

Resume of Zhihong Gao



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Qualifications

Ph.D. Horticulture, China Agricultural University, Beijing, China 2003

Master Degree, Horticulture, Nanjing Agricultural University, Nanjing, China 1997

Professional Experience

Professor, College of Horticulture, Nanjing Agricultural University, January 2013 – present.

Associate Professor, College of Horticulture, Nanjing Agricultural University, April 2004 –
December 2012.

Lecturer, College of Horticulture, Nanjing Agricultural University, December 1999 – March 2004.

Scholar, University of Sydney in Australia, February 2004 – June 2004.

Scholar, Chiba University in Japan, April 2006 – March 2007.

Assistant Lecturer, College of Horticulture, Nanjing Agricultural University, August 1997 – November 1999.

Research interests:

I am interested in germplasm collection and evaluation, the molecular mechanism of pistil abortion and the seasonal dormancy release of Japanese apricot (*Prunus mume* Sieb. et Zucc). We have established the National field GenBank for Japanese apricot.

Selected Publication (2012-present)

1. Jie Gao, Xiaopeng Ni, Hantao Li, Faisal Hayat1, Ting Shi, **Zhihong Gao***. miR169 and PmRGL2 synergistically regulate the NF-Y complex to activate dormancy release in Japanese apricot (*Prunus mume* Sieb. et Zucc.). *Plant Molecular Biology*, 2020, <https://doi.org/10.1007/s11103-020-01070-3>
2. Ting Shi, Shahid Iqbal, Aliya Ayaz, Yang Bai, Zhenpeng Pan, Xiaopeng Ni, Faisal Hayat, Muhammad Saqib Bilal, Muhammad Khuram Razzaq and **Zhihong Gao***. Analyzing Differentially Expressed Genes and Pathways Associated with Pistil Abortion in Japanese Apricot via RNA-Seq, *Genes*, 2020, 11, 1079
3. Shahid Iqbal, Zhenpeng Pan, Xinxin Wu, Ting Shi, Xiaopeng Ni, Yang Bai, Jie Gao, Muhammad Khalil-ur-Rehman, **Zhihong Gao***. Genome-wide analysis of PmTCP4 transcription factor binding sites by ChIP-Seq during pistil abortion in Japanese apricot. *The Plant Genome*, 2020; e20052. <https://doi.org/10.1002/tpg2.20052>
4. Shahid Iqbal, Xiaopeng Ni, Muhammad Saqib Bilal, Ting Shi, Muhammad Khalil-ur-Rehman, Pan Zhenpeng, Gao Jie, Muhammad Usman, **Zhihong Gao*** Identification and expression profiling of sugar transporter genes during sugar accumulation at different stages of fruit development in apricot. *Gene*, 2020, 742, 144584 (IF: 2.623)
5. Xinxin Wu, Yong Zhou, Dan Yao, Shahid Iqbal, **Zhihong Gao***, Zhen Zhang. DNA methylation of LDOX gene contributes to the floral colour variegation in peach. *Journal of Plant Physiology* 2020, 246-247: 153116. (IF: 2.825)
6. Ting Shi, Wen Jieluo, Han Taoli, Xuexi Huang, Zhaojun Ni, Haidong Gao, Shahid Iqbal, **Zhihong Gao*** Association between blooming time and climatic adaptation in *Prunus mume*. *Ecol Evol.* 2020, 10:292-306.
7. Song Xue, Ting Shi, Wenjie Luo, Xiaopeng Ni, Shahid Iqbal, Zhaojun Ni, Xiao Huang, Dan Yao, Zhijun Shen and **Zhihong Gao***. Comparative analysis of the complete chloroplast genome among *Prunus mume*, *P. armeniaca*, and *P. salicina*. *Horticulture Research* (2019) 6:89
8. Xinxin Wu, Ting Shi, Shahid Iqbal, Yong Zhang, Lin Liu and **Zhihong Gao***. Genome-wide discovery and characterization of flower development related long non-coding RNAs in *Prunus mume*. *BMC Plant Biology*, 2019, 19:64 <https://doi.org/10.1186/s12870-019-1672-7>
9. Ting Shi, Jie Suna, Xinxin Wu, Jinyang Weng, Pengkai Wang, Hongli Qie, Yinghong Huang, Huakun Wang, **Zhihong Gao***. Transcriptome analysis of Chinese bayberry (*Myrica rubra* Sieb. et Zucc.) fruit treated with heat and 1-MCP. *Plant Physiology and Biochemistry*, 2018, 133, 40-49

