Connecting Growth and Defense: The Emerging Roles of Brassinosteroids and Gibberellins in Plant Innate Immunity

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ABSTRACT **Brassinosteroids (BRs) and gibberellins (GAs) are two groups of phytohormones that regulate many common developmental processes throughout the plant life cycle. Fueled by large-scale 'omics' technologies and the burgeoning field of plant computational biology, the past few years have witnessed paradigm-shifting advances in our understanding of how BRs and GA are perceived and their signals transduced. Accumulating evidence also implicates BR and GA in the coordination and integration of plant immune responses. Similarly to other growth regulators, BR and GA play ambiguous roles in molding pathological outcomes, the effects of which may depend not only on the pathogen's lifestyle and infection strategy, but also on specialized features of each interaction. Analysis of the underpinning molecular mechanisms points to a crucial role of GA-inhibiting DELLA proteins and the BR-regulated transcription factor BZR1. Acting at the interface of developmental and defense signaling, these proteins likely serve as central hubs for pathway crosstalk and signal integration, allowing appropriate modulation of plant growth and defense in response to various stimuli. In this review, we outline the latest discoveries dealing with BR and GA modulation of plant innate immunity and highlight interactions between BR and GA signaling, plant defense, and microbial virulence.**

Key words: hormones; defense; pathogen; plant growth; disease resistance.

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INTRODUCTION

Plant hormones are small signaling molecules that play diverse roles throughout the lifespan of plants. They not only orchestrate intrinsic developmental programs, but also convey environmental inputs and drive adaptive responses to abiotic and biotic stresses. Historically, plant immunity research has focused on the role of three hormones: salicylic acid (SA), jasmonic acid (JA), and ethylene (ET). Upon infection, plants produce a highly specific blend of these 'defense hormones', with the exact combination seemingly depending on the pathogen's lifestyle. In the dicot model plant *Arabidopsis thaliana*, resistance to biotrophic pathogens is usually dependent on SA, whereas necrotrophic pathogens tend to be resisted through a combination of JA and ET signaling (Pieterse et al., 2009). Moreover, interaction between these two pathways is most often antagonistic, which has led many authors to suggest that plant immunity follows a binary model with SA and JA/ET having opposing influences (Bari and Jones, 2009). Although valid for many plant–pathogen interactions, this traditional view is overly generalized, and accumulating findings in both dicot and monocot systems suggest a more complex reality (Pieterse et al., 2012; Van der Ent and Pieterse, 2012). For instance, in rice (*Oryza sativa*), one of the most important food crops worldwide and a model for molecular genetic studies in cereals, disease resistance seems to be controlled by a highly complex signaling network that does not support a dichotomy between the effectiveness of the SA, JA, and ET pathways and the lifestyle of a given pathogen (De Vleesschauwer et al., 2010, 2013; Riemann et al., 2013).

Moreover, new developments indicate that plant defense networking is more than just SA and JA/ET, with

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more integrative models implicating a coordinated range of hormones in configuring the plant's response to pathogen attack. These hormones include abscisic acid (ABA), which is best known for its role in abiotic stress adaptation. Depending on the pathogen type, plant species, and even timing of infection, ABA can act as both a positive and negative regulator of disease resistance, at least in part by feeding into the SA–JA–ET backbone of the plant immune system (Asselbergh et al., 2008; Cao et al., 2011). Other recently identified defense regulators include cytokinins (CKs), auxin, brassinosteroids (BRs), and gibberellins (GAs), all of which have been intensively studied in the context of plant growth and development. Although much remains to be discovered about their precise role and function in plant–microbe interactions, recent data are now beginning to unveil how these 'developmental hormones' modulate host immunity, and how microbe-induced perturbations of these classic growth regulators contribute to virulence (Robert-Seilaniantz et al., 2011; Pieterse et al., 2012). In case of auxin, for instance, it is now well established that the auxin and SA pathways act in a mutually antagonistic manner during plant defense, whereas auxin and JA signaling share many commonalities. Moreover, a growing body of evidence indicates that some pathogens either produce auxin themselves or increase plant auxin biosynthesis upon infection to manipulate the plant's defensive and developmental machinery (Valls et al., 2006; Kazan and Manners, 2009).

In this review, we survey recent progress in deciphering the immune-regulatory role of brassinosteroids (BRs) and gibberellins (GAs), with a special focus on the cellular components and hormone signals involved in regulating crosstalk between BR/GA signaling, plant defense, and microbial virulence. For more detailed information on auxin- and cytokinin-modulated immunity, we refer the reader to a number of excellent recent review papers dealing with these topics (Choi et al., 2011; Naseem and Dandekar, 2012; Denancé et al., 2013).

BRASSINOSTEROIDS: MULTI-TASKERS IN PLANT–MICROBE INTERACTIONS

Role of Brassinosteroids in Plant Physiology

Discovered nearly 40 years ago, brassinosteroids are a unique class of polyhydroxylated steroidal phytohormones with important roles in regulating myriad physiological and developmental processes, including pollen tube elongation, seed germination, photomorphogenesis, flowering, and senescence. To date, more than 50 brassinosteroids have been described, of which brassinolide (BL) and castasterone are the most active forms (Bajguz, 2007). Typically, BR-deficient and BR-insensitive mutants display dwarfism. Underlying this phenotype is the involvement of BRs in controlling cell division, expansion, and even differentiation (for review, see Müssig, 2005; Clouse, 2011; Fridman and Savaldi-Goldstein, 2013). In regard to these physiological effects, BRs often have been shown to interact with other growth regulators, such as GA and auxins (Fridman and Savaldi-Goldstein, 2013). Additionally, a clear role in reaction to abiotic stresses was demonstrated (Bajguz and Hayat, 2009). Recent advances, however, indicate that brassinosteroids are also involved in a complex molecular interaction network that steers host defense responses upon pathogen attack (Choudhary et al., 2012).

BR Signaling in Plants

Over the past decade, molecular genetic studies using *Arabidopsis* (*Arabidopsis thaliana*) and rice (*Oryza sativa*) as model plants have identified numerous genes involved in BR biosynthesis and gene regulation. Together with more recent biochemical approaches, these studies have provided fascinating insights into the various aspects of BR signaling, establishing the BR pathway as one of the best-understood signal transduction pathways in plants (for review, see Li, 2010; Ye et al., 2011; Tong and Chu, 2012; Zhu et al., 2013). According to current concepts, active brassinosteroids such as BL and castasterone bind directly to the extracellular domain of the leucine-rich repeat receptor-like kinase (LRR–RLK) BRI1, thereby inducing a series of biochemical responses, including BRI1 dissociation from the negative regulator BKI1, subsequent heterodimerization of BRI1 with, and activation of, the co-receptor BAK1, phosphorylation of the BRI1-interacting signaling kinase (BSK1), and activation of the protein phosphatase BSU1. These events eventually culminate in inhibition of the shaggy-like kinase BIN2 and resultant activation of the homologous transcription factors (TFs) BZR1 and BES1/BZR2. Finally, activated BZR1 and BES1 migrate to the nucleus where they bind BR-responsive promoters, causing transcriptional changes that ultimately shape BR-signaling outputs (Tang et al., 2011).

Implications of BR in Basal Defense and Disease Susceptibility

Besides their critical role in orchestrating growth and developmental processes, BRs are also increasingly implicated in plant responses to pathogen attack. However, compared to the well-characterized signaling pathway, the role of BRs in plant defense is less well understood, and even controversial. Although BRs have long been tagged as positive regulators in plant disease resistance, recent findings have revealed many previously unexpected roles of BR in shaping pathological outcomes (Jaillais et al., 2011; Albrecht et al., 2012; Belkhadir et al., 2012; De Vleesschauwer et al., 2012; Nahar et al., 2013; Shi et al., 2013).

Originally, field trials with exogenously administered BRs suggested a positive effect on the resistance of diverse

crops to a broad array of pathogens (Khripach, 2000). This was supported by a report by Nakashita et al. (2003) who studied the impact of exogenously applied BRs on innate immunity. The authors reported a positive but variable effect of BL on disease resistance of tobacco and rice to distinct leaf pathogens in small-scale disease trials. This effect was found to be not only local, but also systemic (Nakashita et al., 2003). More recently, BR application was also shown to protect barley from several *Fusarium* diseases (Ali et al., 2013).

However, the impact of BR on disease resistance is not always positive, as demonstrated by the inability of exogenous BL to alter resistance of *Arabidopsis* to *Pseudomonas syringae* pv. *tomato* (*Pto*) and *Alternaria brassicicola* (Albrecht et al., 2012). Moreover, two recent studies revealed that BL pre-treatment renders rice hypersusceptible to the root pathogens *Pythium graminicola* and *Meloidogyne graminicola*, unmasking BRs as potential negative regulators of plant immunity (De Vleesschauwer et al., 2012; Nahar et al., 2013). In the case of *P. graminicola*, it was even suggested that the pathogen hijacks the rice BR machinery to promote infection, thus exploiting BRs as virulence factors (De Vleesschauwer et al., 2012). More examples of BR effects on distinct plant–pathogen interactions are reviewed by Bajguz and Hayat (2009).

Together, these apparently conflicting findings clearly illustrate the importance of BR homeostasis in the establishment of plant immunity. Given the central importance of BRs in regulating plant size, these observations are compatible with the idea that BRs merge immune system function with normal growth and developmental programs, thus serving as important regulators of the innate trade-off between disease resistance and plant growth. Although initially seen as mainly positive players in disease resistance, the situation now seems more complicated with positive, negative as well as neutral BR effects being reported. Other plant hormones, such as SA, JA, and ET, can also have diverse effects on disease resistance and, for many pathosystems, the effectiveness of the SA/JA/ET pathways can be linked to the lifestyle of the invading pathogen (i.e. biotrophy, hemibiotrophy, and necrotrophy). In contrast, the effects of BR are seemingly independent of either the plant species or the type of pathogen involved, suggesting that BRs function as complex multifaceted regulators of plant immunity, with apparently divergent outcomes.

Molecular Mechanisms of BR-Mediated Immunity

Although much remains to be revealed about the precise mechanisms via which BRs dictate the output of plant–pathogen interactions, exciting new developments connect BRs to a wide variety of defense-related pathways involved in innate immunity triggered by conserved microbial signatures, microbial-induced cell death, hormone signaling, oxidative metabolism, and secondary metabolite production (Figure 1).

BRs Modulate the Efficiency of PAMP-Triggered Immunity

To date, most studies aimed at understanding how BR molds pathological outcomes have focused on the role of the LRR–RLK BAK1. Originally identified as a co-receptor for BRI1 and, hence, a positive regulator of BR responses, BAK1 appears to be positioned at the intersection of multiple signaling routes. Indeed, besides its role in BR signaling, BAK1 is also involved in the regulation of microbe-induced cell death (Kemmerling et al., 2007), and interacts physically with various pattern recognition receptors (PRRs), including the flagellin receptor FLS2, to drive so-called PAMP-triggered immunity (PTI) (Fradin et al., 2009; Bar et al., 2010; Chaparro-Garcia et al., 2011).

