## **Gu Chao**

### Areas of Research

Fruit development and ripening, Self-incompatibility, Molecular breeding

#### **Contact Information**

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## **Research Interests**

## Self-incompatibility, fruit ripening, fruit size, New cultivar breeding

The objective of our researches is to explore the molecular mechanism of fruit development and ripening and then used for serving new cultivar breeding. The details are as follows:

#### 1. Self-incompatibility

Self-incompatibility is one of natural barriers to inhibit self-fertilization and thus promoting cross-fertilization. This trait is controlled by a locus, named S-locus. This locus contains at least two alleles. S-RNase is stylar-S determinant, and *SFB/SLF* genes are deemed as the good candidates for pollen-S determinant. However, many SFB/SLF genes are detected in the S-locus, it is unclear which of these genes are involved in self-incompatibility reaction.

#### 2. Fruit size and fruit ripening

It is puzzled why fruit is generated after fertilization, why fruit is expanded during fruit development and then ripening. To explore these puzzles, multi-omics study will be conducted to identify the genes involved in the biosynthesis of secondary metabolites, fruit size, and fruit ripening. Combining transgene, protein-protein interaction, and protein-DNA interaction evidences, the molecular network regulating fruit development and ripening will be drafted in the future.

### 3. New cultivar breeding

All researches should be applied in field to improve productivity. Based on the above studies, we will develop the molecular markers to assist traditional breeding. Moreover, new varieties will be created by artificial mutagenesis or gene-editing technology.

# **Education Background**

Bachelor: Anhui Science and Technology University

Master: Nanjing Agricultural University

# Work experience

Assistant/Associate Professor, Wuhan Botanical Garden of China Academy of Sciences, 2011-2015

Associate Professor, Nanjing Agricultural University, 2015-

## **Selected Publication**

**Gu C**<sup>†</sup>, Xu HY<sup>†</sup>, Zhou YH<sup>†</sup>, Yao JL, Xie ZH, Chen YY, Zhang SL\*. Accepted. Multiomics analyses unveil the involvement of microRNAs in pear fruit senescence under high- or low-temperature conditions. Horticulture Research

Pei MS, Cao SH, Wu L, Wang GM, Xie ZH, **Gu C\***, Zhang SL\*. 2020. Comparative transcriptome analyses of fruit development among pears, peaches, and strawberries provide new insights into single sgmoid patterns. BMC Plant Biology 20:108.

**Gu C\***, Guo ZH, Cheng HY, Zhou YH, Qi KJ, Wang GM, Zhang SL. 2019. A HD-ZIP II HOMEOBOX transcription factor, PpHB.G7, mediates ethylene biosynthesis during fruit ripening in peach. Plant Science 278:12-19.

**Gu C**, Wang L, Wang W, Zhou H, Ma B, Zheng H, Fang T, Ogutu C, Vimolmangkang V, Han Y\*. 2016. Copy number variation of a gene cluster encoding endopolygalacturonase mediates flesh texture and stone adhersion in peach. Journal of Experimental Botany 67:1993-2005.