# **Physiological Characteristics and Transcriptome Analysis of Mixed Catkins Differentiation of** *Castanea mollissima*

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#### Introduction

*Castanea mollissima* is an important monoecious fruit crop with high economic and ecological value in China. It has unisexual catkins and mixed catkins, in which the mixed catkins can differentiate into male and female flowers. As we know, chestnut has an imbalance of the ratio of male and female flowers, contributing to the low yield of this species. However, the mechanisms involved in the development of mixed catkins are still not clear. Thus, revealing the molecular mechanism of C. mollissima 'Tanqiao' mixed catkins differentiation is of great significance for improving its fruit yield.



### Objiective

≻Clarify the cytological process of female and male flower development of C. mollissima 'Tanqiao'.

Explore the change characteristics of hormone content during the development of male and female flowers of C. *mollissima* 'Tanqiao'.

Screen several genes related to the differentiation of male and female flowers in the mixed catkins of C. *mollissima* 'Tanqiao'.

### **Materials and Methods**

### ≻Materials

Different stages of male and female flowers in C.

# Result

≻The female flower differentiation of C. *mollissima* 'Tanqiao' was divided into 8 stages (Fig.3A), and the male flower could be divided into 9 stages (Fig.3B).

The development of male and female flowers of C. *mollissima* 'Tanqiao' is closely related to plant hormone synthesis and transduction. The high contents of Salicylic acid (SA), gibberellin (GA<sub>3</sub>) and abscisic acid (ABA) promoted male flowers development (Fig.4A, B, C), while the dynamic changes of Zeatin (ZT) and jasmonic acid (JA) promoted female flowers morphogenesis (Fig.4D, E).

> The JA synthesis gene AOS3, the ZT-related gene CKX3, and UGTK4/5 were crucial genes in the development of female flower regulation. The GA biosynthesis-related genes  $GA_3OXI$ ,  $GA_2OX2$ , ABA synthesis pathway genes CYP707A1/2, and SA signaling gene TGA10 were the key genes in regulating male flower development (Fig.5). ≻Through WGCNA analysis, 10 genes were excavated, among which *IDD7* gene may be the key gene for female flower development of C. mollissima 'Tanqiao' (Fig.6).



#### mollissima 'Tanqiao' as shown in Fig. 1 and Fig. 2.



**Fig.1 Female flower** material of different stage



**Fig.2 Male flower** material of different stage

### >Methods

The development of C. mollissima 'Tanqiao' mixed catkins were investigated by the microscope method. We measured the eight types of hormones by the high performance liquid chromatography and enzyme-linked immunosorbent assay during its differentiation. Futhermore, we carried out RNA-Seq assays aimed at identifying differentially expressed genes responsible for male and female flower development in *C. mollissima*.



Fig.5 Heat map of differential gene expression trend of hormone synthesis and signal transduction genes related to flower development



M4(male flower flowering stage).

**Fig.6 Core gene coexpression network;** CMV\_002842 (*IDD*7).

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## Conclusion

 $\succ$ Our experimental results indicated plant hormone SA, GA played an major role in the process of male flower development. ZT and JA yet played an important role in the process of female flower development.

≻Zinc-finger protein transcription factor *IDD7* and phytohormone-related genes *CYP707A1/2*, *TGA10*, *AOS3*, *UGTK4/5*,  $GA_3OX1, GA_2OX2, CKX3$  were high related to the differentiation of male and female flowers in the mixed catkins of C. mollissima 'Tanqiao'.