In view of this, it was long speculated that BR would either increase plant immunity through BAK1 activation or, alternatively, antagonize plant defenses through competition for BAK1. However, recent work by Albrecht et al. (2012) revealed that exogenously administered BR does not reinforce PTI responses in *Arabidopsis*, but instead unidirectionally antagonizes FLS2-mediated immune signaling (Albrecht et al., 2012; Belkhadir et al., 2012). Moreover, it was shown that BAK1 is not rate-limiting and that BR-controlled inhibition takes place downstream and independently of BAK1 by a so far unknown mechanism (Albrecht et al., 2012). Besides, null *bak1* mutants expressing the hypermorphic *bak1*^{elg} allele showed enhanced BR signaling but failed to mount resistance to *Pto* DC3000 upon treatment with the flagellin epitope flg22 (Jaillais et al., 2011). Another mutation in BAK1 (*bak1-5*) did not impair BR signaling, but compromised PTI signaling, resulting in hypersusceptibility to a weakly virulent *Pto* DC3000 mutant deficient in production of the phytotoxin coronatine (Schwessinger et al., 2011). This adds to the hypothesis that BAK1 pathway specificity is regulated by differential phosphorylation and extracellular domain interactions between receptor and co-receptor (Kemmerling et al., 2007; Oh et al., 2010; Jaillais et al., 2011; Schwessinger et al., 2011). Together with previous studies (Chinchilla et al., 2009), these data also suggest that BAK1 function in cell death control and innate immunity is independent of its function in BR signaling.

At the same time, recent findings by Belkhadir et al. (2012) point to a more complex scenario. By tuning the BR pathway response in *Arabidopsis*, these authors elegantly demonstrated that BR can act both antagonistically and synergistically with PTI responses. Conditions of excess and depleted endogenous BR content as well as increased BR signaling triggered by BRI1 overexpression all attenuated BAK1-mediated PTI, suggesting the existence of a narrow range of BR concentrations that prime innate immunity. In contrast, in plants expressing the hypermorphic *BRI1*^{sud1}

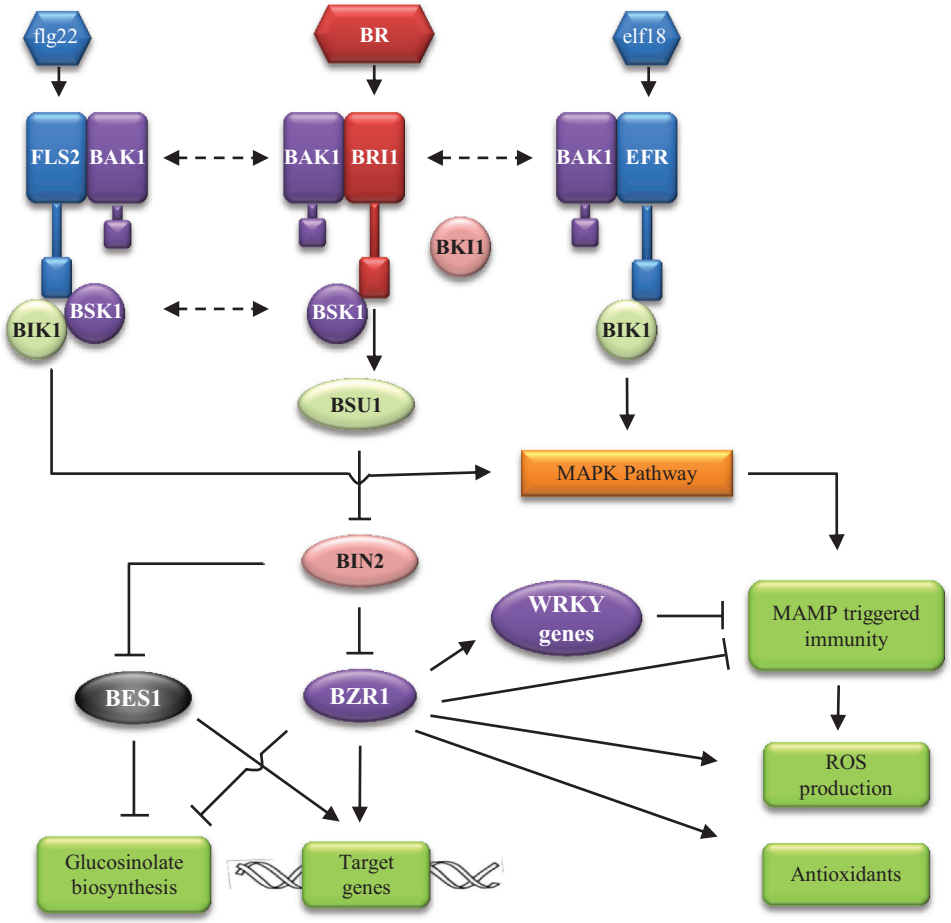

Figure 1 Model Illustrating Molecular Mechanisms by which BR Orchestrates Plant Disease Resistance.

The BR-signaling pathway is linked to PTI on three different levels by sharing the components BAK1 and BSK1 and via BZR1-steered negative regulation of PAMP-triggered immune responses. Downstream in the BR-signaling pathway, core TFs BES1 and BZR1 transduce the BR signal to the nucleus where they alter gene expression, regulate ROS and antioxidant production, and suppress glucosinolate biosynthesis.

allele, flg22-triggered PTI signaling was enhanced in a BAK1-dependent manner. Despite these enhanced PTI responses, *BRI1*^{sud1} plants displayed enhanced susceptibility to the obligate biotrophic pathogen *Hyaloperonospora arabidopsidis*, whereas the same slight increase in BR signaling enhanced resistance in *bak1* mutant plants. Overall, these data not only support a scenario wherein BAK1 acts as a mediator for the synergistic activities of BRs on PTI responses, but also indicate that BR can act on plant defenses independently of BAK1.

Interestingly, two recent papers have shed more light on the molecular mechanisms via which BR suppresses PTI responses in a BAK1-independent manner. In the first study, Lozano-Duràn et al. (2013) propose that BR antagonism of PTI happens downstream of BIN2 and that the key BR transcription factor BZR1 is required and sufficient for the suppression of PAMP-induced immune signaling. BZR1 activates several WRKY genes, which subsequently act as co- and secondary negative regulators of PAMP-triggered reactive oxygen species (ROS) production and gene expression, independently of MAPK signaling. The authors propose a model in which BZR1 and WRKY40 cooperate to down-regulate the expression of defense-related gene expression. The second study by Shi et al. (2013) focuses on the role of the BRI1-associated signaling kinase BSK1. Acting as a crucial BRI1 substrate in the BR-signaling pathway, BSK1 also serves as a positive regulator of flg22-induced ROS production and SA accumulation by physically interacting with FLS2. Moreover, inhibition of BSK1 increased susceptibility to both virulent and avirulent pathogens (Shi et al., 2013). Although this would imply that negative BR-PTI crosstalk may also occur upstream of BIN2, these findings suggest that competition for BSK1 between the BRI1 and FLS2 signaling pathways could add to the BAK1-independent negative effect of BR on the flg22-response.

Recently, the receptor-like cytoplasmic kinase Botrytis-Induced Kinase 1 (BIK1) was added to the list of signaling components shared by the BR and PTI pathways (Lin et al., 2013). Although BIK1 negatively regulates the BR-signaling pathway and positively regulates the FLS2–PTI signaling

pathway, its functions in both processes are mechanistically uncoupled. Consistently with FLS2–BIK1 complex dynamics in flagellin signaling, BIK1 associates with BRI1, and is released from the BRI1 receptor upon BR treatment. However, in contrast to BAK1-dependent FLS2–BIK1 dissociation, BAK1 is dispensable for BRI1–BIK1 dissociation. Moreover, unlike FLS2 signaling, which depends on BAK1 to phosphorylate BIK1, BRI1 directly phosphorylates BIK1 to transduce BR signaling. Thus, BIK1 relays the signaling in plant immunity and BR-mediated growth via distinct phosphorylation by BAK1 and BRI1, respectively.

BRs Orchestrate Crosstalk among Defense-Signaling Pathways

Associations between BR signaling and innate immunity have also been found in hormonal crosstalk, as reviewed by Choudhary et al. (2012). Following stress perception, BRs interact with a range of hormones, such as SA, JA, ABA, auxins, and GA. In many cases, the nature and direction of these hormone signal interactions can be rapidly adjusted, depending on the prevailing conditions, equipping the plant with a powerful regulatory mechanism to fine-tune its defense response to the type of stress encountered. This is nicely exemplified in rice where BRs enhance resistance to foliar pathogens in an SA-independent manner, yet, antagonize SA-mediated defenses to the root pathogen *P. graminicola* (Nakashita et al., 2003; De Vleesschauwer et al., 2012). Furthermore, several SA-marker genes were found to be induced upon BL treatment in *Arabidopsis*, raising the prospect of synergistic BR–SA crosstalk as well (Divi et al., 2010). In addition, BRs negatively interact with JA in the regulation of growth processes in *Arabidopsis* (Choudhary et al., 2012) and, accordingly, disable JA-induced resistance to the rice root knot nematode *M. graminicola* (Nahar et al., 2013). Interestingly, BRs can also cross-communicate with auxins. As auxins are well-known modulators of plant immunity, either directly or via crosstalk with the SA/JA signaling network, bidirectional BR-auxin interplay may also contribute to the ambivalent effects of BRs in disease and resistance (Choudhary et al., 2012; Pieterse et al., 2012). Finally, BRs also interact with GA. In the rice–*P. graminicola* interaction, for instance, BRs were shown to dampen effective immune responses by interfering at multiple levels with GA metabolism (De Vleesschauwer et al., 2012). Operating at both the level of biosynthesis regulation and signal transduction with BR suppressing GA biosynthesis and transcriptionally activating GA repressor genes, this BR–GA antagonism results in indirect stabilization of the rice DELLA protein and GA signaling inhibitor, SLR1 (De Vleesschauwer et al., 2012). More recent findings, however, indicate that crosstalk between BR and GA is also mediated by direct physical interactions between the BZR1 transcription factor and GA-inhibiting DELLA proteins (see below).

BRs Fine-Tune Oxidative and Secondary Metabolism

Evidence for yet another mode of BR action is provided by the ability of BRs to influence the production of ROS (Foreman et al., 2003; Almagro et al., 2009; Bajguz and Hayat, 2009; Xia et al., 2009; Swanson and Gilroy, 2010; Suzuki et al., 2012; Baxter et al., 2014). ROS are secondary messenger molecules generated during development and in response to stress that serve myriad functions, including the activation of phytoalexin biosynthesis and regulation of cell death. The involvement of BR in ROS and antioxidant production and the interplay between BR signaling and ROS signaling is ambiguous. A narrow range of BR concentrations stimulate ROS production by membrane-bound NADPH oxidases, and BR-induced ROS production has been shown to be central in the establishment of stress tolerance (Xia et al., 2010). However, depending on hormone titers, plant age, and the type of tissue, BRs can also stimulate antioxidant production and scavenge ROS (Bajguz and Hayat, 2009; Fariduddin et al., 2013). Finally, BRs may also influence disease resistance by modulating secondary metabolite production, as evidenced by the repressive effect of BZR1 and BES1 on glucosinolate production in *Arabidopsis* (Guo et al., 2013).

In summary, consistently with the apparent multifaceted role of BR in determining the outcome of plant–pathogen interactions, the above-mentioned studies have revealed a wide variety of underpinning mechanisms, ranging from modulation of PAMP perception to downstream signaling and orchestration of oxidative metabolism and production of secondary metabolites. Although the importance of BR in the regulation of plant immunity is evident, the precise mechanism(s) involved and its role in either stimulating disease resistance or susceptibility appears to depend greatly on the plant–attacker combination, indicating that the function of plant growth hormones in pathogen defense cannot easily be generalized. In the upcoming sections, we attempt to distill current literature on the immune-regulatory role of another class of phytohormones, GAs, and highlight how these master growth regulators participate in influencing disease outcomes.

