个人简介

所在单位：园艺学院
学历：博士研究生　学位：博士学位
职称：教授博士生导师
联系方式：wangchen@njau.edu.cn

研究方向：

以葡萄、草莓、石榴等浆果为研究对象，主要从分子生物学、基因组学、表观遗传学、信号转导及栽培生理与品质调控等领域开展以下研究：(1)果实无核性状及保健品质形成的表观调控与信号转导；(2)果树生殖发育细胞生物学与分子生物学；(3)果树激素信号转导与表观调控；(4)现代果树绿色精准化栽培与智慧化生产技术研发；(5)果树分子设计育种与种质创新。

2012年6月，硕博连读（四年）提前毕业并留校任教，同时荣获江苏省优秀博士论文，系国家首批农业产业强镇项目智慧葡萄首席专家、江苏省葡萄科技小院首席专家、江苏省果树种业工程创新中心首席专家、中国园艺学会石榴分会副秘书长、江苏省葡萄协会副秘书长，获批江苏省人才办科技副总。国家/省自然科学基金项目、省自主创新项目、国家博士后项目等国家省部级项目评审专家，《International Journal of Molecular Sciences》、《中外葡萄与葡萄酒》、《生物技术学报》期刊等编委。园艺学院果树学科秘书，负责硕博士面试招生、开题及中期考核评定等事宜。培养硕/博士研究生连年荣获“国家奖学金”、“名人奖学金”及“优秀毕业生”等荣誉。目前，主持国家及省部级项目近30项，以第1/通讯作者发表论文130余篇，其中SCI论文60余篇，主要发表在《PANS》《Plant cell & environment》《The plant biotechnology》《The Plant Journal》《Horticultural plant Journal》等国际知名期刊上。荣获教育部二等奖1项，荣获江苏省高等学校科技进步三等奖1项，发明专利8项，参与选育葡萄新品种3个，以副主编身份出版中文专著6部，参编英文专著2部。获批2个江苏省研究生工作站和3个江苏省科技小院，建立1个果树种业研究中心，协助建设“中以葡萄研究中心”及“中印葡萄研究中心”。与以色列、意大利、巴西、新西兰、印度、埃及等国保持着良好的国际交流与合作关系。

教育背景

2008.9-2012.6	南京农业大学	果树学	博士研究生毕业（硕博连读）	农学博士学位
1993.9-1997.6	河北科技师范学院	果树教育	大学本科毕业	学士学位

工作经历

2012.8-至今　南京农业大学园艺学院　教学科研

兼职信息

《International Journal of Molecular Sciences》《中外葡萄与葡萄酒》《生物技术学报》等期刊编委
江苏省葡萄协会，常务理事、副秘书长
中国园艺学会石榴分会，副秘书长
江苏省细胞与发育生物学学会，委员

授课信息

葡萄营养与保健(本科生课程)
水果与健康(本科生课程)
果树育种学(本科生课程)
园艺植物分子生物学(本科生课程)
园艺作物栽培学实验(本科生课程)

知识产权

【专利】王晨,陆爱华,张志昌,张演义,房经贵,徐卫东，一种葡萄园更换品种的方法，ZL202011593782.6，2023

【专利】王晨,叶东东,宣旭娴,吴伟民,王西成,房经贵,肖迎珂，一种鉴定葡萄果实无核的主效QTL 位点的 SSR 分子标记开发和应用，ZL202111382093.5，2022

【专利】房经贵,吴琦琦,郑斌,刘嘉凝,李飞跃,上官凌飞,王晨,王亚宁,于沐成，一种葡萄品种的鉴定方法，ZL202410288373.7，2024

【专利】房经贵,王晨,张孜博,刘志龙,上官凌飞,卢素文，一种确定氮磷复合肥与单肥的分步精准组合施肥的方法及应用，ZL202211408713.2，2023

【专利】巩培杰,房经贵,张孟伟(学),王晨,徐卫东(外),上官凌飞，植物病原菌孢子收集装置，ZL201921856001.0，2020

【专利】上官凌飞,张成(学),房经贵,王晨，一种检测盐胁迫对葡萄伤害程度的引物及其应用，ZL201610593036.4，2019

科研项目

主持项目 16 项，其中国家级 4 项，其他 12 项
参与项目 8 项，其中国家级 2 项，省部级 3 项，地市级 3 项

主要论著：

1. 以副主编身份编著《葡萄分子生物学》、《果树志．石榴卷》、《葡萄分子耕田》、《葡萄自育品种》《葡萄设施栽培与病虫害防治图解》《草莓设施栽培与病虫害防治图解》《英汉汉英果树品种词汇》等七部.
2. 参编英文论著:

1) **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.
2) **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.

