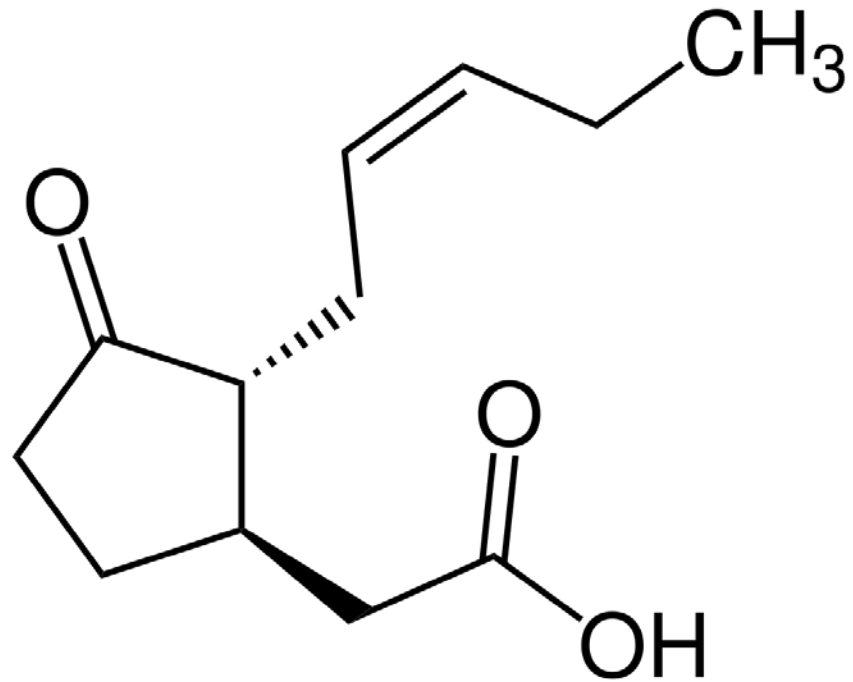


Jasmonates
Jasmonic acid (JA)



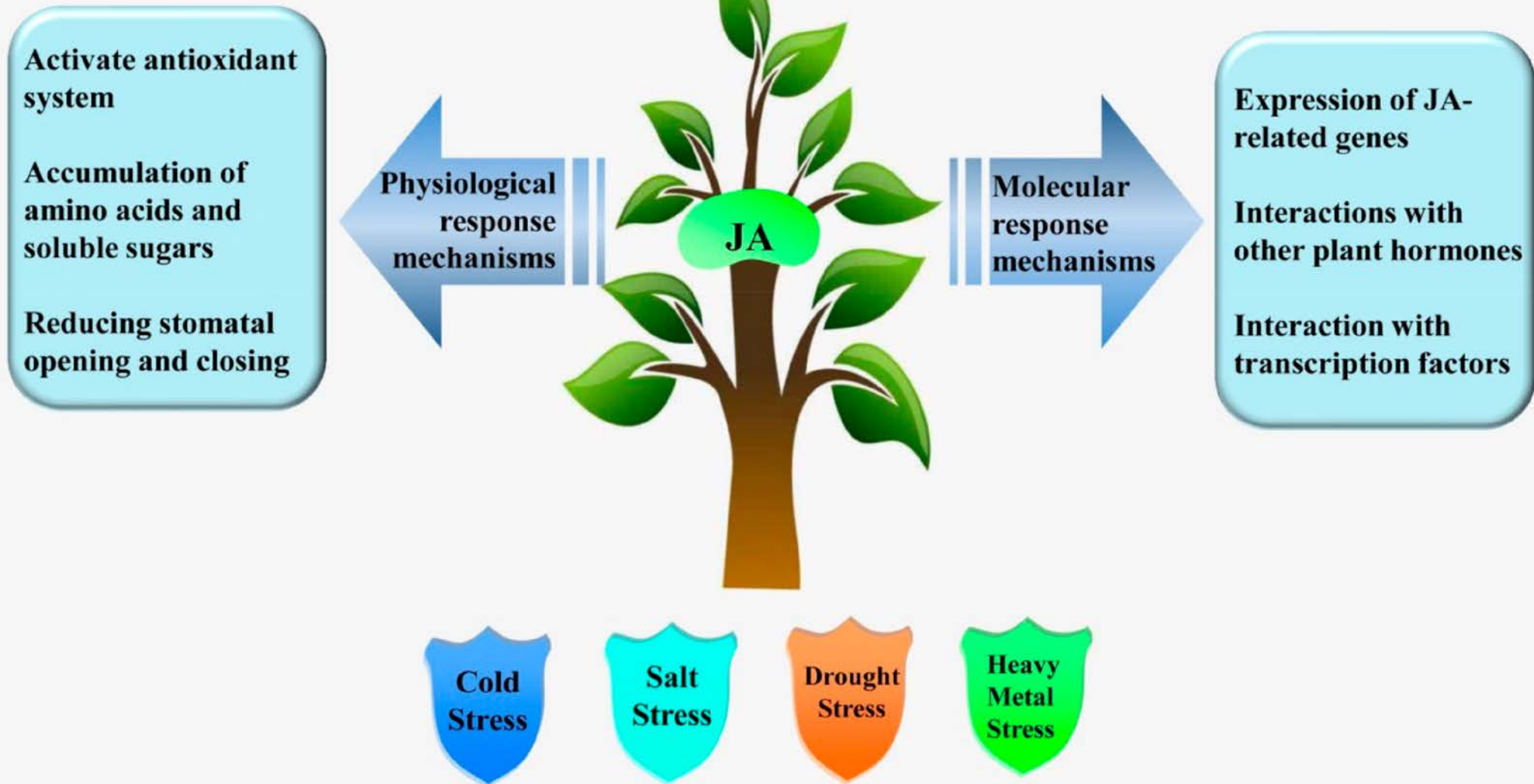
Function of jasmonates

- **Adaptation to environmental stress**
- **Activation of plant defense**
- **Regulation of plant development**

