

Qiao Xin



Areas of Research

Genomics & Bioinformatics, Pear population genetics, Dwarfing mechanisms in pear trees.

Contact Information

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Research Interests

Genomics; genome evolution; population genomics, dwarfing mechanism in pear rootstock

1. Genome evolution

The sharp increase of plant genome, transcriptome and epigenome data provide valuable resources to investigate evolutionary consequences of gene and genome duplication in a range of taxa, and unravel common principles underlying duplicate gene retention. I'm interested in using comparative genomics, evolutionary genomics and bioinformatics approaches to study evolution of gene families, gene and genome duplication (WGD) in pear and plant kingdom. We use a combination of publicly available genomic data and new data generated by ourselves and collaborators from diverse plant species.

2. Population genomics

I'm interested in using population genomics methods to study the genetic basis of adaptation and phenotypic diversification evolution in natural pear populations. How does evolution tinker with these genes to generate different phenotypes among species? What is the adaptive significance of the diverse phenotype forms?

3. Dwarfing mechanisms

To attain efficient breeding of new *Pyrus* rootstocks and dwarf cultivars, it is crucial to understand the molecular mechanism responsible for vigor control and precocity. 'Zhonggai 1' [*Pyrus ussuriensis* × *communis*) × spp.] is an excellent pear dwarfing rootstock common in China. It is dwarf itself and has high dwarfing efficiency on most of

main *Pyrus* cultivated species when used as inter-stock. In 2019, the genome of 'Zhongai 1' was released. This assembled genome will help identify genes involved in dwarfism, early flowering, stress tolerance, and commercially desirable fruit characteristics. In the future, we aim to use multiomics approach to study the vigour mechanisms in dwarfing pear rootstocks.

Education Background

Bachelor: Shanxi Agricultural University

Master: Nanjing Agricultural University

Doctor: Nanjing Agricultural University

Work experience

Associate Professor, Nanjing Agricultural University, 2019-

Selected Publication

2020

Zeng W[†], **Qiao Xin**[†], Li Q, Liu C, Wu J, Yin H, Zhang S: Genome-wide identification and comparative analysis of the ADH gene family in Chinese white pear (*Pyrus bretschneideri*) and other Rosaceae species. *Genomics* 2020, 112(5):3484-3496.

Liu C[†], **Qiao Xin**[†], Li Q, Zeng W, Wei S, Wang X, Chen Y, Wu X, Wu J, Yin H et al: Genome-wide comparative analysis of the BAHD superfamily in seven Rosaceae species and expression analysis in pear (*Pyrus bretschneideri*). *BMC Plant Biology* 2020, 20(1):14.

2019

Qiao Xin, Li Q, Yin H, Qi K, Li L, Wang R, Zhang S* and Paterson AH*: Gene duplication and evolution in recurring polyploidization-diploidization cycles in plants. *Genome Biology* 2019, 20:38.

Li Q[†], **Qiao Xin**[†], Yin H, Zhou Y, Dong H, Qi K, Li L, Zhang S*: Unbiased subgenome evolution following recent whole-genome duplication in pear (*Pyrus bretschneideri*). *Horticulture Research* 2019, 6:34.

2018

Qiao Xin, Yin H, Li L, Wang R, Wu J, Wu J, Zhang S*: Different Modes of Gene Duplication Show Divergent Evolutionary Patterns and Contribute Differently to the

Expansion of Gene Families Involved in Important Fruit Traits in Pear (*Pyrus bretschneideri*). *Frontiers in Plant Science* 2018, 9(161).

2015

Qiao Xin, Li M, Li L, Yin H, Wu J, Zhang S*: Genome-wide identification and comparative analysis of the heat shock transcription factor family in Chinese white pear (*Pyrus bretschneideri*) and five other Rosaceae species. *BMC Plant Biology* 2015, 15(1):12.
