# Xiaosan Huang



#### **Areas of Research**

Resource exploitation and utilization, DNA methylation, epigenetics and germplasm innovation.

#### **Contact Information**

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### **Research Interests**

Resource exploitation and utilization; DNA methylation; epigenetics and germplasm innovation

Advances in molecular level study of stress response and transgene research of pear, molecular mechanisms of stress adaptation in plant natural populations, spatial and temporal profiling of DNA methylation induced by drought stress in pear.

## **Education Background**

**Bachelor:** Huazhong Agricultural University **Master:** Huazhong Agricultural University **Doctor:** Huazhong Agricultural University

# Work experience

Lecturer, College of Horticulture, Nanjing Agricultural University, 2011.12-2013.12

Visiting scholar, School of Horticulture and Landscape Architecture, Purdue University, USA, 2015.03-2016.03

Associate professor, College of Horticulture, Nanjing Agricultural University, 2014.01-2018.12

### **Honors and Awards**

Won the "Outstanding Youth Fund" of Jiangsu Province (2017)

"Outstanding Young Backbone Teacher of Qinglan Project" of Jiangsu Province (2016)

"Zhong Shan Academic Rookie" of Nanjing Agricultural University (2013)

"Young Scholar Award" of Dabei Agriculture (2017),

the second "Hua Nai Horticulture Science and Technology Award" of China Horticultural Society (2013; ranking: 5/11)

the first prize of shennong China Agricultural Science and Technology Award in 2016-2017 (ranking: 12/17)

the Excellent Innovation Team Award of Shennong China Agricultural Science and Technology Award in 2018-2019 (ranking: 6/16)

the 7th First Prize of Jiangsu Province Agricultural Technology Promotion (2014;Rank: 16/25) and other awards.

### Selected Publication

Huang Xiaosan, Wang Wei, Zhang Qian, Liu Jihong. 2013. A Basic Helix-Loop-Helix Transcription Factor, PtrbHLH, of *Poncirustrifoliata* Confers Cold Tolerance and Modulates Peroxidase-Mediated Scavenging of Hydrogen Peroxide.Plant Physiology**162 (2)**: 1178-1194.

Li Kongqing, Xing Caihua, Yao Zhenghong, Huang Xiaosan. 2017. PbrMYB21, a novel MYB Protein of *Pyrus betulaefolia*, functions in drought tolerance and modulates polyamine levels by regulating arginine decarboxylase gene. Plant Biotechnology Journal **15(9)**:1186-1203.

Liu Yue, Yang Tianyuan, Lin Zekun, Gu Bingjie, Xing Caihua, Zhao, Liangyi, Dong Huizhen, Gao Junzhi, Xie Zhihua., Zhang, Shaoling and Huang Xiaosan. 2019. A WRKY transcription factor PbrWRKY53 from *Pyrus betulaefolia* is involved in drought tolerance and AsA accumulation. Plant biotechnology journal **17(9)**:1770–1787.

Xing Caihua Liu Yue Zhao Liangyi Zhang Shaoling Huang Xiaosan. 2019.A novel MYB Transcription Factor regulates AsA synthesis and affects cold tolerance. Plant Cell and Environment **42(3)**:832-845.

Huang Xiaosan, Zhang Shaoling, Li Kongqing, Jyothi Thimmapuram ,Xie Shaojun, Jonathan Wren. 2017. ViewBS: a powerful toolkit for visualization of high-throughput bisulfite sequencing data. Bioinformatics **34(4)**:708-709.

Huang Xiaosan, Zhang Qinghua, Zhu Dexin, Fu Xingzheng, Wang Min, Zhang Qian, Takaya Moriguchi, and Liu Jihong. 2015. ICE1 of *Poncirus trifoliata* functions in cold tolerance by modulating polyamine levels through interacting with arginne decaeboxylas. Journal of ExperimentalBotany**66 (11)**:3259-3274.