- **Local responses vs. systemic responses**
- **Travel through vascular system**

- **-Defense:**
 - **Herbivory, necrotrophic (not biotrophic) microorganisms**
 - **Wounding**

Exogenous JA



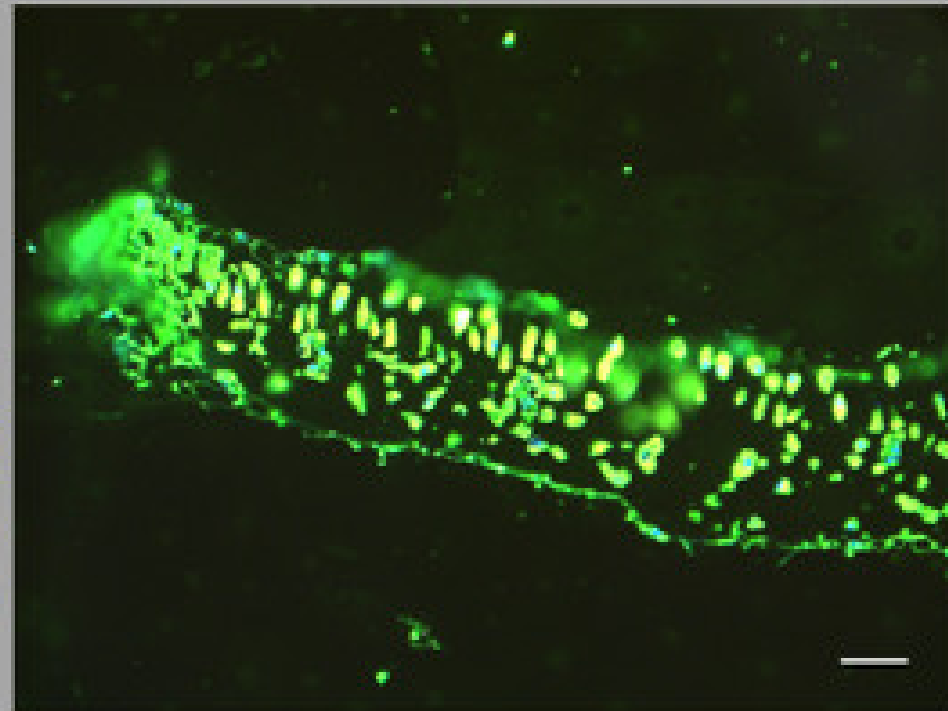
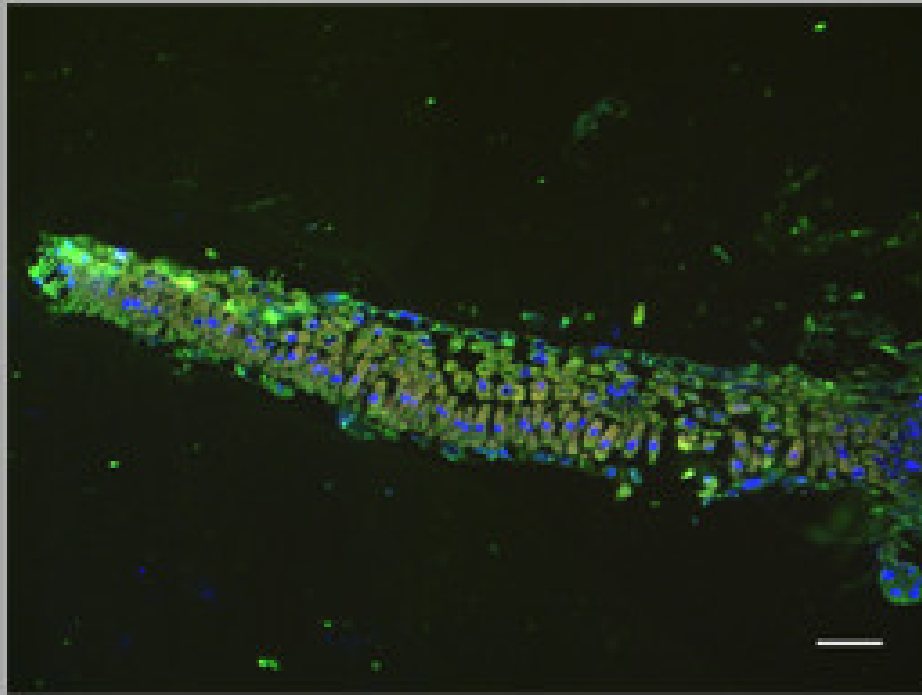
What are defense-related genes/proteins?

