

# Liu Jinyi

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## Areas of Research

Floral organ development, flowering time regulation, plant light signaling and adaptation, gene family/biological pathway evolution and plant genomics.

## Contact Information

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## Research Interests

1. Rose floral organ development and flowering time regulation (seasonal flowering Vs continuous flowering in roses).
  2. Germplasm resources collection and multi-omics evaluation of roses (genome and transcriptome sequencing and metabolite analysis).
  3. Gene family and some specific biological pathway evolution, mainly focus on Rosaceae.
  4. Plant light signaling and evolution, aims to uncover the mechanism of plant shade tolerance and then enhance it for roses through genetics.
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## Education Background

**Bachelor:** Shandong Agricultural University

**Master:** Nanjing Agricultural University

**Doctor:** Nanjing Agricultural University

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## Work experience

Visiting Scholar, University of Tennessee, Knoxville, TN, USA, 2013-2015

PostDoc, Nanjing Agricultural University, Nanjing, China, 2016-2020

Associate Professor, Nanjing Agricultural University, Nanjing, China, 2020-

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## Honors and Awards

Reviewer of Horticulture Research, Tree Genetics & Genomes, Australian Journal of Grape and Wine Research, Horticultural Plant Journal, 3BITC, peer J.

Third place award for the Youth Scholar Forum at the 7th International Horticulture Research Conference.

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## Selected Publication

**Liu Jinyi**, Ren Min, Chen Hui, Wu Silin, Yan Huijun, Jalal Abdul, Wang Changquan \*. 2020. Evolution of *SHORT VEGETATIVE PHASE (SVP)* genes in Rosaceae: Implications of lineage-specific gene duplication events and function diversifications with respect to their roles in processes other than bud dormancy. *The Plant Genome*. <https://doi.org/10.1002/tpg2.20053>

Ren Haoran #, Bai Mengjuan #, Sun Jingjing #, **Liu Jinyi** # (co-first author), Ren Min, Dong Yuwei, Wang Na, Ning Guogui, Wang Changquan \*. 2020. RcMYB84 and RcMYB123 mediate jasmonate-induced defense responses against *Botrytis cinerea* in rose (*Rosa chinensis*). *The Plant Journal*, DOI: 10.1111/tbj.14871

Bai Mengjuan #, Sun Jingjing #, **Liu Jinyi** # (co-first author), Ren Haoran, Wang Kang, Wang Yanling, Wang Changquan \*, Katayoon Dehesh\*. 2019. The B-box protein BBX19 suppresses seed germination via induction of ABI5. *The Plant Journal* 99:1192-1202.

**Liu Jinyi**, Chu Jinjin, Ma Chuangju, Jiang Yueting, Ma Yuanchun, Xiong Jinsong and Zong-Ming (Max) Cheng\*. 2019. Overexpression of an ABA-dependent grapevine bZIP transcription factor, VvABF2, enhances osmotic stress in *Arabidopsis*. *Plant Cell Reports* 38:587-596.

**Liu Jinyi**, Fu Xiaodong, Dong Yuwei, Lu Jun, Ren Min, Zhou Ningning, Wang Changquan \*. 2018. MIKCC-type MADS-box genes in *Rosa chinensis*: the remarkable expansion of ABCDE model genes and their roles in floral organogenesis. *Horticulture Research* 5:25.

Xi Yue #, **Liu Jinyi** # (co-first author), Dong Chao, Zongming (Max) Cheng\*. 2017. The CBL and CIPK Gene Family in Grapevine (*Vitis vinifera*): Genome-Wide Analysis and Expression Profiles in Response to Various Abiotic Stresses. *Frontiers in Plant Science* 8:978.

**Liu Jinyi**, Chen Nana, Xiong Jinsong, Zong-Ming (Max) Cheng\*. 2016. Genome-wide identification, annotation and expression profile analysis of SnRK2 gene family in grapevine. *Australian Journal of Grape and Wine Research* 22:478-488.

**Liu Jinyi**, Chen Nana, Joshua N Grant, Zong-Ming (Max) Cheng, C. Neal Stewart Jr, and Tarek Hewezi\*. 2015. Soybean kinome: Functional classification and gene expression patterns. *Journal of Experimental Botany* 66 (5):1-16.

**Liu Jinyi**, Chen Nana, Chen Fei, Cai Bin, Silvia Dal Santo, Giovanni Battista Tornielli, Mario Pezzotti and Zong-Ming (Max) Cheng\*. 2014. Genome-wide analysis and expression profile of the bZIP transcription factor gene family in grapevine (*Vitis vinifera*). *BMC genomics* 15:281.

**Liu Jinyi**, J. Hollis Rice, Chen Nana, Thomas J. Baum, Tarek Hewezi\*. 2014. Synchronization of developmental processes and defense signaling by growth regulating transcription factors. *PloS One* 9(5):e98477.

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