

## Wang Chen

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### Areas of Research

Molecular biology and epigenetics, hormone signal transduction of reproductive development, fruit nutritional quality and human health care, and genetic breeding of grapevine.

### Contact Information

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## Research Interests

✧ *Regulatory mechanism of reproductive development (especially seedless berry formation)*

Our lab has demonstrated the key roles of miRNAs on guiding grape seedless berry development by modulating parthenocarpy, stenospermocarpic and seed stone development. We are now interested in the physiological, molecular biological and epigenetic mechanisms underlying the miRNA-mediated grape seedless berry formation.

✧ *Hormone signal transduction*

We found the primarily signal network of GA cross-interacting with other hormones such as GA, IAA and CTK to regulate grape reproductive development, especially seed/seedless berry formation, and we have been studying the signal pathways of miRNAs responsive to hormones in modulating reproductive development to enrich hormone signal transduction mechanisms.

✧ *Fruit nutritional quality and human health care*

We focus on the regulatory mechanisms of fruit quality, especially health components such as procyanidine, resveratrol and ascorbic acid accumulation in grape berries.

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## Education Background

2010-2012 Ph.D in Pomology, College of Horticulture, University of Nanjing Agricultural

University China

2008-2010 M.S. in Pomology, College of Horticulture, University of Nanjing Agricultural University China

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## Work experience

2020-present Professor, College of Horticulture, Nanjing Agricultural University, China

2014-2015 Postdoctor, Volcanic Center, ARO, Israel

2014-2019 Associate Professor, College of Horticulture, Nanjing Agricultural University, China

2012-2013 Lecturer, College of Horticulture, Nanjing Agricultural University, China

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## Honors and Awards

- ✧ Second prize for scientific progress, Ministry of Education, China (2019)
  - ✧ Leader 5000 Excellent Paper, Ministry of Education, China (2014)
  - ✧ The Excellent Doctoral Thesis of Jiangsu Province, China (2013)
  - ✧ The Star of Doctor in Nanjing Agricultural University, China (2012)
  - ✧ The 'Jin Sanbao' scholarship Nanjing Agricultural University, China (2011)
  - ✧ The first-class scholarship in Nanjing Agricultural University, China (2009, 2010, 2011)
  - ✧ The 'Chen Yuguang' scholarship in Nanjing Agricultural University, China (2009)
  - ✧ The Merit Student award in Nanjing Agricultural University, China (2009)
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## Selected Publication (\* corresponding author)

### Books:

1. **Wang Chen**, Leng Xiangpeng, Zhang Wenying, Fang Jinggui. 2017. The regulatory and signaling roles of glutathione in modulating abiotic stress responses and tolerance. *Glutathione in Plant Growth, Development and Stress Tolerance*, Chapter 7, Springer International Publishing AG;
2. **Wang Chen**, Fang Jinggui. 2015. miR-RACE: An Effective Approach to Accurately Determine the Sequence of Computationally Identified miRNAs. In: Mathieu Rederstorff eds. *Small Non-Coding RNAs: Methods and Protocols*, Chapter 16, Humana Press 1296:109-118.
3. **Wang Chen**, Fang Jinggui. 2015. RLM-RACE, PPM-RACE and qRT-PCR, an integrated strategy to accurately validate miRNA target genes. In: Mathieu Rederstorff eds. *Small Non-Coding RNAs: Methods and Protocols*, Chapter 16, Humana Press. 1296:175-186.

### Papers:

1. Wenran Wang, Yunhe Bai, Padmalatha Koilkonda, Le Guan, Yaxian Zhuge, Xicheng Wang, Zhongjie Liu, Haifeng Jia, **Chen Wang\***, Jinggui Fang. Genome-wide identification and characterization of Gibberellin Metabolic and Signal Transduction (GA MST) pathway mediating seed and berry development (SBD) in Grape (*Vitis vinifera* L.). *BMC Plant Biology*. 2020, 20:384.