- PR1 (pathogenesis related 1 protein): salicylic acid marker
- PDF1.2: JA marker
- Antioxidant enzymes
- Proteinase inhibitors
- Cell wall strengthening enzymes (callose deposition)
- Enzymes involved in secondary metabolites (toxin, e.g. nicotine, etc.)
- Enzymes involved in volatile biosynthesis
- Defense hormone synthesis and signaling
- Cell death-related genes (local response)
- Long distance transport of threat information (systemic signaling)

JA is rapidly induced after stress application: here wounding

control

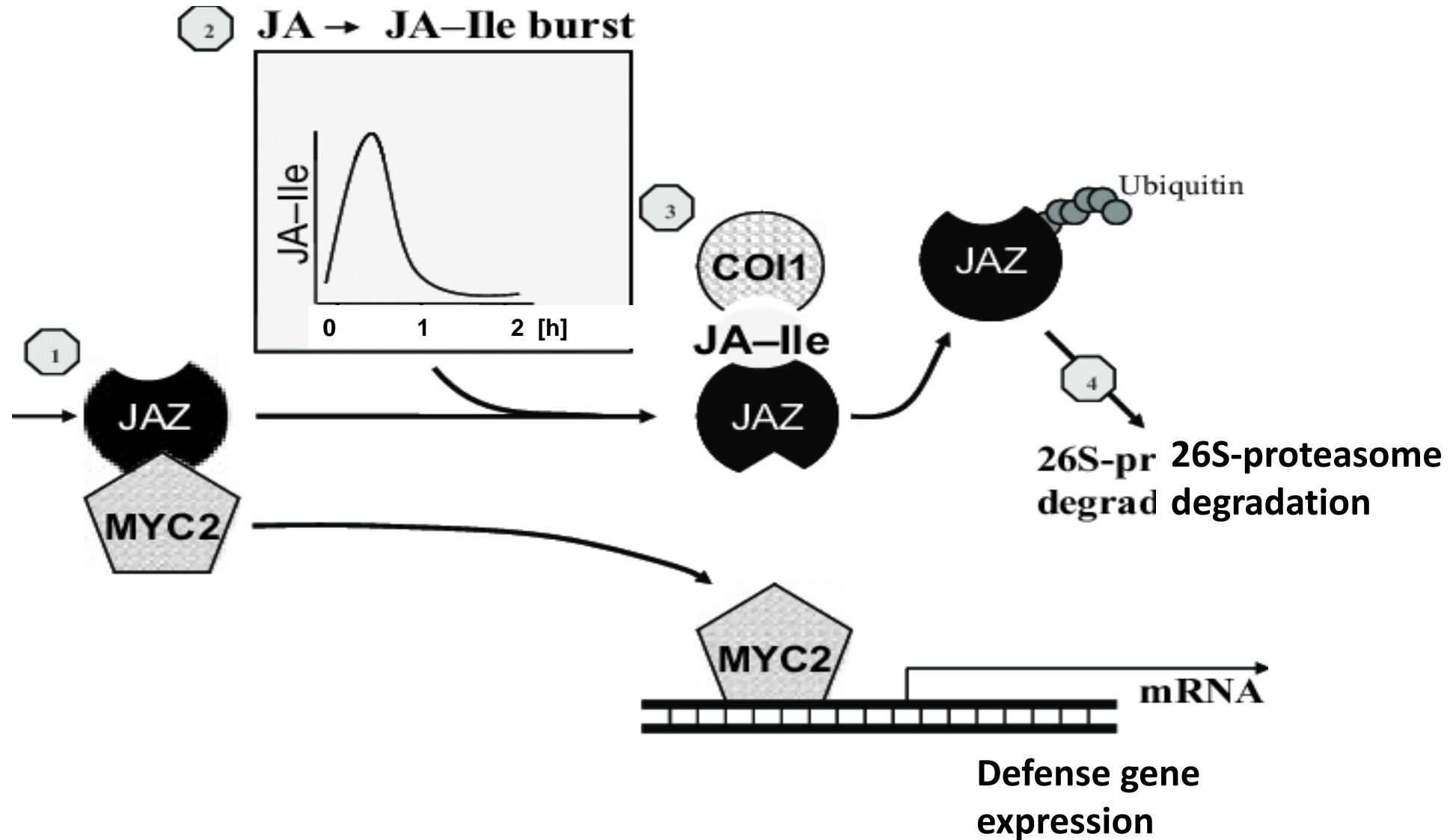
20 min after mechanical wounding



(Antibody from Agrisera)

