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.

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.”

Reference


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