GA AND DELLA PROTEINS: NOVEL MASTER REGULATORS OF PLANT IMMUNITY

GAs: Pivotal Growth Regulators and Architects of the First Green Revolution

Gibberellins (GAs) are tetracyclic diterpenoid plant hormones that act at all stages in the plant life cycle by promoting germination, hypocotyl elongation, root, leaf, stem and fruit growth, greening of leaves, flowering, and flower and seed

development (Hauvermale et al., 2012). The origin of research into GAs can be traced back to Japanese plant pathologists in the late 1800s that were studying a devastating rice disease referred to as 'bakanae' (foolish seedling). Symptoms of the disease included excessive seedling elongation, slender leaves, and stunted roots. In 1938, Yabuta and his associate Yusuke Sumiki tied the elongation of bakanae rice to a substance derived from the fungal pathogen *Gibberella fujikuroi* (teleomorph: *Fusarium moniliforme*) and named the compound after the pathogen it was isolated from: gibberellin.

Although it was not until the mid-1950s that researchers became aware of GAs as naturally occurring substances in higher plants, the involvement of GAs in determining plant stature has since revolutionized modern agriculture. During the first Green Revolution, breeding programs capitalized on increasing crop productivity by selecting semi-dwarf varieties that responded well to nitrogen fertilization without lodging and displayed increased partitioning of assimilates into grains (Khush, 2001). It was subsequently discovered that most Green Revolution varieties harbored mutations affecting GA synthesis. These mutants include the 'miracle' rice line IR8, which produced record yields throughout Asia and was found to contain a defective GA20 oxidase gene (Monna et al., 2002; Sasaki et al., 2002; Spielmeyer et al., 2002). Through extensive physiological and molecular genetic studies of mutant plants impaired in GA perception, biosynthesis, or signaling, it is now clear that GAs are master regulators of plant growth, particularly in response to environmental conditions such as light, flooding, temperature and salt, and biotic stress (Claeys et al., 2013; Colebrook et al., 2014).

GA Signaling in Plants: Of Molecular Glue and DELLA Repression

As with BRs, research over the past few years has uncovered the principal steps associated with GA perception and signal transduction in *Arabidopsis* and rice. According to the canonical GA signaling model, GA promotes plant growth and development by inducing the degradation of DELLAs, a class of nuclear growth-repressing proteins. In rice, binding of GA to the soluble GA receptor GID1 causes the GID1 N-terminal lid domain to act as molecular glue and interact with the single DELLA protein, SLENDER RICE 1 (SLR1) (Ueguchi-Tanaka et al., 2007; Murase et al., 2008). Subsequently, the stabilized trimeric complex consisting of GA, GID1, and SLR1 is targeted for polyubiquitination by the F-box protein GID2, which leads to rapid degradation of SLR1 by the 26S proteasome and resultant relief of the SLR1-imposed growth restraint (Gao et al., 2011). A similar yet more complicated pathway is operative in *Arabidopsis* with three GA receptors (GID1a, GID1b, and GID1c), five DELLA proteins (RGA, GAI, RGL1, RGL2, and RGL3), and the F-box protein SLY1 (Hauvermale et al., 2012).

Implications of GA and DELLAs in Basal Defense and Disease Susceptibility

Despite being first discovered in a fungal plant pathogen, GAs and their signaling components have only recently been implicated in plant responses to pathogen attack. Among the first to suggest a role for GA in plant immunity were Zhu et al. (2005), who reported that the outer capsid protein P2 of the rice dwarf virus interacts with plant ent-kaurene oxidases, leading to decreased GA levels in the infected plants.

However, GA-related immunity research failed to gain momentum until it was shown that *Arabidopsis* mutants lacking four of the five DELLAs exhibited high levels of SA-dependent resistance when challenged with the hemibiotrophic pathogen *P. syringae* (Navarro et al., 2008). In contrast, quadruple DELLA mutants showed attenuated induction of the JA-reporter gene *PDF1.2*, which correlated with enhanced susceptibility against the necrotrophic fungus *Alternaria brassicola* (Navarro et al., 2008). On the basis of these and other findings, it has been contemplated that DELLAs modulate the balance of SA/JA signaling during plant immunity, promoting JA perception and/or signaling, and repressing SA biosynthesis and signaling (Navarro et al., 2008). This ambivalent role of DELLAs also seems well conserved in monocot species as experiments with defined wheat and barley lines differing in DELLA status revealed a similar resistance trade-off with increased susceptibility to biotrophs and enhanced resistance to necrotrophs (Saville et al., 2012).

In rice, strikingly different results have been obtained in that exogenously administered GA was found to lower resistance to the hemibiotrophic rice pathogens *Magnaporthe oryzae* (*Mo*) and *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) (Yang et al., 2008; Qin et al., 2013). Moreover, transgenic rice overexpressing Elongated Uppermost Internode (EUI), a GA deactivating enzyme, accumulated low levels of GA and SA and displayed enhanced resistance to *Mo* and *Xoo*, whereas loss-of-function mutations in EUI were more vulnerable to these pathogens (Yang et al., 2008). These phenotypes and additional analyses of rice mutants compromised in GA perception or synthesis suggest that GA impairs (hemi)biotroph resistance in rice (Tanaka et al., 2006; Qin et al., 2013). However, GA can also act positively on rice immunity as shown for the necrotrophic rice root rot pathogen *P. graminicola* (De Vleesschauwer et al., 2012). Therefore, in contrast with the situation in *Arabidopsis*, barley, and wheat, rice GA signaling appears to promote resistance to necrotrophs and susceptibility to (hemi)biotrophs.

Emerging from these studies is the view that GAs play ambiguous roles in the plant innate immune signaling network. In some cases, they contribute to the development of disease symptoms, whereas in other cases they are required for defense responses and induction of plant resistance.

Much like BRs and the classic defense hormones SA, JA, and ET, GAs thus seem to behave as multifaceted regulators of plant immunity, the effect of which may differ not only on the plant species and type of pathogen involved, but also on specialized features of each interaction.

Mechanisms of GA- and DELLA-Mediated Plant Immunity

Whilst offering a first insight into the immune-regulatory role of GA and DELLAs, most of above-mentioned reports have only scratched the surface and much remains to be learned about the precise mechanisms via which GA and DELLAs modulate plant immunity. However, fueled by large-scale proteomic analyses and recent advances in computational biology, exciting new progress is now beginning to unveil the molecular secrets of GA and DELLA protein action.

GA and DELLAs Contribute to Fine-Tuning of ROS Production

Although earlier studies provided circumstantial evidence connecting GA to the regulation of phytoalexin biosynthesis and the expression of pathogenesis-related proteins (Zhu et al., 2005; Tanaka et al., 2006), Achard et al. (2008) made a first inroad into the molecular underpinnings of GA-mediated immunity by showing that DELLAs modulate ROS production during periods of adversity. In contrast with GA-induced oxidative stress (Fath, 2001; Schopfer, 2001), DELLAs elevate the induction of genes involved in ROS detoxification, thus reducing ROS levels and restraining plant cell death. Upon attack by a necrotrophic pathogen, such DELLA-mediated cell death restriction contributes to enhanced disease resistance, as was shown for the gray mold pathogen *Botrytis cinerea* and the mutualist fungus *Piriformospora indica* (Achard et al., 2008; Jacobs et al., 2011). Implicit here is the view that necrotrophic pathogens such as *G. fujikuroi* exploit GAs as virulence factors to degrade DELLAs and establish host susceptibility, not only by interfering with SA/JA-dependent defenses as described above, but also by tilting the ROS-controlled life-or-death balance towards death. Moreover, considering the intricate interaction of ROS and SA in a self-amplifying system (Shirasu et al., 1997), it has been hypothesized that attenuation of SA signaling by DELLAs results, at least in part, from diminishing ROS levels (Grant and Jones, 2009).

GA Signaling Orchestrates Cell Wall Development and Modifies Carbon and Energy Metabolism

Plant defense is a highly energy-intensive process (Bolton, 2009). Although pathogen recognition and downstream immune signaling have been intensively studied, the question of how plants are able to recruit energy to fuel defense responses has received only scant attention. Mounting evidence, however, indicates that large carbon and nitrogen fluxes into secondary metabolism during the immune response cannot occur without influencing reactions in primary metabolism (Bolton, 2009; Seifi et al., 2013a, 2013b).

Noteworthy in this respect is a recent study that investigated the effect of GA on carbon and energy metabolism during rosette growth in *Arabidopsis* (Ribeiro et al., 2012). Combined metabolite profiling and translational analyses revealed that low GA regimes modulate global changes in primary metabolism, thereby uncoupling growth from carbon availability. Likewise, overexpressing gain-of-function versions of the *Arabidopsis* DELLA proteins GAI and RGL1 in transgenic poplar trees had profound consequences on cellular metabolism, suggesting increased respiration in roots and reduced carbox flux through the lignin biosynthetic pathway in shoots as well as a shift towards defense compounds associated mainly with the phenylpropanoid pathway (Busov et al., 2006). By analogy with auxin-mediated disease susceptibility (Zhang et al., 2007), GA may thus modify plant metabolism profiles, resulting in decreased production of antimicrobial compounds or increased nutrient efflux favoring microbes.

Interestingly, GA-induced metabolism changes may also result in cell wall modification, the role of which in plant immunity is well documented (Nishimura et al., 2003; Hernandez-Blanco et al., 2007; Curvers et al., 2010). GA and DELLA have long been known to respectively induce and repress cell wall relaxation by altering the expression of xyloglucan endotransglucosylase/endohydrolases (XTHs) and expansins (Ogawa, 2003; Gallego-Bartolomé et al., 2011; Park et al., 2013). Although loosening the cell wall is a vital process during growth and development, it may also render the plant more vulnerable to biotic intruders by facilitating pathogen entry or allowing enhanced nutrient leakage. Indeed, recent evidence showed that rice plants overexpressing expansin genes become more vulnerable to *Xoo* and *Mo*, two pathogens that exploit GAs as virulence factors and are sensitive to DELLA-mediated defenses (Tanaka et al., 2006; Ding et al., 2008; Yang et al., 2008; Fu et al., 2011). These findings raise the possibility that DELLAs may induce disease resistance, at least in part, by counteracting pathogen-induced cell wall disturbance.

DELLAs Mediate Stress-Induced Cell Differentiation and Direct Immunity-Associated Changes in Plant Cytoskeleton Architecture

Cell divisions, including meiosis, mitosis, and endoreduplication, are essential processes for both vegetative and reproductive development in plants. The anaphase-promoting complex/cyclosome (APC/ C) is an evolutionarily conserved E3 ubiquitin ligase critical for cell cycle progression by

degrading cell cycle proteins (Inzé and De Veylder, 2006). A recent study by Bao et al. (2013) revealed an unexpected effect of APC/C activity on plant immunity by showing that deregulation of two negative APC/C regulators, *OSD1* and its homolog *UVI4*, is associated with activation of disease resistance genes and enhanced immunity to *Pto* (Bao et al., 2013). Interestingly, *UVI4* was also found to be down-regulated following DELLA stabilization, resulting in mitotic exit and onset of endoreduplication (Claeys et al., 2013). While the causality of DELLA stabilization on plant disease resistance is by no means clear, these findings suggest a potential role of DELLAs in plant immunity by interfering with cell cycle-dependent expression of immunity genes.

