation of nitrogen-fixing nodules. The process is triggered by a lipochitooligosaccharide signal molecule (Nod factor) secreted by *Rhizobium*. **Rene Guerts *et al.*** infer skeletal plant signaling pathways that are employed by *Rhizobia* to establish a symbiotic relationship with *Lotus japonicus* or *Medicago truncatula*. Several of the recently identified plant components in rhizobial symbiosis are also required for the formation of mycorrhiza, a widespread form of endosymbiosis in higher plants, thus indicating the existence of overlapping signaling pathways. Interestingly, evidence is emerging that

Nod factor signaling partially overlaps with the thigmotropic response of root hairs, thereby illustrating how nature utilizes the same building blocks to regulate signaling in response to different cues.

Both plants and animals recognize potential pathogens by detecting a wide range of conserved pathogen-associated molecular patterns (PAMPs) using so-called pattern-recognition receptors. [Cyril Zipfel and Georg Felix](#) discuss emerging evidence that this form of innate immunity is the result of convergent evolution, despite structural and functional similarities shared by the proteins involved in pathogen perception and signal transduction. Likewise, there is evidence for the evolution of a convergent repertoire of PAMPs detected by different organisms.

The existence of an elaborate surveillance system for PAMPs in plants (see the review by [Zipfel and Felix](#)) raises the question of how microbial pathogens counter this non-self radar system during pathogenesis. [Kinya Nomura et al.](#) highlight recent advances in our understanding of the diversity of mechanisms by which *Pseudomonas syringae* effectors suppress host defense and cell death pathways. Indeed, mechanisms and strategies of defense suppression are developing into a research field of their own, and this will have an increasing impact in the future on our understanding of the molecular basis of pathogenesis.

[Tony Schillmiller and Gregg Howe's](#) review of systemic signaling in the wound response integrates molecular, biochemical and cell biology data to bring us a perspective on progress and outstanding questions in the one of the hottest areas of long-distance signaling in plants.

Unlike other recent reviews with a focus on the molecular genetic basis of systemic acquired resistance (SAR), [Pierre Fobert and Charles Després](#) critically review recent findings implicating changes in cellular redox status as a driving force to regulate the activity of key SAR signaling components. Although current studies emphasize the importance of the oxidative phase in mediating defense responses, the authors make a case for future investigations into the balance between oxidative and reducing conditions in SAR control.

[Marcel Wiermer, Bart Feys and Jane Parker](#) portray a 'trio infernal' — a regulatory hub in plant immunity that involves the sequence-related and interacting proteins EDS1, PAD4 and SAG101. Recent work points to a fundamental role for these proteins in transducing redox signals in response to both biotic and abiotic stress. Although the trio infernal shares homology with acyl hydrolases, the authors discuss new findings that make catalytic activity unlikely and instead propose a role for these proteins in the re-location and shipping of oxygenated lipids inside plant cells.

Nitric oxide (NO) has been recruited as a versatile signaling molecule for the regulation of multiple plant processes, including germination, growth, reproduction and disease resistance. [Massimo Delledone](#) focuses his review on the use of NO in plants to organize redox signaling in cellular processes, in particular during disease resistance responses. Clearly, the identification of direct targets of NO remains one of the major future challenges for understanding NO function in biotic stress. The review by [Miguel Torres and Jeff Dangl](#) gives a good update on what is known about the enzymatic production of reactive oxygen intermediates (ROI) by plant respiratory burst oxidase homologs and on the roles of calcium signaling in ROI generation. The NADPH-dependent oxidase homologs are one source of ROI production in plants and generate nearly all of the ROIs in response to avirulent bacterial or oomycete pathogens. Similar to NO, plant respiratory burst oxidase homologs have been recruited as signaling module for other biological processes, including cell expansion during root hair formation or ABA-mediated stomata closure upon abiotic stress. This re-utilization of the same module in different biological processes appears widespread and might serve as a general design principle in the evolution of novel biological traits.

Caspases, a subgroup of cysteine proteases, serve a role as executioners in programmed cell death in animals. Although caspase-like activities have been shown to be required for the initiation of programmed cell death in plants, including cell death in immune responses, the corresponding genes remained elusive for many years. [Ikuko Hara-Nishimura et al.](#) review recent findings indicating that vacuolar processing enzyme (VPE) in plants functions as a cysteine protease that shares several enzymatic properties with caspases and exerts a critical role in disease resistance to multiple plant pathogens.

[Brigitte Mauch-Mani and Felix Mauch](#) provide an articulate perspective on the functions of the abiotic stress hormone abscisic acid in plant disease resistance responses. Much neglected in the past, molecular genetic evidence now provides strong evidence that abscisic acid affects disease resistance by negatively interfering at multiple levels with biotic stress signaling.

[Patrice Dunoyer and Olivier Voinnet](#) capture the current excitement surrounding small RNAs, pathogenesis and genome remodeling. Their review, at times speculative, extends to an innovative model of *R*-gene regulation, and evokes many new experiments aimed at testing how RNA-derived regulators could both protect the host and also provide targets for the pathogen. This is then linked to possibly heritable effects on both host and virus genomes.

[Ian Toth and Paul Birch's](#) review presents the clear and well-argued opinion that soft rot erwinias should no

longer be thought of as brute force pathogens. The argument is that these bacteria make the transition from a biotrophic to a necrotrophic lifestyle, and that we will understand this better as we unravel data from the genome project.

The review by [Bill Foley and Ben Moore](#) links ecological and molecular aspects of plant defense against vertebrate herbivores, and highlights their counter-adaptive measures. The review is illustrated with a beautiful example of leaf chemistry and specialization of Australian marsupial folivores.

[Gustavo Romero and Woodruff Benson](#) give a fascinating and colorfully illustrated perspective on the occurrence and roles of 'domatia'. These are structures that the plant provides for mutualist arthropods, typically predaceous

or fungivorous mites. Not surprisingly, domatia can be invaded by other mite species that 'squat' the structures for their own ends without bringing benefits to the plant.

[Jim Kolmer](#) gives us the big picture on spore dispersal by fungal rust pathogens. Urediniospores, typically a little over 20 μm in length, can traverse huge distances in the wind, spreading across continents and over seas. Tracking the rust fungi is critical to ensuring stable production of one of the world's most vital staples: wheat.

The majority of plants in nature harbor fungal endophytes. The article by [Christine Müller and Jochen Krauss](#) gives a balanced perspective on the good and evil wrought by these organisms in grasses. The review links endophytes to the plants' survival in complex communities where there are many biotic and abiotic variables.

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