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PLANT BIOLOGY

# Arabidopsis Jasmonate Signaling Pathway

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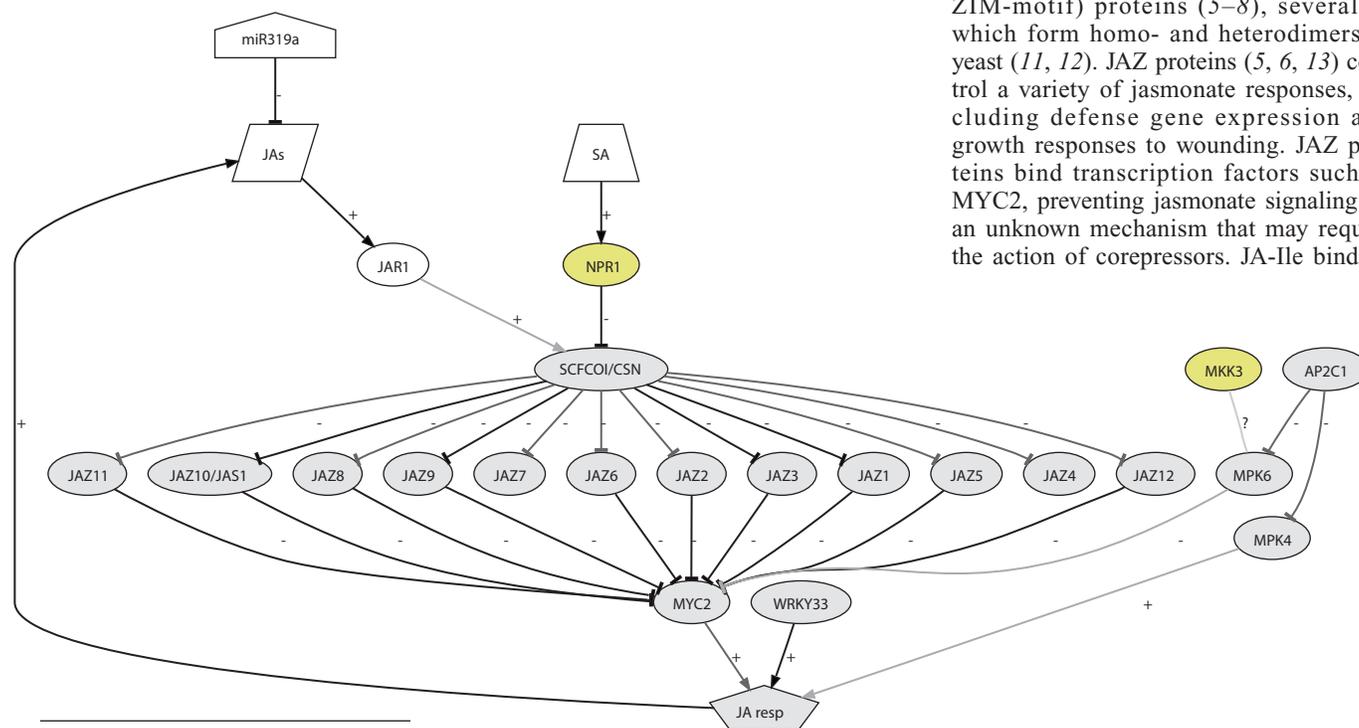
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Jasmonates control defense gene expression, growth, and fertility throughout the plant kingdom and have been studied extensively in *Arabidopsis thaliana*. The pro-hormone jasmonic acid (JA) is conjugated to amino acids such as isoleucine to form the active hormone jasmonoyl-isoleucine (JA-Ile). A series of breakthroughs has identified the SCF [SCF consists of four subunits: a cullin, SKP1 (S-phase kinase-associated protein 1), a RING finger protein (RBX1/HRT1/ROC1), and an F-box protein] CORONATINE INSENSITIVE1 (COI1) E3 ubiquitin ligase complex and the JASMONATE ZIM-DOMAIN (JAZ) proteins as central components in the perception of and transcriptional response to JA-Ile. JAZ proteins (most probably as dimers) bind transcription factors such as MYC2 before JA-Ile production. JA-Ile binds to COI1 to facilitate the formation of COI1-JAZ complexes, leading to ubiquitination and subsequent degradation of JAZ proteins. The degradation of JAZ proteins liberates transcription factors that function in the presence of the RNA polymerase II coregulatory complex Mediator to permit the expression of a number of jasmonate-regulated genes. Recent developments include the identification of COI1 as a receptor for jasmonates. Upstream of the signaling events, microRNA319 (miR319) negatively regulates the production of JA and JA-derived signals.

## Description

This record contains information specific to the *Arabidopsis* Jasmonate Signaling Pathway.