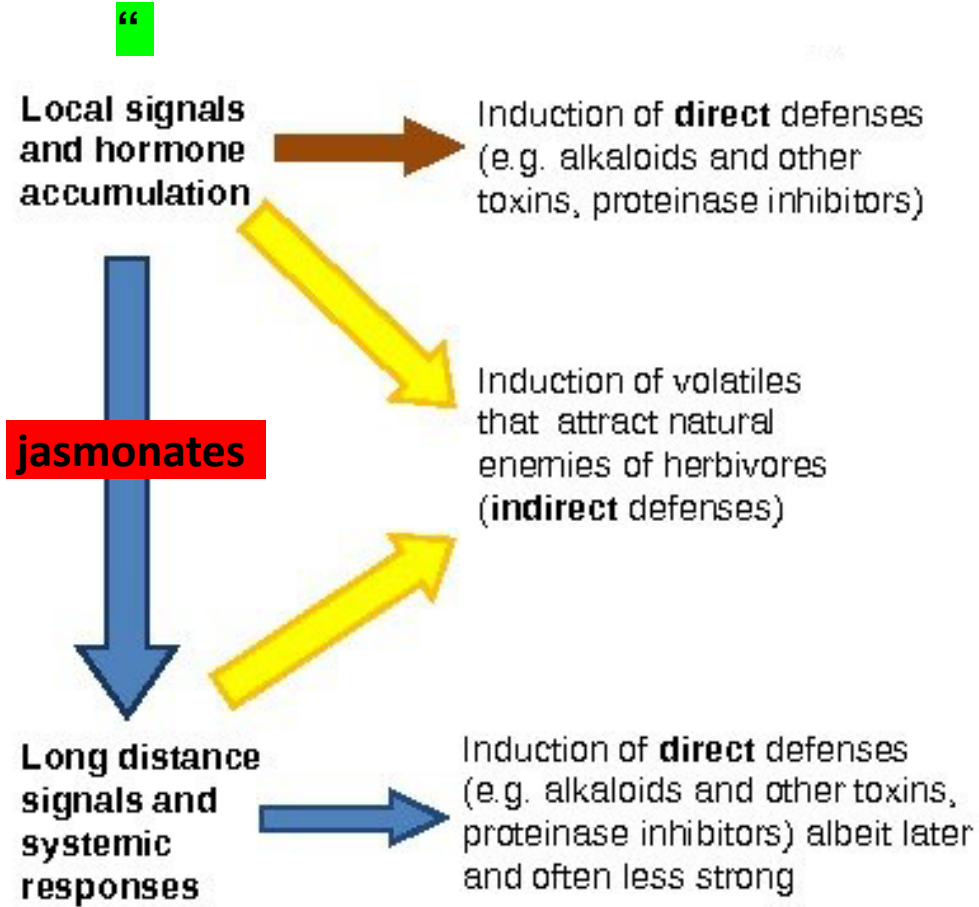
bars = 50 μ m

JA-Ile burst 30 min after stress application



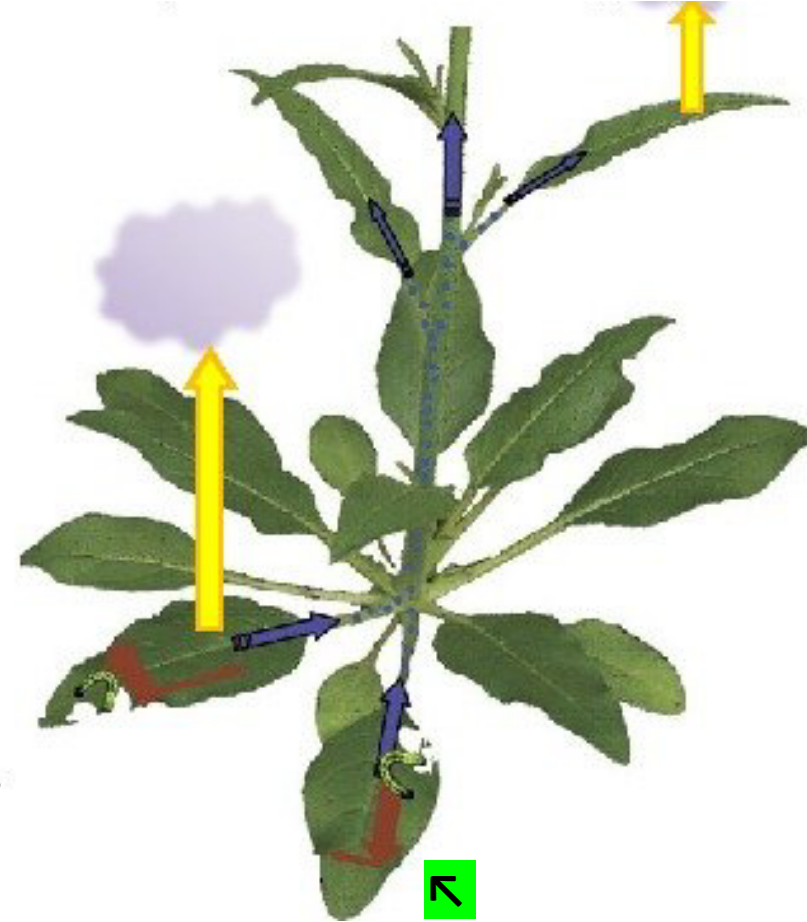
JA induces systemic resistance

e.g. herbivore attack



Distal leaf is alarmed.

