

## **Domestication of double flowered Camellias: sequence variation and expression analyses of the *AGMAOUS* homolog**

Ziyan Nie, Tao Lyu, Zhengqi Fan, Xinlei Li, Jiyuan Li, Hengfu Yin\*

Research Institute of Subtropical Forestry, Chinese Academy of Forestry, Hangzhou, Zhejiang, China 311400

\*contact: hfyin@caf.ac.cn

Cultivated *Camellia* varieties are multifarious in floral shapes, and distinct double flower forms are remarkably attractive to breeders. The C class homeotic genes play essential roles in the regulation of stamen and carpel identity in various plants. Tinkering the function of C class genes can lead to the development of extra petals, which is a key domestication path of double flower (DF) formation. We have found that the modification of expression patterns of C class homolog in *Camellia japonica* (*CjAG*) was involved in DF development. Here, we have performed sequence analysis of *CjAG* and identified a polymorphic region near the 3' end of coding sequence; targeted sequencing in wild and multiple DF cultivars has revealed that this region is highly variable suggesting a functional diversification of different alleles. We propose that the determination of the region can serve as a molecular evidence to trace the origins of cultivated Camellias with different floral forms.