

Beyond pathogens: microbiota interactions with the plant immune system

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Plant immune receptors perceive microbial molecules and initiate an array of biochemical responses that are effective against most invaders. The role of the plant immune system in detecting and controlling pathogenic microorganism has been well described. In contrast, much less is known about plant immunity in the context of the wealth of commensals that inhabit plants. Recent research indicates that, just like pathogens, commensals in the plant microbiome can suppress or evade host immune responses. Moreover, the plant immune system has an active role in microbiome assembly and controls microbial homeostasis in response to environmental variation. We propose that the plant immune system shapes the microbiome, and that the microbiome expands plant immunity and acts as an additional layer of defense against pathogenic organisms.

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Introduction

Scientists have studied the molecular aspects of plant immunity since the mid-1980s. Investigation of how plants

recognize, respond, and limit the growth of invading organisms, and the strategies used by pathogens to counteract plant immunity led to a conceptual framework of the plant immune system [1]. Briefly, plants possess receptors that recognize non-self or modified-self molecules which indicate the presence of potential invaders. A first layer of pattern recognition receptors (PRRs) located in the plasma membrane perceives the presence of extracellular molecules, which are often conserved across whole classes of microbes (e.g. fungal chitin or bacterial flagellin) and are thus known as Microbe-Associated Molecular Patterns (MAMPs). Recognition of MAMPs leads to an immune response known as MAMP-triggered immunity (MTI), which is sufficient to halt the proliferation of most microbes. However, adapted pathogens have evolved effector molecules to interfere with MTI and host physiology. The clear dichotomy between extracellular MAMPs and intracellular effectors is, however, increasingly blurred [2]. In turn, plants deploy a second level of receptors to counteract adapted pathogens. These receptors belong to the family of NLR proteins (Nucleotide-binding Leucine-rich Repeat) and function as intracellular sensors that recognize the presence of specific effector proteins. Direct or indirect perception of pathogen effectors by a correspondingly specific host NLR protein activates the Effector-triggered immunity (ETI), which is a robust disease-resistance response that often includes localized host cell death and systemic defense signaling. Complex interplay between plant hormones that control defense versus growth trade-offs are a major part of the plant immune system [3].

Though this model provides a good overview of the fundamental principles governing plant immunity, it is based on the interaction of plants with pathogenic microbes. However, it is clear that plants establish intimate relationships with diverse commensal microorganisms, forming complex communities in both above-ground and below-ground tissues (i.e. microbiomes), which vary across host plants and environments. In fact, most microbes with which plants interact are non-pathogenic [4], yet many of them express molecules that are potentially recognized by the plant immune system. Thus, one major question of plant microbiome research is whether and how the plant immune system distinguishes commensals from pathogens during microbiome assembly. Are the strategies used by pathogenic microbes to evade plant immunity applicable in the context of microbiomes? Can the microbiome contribute to plant immunity? How does environmental variation shape the interaction between plant immunity and the microbiome?

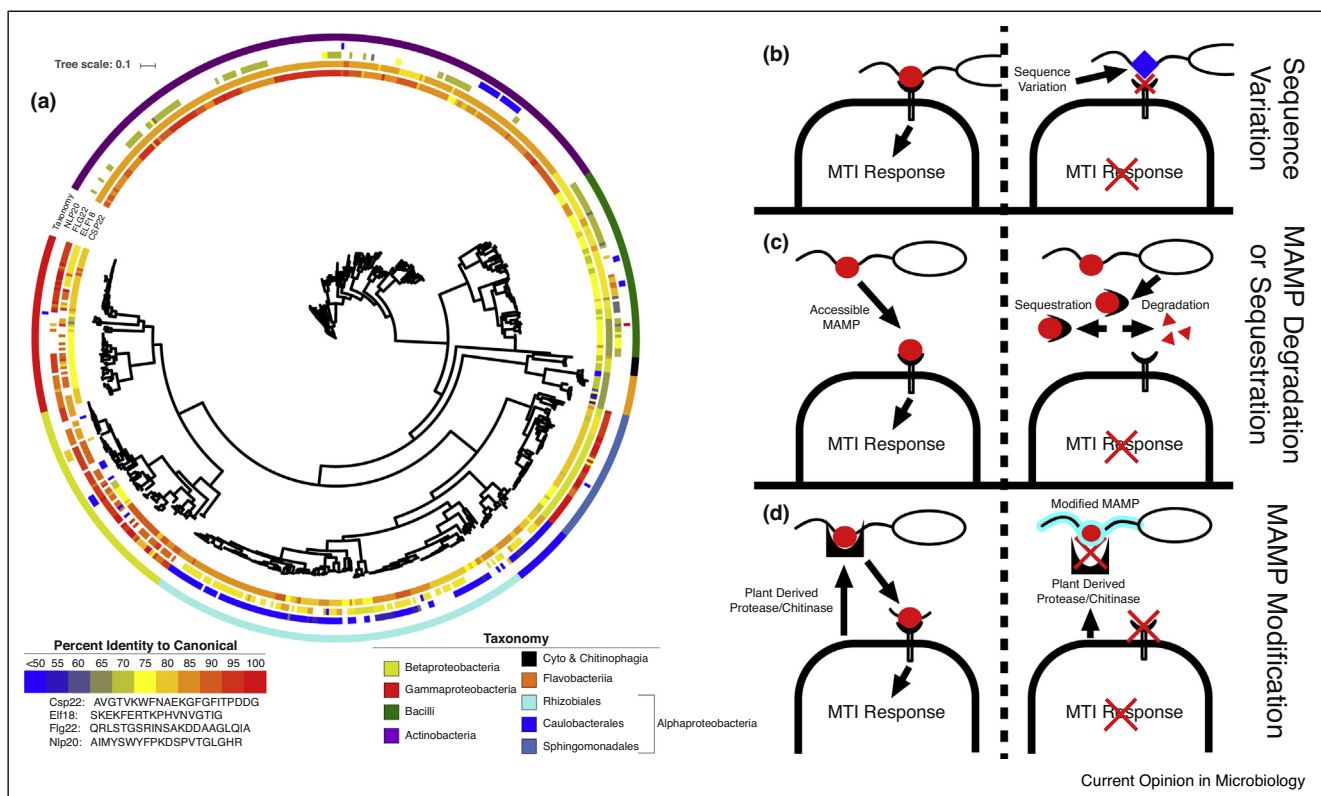
These are some of the key questions in an emerging field that has gained increasing attention recently [5**]. Here, we review the most recent studies and novel concepts referring to the interaction between the plant immune system and the microbiome, focusing largely on the utility of *Arabidopsis* and its relatives as a tractable model for these studies.

Evidence for the participation of the plant immune system in microbiome assembly

Plants host microbiomes whose composition differs from the surrounding environment [6–9], yet the mechanisms governing the recruitment of these microbes are largely unknown. The holobiont framework proposes that plants and their collective microbiome form a single entity subject to evolutionary processes [10,11], which implies that plants have adapted ways to distinguish their evolutionary partners from other microorganisms. Alternatively, the assembly of at least some of the plant microbiome may represent mere niche filling, a process influenced by plant traits but of minor adaptive importance for the plant host. Regardless of the proposed adaptive value of the plant microbiome as a whole,

it is obvious that some fraction of the commensal community has adaptive value to the host. It is also commonly hypothesized that plants can distinguish between pathogenic and commensal microbes. In fact, in an analysis of closely related commensal and pathogenic *Pseudomonas* strains, the transition between lifestyles is based on the gain/loss of only a very few virulence islands [12*]. Additionally, inspection of 627 bacterial genomes derived from healthy *Arabidopsis* roots and leaves revealed that 608 bacteria (97%) have the potential to produce putatively immunogenic MAMPs (Figure 1a). Many of these bacteria share identical MAMP variants to known pathogens, indicating that the MTI response shown to repress the growth of pathogens [13] is potentially activated in response to commensals as well. This begs the question of how commensals avoid or suppress MTI. It is plausible that MTI can both inhibit pathogens and maintain microbiome homeostasis by gating microbes ‘in’ or ‘out’ upon intimate contact with the host. In this view, MTI functions as a general mechanism used by plants to control the assembly of their microbiota. In support, *Arabidopsis* multi-mutants defective in MAMP recognition and

Figure 1



Commensal MAMP profiles and potential mechanism used by microorganisms to evade the plant immune system.