10. Shaolei Guo, Shahid Iqbal, Ruijuan Ma, Juan Song, **Mingliang Yu***, **Zhihong Gao***. High-density genetic map construction and quantitative trait loci analysis of the stony hard phenotype in peach based on restriction-site associated DNA sequencing. *BMC Genomics*, 2018, 19:612
11. Xiaoming Lou, Huakun Wang, Xiaopeng Ni, **Zhihong Gao***, Shahid Iqbal Integrating proteomic and transcriptomic analyses of loquat (*Eriobotrya japonica* Lindl.) in response to cold stress. *Gene*, 2018(677:57-65
12. Xiaopeng Ni, Song Xue, Wanxu Wang, Zhaojun Ni, Muhammad Khalil-ur-Rehman and **Zhihong Gao***. Candidate genes associated with red colour formation revealed by comparative genomic variant analysis of red- and green-skinned fruits of Japanese apricot (*Prunus mume*) *PeerJ* 2018, 6: e4625; DOI 10.7717/peerj.4625
13. Lin Lv, Ximei Huo, Luhua Wen, **Zhihong Gao***, Khalil-ur-Rehman M. Isolation and Role of PmRGL2 in GA-mediated Floral Bud Dormancy Release in Japanese Apricot (*Prunus mume* Siebold et Zucc.). *Front. Plant Sci.* 2018, 9:27. doi: 10.3389/fpls.2018.00027
14. Wanxu Wang, Ting Shi, Xiaopeng Ni, Yanshuai Xu, Shenchun Qu, **Zhihong Gao***. The role of miR319a and its target gene TCP4 in the regulation of pistil development in *Prunus mume*. *Genome*, 2018, 61: 43–48 dx.doi.org/10.1139/gen-2017-0118
15. Xianbin Gu, **Zhihong Gao***, Yichao Yan, Xiuyun Wang, Yushan Qiao, Yuhua Chen* RdreB1BI enhances drought tolerance by activating AQP-related genes in transgenic strawberry. *Plant Physiology and Biochemistry*, 2017,119:33-42
16. Xinxin Wu, Qinghua Gong, Xiaopeng Wu, **Zhihong Gao***. UFGT: The Key Enzyme Associated with the Petals Variegation in Japanese Apricot. *Front. Plant Sci.* 8:108.doi: 10.3389/fpls.2017.0010
17. Huang Zhigang, Shi Ting, Zheng Binglian, Yumul Rae Eden, Liu Xigang, You Chenjiang, **Gao Zhihong**, Xiao Langtao, Chen Xuemei. *APETALA2* antagonizes the transcriptional activity of *AGAMOUS* in regulating floral stem cells in *Arabidopsis thaliana* [J]. *New Phytol*, 2016:
18. Zhuang W B, Cai B H, **Gao ZH***, Zhang Z. Determination of chilling and heat requirements of 69 Japanese apricot cultivars. *European Journal of Agronomy*, 2016,74: 68-74
19. Zhuang W, **Gao ZH***, Wen L H, Huo X M, Cai B H, Zhang Z. Metabolic changes upon flower bud break in Japanese apricot are enhanced by exogenous GA4. Citation: *Horticulture Research*, 2015, 2, 15046, doi:10.1038/hortres.
20. Song J, **Gao ZH***, Huo X M, Sun H L, Xu Y S, Shi T, Ni Z J. Genome-wide identification of the auxin response factor (ARF) gene family and expression analysis of its role associated with pistil development in Japanese apricot (*Prunus mume* Sieb.et Zucc). *Acta Physiol Plant*, 2015, 37:145
21. Song S, Shao J, **Gao ZH***, Sun HL. Evaluation of the antifungal activity of the acetone extract of Japanese apricot fruit. *Journal of Chemical and Pharmaceutical Research*, 2014, 6(11):156-160
22. Wang PP, **Gao ZH***, Ni ZJ, Zhang Z, Cai BH. Self-compatibility in ‘Zaohong’ Japanese apricot is associated with the loss of function of pollen S genes. *Mol Biol Rep* (2013) 40:6485–6493
23. Zhuang WB, **Gao ZH***, Wang LJ, Zhong WJ, Ni ZJ, Zhang Z. Comparative proteomic and transcriptomic approaches to address the active role of GA4 in Japanese apricot flower bud dormancy release. *Journal of Experimental Botany*, 2013 doi:10.1093/jxb/ert284
24. Zhong WJ, **Gao ZH***, Zhuang WB, Shi T, Zhang Z, Ni ZJ. Genome-wide expression profiles of seasonal bud dormancy at four critical stages in Japanese apricot. *Plant Mol Biol*, 2013: 83:247-264
25. **Gao ZH***, Wang PP, Zhuang WB, Zhang Z. Sequences Analysis of New S-RNase and SFB alleles in Japanese Apricot (*Prunus mume*). *Plant Molecular Biology Reporter*, 2013, 31: 751-762
26. Wang PP, **Gao ZH***, Ni ZJ, Zhuang WB, Zhang Z. Isolation and identification of new pollen-specific SFB genes in Japanese apricot (*Prunus mume*). *Genet. Mol. Res.* 2013, 12 (3): 3286-3295
27. Zhuang WB, Shi T, **Gao ZH***, Zhang Z, Zhang Z. Differential expression of proteins associated with