Huang Xiaosan, Luo Tao, Fu Xingzheng, Fan Qijun, and Liu Jihong. 2011. Cloning and molecular characterization of a mitogen-activated protein kinase gene from *Poncirus trifoliata* whose ectopic expression confers dehydration/drought tolerance in transgenic tobacco. Journal of Experimental Botany 62 (14): 5191-5206.

Huang Xiaosan, Li Kongqing, Xu Xiaoyong, Yao Zhenghong, Jin Cong, Zhang Shaoling. 2015. Genome-wide analysis of WRKY transcription factors in white pear (*Pyrus bretschneideri*) reveals evolution and patterns under drought stress. BMC Genomics **16(1)**:1104.

Gong Xin, Zhao Liangyi, Song Xiaofei, Lin Zekun, Gu Bingjie, Yan Jinxuan, Zhang Shaoling, Tao Shutian, and Huang Xiaosan. 2019.Genome-wide analyses and expression patterns under abiotic stress of NAC transcription factors in white pear (*Pyrus bretschneideri*). BMC Plant Biology **19(1)**:161.

Huang Xiaosan, Liu Jihong, and Chen Xuejun. 2010. Overexpression of PtrABF gene, a bZIP transcription factor isolated from *Poncirus trifoliata*, enhances dehydration and drought tolerance in tobacco via scavenging ROS and modulating expression of stress-responsive genes. BMC Plant Biology **10**:230.

Jin Cong, Huang Xiaosan, Li Kongqing, Yin Hao, Li Leiting, Yao Zhenghong, and Zhang Shaoling. 2016. Overexpression of a bHLH1 transcription factor of *Pyrus ussuriensis* confers enhanced cold tolerance and increases expression of stress-responsive genes. Frontiers in Plant Science **7**:441.

Jin Cong, Li Kongqing, Xu Xiaoyong, Zhang Huping, Chen Huixian, Chen Yuhong, Hao Jing, Wang Yang, Huang Xiaosan, and Zhang Shaoling. 2017.A novel NAC transcription factor, PbeNAC1, of *Pyrus betulifolia* confers cold and drought tolerance via interacting with PbeDREBs and activating the expression of stress-responsive genes. Frontiers in Plant Science **8**:1049.

Zhao Liangyi, Yang Tianyuan, Xing Caihua, Dong Huizheng, Huang Xiaosan. 2019. The beta-amylase PbrBAM3 from pear (*Pyrus betulaefolia*) regulates soluble sugar accumulation and ROS homeostasis in response to cold stress. Plant Science **287**:110184.

Dong Huizhen, Wang Chunmeng, Xing Caihua, Yang Tianyuan, YanJinxuan, Gao Junzhi, Li Dingli, Wang Ran, Blumwald Eduardo, Zhang Shaoling, Huang Xiaosan. 2019. Overexpression of PbrNHX2 gene, a Na+/H+ antiporter gene isolated from *Pyrus betulae folia*, confers enhanced tolerance to salt stress via modulating ROS levels. Plant Science **285**:14-25.

Huang Xiaosan,Li Kongqing,Jin Cong,Zhang Shaoling. 2015. ICE1 of *Pyrus ussuriensis* functionsin cold tolerance by enhancing PuDREBa transcriptional levels through interacting with PuHHP1. Scientific Reports**5**:17620.

QiXiaoxiao,HuShi, Zhou Hongsheng,Liu Xing,WangLifen,ZhaoBiying,HuangXiaosan,ZhangShaoling. 2018. A MADS-box

transcription factor of 'Kuerlexiangli' (*Pyrus sinkiangensis* Yu) PsJOINTLESS gene functions in floral organ abscission. Gene **642**:163-171.

Zhao Liangy, Xin Gong,Gao Junzhi,Dong Huizhen, ZhangShaoling,Tao Shutian,Huang Xiaosan. 2019.Transcriptomic and evolutionary analyses of white pear (*Pyrus bretschneideri*) β-amylase genes reveals their importance for cold and drought stress responses. Gene **689**:102-113.