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Distinguished Professor Teh-hui Kao

(Intercollege Graduate Degree Program in Plant Biology, Penn State University) S-RNase-Based Self-Incompatibility in *Petunia*: a Complex Mechanism of Self/Non-Self Recognition between Pollen and Pistil

Self-incompatibility allows the pistil to reject self-pollen to prevent inbreeding and accept non-self pollen for outcrossing. Over the past three decades, my lab has been using *Petunia inflata* as a model to study the type of self-incompatibility that has so far been found in the Solanaceae and two other families. Self/non-self recognition is regulated by the highly polymorphic S-locus (e.g., >30 S-haplotypes have been reported in *Petunia*). Matching of the S-haplotype carried by the pollen and one of the S-haplotypes present in the pistil results in inhibition of self-pollen tube growth in the upper segment of the pistil. The S-locus houses the S-RNase gene for pistil specificity¹⁾ and multiple S-locus F-box (SLF) genes for pollen specificity^{2, 3)}. We have used pollen transcriptome analysis to identify a total of 17 SLF genes in S_2 -haplotype and S_3 -haplotype⁴⁾, and used co-immunoprecipitation and mass spectrometry to show that all these SLF proteins are assembled into similar SCF complexes, which contain a conventional Rbx1 (named PiRBX1), a pollen-specific Cullin1 (named PiCUL1-P) and a pollen-specific Skp1-like protein (named PiSSK1)⁵⁾. According to the collaborative non-self recognition model³⁾, for a given S-haplotype, each SCF complex interacts with a subset of non-self S-RNases, determined by the SLF protein it contains, to mediate their ubiquitination and degradation via the 26S proteasome. A complete suite of SCF complexes is required to detoxify all non-self S-RNases to allow cross-compatible pollinations. We have used a transgenic functional assay²⁾ to determine the interaction relationships of SLF proteins of S_2 -haplotype and S_3 -haplotype with 11 S-RNases. So, far 137 interaction relationships have been determined. We have used a chimeric gene approach to identify candidate amino acids responsible for differential interactions between SLF proteins and S-RNases⁶). We have used CRISPR/Cas9 genome editing to examine the roles of S_2 -SLF1, PiCUL1-P and PiSSK1⁷, and the results fully support the collaborative non-self recognition model and the interaction relationships between SLF proteins and S-RNases determined by the genetic approach.

References

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