(a) Bacteria isolated from healthy *Arabidopsis* plants harbor potentially immunogenic MAMPs while others show large divergence from the canonical, which may contribute to evasion of the plant immune system. The tree includes 627 *Arabidopsis*-derived isolates and was generated by pruning the 3837 microbial tree in Levy *et al.* [29*]. MAMP genes were identified using custom built profile hidden Markov models and the MAMPs were identified after aligning all MAMP genes with MUSCLE [105,106]. Percent identity was calculated using edit distance. The tree was generated with iTOL [107]. The canonical sequences are from *Micrococcus lysodeikticus* (csp22) [108], *Escherichia coli* (elf18) [109], *Pseudomonas syringae pv tabaci* (flg22) [36], and *Phytophthora parasitica* (nlp20) [110]. MAMP divergence could lead to plant immune evasion by (b) sequence variation, (c) MAMP degradation or sequestration, or (d) MAMP modification as detailed in the text.

downstream MTI signaling exhibit reduced defense against an avirulent mutant of a normally pathogenic *Pseudomonas syringae* strain and are unable to maintain normal leaf endophytic bacterial communities under high humidity. Inability to regulate the growth of endophytic bacterial communities led to mild chlorosis and necrosis in some leaves, resembling dysbiosis [14^{••}]. This indicates that plants control the growth of microbial populations with their immune system in order to maintain their own health.

Strategies used by the microbiome to evade or suppress plant immunity

Plant immune receptors do not distinguish between microbial lifestyles and recognize ligands that can be present in both pathogens and commensals [15[•]]. Evasion or suppression of host immune responses is a hallmark of successful pathogens. Likewise, colonization by individual members of the plant microbiome, the essence of community assembly, likely requires strategies to avoid or interfere with plant immunity [16]. Recent work highlights differences and similarities between commensals and pathogens in the strategies used to suppress or evade the plant immune system.

MTI suppression is used by pathogenic microbes to bypass the plant immune system [1] but has also recently been reported for non-pathogenic microbes [17[•],18–20]. The beneficial rhizobacterium *Pseudomonas simiae* WCS417 promotes plant growth and suppresses part of the transcriptional response that is triggered by the bacterial MAMP flg22 [15[•],21]. Similarly, specific *Rhizobiales* strains that colonize Arabidopsis roots are able to prevent responses that are triggered by the same MAMP [22^{••}]. Endophytes can also prevent MAMP-triggered cytosolic calcium influx in Arabidopsis [23[•]]. A recent study found that the plant growth-promoting bacterium *Pseudomonas capeferrum* WCS358 produces organic acids that lower the extracellular pH and interfere with the response to flg22 [24[•]]. Recent research also indicates that mutualistic fungi gain access to plant tissues by manipulating innate plant immunity [25]. Yet, the mechanisms involved in the suppression of immune responses by commensals and mutualists are still largely unexplored. The type III secretion system (T3SS) is a common feature among pathogenic bacteria and it can also be found in non-pathogenic strains [26–28]. Nevertheless, genes encoding this effector-delivery machinery are rare in the genomes of plant-associated commensal bacteria [29[•]]. This may reflect the apparently weak host specialization of most plant-associated commensals [30]. Thus, a diversity of alternative strategies to interfere with the host immune responses, particularly on the extracellular battleground of MTI, are expected to be found in plant microbiomes.

MTI evasion is another strategy used by both pathogenic and commensal microbes to colonize the plant. Microbes have evolved at least three mechanisms to evade MTI: I)

MAMP divergence, II) MAMP degradation/sequestration, and III) MAMP modification.

MAMP divergence

Microbes might evade MTI by evolving MAMP variants that no longer bind to or activate the corresponding plant PRR (Figure 1b). This evasion is at face value likely to be counter-adaptive, since alteration of MAMP sequences and structures may impair the positive function of the microbial MAMP-containing molecule. For example, some flg22 variants that lose immunogenicity also lose motility [31]. Nevertheless, diverse, potentially immune evasive MAMP variants are widespread in certain bacterial taxa. This distribution is likely to be MAMP-dependent (Figure 1a): 26% of the flg22 peptide epitopes found in Arabidopsis-associated bacterial isolates have at least 50% sequence divergence from the canonical active sequence, while less than 1% of elf18 variants identified diverge from the canonical epitope by at least 50%. This suggests that flg22 recognition imposes stronger bacterial fitness defects and/or that the flg22 region is more amenable to variation than elf18, and/or that there are differential stringencies in the requirements for MAMP recognition. Consistent with the first hypothesis, the elf18 receptor EFR is not expressed in Arabidopsis roots, while FLS2 is [21,32]. The MTI response produced by MAMP sequences divergent from the respective canonical sequences is still relatively unknown. In parallel to the MAMP sequence diversity found across plant-associated bacteria, Arabidopsis and tomato lines display large variation in their response to different MAMPs and even to the same MAMP variant, indicating that MAMP recognition across plant populations is evolving [33–35]. Thus, recognition may be driven by the MAMP repertoire of local commensal and beneficial microbes, not just pathogens [15[•],22^{••},36]. Tolerance for the former must be balanced by intolerance of the latter.

MAMP degradation/sequestration

Even if microbes express an immunogenic MAMP, they may have mechanisms to evade MTI. Microbes have evolved proteases that digest their MAMPs or proteins that sequester MAMPs to hide them from plant receptors (Figure 1b). The plant pathogen *P. syringae* DC3000 secretes a protease that, through the degradation of flagellin, decreased MTI and increased this strain's growth in Arabidopsis and tomato leaves [37]. Chitin, a conserved component of the cell wall in fungi, is another potent inducer of MTI. Several fungal pathogens have evolved chitin-binding proteins (LysM or inactive chitinases) capable of sequestering free chitin fragments to prevent the activation of plant PRRs [38–40]. Although this mechanism has been only demonstrated for pathogens thus far, LysM and presumably inactive chitinases are found throughout the fungal kingdom and, therefore, commensals may apply this method of evasion as well.

MAMP modification

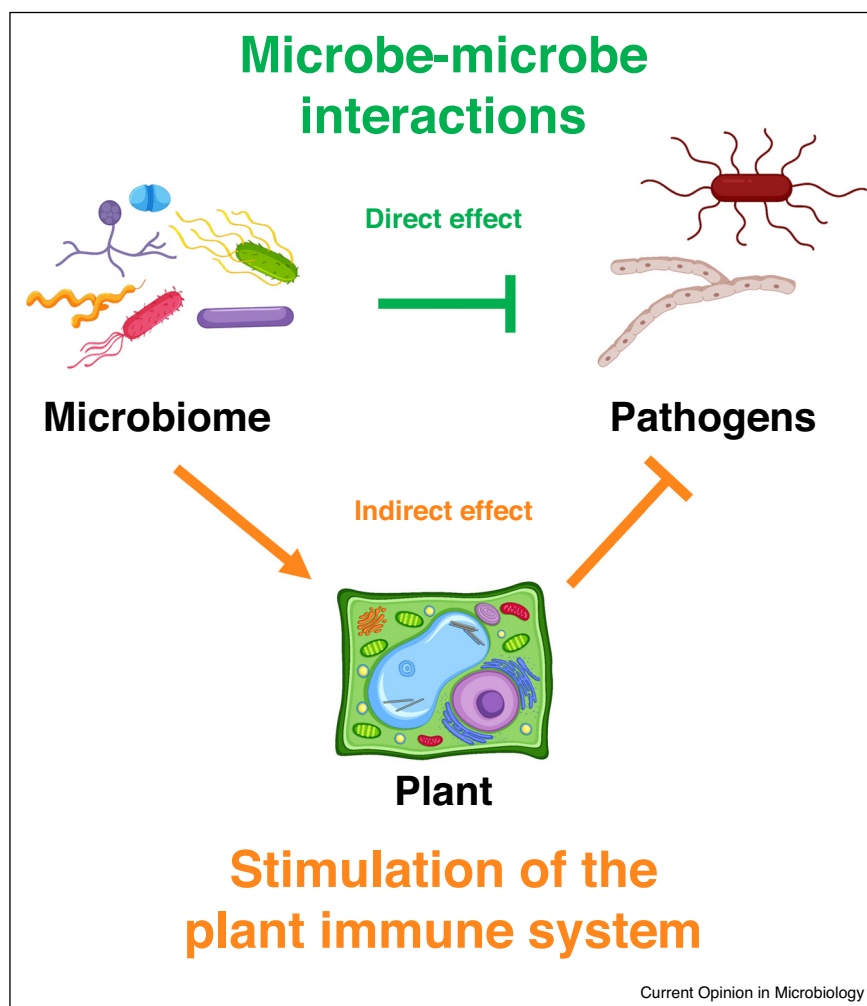
Another strategy used by microbes to prevent the elicitation of MTI is MAMP modification (Figure 1c). For example, *Nicotiana benthamiana* secretes glycosidases that strip the glycan shield from the bacterial flagellum, allowing plant proteases to release the immunogenic flg22 peptide for recognition by the FLS2 receptor [41^{**}]. In turn, pathogens can evade flg22 recognition by either inhibiting plant glycosidases or by modifying the glycan moieties that cover their flagellum [41^{**}]. Similarly, fungi can escape the plant immune system by deacetylating the chitin in their cell wall into chitosan, which is a weaker inducer of immunity [39]. Because both flg22 and chitin are ubiquitous in plant microbiomes, it is likely that commensals have evolved analogous MAMP modification strategies to evade MTI.