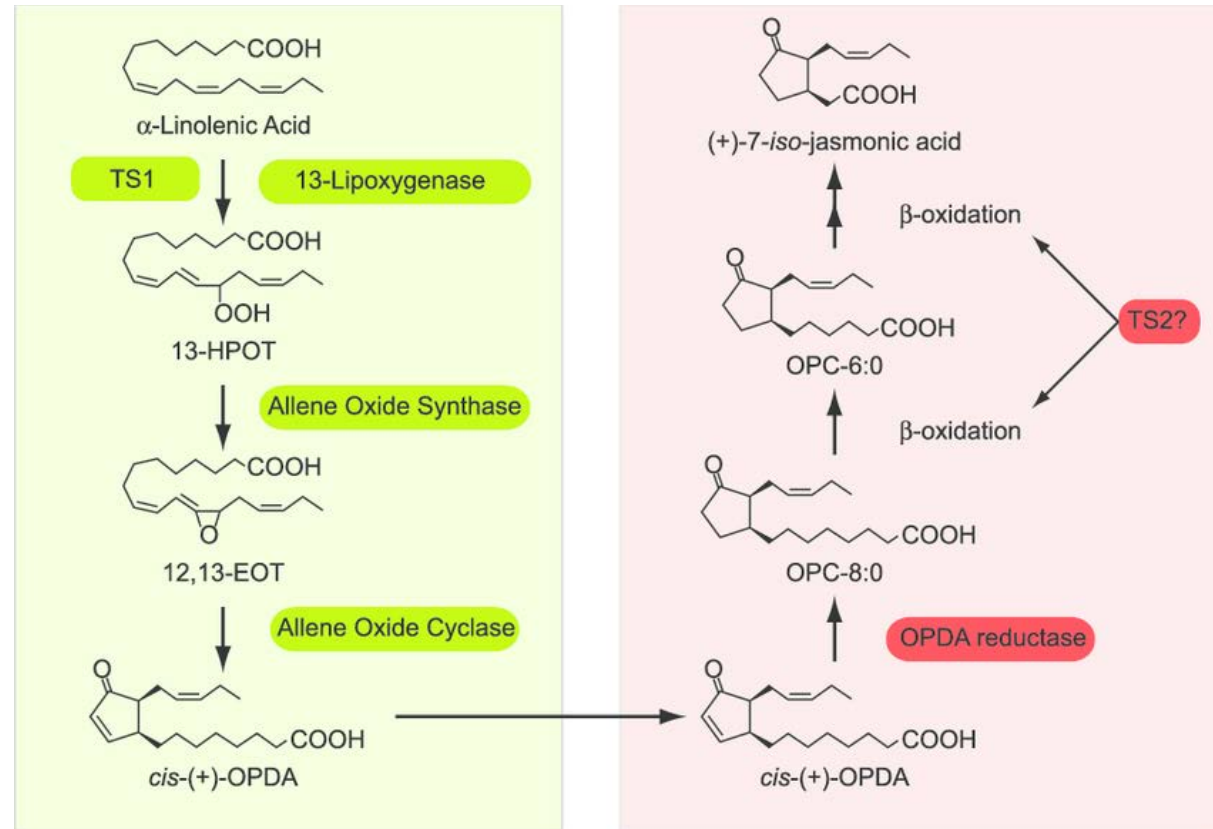
- higher defense level
- „priming“ for later attack



e.g. herbivore attack

Biosynthesis of JA

1



The octadecanoid pathway.

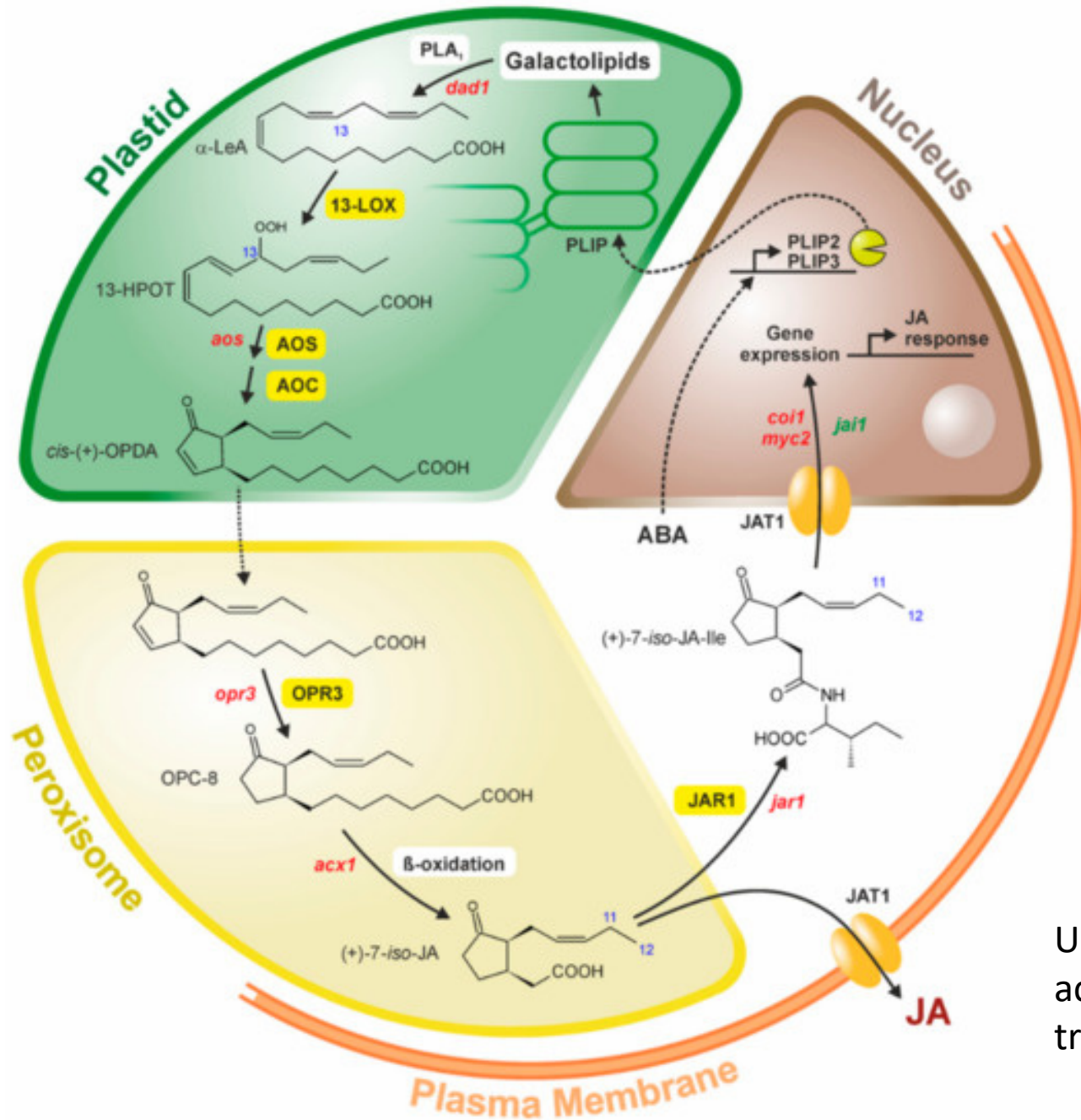
PLASTIDS (green):

