

Figure 1 | Five steps in jasmonate signalling^{1,2}. **a**, JAZ proteins are normally bound to transcription factors and inhibit their activity. **b**, In response to attack, jasmonoyl-isoleucine (JA-Ile, marked with a star) stabilizes the interaction between COI1 and JAZ. **c**, The JAZ protein is probably then modified by ubiquitin (U), so marking it for destruction.

d, JAZ is destroyed, liberating the transcription factors; **e**, this allows transcription of genes that produce proteins involved in defence and development, as well as of JAZ genes to restrain the jasmonate response. (Only the COI1 component of the SCF^{COI1} enzyme complex of which it is a part is shown.)

proteins were unstable *in vivo* when treated with jasmonate, proteins with a truncated carboxyl terminus resisted degradation in response to such treatment.

All of this fits in well with a role for these proteins as repressors that might be destroyed upon perception of jasmonate. The proteins are called JAZ proteins, and they are encoded by approximately 12 genes in *Arabidopsis*. We will know the exact number only when all of them are tested for their roles in jasmonate signalling. Additionally, some of these genes encode multiple proteins that have different abilities to repress jasmonate responses⁵. Why so many JAZ proteins? Perhaps, for one thing, they offer enormous regulatory potential — especially if other hormone-signalling pathways impinge on JAZ gene expression.

Now, at last, we know that the site of jasmonate perception consists of two proteins — COI1 (in the SCF^{COI1} complex) together with one of several JAZ proteins (Fig. 1). In a first regulatory step, a small amount of the jasmonic acid precursor hormone that accumulates is attached enzymatically to molecules such as L-isoleucine, producing an active ligand, jasmonoyl-isoleucine (JA-Ile)⁶. Using an elegant yeast two-hybrid strategy, Thines *et al.*¹ showed that JA-Ile interacts with and stabilizes the COI1-JAZ complex. Then, SCF^{COI1} probably tags the captive JAZ proteins with ubiquitin, condemning them to rapid destruction.

Extending the story, Chini *et al.*² found that the carboxyl terminus of their JAZ protein bound to MYC2, a gene transcription factor involved in jasmonate signalling in *Arabidopsis*. So, after destruction of JAZ proteins, MYC2 can set to work regulating jasmonate-dependent gene expression that activates the plant's defences.

Some fascinating questions remain. Where does JA-Ile bind on the JAZ-COI1 complex? The possibility that COI1 acts as a receptor has already been suggested⁷. How many ligands

derived from jasmonic acid (or introduced into plant cells by pathogens) can bring COI1 and JAZ proteins together? In the scheme of jasmonate signalling, we already know that there is a positive feedback loop where jasmonic acid activates its own synthesis⁴. But it's not good to be in a permanent state of alarm: what puts the brakes on jasmonate signalling? The new data reveal a second type of regulatory loop based

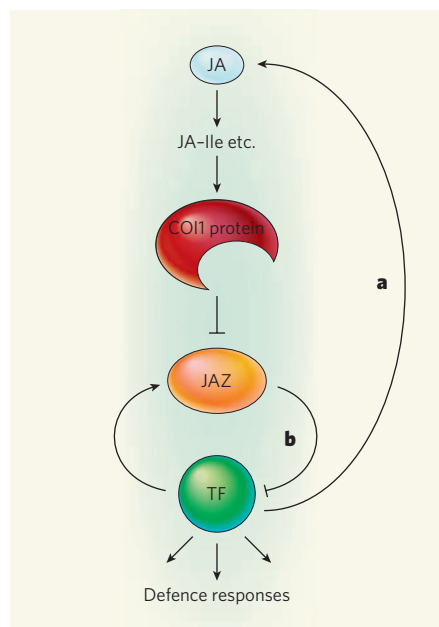


Figure 2 | Primary regulatory cycles in jasmonate signalling. Synthesis of jasmonic acid (JA) is self-promoting (feed-forward loop **a**). Loop **b** is the newly discovered² negative feedback loop involving JAZ proteins and transcription factors (TF) such as MYC2. These two regulatory cycles may be interlocked, but we can expect to find further complexity in the mechanism if, for example, some JAZ proteins bind to transcriptional repressors. Indeed, evidence for secondary regulatory loops already exists. In a regulatory circuit that is not shown here, MYC2 can repress the synthesis of its own transcripts⁹.

on JAZ protein action, whereby jasmonate signalling activates JAZ gene transcription, leading to the downregulation of jasmonate action (Fig. 2). As a thought game, one can imagine similar cycles for each combination of JAZ protein and transcription factor. The importance of these regulatory loops is clear. They bring us to a new level of understanding of how jasmonic acid, the 'cell ingress pro-hormone', activates plant defences in response to cell intrusion.

At this point, researchers working on the developmental hormone auxin must be acknowledged for providing a paradigm for hormone signalling through proteins closely related to COI1 (ref. 7). And it is also intriguing that several JAZ-like genes participate in developmental processes as well as in defence⁸. The new work^{1,2} and a related paper⁵ open possibilities for studying how the fundamental processes of growth control and defence have coevolved, and how they are appropriately managed in complex organisms. In any case, a dynamic yet robust biological security system, tested and shaped over millions of years, has been revealed to us.

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Correction

In "Microbiology: The inside story" by Laurie E. Comstock (*Nature* **448**, 542–544; 2007), methanogenic archaea should have been cited as consumers not of methane but of hydrogen.