The microbiome functions as an extension of the plant immune system

Plant diseases have been traditionally studied as binary associations between a host and a pathogen. In recent years, however, it has become evident that the microbiome can expand plant defensive capabilities and often influences the outcome of plant–pathogen interactions, preventing/mitigating the establishment of diseases by largely unknown mechanisms encompassing the term ‘biocontrol’ [42,43^{*},44–49,50^{*},51]. Importantly, this seems to be largely determined by only two main mechanisms thus far: (I) direct microbe–microbe interactions and (II) stimulation or priming of the plant immune system (Figure 2).

Microbe–microbe interactions play an increasingly evident role in the suppression of pathogens and can

Figure 2



The microbiome expands the plant immune system.

Plant-associated microbes can function as an additional layer of defense against pathogens through at least two mechanisms. First, the microbiome can directly suppress the proliferation of pathogens by producing antimicrobial compounds or through niche competition. Second, the microbiome can indirectly promote resistance against pathogens by stimulating the plant immune system, which in turn becomes more competent to fight off diseases.

serve as a first line of defense against invading organisms in plants. For instance, a molecule secreted by the *Pseudomonas piscium* ZJU60 strain, which was isolated from infected wheat head, antagonizes the fungus *Fusarium graminearum* by inhibiting one of its histone acetyltransferases [50^{*}]. Furthermore, a comprehensive study recently demonstrated that the ability to antagonize other microbes, including pathogens, is a common trait in bacteria isolated from the Arabidopsis leaf microbiome [52]. Genome mining further revealed a high prevalence of a wide variety of unknown biosynthetic gene clusters among inhibitory strains and allowed for the identification of two novel antibiotics [52]. These and other studies show that plant microbiomes are a rich source of pathogen antagonists that work via direct inhibition [53]. Yet, it is likely that many other factors contribute to the direct control of pathogens by the microbiome. In particular, resource competition (niche overlap) with resident microbes has been proposed as an important factor that limits pathogen invasion in plants [54^{*}]. This is analogous to the protective role that commensal microbes play in the animal gut, where invading harmful microbes are out-competed and their growth repressed by the already-established host microbiome [55–57]. Interestingly, Arabidopsis roots are naturally colonized by potentially harmful filamentous eukaryotes that are nevertheless controlled by multiple co-resident bacteria in the context of a multi-kingdom microbiome [58^{**}]. Removal of protective bacteria results in disease, underscoring the importance of microbiome homeostasis and microbe–microbe interactions to plant health.

In addition to the direct inhibition of pathogens described above, commensal microbes can promote host health by stimulating the plant immune system, thus acting indirectly in the suppression of diseases. A well-known form of microbiome-mediated immunity in plants is induced systemic resistance (ISR), a defense response against foliar pathogens and pests triggered by root-associated microorganisms [59]. Required host genetic components of ISR have been uncovered [60–62] and a number of phylogenetically unrelated microbes have been shown to trigger ISR in many different plant species [59]. A hallmark of ISR is the enhanced sensitization rather than the constitutive activation of defense genes [59]. This means that ISR promotes a faster and stronger systemic immune response, but only upon stimulation. Microbiome-mediated disease resistance involving constitutive activation of the plant immune system (a state of alert) has also been reported. A *Sphingomonas melonis* strain isolated from Arabidopsis activates a subset of plant defense genes and promotes immunity against the bacterial pathogen *P. syringae* DC3000 [42,43^{*}]. This protection is lost in the *bak1/bkk1* mutant, indicating that this commensal likely stimulates plant immunity through MAMP recognition by PRRs that rely on BAK1 as a co-receptor [43^{*}]. These studies demonstrate that disease suppression by commensal

microbes can require an intact plant immune system, highlighting the participation of the microbiome in determining the outcome of plant–pathogen interactions.

Recent studies indicate that the plant microbiome is dynamic and responds to the presence of pathogens and pests, supporting the exciting hypothesis that plants actively select protective commensals to fight off diseases under certain circumstances. Arabidopsis grown in native soil from a Dutch field promoted the proliferation of three specific ISR-inducing bacteria in the rhizosphere upon leaf infection with the downy mildew pathogen *Hyaloperonospora arabidopsidis*. Remarkably, these protective bacteria seem to have persisted in the soil and conferred enhanced protection against downy mildew to a subsequent population of plants [63^{*}]. Infection of Arabidopsis leaves with *P. syringae* also resulted in a similar soil-borne legacy that protected a subsequent generation of plants. Supporting the active role of the host in reshaping its microbiome, infected plants displayed altered root exudation profiles that presumably selected for beneficial bacteria [64]. Changes in the microbiome composition and enrichment of potentially beneficial microorganisms have also been observed in barley roots infected with *F. graminearum* [65] and in pepper seedlings infested with whiteflies [66]. Importantly, enrichment of protective microbes in the rhizosphere is associated with the development of disease-suppressive soils, in which plants remain healthy even in the presence of pathogens [67–70]. Thus, microbiome alterations have the potential to affect subsequent generations of plants that germinate in the same soil with consequences for ecological and agricultural processes [71–73].

In sharp contrast to ISR, some root-associated bacteria can make the host plant more susceptible to foliar pathogens. *Pseudomonas* strains that promote resistance against herbivores in Arabidopsis also cause induced systemic susceptibility (ISS) against a hemibiotrophic pathogen [74]. This involves the bacterial production of spermidine, but how this molecule modulates plant immunity is still unclear [75]. Furthermore, arbuscular mycorrhiza fungi also increase the susceptibility of the legume *Astragalus adsurgens* to the foliar pathogen *Erysiphe pisi*, which causes powdery mildew [76]. These studies show that commensal microbes can have pleiotropic effects on the plant immune system, demonstrating that the efficient deployment of immunity-modulating microbes in agriculture will depend on a full understanding of the microbiome effect on plants and both pathogens and other commensals in the context of different environments.

Context-dependent immune modulation shapes the plant microbiome across environments

Since their colonization of terrestrial environments, plants have faced heterogeneous environments that vary

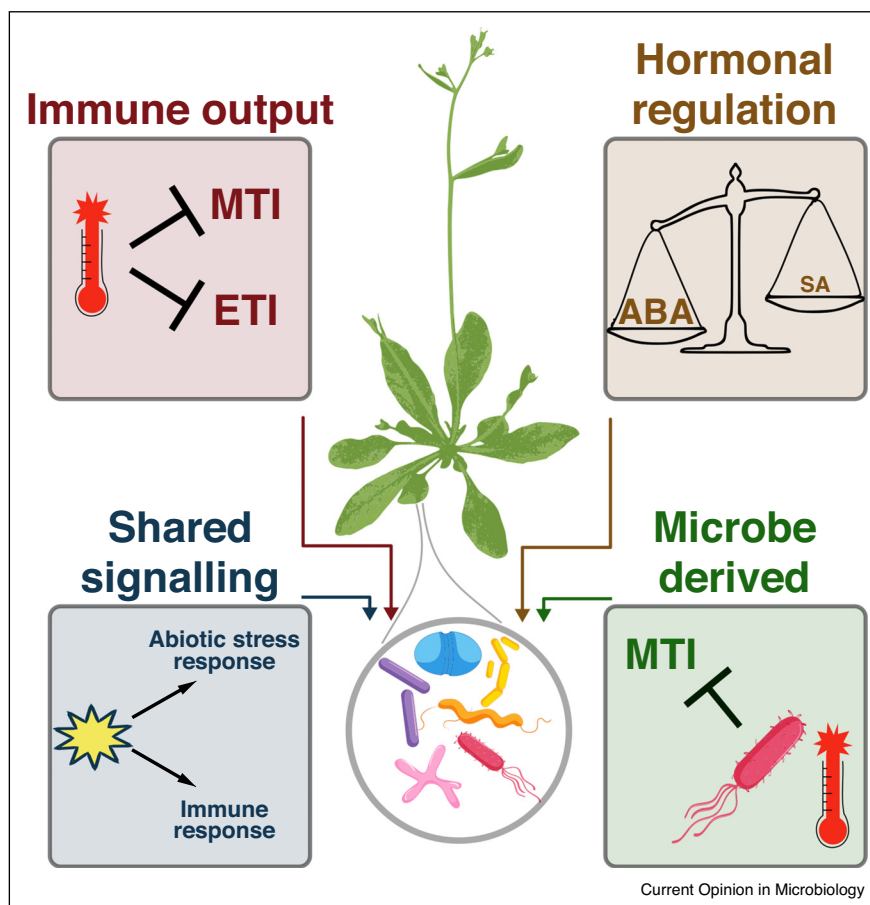
in temperature, water and nutrient availability, and chemical attributes such as salinity, pH and the presence of heavy metals. Plant responses to environmental variation are interconnected with plant immunity [77,78], driven in part by the need for plants to optimally respond to combinations of abiotic stress and pathogen invasion. However, the resultant effects of this interconnectedness on the assembly and function of the plant microbiome are only just being explored.