The first step in jasmonate biosynthesis is the peroxidation of α -linolenic acid (18:3) by 13-lipoxygenase to form (13S)-hydroperoxyoctadecatrienoic acid (13-HPOT). 13-HPOT is transformed into *cis*-(+)-12-oxophytodienoic acid (OPDA) through the sequential action of allene oxide synthase and allene oxide cyclase.

PEROXISOMES (red):

The cyclopentenone ring of OPDA is reduced to 12-oxophytoenoic acid (OPC-8) by OPDA reductase. Next, three beta-oxidation cycles shorten the carboxylic side chain of OPC-8 to produce the 12-carbon JA.

JA-Ile is the active form

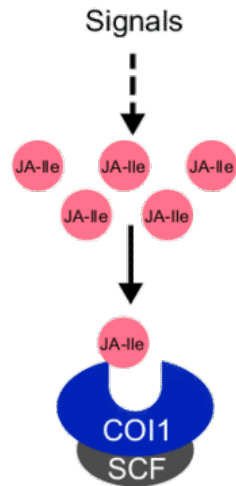


Upon release into the cytosol, JA is conjugated with amino acids by JAR1 or exported by a JA-transporter JAT1. The same transporter allows import of JA-Ile into the nucleus.

JA-Ile signal transduction

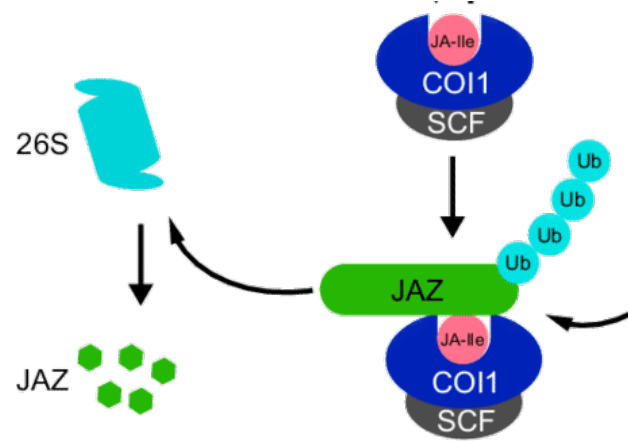
2

JA-Ile binds receptor
COI1



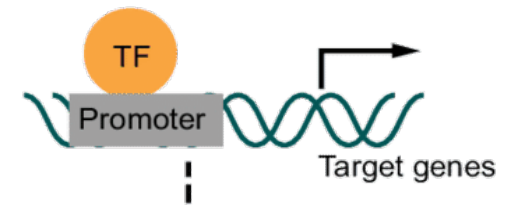
3

JA-receptor complex
degrades JAZ via 26S