2. Zhang Wenyong, Abdelrahman Mostafa, Jiu Songtao, Guan Le, Han Jian, Zheng Ting, Jia Haifeng, Song Changnian, Fang Jinggui, **Wang Chen\***. VvmiR160s/VvARFs interaction and their spatio-temporal expression/cleavage products during GA-induced grape parthenocarp. *BMC Plant biology*, 2019, 19:111
3. Zhang Yanping, Huang Yuqing, **Wang Chen\***, Mu Qian, Jiu Songtao, Zhu Xudong, Zheng Ting, Zhang Kekun, Jia Haifeng, Pervaiz Tariq, and Fang Jinggui\*. Characterization and Identification of PpEIN3 during the Modulation of Fruit Ripening Process by Ectopic Expressions in Tomato[J]. *The Plant Genome*, 2019, 12(3).
4. Cui Mengjie, Wang Wenran, Guo Fengfei, Fan Xiucui, Guan Le, Zheng Ting, Zhu Xudong, Jia Haifeng, Fang Jinggui, **Wang Chen\***, Liu Chonghuai. Characterization and temporal-spatial expression analysis of LEC1 gene in the development of seedless berries in grape induced by gibberellin. *Plant Growth Regulation*, 2019, DOI: 10.1007/s10725-020-00582-8.
5. **Wang Chen\***, Wang Qinglian, Zhu Xudong, Cui Mengjie, Jia Haifeng, Zhang Wenyong, Shen Wenbiao. Characterization on the conservation and diversification of miRNA156 gene family from lower to higher plant species based on phylogenetic analysis at the whole genomic level. *Functional & Integrative Genomics*, 2019, 19:933-952.
6. **Wang Chen\***, Jogaiah S, Zhang Wenyong, Abdelrahman M, Fang Jinggui. 2018. Spatio-temporal expression of miRNA159 family members and their GAMYB target gene during the modulation of gibberellin-induced grapevine parthenocopy. *Journal of experimental botany*, 69(15): 3639-3950.
7. Cui Mengjie, **Wang Chen\***, Zhang Wenyong, Pervaiz T, Haider MS, Tang Wei, Fang Jinggui. 2018. Characterization of Vv-miR156:Vv-SPL pairs involved in the modulation of grape berry development and ripening. *Molecular Genetics Genomics*, 1-22.
8. Wang Mengqi#, Sun Xin#, **Wang Chen\***, Cui Liwen, Chen Lide, Zhang Chaobo, Shangguan Lingfei, Fang Jinggui. 2017. Characterization of miR061 and its target genes in grapevine responding to exogenous gibberellic acid. *Functional & Integrative Genomics*, 17(5): 537-549.
9. Zhao Fanggui#, **Wang Chen#\***, Han Jian, Zhu Xudong, Li Xiaopeng, Wang Xicheng, Fang Jinggui\*. 2017. Characterization of miRNAs responsive to ethylene in grapevine berries at whole genome level. *Functional & Integrative Genomics*, 17: 213-235.
10. Leng Xiangpeng, Wang Peipei, Zhao Pengcheng, Wang Mengqi, Cui Liwen, Shangguan Lingfei, **Wang, Chen\***. 2017. Conservation of microRNA-mediated regulatory networks in response to copper stress in grapevine. *Plant Growth Regulation*, 82(2):293-304.
11. Zeng Jingjue, Zhu Xudong, Haider S. Muhammad, Wang Xicheng, Zhang Cheng, **Wang Chen\***. 2017. Genome-Wide Identification and Analysis of the Type-B Authentic Response Regulator Gene Family in Peach (*Prunus persica*). *Cytogenetic & Genome Research*, 151(1):41.
12. Zhang Cheng, Jia Haifeng, Zeng Jingjue, Perraiz Tariq, Xie Zhenqiang, Zhu Xudong, **Wang Chen\***. 2016. Fertilization of Grapevine Based on Gene Expression. *The Plant Genome*, 9(3).
13. Wang Baoju, Wang Jian, **Wang Chen\***, Shen Wenbiao, Jia Haifeng, Zhu Xudong, Li Xiaopeng. 2016. Study on Modes of Expression and Cleavage Role of miR156b/c/d and its