Environmental variation can modulate plant immunity through a number of non-exclusive mechanisms (Figure 3). First, different environments can directly modulate the expression of plant immune outputs [79,80,81]. For example, exposure to environmental stress can modulate the expression of MTI and ETI-related genes [82–84] and under increased temperature several NLR receptors lose function [85]. Second, hormonal regulators of plant responses to abiotic stress, such as drought and nutrient

availability, typically have an antagonistic effect on plant immunity through the suppression of the jasmonic acid (JA) and salicylic acid (SA) defense pathways [78,86]. Indeed, such effects are so potent that microbial pathogens hijack this interplay to facilitate their invasion [87]. Recent work demonstrates that the antagonistic effect of abiotic responses on plant immunity depends on factors such as plant age and the magnitude and temporal sequence of stressors [88,89,90]. Lastly, shared signaling components can jointly coordinate plant responses to abiotic stress and plant immunity [91,92]. For example, the PRR chitin elicitor receptor kinase 1 (CERK1), is responsible for mounting a plant defense against fungal pathogens but also strongly regulates the expression of genes required for salt stress [93].

Microorganisms may also contribute to the modulation of plant immunity across environments. Translocation of bacterial effectors into the host increases at higher

Figure 3



Environmental variation, including differences in temperature, water, or nutrient availability can modulate plant immunity by a number of mechanisms.

First, different environments can modify the expression plant immune outputs including components of MAMP and effector triggered immunity. Second, crosstalk between abiotic stress hormones (such as abscisic acid) and defense hormones (e.g. salicylic acid) can modulate plant immunity. Third, shared signaling components can lead to joint plant abiotic stress and immune responses. Finally, microbes can modulate plant immunity under particular environments. All of these mechanisms of plant immune modulation have the potential to alter the plant microbiome.

temperatures, which contributes to the suppression of plant immunity [80^{*}]. Furthermore, colonization by the fungal endophyte *Colletotrichum tofieldiae* represses plant immunity but only when host plants are grown under low phosphate conditions [94^{**}]. Finally, members of the γ -proteobacteria eject their polar flagella under nutrient depletion, likely in an attempt to conserve energy under unfavorable conditions [95]. However, because flagellin is an important trigger of plant immunity [36], loss of flagella under particular environments may also lead to modulation of MTI with potential consequences for subsequent microbial colonization. Interestingly, persistence of the endosymbiont *Vibrio fischeri* in the light organ of the Hawaiian bobtail squid, *Euprymna scolopes*, is accompanied by the loss of flagella [96,97], suggesting that environment-dependent modulation of host immunity through MAMP modification may be a signature of associated microorganisms across plant and animal hosts.

The modulation of plant immunity under conditions of environmental or nutrient stress can reshape plant microbiota. In low phosphate conditions, plant immune-related compounds, specifically tryptophan-derived secondary metabolites, are required for the controlled recruitment of the fungal endophyte *C. tofieldiae* [94^{**}]. Additionally, PHR1, the master transcriptional regulator of the plant phosphate starvation response, directly modulates plant immunity via targeting genes in the SA and JA pathways. This crosstalk leads to a dampening of plant immune responses and a perturbed root microbiome [92^{**}]. A root-exuded coumarin that is produced by Arabidopsis during iron starvation or in the presence of ISR-inducing bacteria [75] exerts a selective antimicrobial effect in the rhizosphere, suppressing fungal pathogens and reshaping the microbiome to possibly select beneficial microbes [67,76]. In response to iron starvation, plants synthesize and exude coumarins into the rhizosphere, which not only help mobilize iron in soil [98] but also reshape the composition of the root microbiome through their antimicrobial activity [91^{**},99^{**}]. PBS3, which modulates plant immunity under abiotic stress in an age-dependent manner, also reshapes the composition leaf bacterial communities [88^{*}].

While growing evidence supports the idea that context-dependent immune modulation can reshape plant microbiota, the consequences, whether positive or negative, of such microbiome reshaping for plant performance remain relatively untested. Coumarins exuded by plants under iron depletion selectively inhibit the growth of pathogenic fungi while maintaining plant-growth promoting *Pseudomonas* species and other microbes [91^{**}]. These coumarin-selected microbes may benefit plants by increasing plant tolerance to iron starvation. Similarly, plants may benefit from the alterations to their microbiota under stresses such as herbivory [66], drought [100] and pathogen attack [63^{*}]. Though in these

examples the mechanism underlying microbiome alterations was not determined. Under low phosphate conditions, recruitment of the fungal endophyte *C. tofieldiae* increased the biomass of Arabidopsis plants [94^{**}]. However, synthetic community experiments showed that a bacterial taxon enriched in Arabidopsis roots under phosphate starvation reduced plant performance as measured by shoot phosphate accumulation [101]. A recent study demonstrated that triterpenes produced by Arabidopsis are major determinants of the root bacterial microbiome [102^{**}]. These molecules act as antibiotics or proliferation agents depending on the bacteria taxa and selectively regulate the composition of the root microbiota. Importantly, triterpene biosynthesis can be induced in response to abiotic stresses as well as during pathogen and herbivore attack [103]. These examples highlight that microbiome alteration across environments, mediated in part by plant immune modulation, can have both positive and negative effects on plant performance.

Conclusions

Our knowledge of the plant immune system has been primarily built based on decades of study of plant–pathogen interactions. This knowledge is now being revisited, tested and structured in the context of microbiomes, revealing exciting differences and similarities. Research thus far indicates that the plant immune system mediates interactions with pathogenic and commensal microbes alike. Most MAMPs that are recognized by plant immune receptors are commonly found in pathogens and commensals, indicating that colonization of plant tissues by microorganisms involves suppression and/or evasion of the host immune system, regardless of their lifestyle. Indeed, recent work demonstrates that many commensal bacteria can suppress MTI. Future research should focus on determining the mechanisms of this suppression and its significance to microbiome assembly. Equally important is the interaction between pathogens and the community of commensals that inhabit plants. We propose that the microbiome functions as an additional layer of the plant immune system and can suppress diseases directly via microbe–microbe interactions or indirectly via stimulation of plant immunity. We predict that pathogens must have evolved strategies to overcome the immune barrier imposed by the microbiome. Finally, the plant immune system is intricately linked with environmental and nutrient responses, and altered microbial communities are often seen in the face of environmental changes [71,92^{**},104]. A relevant direction is to investigate how context-dependent immune modulation shifts the composition of plant microbiota and how this helps plants to thrive under stress conditions across various environments. Determining the underlying mechanisms and the resultant plant effects of the complex interplay between plant immunity and microbiota are important goals to advance the field of plant–microbe interactions.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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References and recommended reading

Papers of particular interest, published within the period of review, have been highlighted as:

- of special interest
- of outstanding interest

1. Jones JD, Dangl JL: **The plant immune system.** *Nature* 2006, **444**:323-329.
 2. Thomma BP, Nurnberger T, Joosten MH: **Of PAMPs and effectors: the blurred PTI-ETI dichotomy.** *Plant Cell* 2011, **23**:4-15.
 3. Berens ML, Berry HM, Mine A, Argueso CT, Tsuda K: **Evolution of hormone signaling networks in plant defense.** *Annu Rev Phytopathol* 2017, **55**:401-425.
 4. Vorholt JA: **Microbial life in the phyllosphere.** *Nat Rev Microbiol* 2012, **10**:828-840.
 5. Hacquard S, Spaepen S, Garrido-Oter R, Schulze-Lefert P: **Interplay between innate immunity and the plant microbiota.** *Annu Rev Phytopathol* 2017, **55**:565-589.
- The seminal review in the field to date, this paper summarizes a series of models that could be experimentally approached to dissect microbiome interaction with the plant immune system.
6. Hacquard S, Garrido-Oter R, Gonzalez A, Spaepen S, Ackermann G, Lebeis S, McHardy AC, Dangl JL, Knight R, Ley R *et al.*: **Microbiota and host nutrition across plant and animal kingdoms.** *Cell Host Microbe* 2015, **17**:603-616.
 7. Bulgarelli D, Rott M, Schlaeppi K, Ver Loren van Themaat E, Ahmadinejad N, Assenza F, Rauf P, Huettel B, Reinhardt R, Schmelzer E *et al.*: **Revealing structure and assembly cues for Arabidopsis root-inhabiting bacterial microbiota.** *Nature* 2012, **488**:91-95.
 8. Bai Y, Muller DB, Srinivas G, Garrido-Oter R, Potthoff E, Rott M, Dombrowski N, Munch PC, Spaepen S, Remus-Emsermann M *et al.*: **Functional overlap of the Arabidopsis leaf and root microbiota.** *Nature* 2015, **528**:364-369.
 9. Lundberg DS, Lebeis SL, Paredes SH, Yourstone S, Gehring J, Malfatti S, Tremblay J, Engelbrekton A, Kunin V, Del Rio TG *et al.*: **Defining the core Arabidopsis thaliana root microbiome.** *Nature* 2012, **488**:86-90.
 10. Vandenkoornhuysen P, Quaiser A, Duhamel M, Le Van A, Dufresne A: **The importance of the microbiome of the plant holobiont.** *New Phytol* 2015, **206**:1196-1206.
 11. Hassani MA, Duran P, Hacquard S: **Microbial interactions within the plant holobiont.** *Microbiome* 2018, **6**:58.
 12. Melnyk RA, Hossain SS, Haney CH: **Convergent gain and loss of genomic islands drive lifestyle changes in plant-associated Pseudomonas.** *ISME J* 2019, **13**:1575-1588.
- A great example of comparative genomics where the authors show that differences between commensal and pathogenic strains of bacteria are due to virulence islands, and these genes are convergently gained or lost. The genes necessary for commensal lifestyle are also not from the type three secretion system, indicating that microbes have likely evolved type III-independent mechanisms to evade MTI. Also, the overall genomic similarity of the microbes indicates that commensal and pathogenic strains may not be differentiable by the plant.
13. Li X, Lin H, Zhang W, Zou Y, Zhang J, Tang X, Zhou JM: **Flagellin induces innate immunity in nonhost interactions that is suppressed by Pseudomonas syringae effectors.** *Proc Natl Acad Sci U S A* 2005, **102**:12990-12995.
 14. Xin XF, Nomura K, Aung K, Velasquez AC, Yao J, Boutrot F, Chang JH, Zipfel C, He SY: **Bacteria establish an aqueous living space in plants crucial for virulence.** *Nature* 2016, **539**:524-529.
- This study elegantly shows how the environment influences the plant immune system. It shows, through the use of Arabidopsis mutants, that the plant immune system is needed to maintain the normal growth of commensal bacteria.
15. Stringlis IA, Proietti S, Hickman R, Van Verk MC, Zamioudis C, Pieterse CMJ: **Root transcriptional dynamics induced by beneficial rhizobacteria and microbial immune elicitors reveal signatures of adaptation to mutualists.** *Plant J* 2018, **93**:166-180.
- The beneficial rhizobacterium *Pseudomonas simiae* WCS417 suppresses the flg22-induced transcriptional response in Arabidopsis roots. Moreover, the flg22 peptide from this beneficial strain is as immunogenic as the 'canonical' one from *P. aeruginosa*.
16. Zamioudis C, Pieterse CM: **Modulation of host immunity by beneficial microbes.** *Mol Plant Microbe Interact* 2012, **25**:139-150.
 17. Liu Z, Beskrovnyaya P, Melnyk RA, Hossain SS, Khorasani S, O'Sullivan LR, Wiesmann CL, Bush J, Richard JD, Haney CH: **A genome-wide screen identifies genes in rhizosphere-associated pseudomonas required to evade plant defenses.** *mBio* 2018, **9**.
- This paper introduces a novel technique capable of uncovering genes necessary to evade plant defenses. This same technique could be applied to uncover the genes necessary for beneficial interactions, or the mechanisms used by different lineages to colonize the plant microbiome. This paper also shows that the dampening of MTI is important for colonizing the plant microbiome, as two of the seven genes they found in their screen perform this function.
18. Plett JM, Kempainen M, Kale SD, Kohler A, Legue V, Brun A, Tyler BM, Pardo AG, Martin F: **A secreted effector protein of Laccaria bicolor is required for symbiosis development.** *Curr Biol* 2011, **21**:1197-1203.
 19. Liang Y, Cao Y, Tanaka K, Thibivilliers S, Wan J, Choi J, Kang C, Qiu J, Stacey G: **Nonlegumes respond to rhizobial nod factors by suppressing the innate immune response.** *Science* 2013, **341**:1384-1387.
 20. Plett JM, Daguerre Y, Wittulsky S, Vayssieres A, Deveau A, Melton SJ, Kohler A, Morrell-Falvey JL, Brun A, Veneault-Fourrey C *et al.*: **Effector MiSSP7 of the mutualistic fungus Laccaria bicolor stabilizes the Populus JAZ6 protein and represses jasmonic acid (JA) responsive genes.** *Proc Natl Acad Sci U S A* 2014, **111**:8299-8304.
 21. Millet YA, Danna CH, Clay NK, Songnuan W, Simon MD, Werck-Reichhart D, Ausubel FM: **Innate immune responses activated in Arabidopsis roots by microbe-associated molecular patterns.** *Plant Cell* 2010, **22**:973-990.
 22. Garrido-Oter R, Nakano RT, Dombrowski N, Ma KW, AgBiome T, McHardy AC, Schulze-Lefert P: **Modular traits of the rhizobiales root microbiota and their evolutionary relationship with symbiotic rhizobia.** *Cell Host Microbe* 2018, **24**:155-167 e155.
- The authors perform large scale comparative genomics to identify commensal Rhizobiales that can interfere with MAMP-triggered responses in Arabidopsis. They find that this trait is strain-specific and is separable from the root growth promotion ability that is characteristic of Rhizobiales.
23. Lammertz M, Kuhn H, Pfeilmeier S, Malone J, Zipfel C, Kwaaitaal M, Lin NC, Kvitko BH, Panstruga R: **Widely conserved attenuation of plant MAMP-induced calcium influx by bacteria depends on multiple virulence factors and may involve desensitization of host pattern recognition receptors.** *Mol Plant Microbe Interact* 2019, **32**:608-621.

A number of plant-associated bacteria can suppress MAMP-triggered immunity in *Arabidopsis*, indicating that this may be a common feature among non-pathogenic strains.