proteasomes



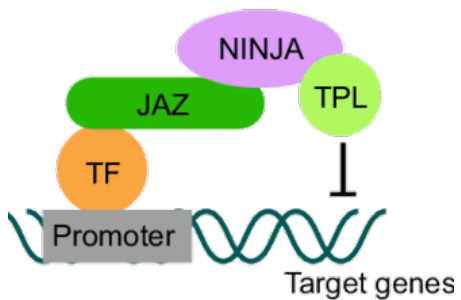
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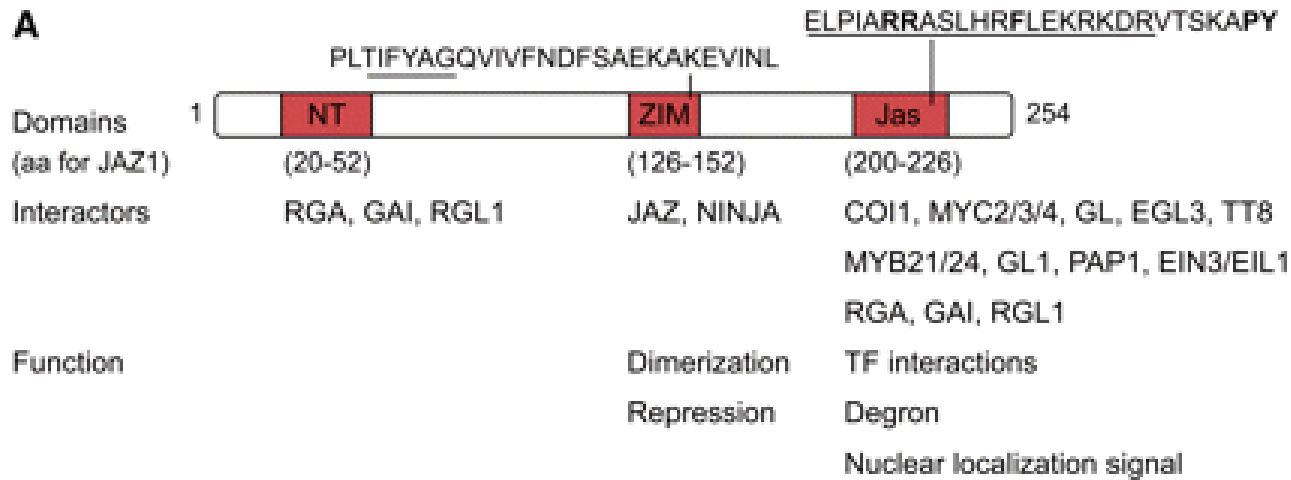
JA-responsive genes
are expressed



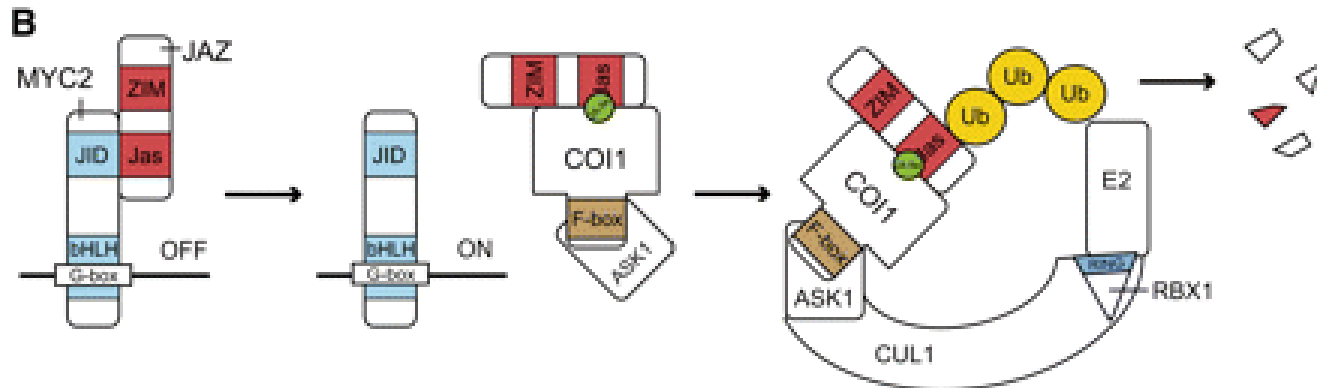
1

JAZ repressors prevent
transcription





JAZ degradation allows MYC2-mediated activation of JA genes (details)



JAZ Domain Structure and JA-Ile–Triggered Degradation by the Ubiquitin-Proteasome Pathway.

(A) Schematic representation of the JAZ1 protein and its conserved domains. Known protein interactors and functions are depicted. The TIFY motif for the ZIM domain and the JAZ degren for the Jas domain are underlined.

(B) In the absence of JA-Ile, JAZ binds MYC2 and represses gene expression. COI1-SKP may form a substrate adaptor that, with JA-Ile and InsP5 as a cofactor, binds the Jas domain of JAZ proteins. Upon formation of the SCF^{COI1} E3 ligase complex, JAZ1 is polyubiquitinated, which marks it for degradation by the 26S proteasome.