- Target Gene Vv-SPL9 During the Whole Growth Stage of Grapevine. *Journal of Heredity*, 1-13.
14. Zhu Xudong, LengXiangpeng, Sun Xin, Mu Qian, Wang Baoju, Li Xiaopeng, **Wang Chen\***, Fang Jinggui 2015. Discovery of conservation and diversification of genes by phylogenetic analysis based on global genomes. *The Plant Genome*, 8(2).
  15. Leng Xiangpeng, Han Jian, Wang Xiaomin, Zhao Mizhen, Sun Xin, **Wang Chen\***, Fang Jinggui. 2015. Characterization of a calmodulin-binding Transcription Factor from Strawberry (*Fragaria &times; ananassa*). *The Plant Genome*, 8(2).
  16. Zhang Cheng, Wu Weimin, Wang Xicheng, Fang Jinggui, **Wang Chen\***. 2015. Functional conservation analysis and expression modes of grape anthocyanin synthesis genes responsive to the low temperature stress. *Gene*, 574(1): 168-177.
  17. LengXiangpeng, Song Changnian, Han Jian, ShangguanLingfei, Fang Jinggui, **Wang Chen\***. 2015. Determination of the precise sequences of computationally predicted miRNAs in *Citrus reticulata* by miR-RACE and characterization of the related target genes using RLM-RACE. *Gene*, 575(2): 498-505.
  18. **Wang Chen**, Leng XP, Zhang YY, Kayesh E, Zhang YP, Sun X, Fang J G\*. 2014. Transcriptome-wide analysis of dynamic variations in regulation modes of grapevine microRNAs on their target genes during grapevine development. *Plant Molecular Biology*, 84:269-285.
  19. **Wang Chen**, Han J, Shangguan LF, Yang G, Kayesh E, Zhang YY, Leng XP, Fang JG\*. 2014. Depiction of grapevine phenology by genes expression information and test of its workability in guiding fertilization. *Plant Molecular Biology Reporter*. 5: 1070-1084.
  20. Han J, Fang JG, **Wang Chen\***, Yin YL, Sun X, Leng XP, Song CN. 2014. Grapevine microRNAs responsive to exogenous gibberellin. *BMC Genomics*, 15:111.
  21. Xin Sun, Yanping Zhang, Xudong Zhu, Nicholas KibetKorir, Ran Tao, **Chen Wang\***, Jinggui Fang\*. 2014. Advances in identification and validation of plant microRNAs and their target genes. *PhysiologiaPlantarum*, 166-173.
  22. Ren GH, Wang BJ, Zhu XD, Mu Q, **Wang Chen\***, Tao R, Fang JG. 2014. Cloning, expression, and characterization of miR058 and its target PPO during the development of grapevine berry stone. *Gene*, 166-173.
  23. Zhang YP, Han J, Liu D, Wen XC, Li Y, Tao R, Peng YB, Fang JG, **Wang Chen\***. 2014. Genome-wide identification and analysis of FK506-binding protein gene family in peach (*Prunuspersica*). *Gene*. 416-424.
  24. **Wang Chen**, Han J, Nicholas KK, Wang XC, Liu H, Li XY, Leng XP, Fang JG\*. 2013. The characterization of target mRNAs for table grapevines miRNAs with an integrated strategy of modified RLM RACE, PPM RACE and qRT-PCRs of cleavage products. *Journal of Plant physiology*,170 (10): 943-957.
  25. **Wang Chen**, Han J, Liu C, Nicholas K, Kayesh E, Shangguan LF, Li X, Fang J. 2012. Identification of microRNAs from Amur grapes (*VitisamurensisRupr.*) by deep sequencing and analysis of microRNA variations with bioinformatics. *BMC Genomics* 13: 122.
  26. **Wang Chen**, Shangguan LF, Nicholas KK, Wang XC, Han J, Song CN, Fang JG. 2011. Characterization of microRNAs identified in a table grapevine cultivar with validation of computationally predicated grapevine miRNAs by miR-RACE. *PLoS ONE*, 6(7): e21259.

27. **Wang Chen**, Wang XC, Nicholas KK, Song CN, Zhang CQ, Li XY, Han J, Fang JG. 2011. Deep sequencing of grapevine flower and berry short RNA library for discovery of novel microRNAs and validation of precise sequences of grapevine microRNAs deposited in miRBase. *Physiologia Plantarum*, 143: 64-81.
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