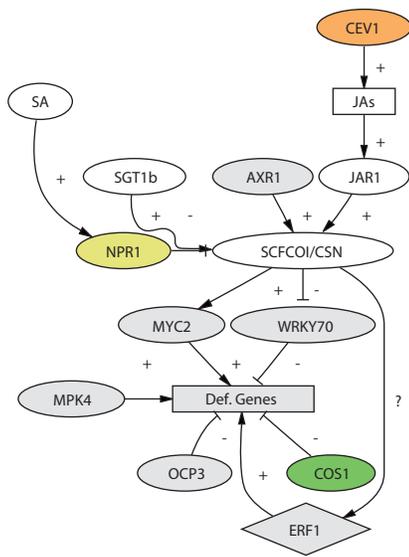
The roles, synthesis, and signaling mechanisms of jasmonic acid (JA) are subjects of intense interest, especially to those in the plant defense field (1–4). JA, a 12-carbon cyclopentanone oxylipin, is activated by its conjugation to hydrophobic amino acids (most notably L-isoleucine) by enzymes such as JAR1. Jasmonoyl isoleucine (JA-Ile) signals through COI1 [CORONATINE INSENSITIVE1 (5–8)], which has been identified as its receptor (9). This allows basic helix-loop-helix (bHLH) transcription factors such as MYC2 to regulate various target genes, including genes involved in defense and development. COI1 is part of an ubiquitin E3 ligase complex, which is itself associated with another large protein complex, the COP9 signalosome (10). JA-Ile binding to COI1 promotes the interaction between the COI1 complex and JAZ (JASMONATE ZIM-motif) proteins (5–8), several of which form homo- and heterodimers in yeast (11, 12). JAZ proteins (5, 6, 13) control a variety of jasmonate responses, including defense gene expression and growth responses to wounding. JAZ proteins bind transcription factors such as MYC2, preventing jasmonate signaling by an unknown mechanism that may require the action of corepressors. JA-Ile binding



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**Fig. 1.** Pathway image captured from the dynamic graphical display of the information in the Connections Map available 19 January 2010. Please see the pathway ([http://stke.sciencemag.org/cgi/cm/stkcm;CMP\\_13931](http://stke.sciencemag.org/cgi/cm/stkcm;CMP_13931)) for a key to the colors and symbols, for details about the pathway components, and to access the underlying data.



**Fig. 2.** Pathway image captured from the dynamic graphical display of the information in the Connections Map available 26 January 2006. Please see the pathway ([http://stke.sciencemag.org/cgi/cm/stkecm;CMP\\_13931](http://stke.sciencemag.org/cgi/cm/stkecm;CMP_13931)) for a key to the colors and symbols, for details about the pathway components, and to view the most current information.

to COI1 promotes ubiquitination of the JAZ proteins, which targets them for proteolysis. The destruction of JAZ proteins depends on the presence of a Jas motif, but some naturally occurring JAZ protein variants, at least some of which are generated by alternative splicing, lack this motif (12, 13). These variants appear to be more stable than full-length JAZ proteins and they, unlike the full-length proteins, can down-regulate jasmonate responses (12). The multiprotein complex Mediator is necessary for the correct transcription of at least some jasmonate-responsive genes (14).

Although the pathway shown here (Fig. 1) represents jasmonate regulation of gene expression in vegetative tissues (leaves), the pathway is expected to show the same basic structure in flowers, where it is required for anther elongation, correct dehiscence, and pollen viability in *Arabidopsis*. Transcriptional profiling has identified genes that are differentially regulated in

jasmonate-deficient *oxophytodienoic acid reductase 3 (opr3)* mutant anthers in response to treatment with methyl jasmonate (15). There are many examples of the effects of jasmonate signaling on plant growth in flowers and in vegetative tissues. For example, new leaves that emerge after a plant is wounded have a higher trichome density than leaves present before wounding. In the absence of wounding, jasmonate can also increase trichome density in newly developing leaves. Increased trichome density in response to methyl jasmonate treatment depends on the bHLH transcription factor GL3 [GLABROUS3 (16)]. Recently, a regulatory mechanism controlling the synthesis of JA (the precursor of JA-Ile) has emerged. microRNA319 (miR319) targets the transcripts of several TCP (teosinte branched1/CYCLOIDEA/PCNA) family transcription factors that bind to and activate the promoters of genes that encode key mediators of JA biosynthesis such as LIPOXYGENASE2 (LOX2). miR319 is thus a negative regulator of JA synthesis (17). For a historic representation of the pathway before the current update, see Fig. 2.

**Pathway Details**

URL: [http://stke.sciencemag.org/cgi/cm/stkecm;CMP\\_13931](http://stke.sciencemag.org/cgi/cm/stkecm;CMP_13931)

Scope: Specific

Organism: plants: *Arabidopsis*

Canonical Pathway: Jasmonate Signaling Pathway ([http://stke.sciencemag.org/cgi/cm/stkecm;CMP\\_13931](http://stke.sciencemag.org/cgi/cm/stkecm;CMP_13931))

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