Genetic Mechanisms of Different Flower Patterning

Dimorphic cleistogamous plants produce both closed (cleistogamous, CL) flowers and open (chasmogamous, CH) flowers on the same individual or on different individuals. However, few studies have investigated the genetic regulation of CH and CL flowering patterning in a naturally cleistogamous species. Pseudostellaria heterophylla demonstrates typical dimorphic cleistogamy, usually producing both CH and CL flowers on the same individual plant that appear in different positions and in different seasons (CH in spring and CL in summer). This species provides an excellent model for investigating the gene regulatory networks that control CH and CL flowering.

Dr. LUO Yan from Xishuangbanna Tropical Botanical Garden (XTBG) and her collaborators used the RNA-Seq platform based on Illumina Hiseq technology to compare the transcriptome of P. heterophylla CH and CL flowers to investigate differences in gene transcription patterns relating to CH and CL flowering processes. They aimed to identify differentially expressed genes involved in the transition from CH to CL flowering in the dimorphic cleistogamous species, and to investigate putative gene regulatory pathways that determine differences between CH and CL patterning and processes.

The researchers identified the homologues of 428 Arabidopsis genes involved in regulating flowering processes and estimated the differential gene expression patterns between CH and CL flowers. Some of those genes involved in gene regulatory networks of flowering processes showed significantly differential expression patterns between CH and CL flowers.

Two types of flower of *Pseudostellaria heterophylla*. a-d Chasmogamous (CH) flowering. **a** Habitat of *P. heterophylla* when producing CH flower. **b** *P. heterophylla* individuals with CH flowers. **c** CH flower is at the apical shoot. **d** SEM images of the early stage of CH flower development, with initiation of floral organs (S = sepal, A = stamen, G = carpel, 1–10 indicate the identified number of floral organs). **e–h** Cleistogamous (CL) flowering. **e** Habitat of *P. heterophylla* when producing CL flower. **f** *P. heterophylla* individuals with CL flowers (CL flowers are under the leaves and cannot be seen). **g** CL flower is in a lateral position on the stem (black arrows). **h** SEM images of the early stage of CL flower development, with initiation of floral organs. Bars show 5 mm in **c** and **g**, 40 μm in **d** and **h**.

They modified the gene expression controlling development as a consequence of environmental changes, leading to altered multiple flower developmental pathways. The researchers then proposed three modules (CO-FT module, STM-AP1 module, and ABCE model) that regulated flowering time, meristem development and patterning in natural populations of *P. heterophylla*.

The study was the first to analyze the flowering GRNs with RNA-seq based transcriptome in a naturally cleistogamous plant for understanding the genetic mechanisms of different flower patterning. It provided a foundation for dissecting the molecular basis of flowering time and patterns in naturally cleistogamous plants.

Their paper, entitled "Genomewide Analysis of Gene Expression Reveals Gene Regulatory Networks that Regulate Chasmogamous and Cleistogamous Flowering in Pseudostellaria heterophylla (Caryophyllaceae)", has been published in *BMC Genomics*.