



Jasmonate Signaling

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Gasperini, D.; Howe, G. A.; Phytohormones in a universe of regulatory metabolites: lessons from jasmonate *Plant Physiol.* (2024) DOI: [10.1093/plphys/kiae045](https://doi.org/10.1093/plphys/kiae045)

Abstract
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Small-molecule phytohormones exert control over plant growth, development, and stress responses by coordinating the patterns of gene expression within and between cells. Increasing evidence indicates that currently recognized plant hormones are part of a larger group of regulatory metabolites that have acquired signaling properties during the evolution of land plants. This rich assortment of chemical signals reflects the tremendous diversity of plant secondary metabolism, which offers evolutionary solutions to the daunting challenges of sessility and other unique aspects of plant biology. A major gap in our current understanding of plant regulatory metabolites is the lack of insight into the direct targets of these compounds. Here, we illustrate the blurred distinction between classical phytohormones and other bioactive metabolites by highlighting the major scientific advances that transformed the view of jasmonate from an interesting floral scent to a potent transcriptional regulator. Lessons from jasmonate research generally apply to other phytohormones and thus may help provide a broad understanding of regulatory metabolite-protein interactions. In providing a framework that links small-molecule diversity to transcriptional plasticity, we hope to stimulate future research to explore the evolution, functions, and mechanisms of perception of a broad range of plant regulatory metabolites.

Mielke, S.; Zimmer, M.; Meena, M. K.; Dreos, R.; Stellmach, H.; Hause, B.; Voiniciuc, C.; Gasperini, D.; Jasmonate biosynthesis arising from altered cell walls is prompted by turgor-driven mechanical compression *Sci. Adv.* **7**, eabf0356, (2021) DOI: [10.1126/sciadv.abf0356](https://doi.org/10.1126/sciadv.abf0356)

Abstract
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Despite the vital roles of jasmonoyl-isoleucine (JA-Ile) in governing plant growth and environmental acclimation, it remains unclear what intracellular processes lead to its induction. Here, we provide compelling genetic evidence that mechanical and osmotic regulation of turgor pressure represents a key

elicitor of JA-Ile biosynthesis. After identifying cell wall mutant alleles in KORRIGAN1 (KOR1) with elevated JA-Ile in seedling roots, we found that ectopic JA-Ile resulted from cell nonautonomous signals deriving from enlarged cortex cells compressing inner tissues and stimulating JA-Ile production. Restoring cortex cell size by cell type-specific KOR1 complementation, by isolating a genetic *kor1* suppressor, and by lowering turgor pressure with hyperosmotic treatments abolished JA-Ile signaling. Conversely, hypoosmotic treatment activated JA-Ile signaling in wild-type plants. Furthermore, constitutive JA-Ile levels guided mutant roots toward greater water availability. Collectively, these findings enhance our understanding on JA-Ile biosynthesis initiation and reveal a previously undescribed role of JA-Ile in orchestrating environmental resilience.

Menna, A.; Dora, S.; Sancho-Andrés, G.; Kashyap, A.; Meena, M. K.; Sklodowski, K.; Gasperini, D.; Coll, N. S.; Sánchez-Rodríguez, C.; A primary cell wall cellulose-dependent defense mechanism against vascular pathogens revealed by time-resolved dual transcriptomics *BMC Biol.* **19**, 161, (2021) DOI: [10.1186/s12915-021-01100-6](https://doi.org/10.1186/s12915-021-01100-6)