发表的主要 SCI/期刊论文(*通讯作者)：

1. **Wang Chen***, Xuan Xuxian, Wang Wenran, Ehsan Sadeghnezhad, Linjia Luo, Peijie Gong, Qiqi Wu, Ruiqiang Chao, Xinpeng Chen, Mucheng Yu, Ziyang Qi, Xiaowen Zhang, Fei Wang, Tianyu Dong, Yanhua Ren, Laisheng Meng, Jinggui Fang. ***Plant, Cell & Environment***, 2025. DOI:10.1111/pce.15570 (通讯作者)
2. Xuan xuxian, , Ziyang Qu, Ehsan Sadeghnezhad, Zhenqiang Xie, Ziyang Qi, Hui Yang, Xiuling Song, Mucheng Yu, Linjia Luo, Rana Badar Aziz, Yanping Zhang, Peijie Gong, Jinggui Fang, **Chen Wan**g*. Competitive action network of polyamines metabolic and

ethylene biosynthesis pathways in gibberellin-induced parthenocarpic berries during grape fruit setting. ***Horticultural Plant Journal***, 2025, https://doi.org/10.1016/j.hpj.2024.07.002. (通讯作者)

3. Bao Qin-Xin,Mu Xin-Rong,Tong Chen,Li Cong,Tao Wen-Zhe,Zhao Sheng-Ting,Liu Yu-xin,Wang Wan-Ni,Wei Yu-ting,Yu Fu-Huan,Wang Jing-wen,Sun Zhi-Lan,Fan Bing-Ling,Sun Jia,**Wang Chen***, Meng Lai-Sheng*. Sugar status in preexisting leaves determines systemic stomatal development within newly developing leaves, ***Proceedings of the national academy of sciences of the United States of America*（PANS）**,2023,120(24) (通讯作者)
4. Yao Zimeng, Chen Wuhui*, **Wang Chen***. Sucrose transporter systems in cotyledons (or pre-existing leaves), as integrators of multiple signals, regulate stomatal development of all leaves. ***Plant Physiology and Chemistry***, 2025, 224, 109968. (通讯作者)
5. **Wang Chen***, Jogaiah S, Zhang Wenying, Abdelrahman M, Fang Jinggui. 2018. Spatio-temporal expression of miRNA159 family members and their GAMYB target gene during the modulation of gibberellin-induced grapevine parthenocapy. ***Journal of experimental botany***, doi:10.1093/jxb/ery172. (通讯作者)
6. Luo Linjia, Zhao Pengcheng, Su Ziwen, Huang Yuqing, Zhang Yanping, Mu Qian, Xuan Xuxian, Qu Ziyang, Yu Mucheng, Qi Ziyang, Aziz Rana Badar, Gong Peijie, Xie Zhenqiang, Fang Jinggui, **Wang Chen***.Characterization and Potential Action Mode Divergences of Homologous ACO1 Genes during the Organ Development and Ripening Process between Non-Climacteric Grape and Climacteric Peach, ***International Journal of Molecular Sciences,***2024,25(2):-(通讯作者)
7. Liu Fei, Aziz Rana Badar,Wang Yumiao,Xuan Xuxian,Yu Mucheng,Qi Ziyang,Chen Xinpeng,Wu Qiqi,Qu Ziyang,Dong Tianyu,Li Shaonan,Fang Jinggui, **Wang Chen***. Identification of VvAGL Genes Reveals Their Network's Involvement in the Modulation of Seed Abortion via Responding Multi-Hormone Signals in Grapevines, ***International Journal of Molecular Sciences,*** 2024,25(18)(通讯作者)
8. Zhang Yanping, Su Ziwen,Luo Linjia,Wang Pengkai,Zhu Xudong,Liu Jiecai, **Wang Chen***. Exogenous auxin regulates the growth and development of peach fruit at the expansion stage by mediating multiple-hormone signaling, ***BMC Plant Biology***,2023,23(1)(通讯作者)
9. Jiu Songtao, Guanle, Leng Xiangpeng, Zhang Kekun,MUHAMMAD SALMAN HAIDER,Yuxiang, Zhu Xudong, Zheng Ting, Ge Mengqing, **Wan Chen**, Jia Haifeng, Shangguan Lingfei,Zhang Caixi,Tang Xiaoping,Abdullah Muhammad,Javed Hafiz Umer,Han jiang,Dong Zhigang,Fang Jinggui.The role of VvMYBA2r and VvMYBA2w alleles of the MYBA2 locus in the regulation of anthocyanin biosynthesis for molecular breeding of grape (Vitis spp.) skin coloration. ***PLANT Biotechnology Journal (PBJ)***,2021,19(6):1216-1239(参与作者)
10. Shi Zhaowan, Tamar Halaly-Basha, Chuanlin Zheng, Michal Sharabi-Schwager, **Chen Wang**, David W. Galbraith, Ron Ophir, Xuequn Pang, Etti Or. Identification of potential post-ethylene events in the signaling cascade induced by stimuli of bud dormancy release in grapevine. ***The Plant Journal***, 2020, doi: 10.1111/tpj.14997. (参与作者)
11. Bai Yunhe, Wang Zhuangwei, Luo Linjia, Xuan Xuxian, Tang Wei, Qu Ziyang, Dong Tianyu, Qi Ziyang, Yu Mucheng, Wu Weimin, Fang Jinggui, **Wang Chen***. Characterization of VvmiR166s-Target Modules and Their Interaction Pathways in Modulation of