24. Yu K, Tichelaar R, Liu Y, Savant N, Lagendijk E, Van Kuijk S, Stringlis I, Van Dijken A, Haney C, Pieterse C: **Plant-beneficial *Pseudomonas* spp. suppress local root immune responses by gluconic acid-mediated lowering of environmental pH.** *Curr Biol* 2019. -D-19-00852.
- Plant-associated bacteria can suppress MAMP-triggered immunity in *Arabidopsis*. This paper shows that *Pseudomonas capeferrum* WCS358 acidifies the extracellular medium via organic acid production to interfere with the plant response to flg22.
25. Shen Q, Liu Y, Naqvi NI: **Fungal effectors at the crossroads of phytohormone signaling.** *Curr Opin Microbiol* 2018, **46**:1-6.
26. Mavrodi DV, Joe A, Mavrodi OV, Hassan KA, Weller DM, Paulsen IT, Loper JE, Alfano JR, Thomashow LS: **Structural and functional analysis of the type III secretion system from *Pseudomonas fluorescens* Q8r1-96.** *J Bacteriol* 2011, **193**:177-189.
27. Stringlis IA, Zamioudis C, Berendsen RL, Bakker P, Pieterse CMJ: **Type III secretion system of beneficial rhizobacteria *Pseudomonas simiae* WCS417 and *Pseudomonas defensor* WCS374.** *Front Microbiol* 2019, **10**:1631.
28. Preston GM, Bertrand N, Rainey PB: **Type III secretion in plant growth-promoting *Pseudomonas fluorescens* SBW25.** *Mol Microbiol* 2001, **41**:999-1014.
29. Levy A, Salas Gonzalez I, Mittelviehhaus M, Clingenpeel S, Herrera Paredes S, Miao J, Wang K, Devescovi G, Stillman K, Monteiro F et al.: **Genomic features of bacterial adaptation to plants.** *Nat Genet* 2017, **50**:138-150.
- A comprehensive comparative genomics study that analyzed thousands of bacterial genomes and revealed features that are commonly found in plant-associated strains. Although the Type-III secretion system is a hallmark of bacterial pathogens, it is relatively rare in commensals, suggesting that these strains use a number of yet undescribed mechanisms to interfere with plant immunity.
30. Thiergart T, Duran P, Ellis T, Garrido-Oter R, Kemen E, Roux F, Alonso-Blanco C, Agren J, Schulze-Lefert P, Hacquard S: **Root microbiota assembly and adaptive differentiation among European *Arabidopsis* populations.** *bioRxiv* 2019. 640623.
31. Naito K, Taguchi F, Suzuki T, Inagaki Y, Toyoda K, Shiraiishi T, Ichinose Y: **Amino acid sequence of bacterial microbe-associated molecular pattern flg22 is required for virulence.** *Mol Plant Microbe Interact* 2008, **21**:1165-1174.
32. Wyrtsch I, Dominguez-Ferreras A, Geldner N, Boller T: **Tissue-specific FLAGELLIN-SENSING 2 (FLS2) expression in roots restores immune responses in *Arabidopsis* fls2 mutants.** *New Phytol* 2015, **206**:774-784.
33. Vetter M, Karasov TL, Bergelson J: **Differentiation between MAMP triggered defenses in *Arabidopsis thaliana*.** *PLoS Genet* 2016, **12**:e1006068.
34. Veluchamy S, Hind SR, Dunham DM, Martin GB, Panthee DR: **Natural variation for responsiveness to flg22, flgII-28, and csp22 and *Pseudomonas syringae* pv. tomato in heirloom tomatoes.** *PLoS One* 2014, **9**:e106119.
35. Roberts R, Mainiero S, Powell AF, Liu AE, Shi K, Hind SR, Strickler SR, Collmer A, Martin GB: **Natural variation for unusual host responses and flagellin-mediated immunity against *Pseudomonas syringae* in genetically diverse tomato accessions.** *New Phytol* 2019, **223**:447-461.
36. Felix G, Duran JD, Volko S, Boller T: **Plants have a sensitive perception system for the most conserved domain of bacterial flagellin.** *Plant J* 1999, **18**:265-276.
37. Pel MJ, van Dijken AJ, Bardoel BW, Seidl MF, van der Ent S, van Strijp JA, Pieterse CM: ***Pseudomonas syringae* evades host immunity by degrading flagellin monomers with alkaline protease AprA.** *Mol Plant Microbe Interact* 2014, **27**:603-610.
38. Fiorin GL, Sanchez-Vallet A, Thomazella DPT, do Prado PFV, do Nascimento LC, Figueira AVO, Thomma B, Pereira GAG, Teixeira P: **Suppression of plant immunity by fungal chitinase-like effectors.** *Curr Biol* 2018, **28**:3023-3030 e3025.
39. Sanchez-Vallet A, Mesters JR, Thomma BP: **The battle for chitin recognition in plant-microbe interactions.** *FEMS Microbiol Rev* 2015, **39**:171-183.
40. de Jonge R, van Esse HP, Kombrink A, Shinya T, Desaki Y, Bours R, van der Krol S, Shibuya N, Joosten MH, Thomma BP: **Conserved fungal LysM effector Ecp6 prevents chitin-triggered immunity in plants.** *Science* 2010, **329**:953-955.
41. Buscaill P, Chandrasekar B, Sanguankiattichai N, Kourelis J, Kaschani F, Thomas EL, Morimoto K, Kaiser M, Preston GM, Ichinose Y et al.: **Glycosidase and glycan polymorphism control hydrolytic release of immunogenic flagellin peptides.** *Science* 2019, **364**.
- A beautifully presented paper which shows that bacterial glycosylation of flagellin provides protection against plant-derived proteases. They further show that plants use specific glycosidases and proteases to remove glycans from bacterial flagellin and to release the MTI-inducing peptide flg22.
42. Innerebner G, Knief C, Vorholt JA: **Protection of *Arabidopsis thaliana* against leaf-pathogenic *Pseudomonas syringae* by *Sphingomonas* strains in a controlled model system.** *Appl Environ Microbiol* 2011, **77**:3202-3210.
43. Vogel C, Bodenhausen N, Gruissem W, Vorholt JA: **The *Arabidopsis* leaf transcriptome reveals distinct but also overlapping responses to colonization by phyllosphere commensals and pathogen infection with impact on plant health.** *New Phytol* 2016, **212**:192-207.
- This study explores the overlapping and unique plant transcriptional responses to colonization by common foliar microbial pathogens and commensals. Foliar colonization by a *Sphingomonas* strain activated plant defense and mediated resistance to the plant pathogen *Pseudomonas syringae* DC3000.
44. Khalaf EM, Raizada MN: **Bacterial seed endophytes of domesticated cucurbits antagonize fungal and oomycete pathogens including powdery mildew.** *Front Microbiol* 2018, **9**:42.
45. Hunziker L, Bonisch D, Groenhagen U, Bailly A, Schulz S, Weisskopf L: ***Pseudomonas* strains naturally associated with potato plants produce volatiles with high potential for inhibition of *Phytophthora infestans*.** *Appl Environ Microbiol* 2015, **81**:821-830.
46. Busby PE, Peay KG, Newcombe G: **Common foliar fungi of *Populus trichocarpa* modify *Melampsora* rust disease severity.** *New Phytol* 2016, **209**:1681-1692.
47. Santhanam R, Luu VT, Weinhold A, Goldberg J, Oh Y, Baldwin IT: **Native root-associated bacteria rescue a plant from a sudden-wilt disease that emerged during continuous cropping.** *Proc Natl Acad Sci U S A* 2015, **112**:E5013-5020.
48. Ritpitakphong U, Falquet L, Vimoltust A, Berger A, Metraux JP, L'Haridon F: **The microbiome of the leaf surface of *Arabidopsis* protects against a fungal pathogen.** *New Phytol* 2016, **210**:1033-1043.
49. Kwak MJ, Kong HG, Choi K, Kwon SK, Song JY, Lee J, Lee PA, Choi SY, Seo M, Lee HJ et al.: **Rhizosphere microbiome structure alters to enable wilt resistance in tomato.** *Nat Biotechnol* 2018.
50. Chen Y, Wang J, Yang N, Wen Z, Sun X, Chai Y, Ma Z: **Wheat microbiome bacteria can reduce virulence of a plant pathogenic fungus by altering histone acetylation.** *Nat Commun* 2018, **9**:3429.
- This study represents one of a few examples of direct microbe-microbe interactions occurring within the plant microbiome. The authors demonstrate that the bacterium *Pseudomonas piscium* directly interferes with the molecular machinery of a *Fusarium* fungal plant pathogen, resulting in reduced virulence and fungal growth.
51. Haney CH, Samuel BS, Bush J, Ausubel FM: **Associations with rhizosphere bacteria can confer an adaptive advantage to plants.** *Nat Plants* 2015, **1**.
52. Helfrich EJN, Vogel CM, Ueoka R, Schafer M, Ryffel F, Muller DB, Probst S, Kreuzer M, Piel J, Vorholt JA: **Bipartite interactions, antibiotic production and biosynthetic potential of the *Arabidopsis* leaf microbiome.** *Nat Microbiol* 2018, **3**:909-919.