In a similar vein, DELLAs have recently also been found to control plant cytoskeleton dynamics by physically interacting with the prefoldin complex, a cochaperone required for tubulin folding (Locascio et al., 2013). In the absence of GA, the prefoldin complex interacts with DELLAs in the nucleus, which severely compromises alpha/beta-tubulin heterodimer availability, affecting microtubule organization. In the presence of GA, however, DELLAs are degraded, which keeps the complex in an active state in the cytosol. Particularly interesting in this regard is a series of recent studies unmasking the cytoskeleton as a dynamic platform for sensing and responding to a diverse array of fungal, bacterial and oomyceteous pathogens (Tian et al., 2009; Lee et al., 2012; Porter et al., 2012; Henty-Ridilla et al., 2013). With transient increases in actin filament density being unveiled as an important contributing factor during PTI (Henty-Ridilla et al., 2013), elucidating whether DELLA-mediated plant immunity involves perturbation of cell cycle regulation is an important challenge ahead.

Straddling the Line: DELLA–JAZ Interactions Balance Plant Growth and Defense

Although the above-mentioned studies also implicate a non-transcriptional mode of action, DELLAs are generally thought of as transcriptional regulators. Yet, the lack of known DNA-binding domains and the moderate enrichment of promoter targets determined by chromatin immunoprecipitation (Zentella et al., 2007; Hauvermale et al., 2012) suggest that DELLAs require additional factors to exert transcriptional activity. In compliance with this concept, DELLAs were recently shown to physically interact with Switch (SWI)/Sucrose Nonfermenting (SNF)-type chromatin-remodeling complexes responsible for modulation of chromatin structure (Sarnowska et al., 2013). Moreover, it is becoming increasingly clear that DELLAs orchestrate growth and developmental processes through direct protein interaction with multiple TF targets. For example, DELLAs mediate hypocotyl elongation by interacting with Phytochrome Interacting Factors (PIFs) (de Lucas et al., 2008; Feng et al., 2008; Gallego-Bartolomé et al., 2010; Hauvermale et al., 2012), and they control floral transition and fruit patterning by respectively binding to Squamosa Promoter Binding-Like (SPL) and Alcatraz (ALC) factors (Arnaud et al., 2010; Yu et al., 2012).

In a similar vein, several lines of evidence suggest that DELLAs modulate plant immunity via competitive binding to JA ZIM-domain (JAZ) proteins, a family of JA signaling repressors (Hou et al., 2010; Wild et al., 2012; Yang et al., 2012). JAZ proteins bind and inhibit the activity of a wide array of TFs, including the key JA transcriptional activator MYC2 (Kazan and Manners, 2012, 2013). Recently, three groups have shown that DELLAs compete with MYC2 for binding to JAZs, thereby releasing free MYC2 to activate JA-responsive gene expression and enhance resistance to necrotrophic pathogens (Navarro et al., 2008; Hou et al., 2010; Wild et al., 2012; Yang et al., 2012). In the presence of GA, however, DELLAs are rapidly degraded, leading to inhibitory JAZ–MYC2 interactions and disruption of JA signaling (Figure 2). This so-called 'relief of repression' model not only elegantly explains how plants mediate the balance between growth and defense, but also offers novel insights into how GA may disable JA-mediated pathogen resistance by degrading DELLAs and releasing JAZs to bind and inhibit MYC2 (Navarro et al., 2008; Hou et al., 2010).

Interestingly, MYC2 can also modulate the level of the DELLA protein RGL3. Unlike other DELLAs, *RGL3* is induced by JA in a MYC2-dependent fashion. In turn, JA-induced RGL3 interacts with JAZs and releases MYC2 to enhance JA-responsive gene expression (Wild et al., 2012). Therefore, DELLAs seem to positively regulate JA responses not only through blocking JAZ repressor action, but also through acting directly as JA-responsive regulators. Importantly, phenotypic analyses revealed that the *rgl3-5* mutant exhibits enhanced susceptibility to the necrotroph *Botrytis cinerea* and increased susceptibility to the hemibiotroph *Pto*, demonstrating the biological significance of this mechanism. Moreover, the finding that *RGL3* expression is strongly induced by *Pto* but not by a mutant strain defective in production of coronatine, a JA-mimicking phytotoxin, raises the possibility that pathogens co-opt the JA pathway to modulate DELLA expression *in planta* (Wild et al., 2012).

The Spider in the Web: Do DELLAs Act as a Nexus for Pathway Crosstalk and Signal Integration?

Together, the above-mentioned studies clearly establish the importance of DELLA in the regulation of JA–GA crosstalk and the conflicting association between plant growth and defense. However, this may not be the end of the story, as rapidly accumulating evidence suggests that DELLAs serve as main hubs within an intricate signaling network, integrating, transmitting, and processing multiple environmental signals and developmental cues (Hauvermale et al., 2012; Kazan and Manners, 2012; Hou et al., 2013).

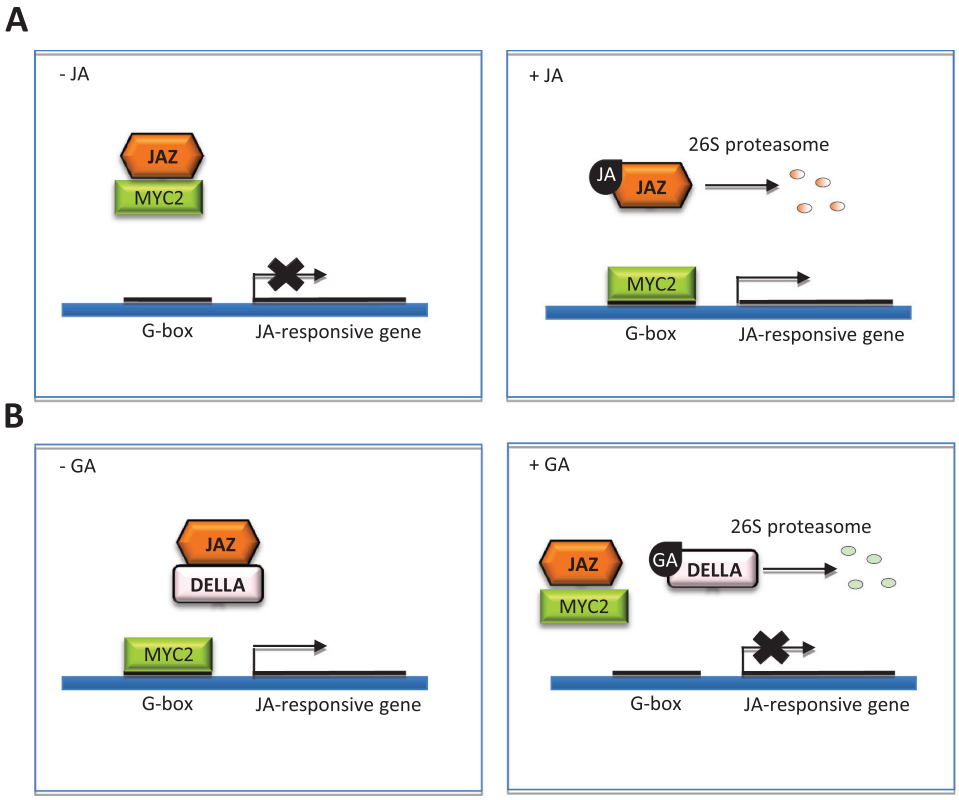

Figure 2 'Relief of Repression' Model Illustrating how DELLA–JAZ Interactions Orchestrate JA Signaling.

(A) In the absence of JA, stabilized JAZs sequester and inhibit the JA transcriptional activator MYC2, thereby preventing JA-responsive gene expression. JA promotes degradation of JAZs by the 26S proteasome, thus releasing free MYC2 to trigger expression of JA-responsive genes via binding to G-box motifs.

(B) Without GA, stabilized DELLAs compete with MYC2 for binding to JAZs, which in turn liberates MYC2 to activate JA-responsive genes. In the presence of GA, DELLAs are rapidly degraded, enabling JAZs to bind MYC2 and block JA signaling output.

Because of their well-studied growth-repressing properties and their accumulation in response to biotic and abiotic stresses (Achard et al., 2006, 2008; Navarro et al., 2008), DELLA proteins have long been hypothesized to act at the interface of developmental, physiological, and stress signaling. In support of this assumption, a large body of data indicates that DELLAs lie at the node of multiple hormone signaling pathways. The effect of GA on DELLA is probably the most important and the most direct; however, several other hormones have been shown to regulate plant growth by affecting DELLA levels. Auxin, for instance, is well known to promote root growth by triggering GA-induced DELLA proteolysis, whereas JA, ABA, cytokinin, and ET all enhance DELLA stabilization, and delay its degradation by GA (Fu and Harberd, 2003; Vriezen et al., 2004; Brenner et al., 2005; Achard et al., 2007; Wild et al., 2012; Yang et al., 2012). Moreover, DELLA may also serve as a point of integration of hormone and metabolite signaling based on recent findings that sucrose, but not glucose, stabilizes DELLA to repress growth and induce anthocyanin biosynthesis in *Arabidopsis* (Li et al., 2013).

Other than harmonizing signals from multiple upstream effectors, DELLAs also interact with a variety of regulatory TFs, thus controlling the expression of a multitude of genes functioning in myriad cellular activities and biological processes (de Lucas et al., 2008; Feng et al., 2008). Thus far, most attention has been paid to the above-mentioned DELLA–JAZ interaction and its role in orchestrating GA–JA signal interactions. However, with an increasing number of TFs and other proteins being identified as binding targets of JAZs, JAZ proteins appear to be main hubs for orchestrating not only multiple JA downstream processes, but also the interplay between JA and many other phytohormones, including SA, ET, ABA, and GA (Qi et al., 2011; Song et al., 2011; Kazan and Manners, 2012). Therefore, interactions with single JAZ proteins may enable DELLA to tap into multiple hormone signaling pathways and control the outcome of multidimensional signal interactions.

Interestingly, three recent studies have revealed similar interactions with the key BR-regulatory TF BZR1, further diversifying DELLA's functional portfolio. Analogous to the mechanism described for JAZs and PIFs, DELLAs sequester

BZR1 into inactive protein complexes, thereby inhibiting its DNA-binding activity and ultimately blocking BR signal transduction (Bai et al., 2012; Gallego-Bartolomé et al., 2012; Li et al., 2012). In addition, large-scale chip–chip experiments have identified a few thousand BZR1 targets, including numerous defense-related proteins such as the flg22 receptor *FLS2*, as well as PIF4, a dark- and heat-activated TF which together with BZR1 controls a central transcription network involved in cell elongation and seedling photomorphogenesis (Sun et al., 2010; Yu et al., 2011; Oh et al., 2012). Through its ability to inhibit BZR1 and PIF4 individually and target the BZR1–PIF4 heterodimer, DELLA also impinges on this core transcription module, thereby enabling coordinated regulation of growth and development by GA, BR, temperature, and light signals (Bai et al., 2012).

In summary, the emerging roles of BZR1, PIFs, and JAZs as coordinators of a wide network of (hormone) signaling crosstalk illustrate the functional versatility of these proteins. Considering the intricate interconnection of DELLAs with each of these regulators, it is tempting to speculate that the balance of DELLA–BZR1/PIF/MYC2 interaction acts as a central command system that integrates responses from independent hormones and signals of adverse conditions, permitting flexible and appropriate modulation of plant growth and defense in response to diverse stimuli. Moreover, considering the combinatorial diversity in DELLA–MYC2/PIF/BZR1 interactions and the ability of each protein to control a vast array of both common and unique target genes, this decision module may not only accept different inputs, but also send out branched outputs. In Figures 3 and 4, we propose a model for how dynamic DELLA–TF interactions may fine-tune the interplay and balance of plant defense and growth responses mounted through multiple signaling pathways in the model plants *Arabidopsis* and rice.