Gibberellic-Acid-Induced Grape Seedless Berries. ***International Journal of Molecular Sciences***,2023,24(22):-(通讯作者)

12. Sheng Zilu,Xuan XuXian,Wang Fei,Sadeghnezhad Ehsan,Gong Peijie,Xiao Yingke,Dong Tianyu,Zhang Peian,Wang Xicheng,Fang Jinggui, **Wang Chen***. Identification and Characterization of AUXIN Response Factor Gene Family Reveals Their Regulatory Network to Respond the Multi-Hormones Crosstalk during GA-Induced Grape Parthenocarpic Berry, ***International Journal of Molecular Sciences***,2022,23(19)(通讯作者)
13. Wang Peipei, Xuan Xuxian, Su Ziwen,Wang Wenran,Abdelrahman, Mostafa,Jiu Songtao,Zhang Xiaowen,Liu Zongjie,Wang Xicheng, **Wang Chen***.Identification of miRNAs-mediated seed and stone-hardening regulatory networks and their signal pathway of GA-induced seedless berries in grapevine (*Vitis vinifera* L.), **BMC PLANT BIOLOGY**,2021,21(1): (通讯作者)
14. 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. (通讯作者)
15. Zhang Wenying, 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 parthenocarpy. ***BMC Plant Biology***, 2019, 19:111(通讯作者)
16. 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). (通讯作者)
17. Cui Mengjie, Wang Wenran, Guo Fengfei, Fan Xiucai, Guan Le, Zheng Ting, Zhu Xudong, Jia Haifeng, Fang Jinggui, **Wang Chen***. 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. (通讯作者)
18. **Wang Chen***, Jogaiah S, Zhang Wenying, Abdelrahman M, Fang Jinggui. 2018. Spatio-temporal expression of miRNA159 family members and their GAMYB target gene during the modulation of gibberellin-induced grapevine parthenocapy. ***Journal of experimental botany***, doi:10.1093/jxb/ery172. (通讯作者)
19. Cui Mengjie, **Wang Chen***, Zhang Wenying, 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. (通讯作者)
20. Wang Menqi#, 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. (通讯作者)
21. 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. (通讯作者)
22. 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. (通讯作者)

