GENETICS

Stratospheric order mutants

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Many *Arabidopsis* genes are still not associated with a biological function. Reverse genetics, applied mostly through insertional mutagenesis and recently with genome editing, is a powerful approach to assign a function to one gene. Unfortunately, the redundancy of plant genomes often makes it necessary to mutate several genes before obtaining a phenotype. The amount of time-consuming background work makes it difficult to produce high-order mutants. However, two recent studies, on abscisic acid (ABA) and immune signalling, used mutants of a level likely unseen before.

Jian-Kang Zhu and collaborators produced plants mutated on 12 (duodecuple) and all 14 (quattuordecuple) members of the PYR/PYL family of *Arabidopsis* ABA receptors, by combining insertion mutants and multiplex CRISPR–Cas9. The plants were extremely insensitive to ABA for various processes, such as stomatal closure, germination and senescence, but unexpectedly some ABA-independent responses to osmotic stress were enhanced.

Another project, headed by Jian-Min Zhou, focused on receptor-like cytoplasmic kinases (RLCK) subfamily VII. Members of this subfamily seem to connect membrane perception of pathogen signals to downstream events, such as MAPK activation. There are 46 RLCK VII in *Arabidopsis*, distributed in 9 subgroups. Once again combining insertion and CRISPR–Cas9 mutants, the authors produced high-order mutants for each subgroup. They characterized their response to various patterns, and found, for example, that one subgroup is necessary for chitin signalling.

These studies show that old and new techniques can be merged to obtain genetic tools that were unreachable only a few years before. It is now possible to knock out entire gene families and, hopefully, this will help to reduce the percentage of *Arabidopsis* genes with unknown function.

 Guillaume Tena

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