CONCLUSIONS AND FURTHER PERSPECTIVES

Contrary to the relative wealth of information on how BR and GA are perceived and their signals transduced, their role and significance in the regulation and integration

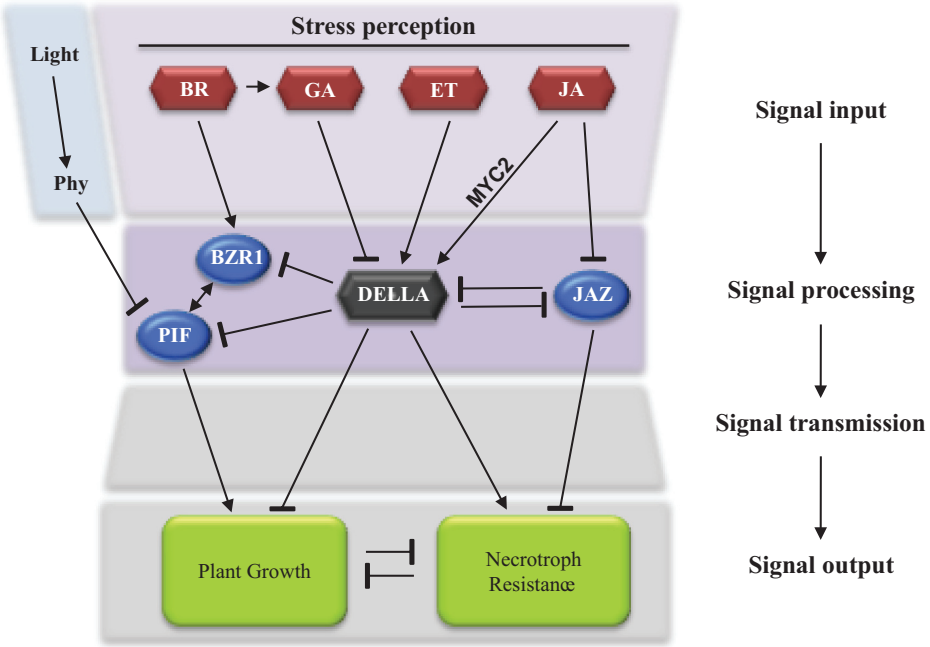

Figure 3 Model Describing how the PIF–BZR1–DELLA–JAZ Decision Module Integrates and Processes Various Environmental and Developmental Cues to Balance Plant Growth and Defense to Necrotrophic Pathogens in *Arabidopsis thaliana*.

Perception of environmental stress signals triggers asymmetric activation of phytochrome (Phy), BR, GA, ET, and JA signaling to modulate the levels of PIFs, BZR1, DELLAs, and JAZs, respectively. BZR1 and PIFs form a functional complex that regulates large suites of genes contributing to cell growth, whereas JAZ proteins bind and inhibit numerous TF targets to suppress JA-induced processes, including resistance to necrotrophic pathogens. DELLAs, on the other hand, physically interact with BZR1, PIFs, and JAZs to inhibit their DNA-binding ability and, hence, block their transcription activity. We propose that the dynamic nature and balance of DELLA–TF interactions act as a central rheostat, enabling plants to flexibly tailor the allocation of limited resources into growth and/or defense responses.

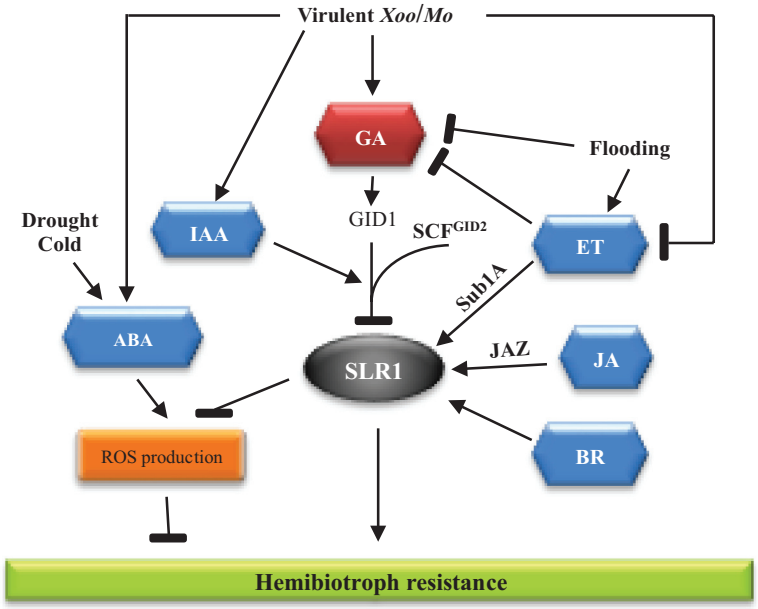

Figure 4 The DELLA Protein SLR1 Coordinates and Adjusts Interplay between Environmental and Phytohormonal Signals to Shape the Immune Response of Rice (*Oryza sativa*).

In contrast with DELLA-mediated necrotroph resistance in *Arabidopsis*, SLR1 mounts resistance to (hemi)biotrophic rice pathogens such as the blast fungus *Magnaporthe oryzae* (*Mo*) and the bacterial leaf blight pathogen *Xanthomonas oryzae* pv. *oryzae* (*Xoo*). The model provides a mechanistic framework for abiotic stress (ABA)-induced susceptibility (Koga et al., 2004; Jiang et al., 2010) to *Xoo* and *Mo*, as well as for immunity triggered by JA (Mei et al., 2006; Riemann et al., 2013), BR (Nakashita et al., 2003), and/or flooding-induced ET (Singh et al., 2004), but also may explain how virulent strains of *Mo* and *Xoo* can attenuate SLR1-orchestrated immunity by hijacking the GA and/or IAA machinery in order to promote GID2-mediated degradation of SLR1 by the 26S proteasome (Ding et al., 2008; Domingo et al., 2009; Fu et al., 2011). Manipulation of ABA signaling by *Xoo* and *Mo* was shown by Xu et al. (2013) and Jiang et al. (2010), respectively. Blunt lines indicate antagonistic interactions; arrowheads depict positive interactions. GA, gibberellic acid; IAA, indole acetic acid; ABA, abscisic acid; ET, ethylene; JA, jasmonic acid; BR, brassinosteroids; ROS, reactive oxygen species.

of plant immune responses have long been ignored. Emerging from the studies reviewed here is a complex picture whereby GA and BR play a widespread and ambivalent role in plant defense, acting as either positive or negative regulators of disease resistance by interfering at multiple levels with biotic stress signaling cascades. Moreover, exciting new developments suggest that a number of GA/BR-regulatory elements such as DELLAs and BZR1 constitute central nodes within the hard wiring of the plant's signaling network. Situated at the interface of developmental and defense signaling, these proteins likely serve as main hubs for pathway crosstalk and signal integration, allowing flexible and appropriate modulation of plant growth and defense in response to various endogenous and exogenous cues.

Despite these paradigm-shifting advances, our understanding of precisely how BR and GA impact plant innate immunity is still lagging far behind that of the classic defense hormones SA, JA, and ET. For instance, there is little if no information available about the spatiotemporal dynamics of BR and GA during a given plant–microbe interaction, the dynamics and stability of DELLA and BZR1 protein complexes in response to pathogen attack remain elusive, and there is still much to be learned about the function and action of many of the downstream DELLA/BZR1 target genes. In addition, there is a paucity of knowledge on the causality of DELLA stabilization on disease resistance and it remains to be tested whether the temporal oscillation of DELLA accumulation and BR synthesis may contribute to the circadian rhythm of plant immunity (Arana et al., 2011; Wang et al., 2011; Belkhadir et al., 2012).

Moreover, it will be very interesting to assess whether GA and BR signaling are sites of manipulation by pathogens during infection. Although unequivocal evidence is still lacking, several authors have suggested that pathogens may deploy specific effectors to modify the host's GA and BR homeostasis for their own advantage (Shan et al., 2008; De Vleesschauwer et al., 2012). In addition, plant pathogens may produce GA or BR themselves to trick the plant into activating inappropriate responses. Genome sequencing of the obligate biotroph *Albugo laibachii*

revealed the presence of a near-complete BR biosynthesis pathway (Kemen et al., 2011), while several *Fusarium* species are known to produce toxins that resemble brassinosteroids (Robert-Seilaniantz et al., 2007). Furthermore, several fungal and bacterial species synthesize GA or GA-like compounds that are chemically similar to plant GAs and have similar effects on plant physiology (Bottini et al., 2004; Kawaide, 2006). Since pathogens that are deficient in hormone production do not display a strong growth phenotype, it is tempting to speculate that pathogens produce BR and GA or mimics thereof to tap into the plant's defense-signaling network and subdue host immunity.

In conclusion, despite significant progress made over recent years, we are only just beginning to understand the immune-regulatory roles of BR and GA. Given their apparent pluriform function in plant disease and resistance, unraveling the complexity of BR- and GA-modulated disease resistance will prove a hard nut to crack. However, elucidating the molecular mechanisms via which GA and BR interact with and feed into the plant immune network will not only advance our fundamental understanding of how plants integrate and balance immune system function and normal growth signals in response to the environment, but, ultimately, also will be instrumental in developing novel strategies for biologically based, environmentally friendly, and durable disease control in various agricultural settings.

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REFERENCES

Achard, P., Baghour, M., Chapple, A., Hedden, P., Van Der Straeten, D., Genschik, P., Moritz, T., and Harberd, N.P. (2007). The plant stress hormone ethylene controls floral transition via DELLA-dependent regulation of floral meristem-identity genes. Proc. Natl Acad. Sci. U S A. **104**, 6484–6489.

Achard, P., Cheng, H., De Grauwe, L., Decat, J., Schoutteten, H., Moritz, T., Van Der Straeten, D., Peng, J., and Harberd, N.P. (2006). Integration of plant responses to environmentally activated phytohormonal signals. Science. **311**, 91–94.

Achard, P., Renou, J.-P., Berthomé, R., Harberd, N.P., and Genschik, P. (2008). Plant DELLAs restrain growth and promote survival of adversity by reducing the levels of reactive oxygen species. Curr. Biol. **18**, 656–660.

Albrecht, C., Boutrot, F., Segonzac, C., Schwessinger, B., Gimenez-Ibanez, S., Chinchilla, D., Rathjen, J.P., de Vries, S.C., and Zipfel, C. (2012). Brassinosteroids inhibit pathogen-associated molecular pattern-triggered immune signaling independent of the receptor kinase BAK1. Proc. Natl Acad. Sci. U S A. **109**, 303–308.

Ali, S.S., Kumar, G.B.S., Khan, M., and Doohan, F.M. (2013). Brassinosteroid enhances resistance to fusarium diseases of barley. Phytopathology. **103**, 1260–1267.

Almagro, L., Gómez Ros, L.V., Belchi-Navarro, S., Bru, R., Ros Barceló, A., and Pedreño, M.A. (2009). Class III peroxidases in plant defence reactions. J. Exp. Bot. **60**, 377–390.

Arana, M.V., Marin-de-la Rosa, N., Maloof, J.N., Blazquez, M.A., and Alabadi, D. (2011). Circadian oscillation of gibberellin signaling in *Arabidopsis*. Proc. Natl. Acad. Sci. U S A. **108**, 9292–9297.

