Plant genetics

Self-recognition in pollination

Studies reveal a new way for plants to distinguish self from non-self during pollination

Genetic diversity is crucial for ensuring the fitness of a species. One way plants promote diversity is by preventing inbreeding — also known as self-fertilization. Previous research demonstrated that *Petunia* uses a non-self-recognition system in which a pollen protein called S-locus F-box (SLF) interacts with a protein in the style S-RNase. S-RNase is toxic, and it prevents pollen-tube growth unless it is degraded by an SLF protein. Thus, pollen SLF functions by recognizing non-self S-RNases and degrading them, thereby allowing growth to continue.

However, researchers have been puzzled as to why the genetic diversity of the SLF gene is much lower than that of S-RNases in *Petunia*. According to Seiji Takayama of NAIST in Japan, "it remained a mystery how SLF recognizes a large repertoire of non-self female determinants." To shed light on this enigma, Takayama and colleagues sought to determine the molecular mechanism of self-recognition in *Petunia*.

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The scientists solved this mystery when they discovered that, unlike pollen of other plant species, *Petunia* pollen expresses not one, but multiple SLF-like proteins. At the start of their work, the team discovered several SLF-like genes that are expressed in pollen. But this was just the beginning. "It was tough work to show that each SLF recognizes and detoxifies a subset of non-self S-RNases," Takayama explains. "To search for the actual targets [S-RNases] of each SLF, we had to make several hundred transgenic plants."

Ultimately, they showed that these SLF proteins work together to recognize and degrade diverse S-RNases to promote non-self recognition. According to Takayama, the data provided convincing evidence that *Petunia* uses a 'collaborative non-self recognition model', which had never been described for other types of plants.

Since making these pioneering discoveries, the team has continued to uncover the molecular mechanism of collaborative non-self recognition. Takayama notes that during the research, "we identified six SLF genes." They then "thoroughly searched for SLFs using next-generation sequencing and found that 16–20 SLFs collaboratively function to detoxify non-self S-RNases."

They also "found evidence of gene conversion events," Takayama says. He considers these events to be "essential to the constitution of this 'non-self recognition' system and also to contribute to self-compatible mutation." The results of this work were recently published in *Nature Plants*.

All of this work was facilitated by NAIST which, according to Takayama, provided "a quiet and calm atmosphere suitable for scientific research, properly maintained research facilities, and leading-edge shared equipment."

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Close-up image of a petunia flower.

Reference

1. Kubo, K. *et al.* (2010) Collaborative non-self recognition system in S-RNase-based self-incompatibility. *Science* **330**, 796-799 (2010).

More information about the group's research can be found at the Intercellular Communications Laboratory webpage:
http://bsw3.naist.jp/eng/courses/courses102.html