- seasonal bud dormancy at four critical stages in Japanese apricot. *Plant Biology*, 120(1), 2012 pp 123-130
28. **Gao ZH***, Shi T, Luo XY, Zhang Z, Zhuang WB, Wang LJ. High-Throughput Sequencing of small RNAs and Analysis of Differentially Expressed microRNAs Associated with Pistil Development in Japanese apricot, *BMC Genomics*, (13), 2012, p 371
 29. Shi T, **Gao ZH***, Wang LJ, Zhang Z, Zhuang WB, Sun HL, Zhong WJ. Identification of differentially-expressed genes associated with pistil abortion in Japanese apricot by genome-wide transcriptional analysis. *Plos ONE*, 2012, 2012, 7(10): 47810 (SCI, IF=4.09(2011))
 30. Shi T, Zhuang WB, Zhang Z, Sun HL, Wang LJ, **Gao ZH***. Comparative proteomic analysis of pistil abortion in Japanese apricot (*Prunus mume* Sieb. et Zucc). *Journal of Plant Physiology*, 169(13), 2012 pp 1301-1310
 31. Gao ZH*, Luo XY, Shi T, Cai B, Zhang Z, Cheng ZM, Zhuang WB. Identification and Validation of Potential Conserved microRNAs and Their Targets in Peach (*Prunus persica*), *Molecules and Cells*, 2012, 34(3):239-49
 32. Gao ZH*, Zhuang WB, Wang LJ, Shao J, Luo XY, Cai BH, Zhang Z*. 2012. Evaluation of Chilling and Heat Requirements in Japanese Apricot with Three Models *HORTSCIENCE*, 2012, 47(12):1-6.
 33. Wang PP, Shi T, Zhuang WB, Zhang Z, **Gao ZH***. Determination of S-RNase genotypes and isolation of four novel S-RNase genes in Japanese apricot (*Prunus mume* Sieb. et Zucc.) native to China. *Journal of Horticultural Science & Biotechnology*, 2012 87 (3):266-270