Arnaud, N., Girin, T., Sorefan, K., Fuentes, S., Wood, T.A., Lawrenson, T., Sablowski, R., and Østergaard, L. (2010). Gibberellins control fruit patterning in *Arabidopsis thaliana*. Genes Dev. **24**, 2127–2132.

Asselbergh, B., De Vleesschauwer, D., and Höfte, M. (2008). Global switches and fine-tuning: ABA modulates plant pathogen defense. Mol. Plant Microbe Interact. **21**, 709–719.

Bai, M.Y., Shang, J.X., Oh, E., Fan, M., Bai, Y., Zentella, R., Sun, T.P., and Wang, Z.Y. (2012). Brassinosteroid, gibberellin and phytochrome impinge on a common transcription module in *Arabidopsis*. Nat. Cell Biol. **14**, 810–817.

Bajguz, A. (2007). Metabolism of brassinosteroids in plants. Plant Physiol. Biochem. **45**, 95–107.

Bajguz, A., and Hayat, S. (2009). Effects of brassinosteroids on the plant responses to environmental stresses. Plant Physiol. Biochem. **47**, 1–8.

Bao, Z., Yang, H., and Hua, J. (2013). Perturbation of cell cycle regulation triggers plant immune response via activation of disease resistance genes. Proc. Natl Acad. Sci. U S A. **110**, 2407–2412.

Bar, M., Sharfman, M., Ron, M., and Avni, A. (2010). BAK1 is required for the attenuation of ethylene-inducing xylanase (Eix)-induced defense responses by the decoy receptor LeEix1. Plant J. **63**, 791–800

Bari, R., and Jones, J. (2009). Role of plant hormones in plant defence responses. Plant Mol. Biol. **69**, 473–488.

Baxter, A., Mittler, R., and Suzuki, N. (2014). ROS as key players in plant stress signalling. J. Exp. Bot. **65**, 1229–1240.

Belkhadir, Y., Jaillais, Y., Epple, P., Balsemão-Pires, E., Dangl, J.L., and Chory, J. (2012). Brassinosteroids modulate the efficiency of plant immune responses to microbe-associated molecular patterns. Proc. Natl Acad. Sci. U S A. **109**, 297–302.

Bolton, M.D. (2009). Primary metabolism and plant defense: fuel for the fire. Mol. Plant. Microbe. Interact. **22**, 487–497.

Bottini, R., Cassán, F., and Piccoli, P. (2004). Gibberellin production by bacteria and its involvement in plant growth promotion and yield increase. Appl. Microbiol. Biotechnol. **65**, 497–503.

Brenner, W.G., Romanov, G.A., Köllmer, I., Bürkle, L., and Schmülling, T. (2005). Immediate-early and delayed cytokinin response genes of *Arabidopsis thaliana* identified by genome-wide expression profiling reveal novel cytokinin-sensitive processes and suggest cytokinin action through transcriptional cascades. Plant J. **44**, 314–333.

Busov, V., Meilan, R., Pearce, D.W., Rood, S.B., Ma, C., Tschaplinski, T.J., and Strauss, S.H. (2006). Transgenic modification of gai or rgl1caus es dwarfing and alters gibberellins, root growth, and metabolite profiles in *Populus*. Planta. **224**, 288–299.

Cao, F.Y., Yoshioka, K., and Desveaux, D. (2011). The roles of ABA in plant–pathogen interactions. J. Plant Res. **124**, 489–499.

Chaparro-Garcia, A., Wilkinson, R.C., Gimenez-Ibanez, S., Findlay, K., Coffey, M.D., Zipfel, C., Rathjen, J.P., Kamoun, S., and Schornack, S. (2011). The receptor-like kinase SERK3/BAK1 is required for basal resistance against the late blight pathogen phytophthora infestans in *Nicotiana benthamiana*. PLoS One. **6**, e16608.

Chinchilla, D., Shan, L., He, P., de Vries, S., and Kemmerling, B. (2009). One for all: the receptor-associated kinase BAK1. Trends Plant Sci. **14**, 535–541.

Choi, J., Choi, D., Lee, S., Ryu, C.M., and Hwang, I. (2011). Cytokinins and plant immunity: old foes or new friends? Trends Plant Sci. **16**, 388–394.

Choudhary, S.P., Yu, J.-Q., Yamaguchi-Shinozaki, K., Shinozaki, K., and Tran, L.-S.P. (2012). Benefits of brassinosteroid crosstalk. Trends Plant Sci. **17**, 594–605.

Claeys, H., De Bodt, S., and Inzé, D. (2013). Gibberellins and DELLAs: central nodes in growth regulatory networks. Trends Plant Sci., 29 October, 10.1016/j.tplants.

Clouse, S.D. (2011). Brassinosteroid signal transduction: from receptor kinase activation to transcriptional networks regulating plant development. Plant Cell. **23**, 1219–1230.

Colebrook, E.H., Thomas, S.G., Phillips, A.L., and Hedden, P. (2014). The role of gibberellin signalling in plant responses to abiotic stress. J. Exp. Bot. **217**, 67–75.

Curvers, K., Seifi, H., Mouille, G., de Rycke, R., Asselbergh, B., Van Hecke, A., Vanderschaeghe, D., Höfte, H., Callewaert, N., Van Breusegem, F., et al. (2010). Abscisic acid deficiency causes changes in cuticle permeability and pectin composition that influence tomato resistance to *Botrytis cinerea*. Plant Physiol. **154**, 847–860.

De Lucas, M., Davière, J.-M., Rodríguez-Falcón, M., Pontin, M., Iglesias-Pedraz, J.M., Lorrain, S., Fankhauser, C., Blázquez, M.A., Titarenko, E., and Prat, S. (2008). A molecular framework for light and gibberellin control of cell elongation. Nature. **451**, 480–484.

De Vleesschauwer, D., Gheysen, G., and Höfte, M. (2013). Hormone defense networking in rice: tales from a different world. Trends Plant Sci. **10**, 555–565.

De Vleesschauwer, D., Van Buyten, E., Satoh, K., Balidion, J., Mauleon, R., Choi, I.-R., Vera-Cruz, C., Kikuchi, S., and Höfte, M. (2012). Brassinosteroids antagonize gibberellin- and salicylate-mediated root immunity in rice. Plant Physiol. **158**, 1833–1846.

De Vleesschauwer, D., Yang, Y., Vera-Cruz, C., and Höfte, M. (2010). Abscisic acid-induced resistance against the brown spot pathogen *Cochliobolus miyabeanus* in rice involves MAP kinase-mediated repression of ethylene signaling. Plant Physiol. **152**, 2036–2052

Denancé, N., Sánchez-Vallet, A., Goffner, D., and Molina, A. (2013). Disease resistance or growth: the role of plant hormones in balancing immune responses and fitness costs. Front Plant Sci. **24**, 155.

Ding, X.H., Cao, Y.L., Huang, L.L., Zhao, J., Xu, C.G., Li, X.H., and Wang, S.P. (2008). Activation of the indole-3-acetic acid-amido synthetase GH3-8supp resses expansin expression and promotes salicylate- and jasmonate-independent basal immunity in rice. Plant Cell. **20**, 228–240.

Divi, U.K., Rahman, T., and Krishna, P. (2010). Brassinosteroid-mediated stress tolerance in *Arabidopsis* shows interactions with abscisic acid, ethylene and salicylic acid pathways. BMC Plant Biol. **10**, 151.

Domingo, C., Andres, F., Tharreau, D., Iglesias, D.J., and Talon, M. (2009). Constitutive expression of OsGH3.1 reduces auxin content and enhances defense response and resistance to a fungal pathogen in rice. Mol. Plant Microbe Interact. **22**, 201–210

Fariduddin, Q., Khalil, R.R.A.E., Mir, B.A., Yusuf, M., and Ahmad, A. (2013). 24-Epibrassinolide regulates photosynthesis, antioxidant enzyme activities and proline content of *Cucumis sativus* under salt and/or copper stress. Environ. Monit. Assess. **185**, 7845–7856.

Fath, A. (2001). Enzymes that scavenge reactive oxygen species are down-regulated prior to gibberellic acid-induced programmed cell death in barley aleurone. Plant Physiol. **126**, 156–166.

Feng, S., Martinez, C., Gusmaroli, G., Wang, Y., Zhou, J., Wang, F., Chen, L., Yu, L., Iglesias-Pedraz, J.M., Kircher, S., et al. (2008). Coordinated regulation of *Arabidopsis thaliana* development by light and gibberellins. Nature. **451**, 475–479.

Foreman, J., Demidchik, V., Bothwell, J.H.F., Mylona, P., Miedema, H., Torres, M.A., Linstead, P., Costa, S., Brownlee, C., Jones, J.D.G., et al. (2003). Reactive oxygen species produced by NADPH oxidase regulate plant cell growth. Nature. **422**, 442–446.

Fradin, E.F., Zhang, Z., Juarez Ayala, J.C., Castroverde, C.D.M., Nazar, R.N., Robb, J., Liu, C.-M., and Thomma, B.P.H.J. (2009). Genetic dissection of *Verticillium* wilt resistance mediated by tomato Ve1. Plant Physiol. **150**, 320–332.

Fridman, Y., and Savaldi-Goldstein, S. (2013). Brassinosteroids in growth control: how, when and where. Plant Sci. **209**, 24–31.

Fu, J., Liu, H., Li, Y., Yu, H., Li, X., Xiao, J., and Wang, S. (2011). Manipulating broad-spectrum disease resistance by suppressing pathogen-induced auxin accumulation in rice. Plant Physiol. **155**, 589–602.

Fu, X., and Harberd, N.P. (2003). Auxin promotes *Arabidopsis* root growth by modulating gibberellin response. Nature. **421**, 740–743.

Gallego-Bartolomé, J., Alabadí, D., and Blázquez, M.A. (2011). DELLA-induced early transcriptional changes during etiolated development in *Arabidopsis thaliana*. PLoS One. **6**, e23918.

Gallego-Bartolomé, J., Minguet, E.G., Grau-Enguix, F., Abbas, M., Locascio, A., Thomas, S.G., Alabadí, D., and Blázquez, M.A. (2012). Molecular mechanism for the interaction between gibberellin and brassinosteroid signaling pathways in *Arabidopsis*. Proc. Natl Acad. Sci. U S A. **109**, 13446–13451.

Gallego-Bartolomé, J., Minguet, E.G., Marín, J.A., Prat, S., Blázquez, M.A., and Alabadí, D. (2010). Transcriptional diversification and functional conservation between DELLA proteins in *Arabidopsis*. Mol. Biol. Evol. **27**, 1247–1256.

Gao, X.-H., Xiao, S.-L., Yao, Q.-F., Wang, Y.-J., and Fu, X.-D. (2011). An updated GA signaling 'relief of repression' regulatory model. Mol. Plant. **4**, 601–606.

Grant, M.R., and Jones, J.D.G. (2009). Hormone (dis)harmony moulds plant health and disease. Science. **324**, 750–752.

Guo, R., Qian, H., Shen, W., Liu, L., Zhang, M., Cai, C., Zhao, Y., Qiao, J., and Wang, Q. (2013). BZR1 and BES1 participate in regulation of glucosinolate biosynthesis by brassinosteroids in *Arabidopsis*. J. Exp. Bot. **64**, 2401–2412.