Abstract
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Background: Cell walls (CWs) are protein-rich polysaccharide matrices essential for plant growth and environmental acclimation. The CW constitutes the first physical barrier as well as a primary source of nutrients for microbes interacting with plants, such as the vascular pathogen *Fusarium oxysporum* (Fo). Fo colonizes roots, advancing through the plant primary CWs towards the vasculature, where it grows causing devastation in many crops. The pathogenicity of Fo and other vascular microbes relies on their capacity to reach and colonize the xylem. However, little is known about the root-microbe interaction before the pathogen reaches the vasculature and the role of the plant CW during this process. **Results:** Using the pathosystem *Arabidopsis*-Fo5176, we show dynamic transcriptional changes in both fungus and root during their interaction. One of the earliest plant responses to Fo5176 was the downregulation of primary CW synthesis genes. We observed enhanced resistance to Fo5176 in *Arabidopsis* mutants impaired in primary CW cellulose synthesis. We confirmed that *Arabidopsis* roots deposit lignin in response to Fo5176 infection, but we show that lignin-deficient mutants were as susceptible as wildtype plants to Fo5176. Genetic impairment of jasmonic acid biosynthesis and signaling did not alter *Arabidopsis* response to Fo5176, whereas impairment of ethylene signaling did increase vasculature colonization by Fo5176. Abolishing ethylene signaling attenuated the observed resistance while maintaining the dwarfism observed in primary CW cellulose-deficient mutants. **Conclusions:** Our study provides significant insights on the dynamic root-vascular pathogen interaction at the transcriptome level and the vital role of primary CW cellulose during defense response to these pathogens. These findings represent an essential resource for the generation of plant resistance to Fo that can be transferred to other vascular pathosystems. **Keywords:** *Arabidopsis*, *Fusarium oxysporum*, *Ralstonia solanacearum*, plant-pathogen interaction, dual-time course transcriptomics, cellulose, ethylene, defense response

Dallery, J.-F.; Zimmer, M.; Halder, V.; Suliman, M.; Pigné, S.; Le Goff, G.; Gianniou, D. D.; Trougakov, I. P.; Ouazzani, J.; Gasperini, D.; O'Connell, R. J.; Inhibition of jasmonate-

mediated plant defences by the fungal metabolite higginsianin B
J. Exp. Bot. **71**, 2910-2921, (2020) DOI: [10.1093/jxb/eraa061](https://doi.org/10.1093/jxb/eraa061)

Abstract
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Infection of *Arabidopsis thaliana* by the ascomycete fungus *Colletotrichum higginsianum* is characterised by an early symptomless biotrophic phase followed by a destructive necrotrophic phase. The fungal genome contains 77 secondary metabolism-related biosynthetic gene clusters (BGCs), and their expression during the infection process is tightly regulated. Deleting CclA, a chromatin regulator involved in repression of some BGCs through H3K4 trimethylation, allowed overproduction of 3 families of terpenoids and isolation of 12 different molecules. These natural products were tested in combination with methyl jasmonate (MeJA), an elicitor of jasmonate responses, for their capacity to alter defence gene induction in *Arabidopsis*. Higginsianin B inhibited MeJA-triggered expression of the defence reporter VSP1p:GUS, suggesting it may block bioactive JA-Ile synthesis or signalling in planta. Using the JA-Ile sensor Jas9-VENUS, we found that higginsianin B, but not three other structurally-related molecules, suppressed JA-Ile signalling by preventing degradation of JAZ proteins, the repressors of JA responses. Higginsianin B likely blocks the 26S proteasome-dependent degradation of JAZ proteins because it inhibited chymotrypsin- and caspase-like protease activities. The inhibition of target degradation by higginsianin B also extended to auxin signalling, as higginsianin B treatment reduced IAA-dependent expression of DR5p:GUS. Overall, our data indicate that specific fungal secondary metabolites can act similarly to protein effectors to subvert plant immune and developmental responses.

Mielke, S.; Gasperini, D.; Plant-Insect Bioassay for Testing
Arabidopsis Resistance to the Generalist Herbivore *Spodoptera*
littoralis (Champion, A. & Laplaze, L., eds.). *Methods Mol. Biol.*
2085, 69-78, (2020) ISBN: 978-1-0716-0142-6 DOI:
[10.1007/978-1-0716-0142-6_5](https://doi.org/10.1007/978-1-0716-0142-6_5)

Abstract
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Jasmonates are essential engineers of plant defense responses against many pests, including herbivorous insects. Herbivory induces the production of jasmonic acid (JA) and its bioactive conjugate jasmonoyl-l-isoleucine (JA-Ile), which then triggers a large transcriptional reprogramming to promote plant acclimation. The contribution of the JA pathway, including its components and regulators, to defense responses against insect herbivory can be evaluated by conducting bioassays with a wide range of host plants and insect pests. Here, we describe a detailed and reproducible protocol for testing feeding behavior of the generalist herbivore *Spodoptera littoralis* on the model plant *Arabidopsis thaliana* and hence infer the contribution of JA-mediated plant defense responses to a chewing insect.

