

research highlights

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Beyond classical genetics

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Life is complex. To understand even some of the limited aspects of living organisms, we have to reduce this complexity to a manageable scale. While there is still ample room for strict reductionist approaches, in fields such as plant immunity the shift to systems biology strategies and large scale data collection has begun. Fumiaki Katagiri and colleagues, writing in *PLoS Genetics*, combine genetic network deconstruction with high-resolution techniques to reveal the inducible immune response in all its beautiful complexity. They conclude that interactions inside the network protect it against microbial interference, making the plant more efficient in its constant fight against fast-evolving pathogens.

The authors study the broad transcriptional and hormonal response induced in *Arabidopsis thaliana* by the peptide flg22, a fragment of bacterial flagellin. They previously demonstrated that the immune network is strongly bottlenecked by four main sectors controlled by ethylene, salicylic acid, jasmonic acid and the *PAD4* (*PHYTOALEXIN DEFICIENT 4*) gene. Mutations disabling a single sector have practically no effect on immunity against



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bacteria, but a quadruple mutant is severely immunocompromised. Now, using a massive data collection approach involving transcriptome and hormone profiling,

Katagiri and colleagues analyse the signalling responses to flg22 with an unseen level of granularity. After filtering, they assess the effect of each sector on several thousands of individual output genes. The conclusion is that the regulation of most of these genes depends on the complex interactions of several sectors, and not on easily predictable linear pathways. Moreover, a high proportion of the flg22 transcriptome is buffered against network interference. For example, a third of the genes are completely unaffected if two of the sectors are disabled.

This high level of resilience is biologically relevant, as continuously evolving pathogens inject effector proteins or molecules that will disable large parts of the plant immune response, and the plant must be resistant to these perturbations to mount an effective defence and survive. An analogy with the decentralized worldwide computer network we call the Internet can be made, as its communication routes are supposed to survive the nuclear destruction of many nodes. Similarly interesting is the fact that the genetic buffering that generates resilience against perturbations also makes plants hard to study with traditional genetics. It is as if plants try to hide their defence mechanisms not only to the pathogens, but also to us.

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