Hauvermale, A.L., Ariizumi, T., and Steber, C.M. (2012). Gibberellin signaling: a theme and variations on DELLA repression. Plant Physiol. **160**, 83–92.

Henty-Ridilla, J.L., Shimono, M., Li, J., Chang, J.H., Day, B., and Staiger, C.J. (2013). The plant actin cytoskeleton responds to signals from microbe-associated molecular patterns. PLoS Pathog. **9**, e1003290.

Hernandez-Blanco, C., Feng, D.X., Hu, J., Sanchez-Vallet, A., Deslandes, L., Llorente, F., Berrocal-Lobo, M., Keller, H., Barlet, X., Sanchez-Rodriguez, C., et al. (2007). Impairment of cellulose synthases required for *Arabidopsis* secondary cell wall formation enhances disease resistance. Plant Cell. **19**, 890–903.

Hou, X.L., Ding, X.H., and Yu, H. (2013). Crosstalk between GA and JA signalling mediates plant growth and defense. Plant Cell Rep. **32**, 1067–1074.

Hou, X., Lee, L.Y.C., Xia, K., Yen, Y., and Yu, H. (2010). DELLAs modulate jasmonate signaling via competitive binding to JAZs. Dev. Cell. **19**, 884–894.

Inzé, D., and De Veylder, L. (2006). Cell cycle regulation in plant development. Annu. Rev. Genet. **40**, 77–105.

Jacobs, S., Zechmann, B., Molitor, A., Trujillo, M., Petutschnig, E., Likpa, V., Kogel, K.H., and Schaefer, P. (2011). Broad-spectrum suppression of innate immunity is required for colonization of *Arabidopsis* roots by the fungus *Piriformospora indica*. Plant Physiol. **156**, 726–740.

Jaillais, Y., Belkhadir, Y., Balsemão-Pires, E., Dangl, J.L., and Chory, J. (2011). Extracellular leucine-rich repeats as a platform for receptor/coreceptor complex formation. Proc. Natl Acad. Sci. U S A. **108**, 8503–8507.

Jiang, C.-J., Shimono, M., Sugano, S., Kojima, M., Yazawa, K., Yoshida, R., Inoue, H., Hayashi, N., Sakakibara, H., and Takatsuji, H. (2010). Abscisic acid interacts antagonistically with salicylic acid signaling pathway in rice–*Magnaporthe grisea* interaction. Mol. Plant. Microbe. Interact. **23**, 791–798.

Kawaide, H. (2006). Biochemical and molecular analyses of gibberellin biosynthesis in fungi. Biosci. Biotechnol. Biochem. **70**, 583–590.

Kazan, K., and Manners, J.M. (2009). Linking development to defense: auxin in plant–pathogen interactions. Trends Plant Sci. **14**, 373–382.

Kazan, K., and Manners, J.M. (2012). JAZ repressors and the orchestration of phytohormone crosstalk. Trends Plant Sci. **17**, 22–31.

Kazan, K., and Manners, J.M. (2013). MYC2: the master in action. Mol. Plant. **6**, 686–703.

Kemen, E., Gardiner, A., Schultz-Larsen, T., Kemen, A.C., Balmuth, A.L., Robert-Seilaniantz, A., Bailey, K., Holub, E., Studholme, D.J., Maclean, D., et al. (2011). Gene gain and loss during evolution of obligate parasitism in the white rust pathogen of *Arabidopsis thaliana*. PLoS Biol. **9**, e1001094.

Kemmerling, B., Schwedt, A., Rodriguez, P., Mazzotta, S., Frank, M., Qamar, S.A., Mengiste, T., Betsuyaku, S., Parker, J.E., Müssig, C., et al. (2007). The BRI1-associated kinase 1, BAK1, has a brassinolide-independent role in plant cell death control. Curr. Biol. **17**, 1116–1122.

Khripach, V. (2000). Twenty years of brassinosteroids: steroidal plant hormones warrant better crops for the XXI century. Ann. Bot. **86**, 441–447.

Khush, G.S. (2001). Green revolution: the way forward. Nat. Rev. Genet. **2**, 815–822.

Koga, H., Dohi, K., and Mori, M. (2004). Abscisic acid and low temperatures suppress the whole plant-specific resistance reaction of rice plants to the infection of *Magnaporthe grisea*. Physiol. Mol. Plant Pathol. **65**, 3–9.

Lee, A.H., Hurley, B., Felsensteiner, C., Yea, C., Ckurshumova, W., Bartetzko, V., Wang, P.W., Quach, V., Lewis, J.D., Liu, Y.C., et al. (2012). A bacterial acetyltransferase destroys plant microtubule networks and blocks secretion. PLoS Pathog. **8**, e1002523.

Li, J. (2010). Regulation of the nuclear activities of brassinosteroid signaling. Curr. Opin. Plant Biol. **13**, 540–547.

Li, Q.-F., Wang, C., Jiang, L., Li, S., Sun, S.S.M., and He, J.-X. (2012). An interaction between BZR1 and DELLAs mediates direct signaling crosstalk between brassinosteroids and gibberellins in *Arabidopsis*. Sci. Signal. **5**, ra72.

Li, Y., Van den Ende, W., and Rolland, F. (2013). Sucrose induction of anthocyanin biosynthesis is mediated by DELLA. Mol. Plant., 16 November, 10.1093/mp/sst16.

Lin, W., Lu, D., Gao, X., Jiang, S., Ma, X., Wang, Z., Mengiste, T., and He, P. (2013). Inverse modulation of plant immune and

brassinosteroid signaling pathways by the receptor-like cytoplasmic kinase BIK1. Proc. Natl Acad. Sci. U S A. **110**, 12114–12119.

Locascio, A., Blázquez, M.A., and Alabadí, D. (2013). Dynamic regulation of cortical microtubule organization through prefoldin–DELLA interaction. Curr. Biol. **23**, 804–809.

Lozano-Durán, R., Macho, A.P., Boutrot, F., Segonzac, C., Somssich, I.E., and Zipfel, C. (2013). The transcriptional regulator BZR1medi ates trade-off between plant innate immunity and growth. Elife. **2**, e00983.

Mei, C., Qi, M., Sheng, G., and Yang, Y. (2006). Inducible overexpression of a rice allene oxide synthase gene increases the endogenous jasmonic acid level, PR gene expression, and host resistance to fungal. Mol. Plant Microbe Interact. **19**, 1127–1137.

Monna, L., Kitazawa, N., Yoshino, R., Suzuki, J., Masuda, H., Maehara, Y., Tanji, M., Sato, M., Nasu, S., and Minobe, Y. (2002). Positional cloning of rice semidwarfing gene, sd-1: rice 'Green revolution gene' encodes a mutant enzyme involved in gibberellin synthesis. DNA Res. **9**, 11–17.

Murase, K., Hirano, Y., Sun, T., and Hakoshima, T. (2008). Gibberellin-induced DELLA recognition by the gibberellin receptor GID1. Nature. **456**, 459–463.

Müssig, C. (2005). Brassinosteroid-promoted growth. Plant Biol. **7**, 110–117.

Nahar, K., Kyndt, T., Hause, B., Höfte, M., and Gheysen, G. (2013). Brassinosteroids suppress rice defense against root-knot nematodes through antagonism with the jasmonate pathway. Mol. Plant Microbe Interact. **26**, 106–115.

Nakashita, H., Yasuda, M., Nitta, T., Asami, T., Fujioka, S., Arai, Y., Sekimata, K., Takatsuto, S., Yamaguchi, I., and Yoshida, S. (2003). Brassinosteroid functions in a broad range of disease resistance in tobacco and rice. Plant J. **33**, 887–898.

Naseem, M., and Dandekar, T. (2012). The role of auxin-cytokinin antagonism in plant–pathogen interactions. PLoS Pathogen. **8**, e1003026.

Navarro, L., Bari, R., Achard, P., Lison, P., Nemri, A., Harberd, N.P., and Jones, J.D.G. (2008). DELLAs control plant immune responses by modulating the balance and salicylic acid signaling. Curr. Biol. **18**, 650–655.

Nishimura, M.T., Stein, M., Hou, B.-H., Vogel, J.P., Edwards, H., and Somerville, S.C. (2003). Loss of a callose synthase results in salicylic acid-dependent disease resistance. Science. **301**, 969–972.

Ogawa, M. (2003). Gibberellin biosynthesis and response during *Arabidopsis* seed germination. Plant Cell Online. **15**, 1591–1604.

Oh, E., Zhu, J.-Y., and Wang, Z.-Y. (2012). Interaction between BZR1 and PIF4 integrates brassinosteroid and environmental responses. Nat. Cell Biol. **14**, 802–809.

Oh, M.-H., Wang, X., Wu, X., Zhao, Y., Clouse, S.D., and Huber, S.C. (2010). Autophosphorylation of Tyr-610 in the receptor kinase BAK1 plays a role in brassinosteroid signaling and basal defense gene expression. Proc. Natl Acad. Sci. U S A. **107**, 17827–17832.

Park, J., Nguyen, K.T., Park, E., Jeon, J.-S., and Choi, G. (2013). DELLA proteins and their interacting RING Finger proteins repress gibberellin responses by binding to the promoters of a subset of gibberellin-responsive genes in *Arabidopsis*. Plant Cell. **25**, 927–943.

Pieterse, C.M.J., Leon-Reyes, A., Van der Ent, S., and Van Wees, S.C.M. (2009). Networking by small-molecule hormones in plant immunity. Nature Chem. Biol. **5**, 308–316.

Pieterse, C.M.J., Van der Does, D., Zamioudis, C., Leon-Reyes, A., and Van Wees, S.C.M. (2012). Hormonal modulation of plant immunity. Annu. Rev. Cell Dev. Biol. **28**, 489–521.

Porter, K., Shimono, M., Tian, M., and Day, B. (2012). *Arabidopsis* Actin-Depolymerizing Factor-4 links pathogen perception, defense activation and transcription to cytoskeletal dynamics. PLoS Pathog. **8**, e1003006.

Qi, T., Song, S., Ren, Q., Wu, D., Huang, H., Chen, Y., Fan, M., Peng, W., Ren, C., and Xie, D. (2011). The Jasmonate-ZIM-domain proteins interact with the WD-Repeat/bHLH/MYB complexes to regulate jasmonate-mediated anthocyanin accumulation and trichome initiation in *Arabidopsis thaliana*. Plant Cell. **23**, 1795–1814.

Qin, X., Liu, J.H., Zhao, W.S., Chen, X.J., Guo, Z.J., and Peng, Y.L. (2013). Gibberellin 20-oxidase gene OsGA20ox3 regulates plant stature and disease development in rice. Mol. Plant Microbe Interact. **26**, 227–239.

Ribeiro, D.M., Araújo, W.L., Fernie, A.R., Schippers, J.H.M., and Mueller-Roeber, B. (2012). Translatome and metabolome effects triggered by gibberellins during rosette growth in *Arabidopsis*. J. Exp. Bot. **63**, 2769–2786.

Riemann, M., Haga, K., Shimizu, T., Okada, K., Ando, S., Mochizuki, S., Nishizawa, Y., Yamanouchi, U., Nick, P., Yano, M., et al. (2013). Identification of rice Allene Oxide Cyclase mutants and the function of jasmonate for defence against *Magnaporthe oryzae*. Plant J. **74**, 226–238.

Robert-Seilaniantz, A., Grant, M., and Jones, J.D. (2011). Hormone crosstalk in plant disease and defense: more than just jasmonate-salicylate antagonism. Annu. Rev. Phytopathol. **49**, 317–343.