Mielke, S.; Gasperini, D.; Interplay between Plant Cell Walls
and Jasmonate Production *Plant Cell Physiol.* **60**, 2629-2637,
(2019) DOI: [10.1093/pcp/pcz119](https://doi.org/10.1093/pcp/pcz119)

Abstract
RIS
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Plant cell walls are sophisticated carbohydrate-rich structures representing the immediate contact surface with the extracellular environment, often serving as the first barrier against biotic and abiotic stresses. Notably, a variety of perturbations in plant cell walls result in upregulated jasmonate (JA) production, a phytohormone with essential roles in defense and growth responses. Hence, cell wall-derived signals can initiate intracellular JA-mediated responses and the elucidation of the underlying signaling pathways could provide novel insights into cell wall maintenance and remodeling, as well as advance our understanding on how is JA biosynthesis initiated. This Mini Review will describe current knowledge about cell wall-derived damage signals and their effects on JA biosynthesis, as well as provide future perspectives.

Schulze, A.; Zimmer, M.; Mielke, S.; Stellmach, H.; Melnyk, C. W.; Hause, B.; Gasperini, D.; Wound-Induced Shoot-to-Root Relocation of JA-Ile Precursors Coordinates Arabidopsis Growth
Mol. Plant **12**, 1383-1394, (2019) DOI:
[10.1016/j.molp.2019.05.013](https://doi.org/10.1016/j.molp.2019.05.013)

Abstract
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Multicellular organisms rely on the movement of signaling molecules across cells, tissues, and organs to communicate among distal sites. In plants, localized leaf damage activates jasmonic acid (JA)-dependent transcriptional reprogramming in both harmed and unharmed tissues. Although it has been indicated that JA species can translocate from damaged into distal sites, the identity of the mobile compound(s), the tissues through which they translocate, and the effect of their relocation remain unknown. Here, we found that following shoot wounding, the relocation of endogenous jasmonates through the phloem is essential to initiate JA signaling and stunt growth in unharmed roots of *Arabidopsis thaliana*. By employing grafting experiments and hormone profiling, we uncovered that the hormone precursor cis-12-oxo-phytodienoic acid (OPDA) and its derivatives, but not the bioactive JA-Ile conjugate, translocate from wounded shoots into undamaged roots. Upon root relocation, the mobile precursors cooperatively regulated JA responses through their conversion into JA-Ile and JA signaling activation. Collectively, our findings demonstrate the existence of long-distance translocation of endogenous OPDA and its derivatives, which serve as mobile molecules to coordinate shoot-to-root responses, and highlight the importance of a controlled redistribution of hormone precursors among organs during plant stress acclimation.

Gasperini, D.; Acosta, I. F.; Farmer, E. E.; Cotyledon Wounding of Arabidopsis Seedlings *Bio Protoc.* **6**, e1712, (2016)
DOI: [10.21769/BioProtoc.1712](https://doi.org/10.21769/BioProtoc.1712)

Abstract
RIS
BibTeX

Damage to plant organs through both biotic and abiotic injury is very common in nature. *Arabidopsis thaliana* 5-day-old (5-do) seedlings represent an excellent system in which to study plant responses to mechanical wounding, both at the site of the damage and in distal unharmed tissues. Seedlings of wild type, transgenic or mutant lines subjected to single or repetitive cotyledon wounding can be used to quantify morphological alterations (e.g., root length, Gasperini et al., 2015), analyze the dynamics of reporter genes in vivo (Larrieu et al., 2015; Gasperini et al., 2015), follow transcriptional changes by quantitative RT-PCR (Acosta et al., 2013; Gasperini et al., 2015) or examine additional aspects of the wound response with a plethora of downstream procedures. Here we illustrate how to rapidly and reliably wound cotyledons of young seedlings, and show the behavior of two promoters driving the expression of β -glucuronidase (GUS) in entire seedlings and in the primary root meristem, following single or repetitive cotyledon wounding respectively. We describe two procedures that can be easily adapted to specific experimental needs.