53. Syed Ab Rahman SF, Singh E, Pieterse CMJ, Schenk PM: **Emerging microbial biocontrol strategies for plant pathogens.** *Plant Sci* 2018, **267**:102-111.
54. Berg M, Koskella B: **Nutrient- and dose-dependent microbiome-mediated protection against a plant pathogen.** *Curr Biol* 2018, **28**:2487-2492 e2483.
- Here the authors perform a series of manipulative experiments to understand the effects of foliar microbial community composition and fertilization on plant resistance to a bacterial plant pathogen. Fertilization of tomato leaves abolishes the effect that a microbial community has to compete with *Pseudomonas syringae* in the phyllosphere. Thus, competition for resources may be a mechanism by which the microbiome antagonizes pathogens.
55. Deriu E, Liu JZ, Pezeshki M, Edwards RA, Ochoa RJ, Contreras H, Libby SJ, Fang FC, Raffatellu M: **Probiotic bacteria reduce salmonella typhimurium intestinal colonization by competing for iron.** *Cell Host Microbe* 2013, **14**:26-37.
56. Maltby R, Leatham-Jensen MP, Gibson T, Cohen PS, Conway T: **Nutritional basis for colonization resistance by human commensal *Escherichia coli* strains HS and Nissle 1917 against *E. coli* O157:H7 in the mouse intestine.** *PLoS One* 2013, **8**:e53957.
57. Kamada N, Kim YG, Sham HP, Vallance BA, Puente JL, Martens EC, Nunez G: **Regulated virulence controls the ability of a pathogen to compete with the gut microbiota.** *Science* 2012, **336**:1325-1329.
58. Duran P, Thiergart T, Garrido-Oter R, Agler M, Kemen E, Schulze-Lefert P, Hacquard S: **Microbial interkingdom interactions in roots promote *Arabidopsis* survival.** *Cell* 2018, **175**:973-983 e914.
- The authors use a number of computational and microbial techniques to characterize the interkingdom microbial interactions occurring in the plant root microbiome. Bacteria in the *Arabidopsis* root microbiome promote plant health by antagonizing filamentous eukaryotes that are also part of the microbiome. This study underscores the importance of microbe-microbe interactions and microbial homeostasis for plant health.
59. Pieterse CM, Zamioudis C, Berendsen RL, Weller DM, Van Wees SC, Bakker PA: **Induced systemic resistance by beneficial microbes.** *Annu Rev Phytopathol* 2014, **52**:347-375.
60. Pieterse CM, van Wees SC, van Pelt JA, Knoester M, Laan R, Gerrits H, Weisbeek PJ, van Loon LC: **A novel signaling pathway controlling induced systemic resistance in *Arabidopsis*.** *Plant Cell* 1998, **10**:1571-1580.
61. Zamioudis C, Hanson J, Pieterse CM: **Beta-glucosidase BGLU42 is a MYB72-dependent key regulator of rhizobacteria-induced systemic resistance and modulates iron deficiency responses in *Arabidopsis* roots.** *New Phytol* 2014, **204**:368-379.
62. Van der Ent S, Verhagen BW, Van Doorn R, Bakker D, Verlaan MG, Pel MJ, Joosten RG, Proveniers MC, Van Loon LC, Ton J *et al.*: **MYB72 is required in early signaling steps of rhizobacteria-induced systemic resistance in *Arabidopsis*.** *Plant Physiol* 2008, **146**:1293-1304.
63. Berendsen RL, Vismans G, Yu K, Song Y, de Jonge R, Burgman WP, Burmolle M, Herschend J, Bakker P, Pieterse CMJ: **Disease-induced assemblage of a plant-beneficial bacterial consortium.** *ISME J* 2018, **12**:1496-1507.
- Infection of *Arabidopsis* with the oomycete *Hyaloperonospora arabidopsidis* induces the recruitment of specific microbial strains in the roots. These strains provide protection against the pathogen and improve plant health, indicating that the plant may selectively recruit beneficial bacteria during pathogen infection. They also show that soils associated with infected plants provide protection to subsequent plant generations.
64. Yuan J, Zhao J, Wen T, Zhao M, Li R, Goossens P, Huang Q, Bai Y, Vivanco JM, Kowalchuk GA: **Root exudates drive the soil-borne legacy of aboveground pathogen infection.** *Microbiome* 2018, **6**:156.
65. Dudenhöffer JH, Scheu S, Jousset A: **Systemic enrichment of antifungal traits in the rhizosphere microbiome after pathogen attack.** *J Ecol* 2016, **104**:1566-1575.
66. Kong HG, Kim BK, Song GC, Lee S, Ryu CM: **Aboveground whitefly infestation-mediated reshaping of the root microbiota.** *Front Microbiol* 2016, **7**:1314.
67. Chialva M, Salvioli di Fossalunga A, Daghino S, Ghignone S, Bagnaresi P, Chiapello M, Novero M, Spadaro D, Perotto S, Bonfante P: **Native soils with their microbiotas elicit a state of alert in tomato plants.** *New Phytol* 2018, **220**:1296-1308.
68. Cha JY, Han S, Hong HJ, Cho H, Kim D, Kwon Y, Kwon SK, Crusemann M, Bok Lee Y, Kim JF *et al.*: **Microbial and biochemical basis of a *Fusarium* wilt-suppressive soil.** *ISME J* 2016, **10**:119-129.
69. Mendes R, Kruijt M, de Bruijn I, Dekkers E, van der Voort M, Schneider JH, Piceno YM, DeSantis TZ, Andersen GL, Bakker PA *et al.*: **Deciphering the rhizosphere microbiome for disease-suppressive bacteria.** *Science* 2011, **332**:1097-1100.
70. Weller DM, Raaijmakers JM, Gardener BB, Thomashow LS: **Microbial populations responsible for specific soil suppressiveness to plant pathogens.** *Annu Rev Phytopathol* 2002, **40**:309-348.
71. Bakker P, Pieterse CMJ, de Jonge R, Berendsen RL: **The soil-borne legacy.** *Cell* 2018, **172**:1178-1180.
72. Bever JD, Westover KM, Antonovics J: **Incorporating the soil community into plant population dynamics: the utility of the feedback approach.** *J Ecol* 1997:561-573.
73. Mariotte P, Mehrabi Z, Bezemer TM, De Deyn GB, Kulmatiski A, Drigo B, Veen GFC, van der Heijden MGA, Kardol P: **Plant-soil feedback: bridging natural and agricultural sciences.** *Trends Ecol Evol* 2018, **33**:129-142.
74. Haney CH, Wiesmann CL, Shapiro LR, Melnyk RA, O'Sullivan LR, Khorasani S, Xiao L, Han J, Bush J, Carrillo J *et al.*: **Rhizosphere-associated *Pseudomonas* induce systemic resistance to herbivores at the cost of susceptibility to bacterial pathogens.** *Mol Ecol* 2018, **27**:1833-1847.
75. Melnyk RA, Beskrovnaya PA, Liu Z, Song Y, Haney CH: **Bacterially produced spermidine induces plant systemic susceptibility to pathogens.** *bioRxiv* 2019:517870.
76. Liu Y, Feng X, Gao P, Li Y, Christensen MJ, Duan T: **Arbuscular mycorrhiza fungi increased the susceptibility of *Astragalus adsurgens* to powdery mildew caused by *Erysiphe pisi*.** *Mycology* 2018, **9**:223-232.
77. Venkatesh J, Kang BC: **Current views on temperature-modulated R gene-mediated plant defense responses and tradeoffs between plant growth and immunity.** *Curr Opin Plant Biol* 2019, **50**:9-17.
78. Pieterse CM, Van der Does D, Zamioudis C, Leon-Reyes A, Van Wees SC: **Hormonal modulation of plant immunity.** *Annu Rev Cell Dev Biol* 2012, **28**:489-521.
79. Velasquez AC, Castroverde CDM, He SY: **Plant-pathogen warfare under changing climate conditions.** *Curr Biol* 2018, **28**:R619-R634.
80. Huot B, Castroverde CDM, Velasquez AC, Hubbard E, Pulman JA, Yao J, Childs KL, Tsuda K, Montgomery BL, He SY: **Dual impact of elevated temperature on plant defence and bacterial virulence in *Arabidopsis*.** *Nat Commun* 2017, **8**:1808.
- This paper takes a comprehensive look at the factors contributing to the breakdown of plant immunity under increased temperatures. The authors find that a combination of plant and bacterial factors responsive to temperature contribute to increased pathogen virulence at elevated temperature.
81. Hua J: **Modulation of plant immunity by light, circadian rhythm, and temperature.** *Curr Opin Plant Biol* 2013, **16**:406-413.
82. Janda M, Lamparova L, Zubikova A, Burketova L, Martinec J, Krckova Z: **Temporary heat stress suppresses PAMP-triggered immunity and resistance to bacteria in *Arabidopsis thaliana*.** *Mol Plant Pathol* 2019.
83. MacQueen A, Bergelson J: **Modulation of R-gene expression across environments.** *J Exp Bot* 2016, **67**:2093-2105.
84. Singh P, Yekondi S, Chen PW, Tsai CH, Yu CW, Wu K, Zimmerli L: **Environmental history modulates *Arabidopsis* pattern-triggered immunity in a HISTONE ACETYLTRANSFERASE1-dependent manner.** *Plant Cell* 2014, **26**:2676-2688.

