

Supplementary Material

Supplemental Table S1. Prediction of conserved structural domains of FLA proteins in *P. deltoids*.

Supplemental Table S2. Prediction of conserved structural domains of FLA proteins in *Salix suchowensis*.

Supplementary Table S3. List of the C and N-terminal signals of *P. deltooides* genes identified by BIG-PI Plant Predictor and SignalP online programs.

Supplementary Table S4. Prediction of C-terminal GPI anchor attachment sites and N-terminal signal peptides in *S. suchowensis* genes identified by BIG-PI Plant Predictor and SignalP online programs, respectively.

Supplemental Table S5. Orthologous genes between *P. deltooides* and *S. suchowensis*.

Supplemental Table S6. Ka, Ks and Ka/Ks values of tandem and segmental duplication gene pairs in *P. deltooides* and *S. suchowensis*.

Supplementary Table S7. Conserved motifs predicted by MEME program in PdeFLA and SsuFLA.

Supplemental Table S8. The proportion of the number of Group I genes in the *FLA* gene family and at the genome-wide level in different species.

Supplementary Table S9. Corresponds to the list of p-values in Figure 6D. That is, the list of p-values corresponding to two-sided Student's t-test of relative gene expression between female pollinated and unpollinated treatments for *S. suchowensis* FLA Group I genes.

Supplementary Table S10. List of primer sequences used in qRT-PCR reactions.

Supplementary Sequence S1. List of the sequences of FLA proteins from eight species: *Corylus avellana* L. (23 members), *Quercus rubra* L. (29 members), *Cinnamomum kanehirae* (23 members), *Cinnamomum kanehirae* (25 members), *Zea mays* L. (26 members), *Cucumis sativus* L. (17 members), *Oryza sativa* L. (27 members,) and *Arabidopsis thaliana* (21 members).

Supplementary Figure S1. Significant ANOVA results on the proportions of Group I genes in woody and herbaceous plants.