Kowalski, A. M.; Gooding, M.; Ferrante, A.; Slafer, G. A.; Orford, S.; Gasperini, D.; Griffiths, S.; Agronomic assessment of the wheat semi-dwarfing gene *Rht8* in contrasting nitrogen treatments and water regimes *Field Crops Res.* **191**, 150-160, (2016) DOI: [10.1016/j.fcr.2016.02.026](https://doi.org/10.1016/j.fcr.2016.02.026)

Abstract
RIS
BibTeX

Reduced height 8 (*Rht8*) is the main alternative to the GA-insensitive *Rht* alleles in hot and dry environments where it reduces plant height without yield penalty. The potential of *Rht8* in northern-European wheat breeding remains unclear, since the close linkage with the photoperiod-insensitive allele *Ppd-D1a* is unfavourable in the relatively cool summers. In the present study, two near-isogenic lines (NILs) contrasting for the *Rht8*/tall allele from Mara in a UK-adapted and photoperiod-sensitive wheat variety were evaluated in trials with varying nitrogen fertiliser (N) treatments and water regimes across sites in the UK and Spain. The *Rht8* introgression was associated with a robust height reduction of 11% regardless of N treatment and water regime and the *Rht8* NIL was more resistant to root-lodging at agronomically-relevant N levels than the tall NIL. In the UK with reduced solar radiation over the growing season than the site in Spain, the *Rht8* NIL showed a 10% yield penalty at standard agronomic N levels due to concomitant reduction in grain number and spike number whereas grain weight and harvest index were not significantly different to the tall NIL. The yield penalty associated with the *Rht8* introgression was overcome at low N and in irrigated conditions in the UK, and in the high-temperature site in Spain. Decreased spike length and constant spikelet number in the *Rht8* NIL resulted in spike compaction of 15%, independent of N and water regime. The genetic interval of *Rht8* overlaps with the compactum gene on 2DS, raising the possibility of the same causative gene. Further genetic dissection of these loci is required.

Gasperini, D.; Chételat, A.; Acosta, I. F.; Goossens, J.; Pauwels, L.; Goossens, A.; Dreos, R.; Alfonso, E.; Farmer, E. E.; Multilayered Organization of Jasmonate Signalling in the Regulation of Root Growth *PLOS Genet.* **11**, e1005300, (2015)
DOI: [10.1371/journal.pgen.1005300](https://doi.org/10.1371/journal.pgen.1005300)

Abstract
RIS

BibTeX

Physical damage can strongly affect plant growth, reducing the biomass of developing organs situated at a distance from wounds. These effects, previously studied in leaves, require the activation of jasmonate (JA) signalling. Using a novel assay involving repetitive cotyledon wounding in *Arabidopsis* seedlings, we uncovered a function of JA in suppressing cell division and elongation in roots. Regulatory JA signalling components were then manipulated to delineate their relative impacts on root growth. The new transcription factor mutant *myc2-322B* was isolated. In vitro transcription assays and whole-plant approaches revealed that *myc2-322B* is a dosage-dependent gain-of-function mutant that can amplify JA growth responses. Moreover, *myc2-322B* displayed extreme hypersensitivity to JA that totally suppressed root elongation. The mutation weakly reduced root growth in undamaged plants but, when the upstream negative regulator *NINJA* was genetically removed, *myc2-322B* powerfully repressed root growth through its effects on cell division and cell elongation. Furthermore, in a JA-deficient mutant background, *ninja1 myc2-322B* still repressed root elongation, indicating that it is possible to generate JA-responses in the absence of JA. We show that *NINJA* forms a broadly expressed regulatory layer that is required to inhibit JA signalling in the apex of roots grown under basal conditions. By contrast, *MYC2*, *MYC3* and *MYC4* displayed cell layer-specific localisations and *MYC3* and *MYC4* were expressed in mutually exclusive regions. In nature, growing roots are likely subjected to constant mechanical stress during soil penetration that could lead to JA production and subsequent detrimental effects on growth. Our data reveal how distinct negative regulatory layers, including both *NINJA*-dependent and -independent mechanisms, restrain JA responses to allow normal root growth. Mechanistic insights from this work underline the importance of mapping JA signalling components to specific cell types in order to understand and potentially engineer the growth reduction that follows physical damage.

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