85. Zhu Y, Qian W, Hua J: **Temperature modulates plant defense responses through NB-LRR proteins.** *PLoS Pathog* 2010, **6**: e1000844.
86. Robert-Seilaniantz A, Grant M, Jones JD: **Hormone crosstalk in plant disease and defense: more than just jasmonate-salicylate antagonism.** *Annu Rev Phytopathol* 2011, **49**:317-343.
87. Mine A, Berens ML, Nobori T, Anver S, Fukumoto K, Winkelmuller TM, Takeda A, Becker D, Tsuda K: **Pathogen exploitation of an abscisic acid- and jasmonate-inducible MAPK phosphatase and its interception by Arabidopsis immunity.** *Proc Natl Acad Sci U S A* 2017, **114**:7456-7461.
88. Berens ML, Wolinska KW, Spaepen S, Ziegler J, Nobori T, Nair A, Kruler V, Winkelmuller TM, Wang Y, Mine A et al.: **Balancing trade-offs between biotic and abiotic stress responses through leaf age-dependent variation in stress hormone cross-talk.** *Proc Natl Acad Sci U S A* 2019, **116**:2364-2373.
- This study explores how plants respond to different stresses simultaneously. Depending on the plant age, biotic and abiotic stresses are differentially prioritized: abiotic stresses can suppress immunity in older leaves via ABA signaling, whereas immune function is maintained in younger leaves. The salicylic acid signaling component PBS3 functions in the cross-talk between abiotic and biotic stresses and also influences the composition of leaf-associated bacterial communities.
89. Gupta A, Hisano H, Hojo Y, Matsuura T, Ikeda Y, Mori IC, Senthil-Kumar M: **Global profiling of phytohormone dynamics during combined drought and pathogen stress in Arabidopsis thaliana reveals ABA and JA as major regulators.** *Sci Rep* 2017, **7**:4017.
90. Bostock RM, Pye MF, Roubtsova TV: **Predisposition in plant disease: exploiting the nexus in abiotic and biotic stress perception and response.** *Annu Rev Phytopathol* 2014, **52**:517-549.
91. Stringlis IA, Yu K, Feussner K, de Jonge R, Van Bentum S, Van Verk MC, Berendsen RL, Bakker P, Feussner I, Pieterse CMJ: **MYB72-dependent coumarin exudation shapes root microbiome assembly to promote plant health.** *Proc Natl Acad Sci U S A* 2018, **115**:E5213-E5222.
- This is one of the first papers to demonstrate that plant mediated alterations to root microbiota may benefit plant performance. Coumarins exuded by roots in the presence of beneficial bacteria and under iron starvation reshape the root microbiome and selectively inhibit pathogenic fungi.
92. Castrillo G, Teixeira PJ, Paredes SH, Law TF, de Lorenzo L, Feltcher ME, Finkel OM, Breakfield NW, Mieczkowski P, Jones CD et al.: **Root microbiota drive direct integration of phosphate stress and immunity.** *Nature* 2017, **543**:513-518.
- This paper comprehensively explores the connections between plant responses to low phosphate, plant immunity, and root microbiota. It represents an important advance in showing that plant responses to phosphate stress are directly linked to immunity and depend on an intact root microbial community.
93. Espinoza C, Liang Y, Stacey G: **Chitin receptor CERK1 links salt stress and chitin-triggered innate immunity in Arabidopsis.** *Plant J* 2017, **89**:984-995.
94. Hiruma K, Gerlach N, Sacristan S, Nakano RT, Hacquard S, Kracher B, Neumann U, Ramirez D, Bucher M, O'Connell RJ et al.: **Root endophyte Colletotrichum tofieldiae confers plant fitness benefits that are phosphate status dependent.** *Cell* 2016, **165**:464-474.
- This paper is an excellent example of a mechanistic study of a plant-microbial interaction. The authors use a number of molecular techniques to elegantly demonstrate that plant-derived secondary metabolites are required for the controlled recruitment and beneficial effects of the fungal endophyte, *Colletotrichum tofieldiae*, under phosphate limited conditions.
95. Ferreira JL, Gao FZ, Rossmann FM, Nans A, Brenzinger S, Hosseini R, Wilson A, Briegel A, Thormann KM, Rosenthal PB et al.: **Gamma-proteobacteria eject their polar flagella under nutrient depletion, retaining flagellar motor relic structures.** *PLoS Biol* 2019, **17**:e3000165.
96. Thompson LR, Nikolakakis K, Pan S, Reed J, Knight R, Ruby EG: **Transcriptional characterization of Vibrio fischeri during colonization of juvenile Euprymna scolopes.** *Environ Microbiol* 2017, **19**:1845-1856.
97. Ruby EG, Asato LM: **Growth and flagellation of Vibrio fischeri during initiation of the sepioid squid light organ symbiosis.** *Arch Microbiol* 1993, **159**:160-167.
98. Palmer CM, Hindt MN, Schmidt H, Clemens S, Guerinot ML: **MYB10 and MYB72 are required for growth under iron-limiting conditions.** *PLoS Genet* 2013, **9**:e1003953.
99. Voges M, Bai Y, Schulze-Lefert P, Sattely ES: **Plant-derived coumarins shape the composition of an Arabidopsis synthetic root microbiome.** *Proc Natl Acad Sci U S A* 2019, **116**:12558-12565.
- Here the authors dissect the effect of plant coumarins on the assembly of root bacteria using a synthetic community approach. They discover that the reactive oxygen species generated by coumarins may be affecting particular members of the root microbiome, giving rise to community level perturbations. This represents an important advance in our understanding of the plant-derived mechanisms shaping microbiome composition.
100. Xu L, Naylor D, Dong Z, Simmons T, Pierroz G, Hixson KK, Kim YM, Zink EM, Engbrecht KM, Wang Y et al.: **Drought delays development of the sorghum root microbiome and enriches for monoderm bacteria.** *Proc Natl Acad Sci U S A* 2018, **115**:E4284-E4293.
101. Finkel OM, Salas-González I, Castrillo G, Spaepen S, Law TF, Jones C, Dangl JL: **The effects of soil phosphorous content on microbiota are driven by the plant phosphate starvation response.** *BioRxiv* 2019:608133.
102. Huang AC, Jiang T, Liu YX, Bai YC, Reed J, Qu B, Goossens A, Nutzmans HW, Bai Y, Osbourn A: **A specialized metabolic network selectively modulates Arabidopsis root microbiota.** *Science* 2019, **364**.
- The Arabidopsis root microbiota is modulated by specialized terpenes produced by the plant. These secondary metabolites can have different effects on different bacterial taxa, contributing to the assembly of specific microbial communities. The results from this paper indicate that plant metabolic diversification occurring across species and environments may be a large determinant of microbiome composition.
103. Thimmappa R, Geisler K, Louveau T, O'Maille P, Osbourn A: **Triterpene biosynthesis in plants.** *Annu Rev Plant Biol* 2014, **65**:225-257.
104. Fitzpatrick CR, Copeland J, Wang PW, Guttman DS, Kotanen PM, Johnson MTJ: **Assembly and ecological function of the root microbiome across angiosperm plant species.** *Proc Natl Acad Sci U S A* 2018, **115**:E1157-E1165.
105. Edgar RC: **MUSCLE: multiple sequence alignment with high accuracy and high throughput.** *Nucleic Acids Res* 2004, **32**:1792-1797.
106. Eddy SR: **Accelerated profile HMM searches.** *PLoS Comput Biol* 2011, **7**:e1002195.
107. Letunic I, Bork P: **Interactive tree of life (iTOL) v4: recent updates and new developments.** *Nucleic Acids Res* 2019, **47**:W256-W259.
108. Felix G, Boller T: **Molecular sensing of bacteria in plants. The highly conserved RNA-binding motif RNP-1 of bacterial cold shock proteins is recognized as an elicitor signal in tobacco.** *J Biol Chem* 2003, **278**:6201-6208.
109. Kunze G, Zipfel C, Robatzek S, Niehaus K, Boller T, Felix G: **The N terminus of bacterial elongation factor Tu elicits innate immunity in Arabidopsis plants.** *Plant Cell* 2004, **16**:3496-3507.
110. Bohm H, Albert I, Oome S, Raaymakers TM, Van den Ackerveken G, Nurnberger T: **A conserved peptide pattern from a widespread microbial virulence factor triggers pattern-induced immunity in Arabidopsis.** *PLoS Pathog* 2014, **10**:e1004491.