# **Ting Shi**



#### Areas of Research

Flower development, flowering molecular biology and genomics in fruit tree, germplasm resources and genetic breeding of *Prunus mume*.

#### **Contact Information**

Office location: Room B7002 Life Sciences

Building (Lab room B7003)

Office phone: 86-025-84395724

Lab location: Room B7003-7005 Life Sciences

Building

Email address: shiting@njau.edu.cn

## **Research Interests**

Flower development, flowering molecular biology and genomics in fruit tree, germplasm resources and genetic breeding of *Prunus mume*.

I work on the flower development, flowering molecular biology and genomics in *Prunus mume*. Some of the problems we are currently working on are described below:

#### 1. Flower development

Reproduction is a critical stage in the flower development process, and its failure causes serious problems affecting fruit quality and yield. Pistil abortion is one of the main factors in unsuccessful reproduction and occurs in many fruit plants. In Japanese apricot, the problem of pistil abortion is very common and affects fruit quality and plant yield; however, its molecular mechanism is not clearly understood. Therefore, in the current study, we used RNA-Seq to identify the differentially expressed genes (DEGs) and pathways actively involved in pistil abortion. A total of 60 transcription factor families such as MADS-box, NAC and TCP showed their role in this process. RT-qPCR assays confirmed that the expression levels were consistent with RNA-Seq results. This study provides an alternative to be considered for further studies and understanding of pistil abortion processes in Japanese apricot, and it provides a reference related to this issue for other deciduous fruit crops.

#### 2. Flowering

Prunus mume blooms earlier than other deciduous fruit trees, but different regions have different blooming periods. The time of anthesis is related to the dormancy period, and a certain amount of chilling promotes bud break and blooming. To identify the

relationship between blooming time and the climatic adaptation of *P. mume* cultivars in China, the nuclear and chloroplast genomes of 19 cultivars from the main cultivation areas of *P. mume* in China were resequenced. Associated with the blooming time groups, 21 selective sweep regions were identified, which could provide evidence supporting the possible model of *P. mume* domestication originating due to natural selection. Furthermore, we identified a flowering gene, *FRIGIDA-LIKE 3* (*FRL3*), seems to affect the blooming time and the climatic adaptation of *P. mume* cultivars. This study is a major step toward understanding the climatic adaptation of *P. mume* cultivars in China.

# **Education Background**

**Bachelor:** Jinling Institute of Technology **Master:** Nanjing Agricultural University **Doctor:** Nanjing Agricultural University

# Work experience

Lecturer, Nanjing Agricultural University, 2014-

## **Honors and Awards**

### Selected Publication

Shi Ting, Iqbal S, Ayaz A, et al. Analyzing Differentially Expressed Genes and Pathways Associated with Pistil Abortion in Japanese Apricot via RNA-Seq. Genes 2020, **11**: 1079.

Shi Ting, Luo Wenjie, Li Hantao, et al. Association between blooming time and climatic adaptation in Prunus mume. Ecol Evol. 2020;**10**(1): 292-306.

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Wang Wanxu, Shi Ting, Ni Xiaopeng, et al. The role of miR319a and its target gene TCP4 in the regulation of pistil development in Prunus mume [J]. Genome, 2018, **61**(1): 43-8.

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Sun Hailong, Shi Ting, Song Juan, et al. Pistil abortion in Japanese apricot (Prunus mume Sieb. et Zucc.): isolation and functional analysis of PmCCoAOMT gene [J]. Acta Physiol Plant, 2016, **38**(5): 114.

Luo Xiaoyan, Shi Ting, Sun Hailong, et al. Selection of suitable inner reference genes for normalisation of microRNA expression response to abiotic stresses by RT-qPCR in leaves, flowers and young stems of peach [J]. Sci Hortic, 2014, **165**: 281-7.

Shi Ting, Gao Zhihong, Wang Liangju, et al. Identification of differentially-expressed genes associated with pistil abortion in Japanese apricot by genome-wide transcriptional analysis [J]. PLoS One, 2012, **7**(10): e47810.

Shi Ting, Zhuang Weibing, Zhang Zhen, et al. Comparative proteomic analysis of pistil abortion in Japanese apricot (Prunus mume Sieb. et Zucc) [J]. J Plant Physiol. 2012, **169**(13), 1301-1310.

Gao Zhihong, Shi Ting, Luo Xiaoyan, et al. High-throughput sequencing of small RNAs and analysis of differentially expressed microRNAs associated with pistil development in Japanese apricot [J]. BMC Genomics, 2012, **13**: 371.