

## SYSTEMS BIOLOGY

## Plant networks

A network of ~6,000 binary protein–protein interactions in *Arabidopsis thaliana* has been generated by testing all pairwise combinations of ~8,000 plant proteins using yeast two-hybrid methodology. This map should aid characterization of some of the many genes with unknown function in this model plant and should provide insights into network evolution.

The overall topology of the map is similar to that of maps generated for other species, including yeast, worms and humans. It shows ‘communities’ of proteins with known shared biological functions and suggests new hypotheses by linking proteins that were previously thought to be involved in separate processes. An example application of the network is provided in a companion paper by Mukhtar *et al.* that examined how proteins from evolutionarily distant bacterial and fungal pathogens interact with the plant immune system: they converge on a small number of highly connected proteins.

*A. thaliana* has a higher proportion of duplicated genes than most non-plant species, so this interactome has provided an ideal opportunity to examine how the connections of paralogues are ‘rewired’ during evolution. The authors found that, after a duplication event, the rate of change in interactions is initially rapid and then slows down; a similar rate change occurs for protein sequence divergence. These findings are consistent with an initially relaxed and then tighter selective pressure on retained paralogues. The *A. thaliana* interactome highlights the role of protein–protein interactions in evolution — an aspect to be explored further by comparing this plant network with those of other species.

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**ORIGINAL RESEARCH PAPERS** *Arabidopsis* Interactome Mapping Consortium. Evidence for network evolution in an *Arabidopsis* interactome map. *Science* **333**, 601–607 (2011) | Mukhtar, M. S. *et al.* Independently evolved virulence effectors converge onto hubs in a plant immune system network. *Science* **333**, 596–601 (2011)