Robert-Seilaniantz, A., Navarro, L., Bari, R., and Jones, J.D. (2007). Pathological hormone imbalances. Curr. Opin. Plant Biol. **10**, 372–379.

Sarnowska, E.A., Rolicka, A.T., Bucior, E., Cwiek, P., Tohge, T., Fernie, A.R., Jikumaru, Y., Kamiya, Y., Franzen, R., Schmelzer, E., et al. (2013). DELLA-interacting SWI3C core subunit of switch/sucrose nonfermenting chromatin remodeling complex modulates gibberellin responses and hormonal cross talk in *Arabidopsis*. Plant Physiol. **163**, 305–317.

Sasaki, A., Ashikari, M., Ueguchi-Tanaka, M., Itoh, H., Nishimura, A., Swapan, D., Ishiyama, K., Saito, T., Kobayashi, M., Khush, G.S., et al. (2002). Green revolution: a mutant gibberellin-synthesis gene in rice: new insight into the rice variant that helped to avert famine over thirty years ago. Nature. **416**, 701–702.

Saville, R.J., Gosman, N., Burt, C.J., Makepeace, J., Steed, A., Corbitt, M., Chandler, E., Brown, J.K.M., Boulton, M.I., and Nicholson, P. (2012). The 'Green Revolution' dwarfing genes play a role in disease resistance in *Triticum aestivum* and *Hordeum vulgare*. J. Exp. Bot. **63**, 1271–1283.

Schopfer, P. (2001). Release of reactive oxygen intermediates (superoxide radicals, hydrogen peroxide, and hydroxyl radicals) and peroxidase in germinating radish seeds controlled by light, gibberellin, and abscisic acid. Plant Physiol. **125**, 1591–1602.

Schwessinger, B., Roux, M., Kadota, Y., Ntoukakis, V., Sklenar, J., Jones, A., and Zipfel, C. (2011). Phosphorylation-dependent differential regulation of plant growth, cell death, and innate immunity by the regulatory receptor-like kinase BAK1. PLoS Genet. **7**, e1002046.

Seifi, H.S., Bockhaven, J. Van, Angenon, G., and Höfte, M. (2013a). Glutamate metabolism in plant disease and defense: friend or foe? Mol. Plant Microbe Interact. **26**, 475–485.

Seifi, H.S., Curvers, K., De Vleesschauwer, D., Delaere, I., Aziz, A., and Höfte, M. (2013b). Concurrent overactivation of the cytosolic glutamine synthetase and the GABA shunt in the ABA-deficient sitiens mutant of tomato leads to resistance against *Botrytis cinerea*. New Phytol. **199**, 490–504.

Shan, L., He, P., Li, J., Heese, A., Peck, S.C., Nürnberger, T., Martin, G.B., and Sheen, J. (2008). Bacterial effectors target the common signaling partner BAK1 to disrupt multiple MAMP receptor-signaling complexes and impede plant immunity. Cell Host Microbe. **4**, 17–27.

Shi, H., Shen, Q., Qi, Y., Yan, H., Nie, H., Chen, Y., Zhao, T., Katagiri, F., and Tang, D. (2013). BR-signaling kinase1phys ically associates with Flagellin Sensing2 and regulates plant innate immunity in *Arabidopsis*. Plant Cell. **25**, 1143–1157.

Shirasu, K., Nakajima, H., Rajasekhar, V.K., Dixon, R.A., and Lamb, C. (1997). Salicylic acid potentiates an agonist-dependent gain control that amplifies pathogen signals in the activation of defense mechanisms. Plant Cell. **9**, 261–270.

Singh, M.P., Lee, F.N., Counce, P.A., and Gibbons, J.H. (2004). Mediation of partial resistance to rice blast through anaerobic induction of ethylene. Phytopathology. **94**, 819–825.

Song, S., Qi, T., Huang, H., Ren, Q., Wu, D., Chang, C., Peng, W., Liu, Y., Peng, J., and Xie, D. (2011). The Jasmonate-ZIM domain proteins interact with the R2R3–MYB transcription factors MYB21 and MYB24 to affect Jasmonate-regulated stamen development in *Arabidopsis*. Plant Cell. **23**, 1000–1013.

Spielmeyer, W., Ellis, M.H., and Chandler, P.M. (2002). Semidwarf (sd-1), 'green revolution' rice, contains a defective gibberellin 20-oxidase gene. Proc. Natl Acad. Sci. U S A. **99**, 9043–9048.

Sun, Y., Fan, X.Y., Cao, D.M., Tang, W., He, K., Zhu, J.Y., He, J.X., Bai, M.Y., Zhu, S., Oh, E., et al. (2010). Integration of brassinosteroid signal transduction with the transcription network for plant growth regulation in *Arabidopsis*. Dev. Cell. **19**, 765–777.

Suzuki, N., Koussevitzky, S., Mittler, R., and Miller, G. (2012). ROS and redox signalling in the response of plants to abiotic stress. Plant. Cell Environ. **35**, 259–270.

Swanson, S., and Gilroy, S. (2010). ROS in plant development. Physiol. Plant. **138**, 384–392.

Tanaka, N., Matsuoka, M., Kitano, H., Asano, T., Kaku, H., and Komatsu, S. (2006). gid1, a gibberellin-insensitive dwarf mutant, shows altered regulation of probenazole-inducible protein (PBZ1) in response to cold stress and pathogen attack. Plant Cell Environ. **29**, 619–631.

Tang, W., Yuan, M., Wang, R., Yang, Y., Wang, C., Oses-Prieto, J.A., Kim, T.W., Zhou, H.W., Deng, Z., Gampala, S.S., et al. (2011). PP2A activates brassinosteroid-responsive gene expression and plant growth by dephosphorylating BZR1. Nat. Cell Biol. **13**, 124–131.

Tian, M., Chaudhry, F., Ruzicka, D.R., Meagher, R.B., Staiger, C.J., and Day, B. (2009). *Arabidopsis* actin-depolymerizing factor AtADF4 mediates defense signal transduction triggered by the *Pseudomonas syringae* effector AvrPphB. Plant Physiol. **150**, 815–824.

Tong, H., and Chu, C. (2012). Brassinosteroid signaling and application in rice. J. Genet. Genomics. **39**, 3–9.

Ueguchi-Tanaka, M., Nakajima, M., Motoyuki, A., and Matsuoka, M. (2007). Gibberellin receptor and its role in gibberellin signaling in plants. Annu. Rev. Plant Biol. **58**, 183–198.

Valls, M., Genin, S., and Boucher, C. (2006). Integrated regulation of the type III secretion system and other virulence determinants in *Ralstonia solanacearum*. PLoS Pathog. **2**, e82.

Van der Ent, S., and Pieterse, C.M.J. (2012). Ethylene: multitasker in plant–attacker interactions. In Annual Plant Reviews: The Plant Hormone Ethylene, McManus, M.T., ed. (Oxford, UK: Blackwell Publishing), pp. 343–377.

Vriezen, W.H., Achard, P., Harberd, N.P., and Van Der Straeten, D. (2004). Ethylene-mediated enhancement of apical hook formation in etiolated *Arabidopsis thaliana* seedlings is gibberellin dependent. Plant J. **37**, 505–516.

Wang, W., Barnaby, J.Y., Tada, Y., Li, H., Tör, M., Caldelari, D., Lee, D.U., Fu, X.D., and Dong, X. (2011). Timing of plant immune responses by a central circadian regulator. Nature. **470**, 110–114.

Wild, M., Daviere, J.M., Cheminant, S., Regnault, T., Baumberger, N., Heintz, D., Baltz, R., Genschik, P., and Achard, P. (2012). The *Arabidopsis* DELLA RGA-LIKE3 is a direct target of MYC2 and modulates jasmonate signaling responses. Plant Cell. **24**, 3307–3319.

Xia, X.-J., Chen, Z., and Yu, J.-Q. (2010). ROS mediate brassinosteroids-induced plant stress responses. Plant Signal. Behav. **5**, 532–534.

Xia, X.J., Wang, Y.J., Zhou, Y.H., Tao, Y., Mao, W.H., Shi, K., Asami, T., Chen, Z., and Yu, J.Q. (2009). Reactive oxygen species are involved in brassinosteroid-induced stress tolerance in cucumber. Plant Physiol. **150**, 801–814.

Xu, J., Audenaert, K., Höfte, M., and De Vleesschauwer, D. (2013). Abscisic acid promotes susceptibility to the rice leaf blight pathogen *Xanthomonas oryzae* pv. *oryzae* by suppressing salicylic acid-mediated defenses. Plos One. **8**, e67413.

Yabuta, T., and Sumiki, Y. (1938). On the crystal of gibberellin, a substance to promote plant growth. J. Agric. Chem. Soc. Japan. **14**, 1526.

Yang, D.L., Li, Q., Deng, Y.W., Lou, Y.G., Wang, M.Y., Zhou, G.X., Zhang, Y.Y., and He, Z.H. (2008). Altered disease development

in the Eui mutants and Eui overexpressors indicates that gibberellins negatively regulate rice basal disease resistance. Mol. Plant. **1**, 528–537.

Yang, D.L., Yao, J., Mei, C.S., Tong, X.H., Zeng, L.J., Li, Q., Xiao, L.T., Sun, T.P., Li, J., Deng, X.W., et al. (2012). Plant hormone jasmonate prioritizes defense over growth by interfering with gibberellin signaling cascade. Proc. Natl Acad. Sci. U S A. **109**, 1192–1200.

Ye, H., Li, L., and Yin, Y. (2011). Recent advances in the regulation of brassinosteroid signaling and biosynthesis pathways. J. Integr. Plant Biol. **53**, 455–468.

Yu, S., Galvão, V.C., Zhang, Y.-C., Horrer, D., Zhang, T.-Q., Hao, Y.-H., Feng, Y.-Q., Wang, S., Schmid, M., and Wang, J.-W. (2012). Gibberellin regulates the *Arabidopsis* floral transition through miR156-targeted SQUAMOSA promoter binding-like transcription factors. Plant Cell. **24**, 3320–3332.

Yu, X., Li, L., Zola, J., Aluru, M., Ye, H., Foudree, A., Guo, H., Anderson, S., Aluru, S., Liu, P., et al. (2011). A brassinosteroid transcriptional network revealed by genome-wide identification of BESI target genes in *Arabidopsis thaliana*. Plant J. **65**, 634–646.

Zentella, R., Zhang, Z.-L., Park, M., Thomas, S.G., Endo, A., Murase, K., Fleet, C.M., Jikumaru, Y., Nambara, E., Kamiya, Y., et al. (2007). Global analysis of DELLA direct targets in early gibberellin signaling in *Arabidopsis*. Plant Cell. **19**, 3037–3057.

Zhang, Z., Li, Q., Li, Z., Staswick, P.E., Wang, M., Zhu, Y., and He, Z. (2007). Dual regulation role of GH3.5 in salicylic acid and auxin signaling during *Arabidopsis–Pseudomonas syringae* interaction. Plant Physiol. **145**, 450–464.

Zhu, J.-Y., Sae-Seaw, J., and Wang, Z.-Y. (2013). Brassinosteroid signalling. Development. **140**, 1615–1620.

Zhu, S., Gao, F., Cao, X., Chen, M., Ye, G., Wei, C., and Li, Y. (2005). The rice dwarf virus P2 protein interacts with ent-kaurene oxidases *in vivo*, leading to reduced biosynthesis of gibberellins and rice dwarf symptoms. Plant Physiol. **139**, 1935–1945.