

Plant genetics

Understanding female reproductive organ formation

A deceptively simple appearance belies the complex genetic interactions that occur during the formation of Arabidopsis thaliana's female reproductive organs

Flowers are not simply nature's decorations, they serve a more practical purpose — as plant reproductive organs. A plant's male reproductive organs, the stamens, are collectively known as the androecium; whereas the stigma, style and ovary are collectively known as the gynoecium, the female counterpart. Mitsuhiro Aida, from the Graduate School of Biological Sciences and colleagues investigated the genetic interactions involved in the formation of the closed structure of the gynoecium.

“Much of our daily food comes from fruits or seeds, all of which are products of the gynoecium,” notes Aida. What makes the gynoecium special is its closed structure; this shields developing seeds from changing environmental conditions, allowing them to flourish. Flowering plants with this closed gynoecium structure have proved to be the most successful plant group because “a delicate fertilization process is able to take place in a more regulated manner under more stable conditions than is possible for plants without a gynoecium,” explains Aida.

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He and colleagues were interested in understanding how the gynoecium formed as a closed structure via the fusion of developmental units similar in form to leaves, known as carpels. Previously, they had been working on the *CUP-SHAPED COTYLEDON* genes, *CUC1* and *CUC2* — investigating their function as developmental regulators. While *CUC1* and *CUC2* influence the development of seeds, over-expression of the genes can be ‘too much of a good thing’ and stop adjacent organs from fusing, which would impede the formation of closed gynoecia.



The *Arabidopsis thaliana* flower; a popular model for plant studies.

As closed gynoecium are common in nature, Aida recalls, “We hypothesized that there should be a factor that maintains appropriate expression of *CUC1* and *CUC2* to ensure proper gynoecium development.” They identified the *SPATULA* gene, *SPT* as the most likely candidate since loss of *SPT* function had been observed to result in plants with split gynoecia. Interestingly, the *SPATULA* gene was named after the strange shape of the mutant gynoecia.

This was followed by an extensive study of *CUC1*, *CUC2* and *SPT* expression and corresponding gynoecium structures amongst wild type and mutant variants of *Arabidopsis thaliana*¹, a Eurasian small flowering plant also known as the thale cress.

The most significant finding was the domain-specific effect of *SPT* on *CUC* expres-

sion — suppressing it in the apical domain (thus ensuring closure in the top section of the gynoecium), while allowing it in the basal domain — facilitating seed development in the bottom section of the gynoecium.

It is possible that these interactions may be responsible for the closed gynoecia in other flowering plants. “Elucidating the functions of *CUC1/CUC2* genes and their regulators in gynoecium development will give us clues on how flowering plants evolved to elaborate reproductive organ systems,” notes Aida.

Reference

1. Nahar, M. A-U., Ishida, T., Smyth, D. R., Tasaka, M. & Aida, M. Interactions of *CUP-SHAPED COTYLEDON* and *SPATULA* genes control carpel margin development in *Arabidopsis thaliana*. *Plant Cell Physiology* **53**, 1134–1143 (2012).