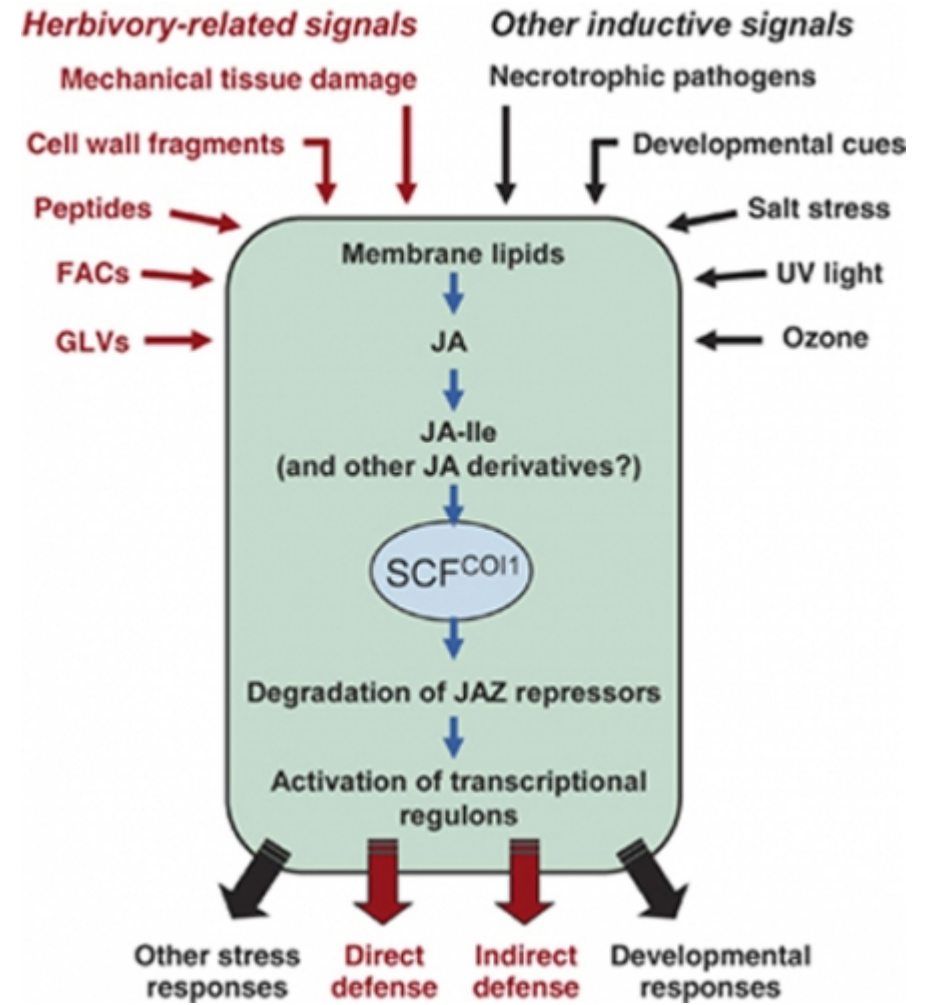
aa, amino acid; NT, N-terminal domain.

Growth-defense balance

Inactivation of JAZ proteins promotes defense on the expense of growth.

growth

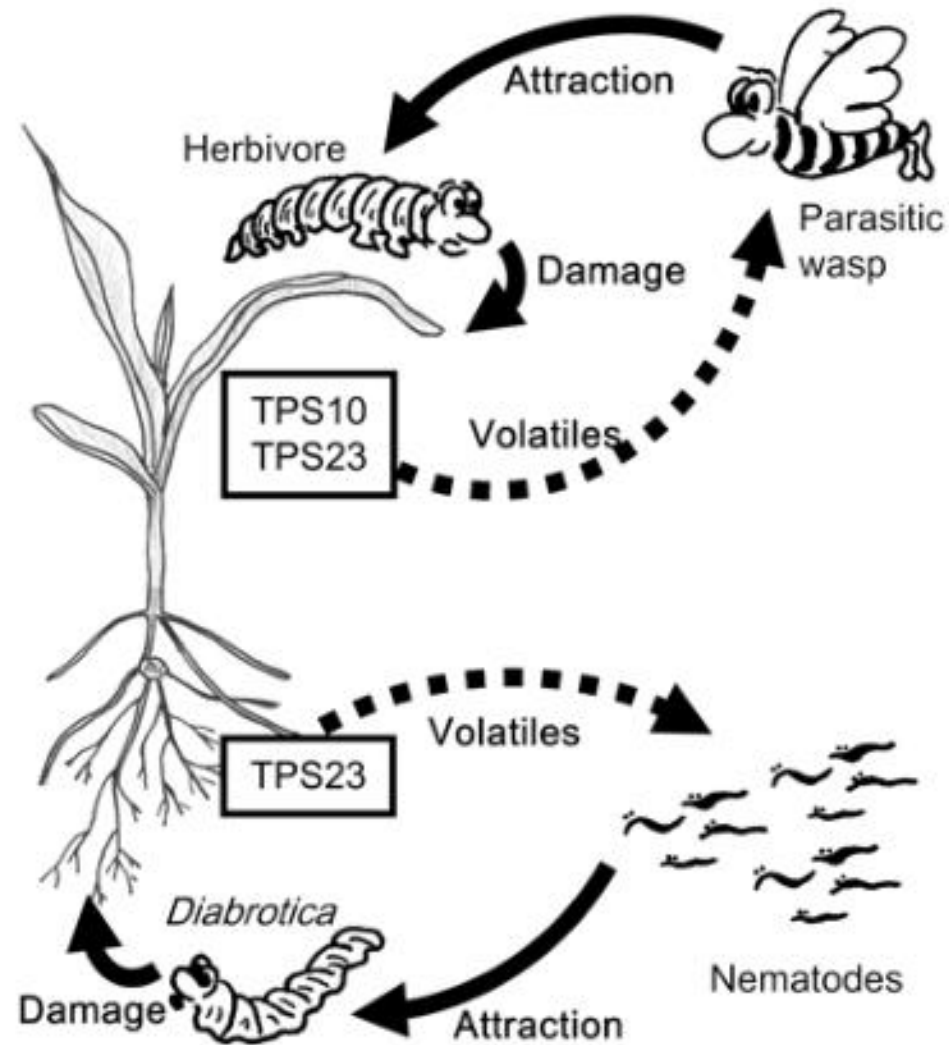
defense



Plant has to decide to invest in either growth or defense.

Jasmonic acid: Plant-insect co-evolution

Tri-trophic interactions



Degenhardt (2009)
Plant Physiology
149:96-102