23. Zeng Jingjue, Zhu Xudong, Haider S. Muhammad, Wang Xicheng, Zhang Cheng, **Chen Wang***. 2017. Genome-Wide Identification and Ana lysis of the Type-B Authentic Response Regulator Gene Family in Peach (Prunus persica). ***Cytogenetic & Genome Research,*** 151(1):41. (通讯作者)
24. 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). (通讯作者)
25. 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. (通讯作者)
26. Fang Jinggui*, Zhu Xudong, Wang Chen, Shangguan Lingfei. 2016. Applications of DNA technologies in agriculture. ***Current Genomics***, 17(4): 379-386.
27. Jia Haifeng, Wang Chen, Zhang Cheng, Muhammad Salman Haider, Zhao Pengcheng, Liu Zhongjie, Shangguan,Lingfei Tariq Pervaiz, Fang Jinggui*. 2016. Functional Analysis of VvBG1 During Fruit Development and Ripening of Grape. ***Journal of Plant Growth Regulation***, 1-13. (通讯作者)
28. Jia Haifeng, Jiu Songtao, Zhang Cheng, **Wang Chen**, Tariq Pervaiz, Liu Zhongjie, Wang Baoju, Cui Liwen, Fang Jinggui*. 2016. Abscisic acid and sucrose regulate tomato and strawberry fruit ripening through the abscisic acid-stress ripening transcription factor. ***Plant Biotechnology Journal.*** 14(10):2045-2065. (参与作者)
29. Zhu Xudong, LengXiangpeng, Sun Xin, Mu Qian, Wang Baoju, Li Xiaopeng, **Wang Chen***. 2015. Discovery of conservation and diversification of genes by phylogenetic analysis based on global genomes. ***The Plant Genome***, 8(2). (通讯作者)
30. 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 × ananassa). ***The Plant Genome***, 8(2). (通讯作者)
31. 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. (通讯作者)
32. 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. (通讯作者)
33. **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. (第 1 作者)
34. **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. (第 1 作者)
35. 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. (通讯作者)

36. 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. (通讯作者)
37. 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. (通讯作者)
38. 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. (通讯作者)
39. **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. (第 1 作者)
40. **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. (第 1 作者)
41. Nicholas KK, Han J, Shangguan LF, **Wang Chen**, Kayesh E, Zhang YY, Fang JG. 2012. Plant variety and cultivar identification: advances and prospects. ***Critical Reviews in Biotechnology***, 33(2):111-125. (参与作者)
42. Wang XC, Guo L, Shangguan LF, **Wang Chen**, Nicholas K K, Yang G, Song CN, Zhang Z, Fang JG. 2012. Analysis of expressed sequence tags from grapevine flower and fruit and development of simple sequence repeat markers. ***Molecular Biology Reports***, 39(6): 6825-6834. (参与作者)
43. Shangguan L, **Wang Chen**, Kayesh E, Zhang Y P, Nicholas K K, Han J, Fang J G. 2012. Review and structural analysis of the evolution of grapevine (Vitisvinifera L.) genes involved in flower and fruit development. ***The Journal of Horticultural Sciences & Biotechnology***, 87(3): 243-249. (参与作者)
44. **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. (第 1 作者)
45. **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. (第 1 作者)
46. Yu H, Song C, Jia Q, **Wang Chen**, Li F, Nicholas K, Zhang X, Fang J. 2011.Computational identification of microRNAs in apple expressed sequence tags and validation of their precise sequences by miR-RACE. ***Physiologia Plantarum***, 141: 56-70. (参与作者)
47. Song C, **Wang Chen**, Zhang CQ, Nicholas KK, Yu HP, Ma ZQ, Fang JG. 2010. Deep sequencing discovery of novel and conserved microRNAs in trifoliate orange (Citrus trifoliata). ***BMC Genomics***, 11: 431. (参与作者)
48. Song CN, Fang JG, **Wang Chen**, Guo L, Nicholas KK, Ma ZQ. 2010. miR-RACE, a new

efficient approach to determine the precise sequences of computationally identified trifoliate orange (Poncirustrifoliata) microRNAs. ***PLoS ONE***, 5(6): e10861. (参与作者)

49. Li X, Shangguan L, Song C, Nicholas K, **Wang Chen**, Gao Z, Shen Y, Fang J. 2010. Analysis of expressed sequence tags from mei (PrunusmumeSieb. et Zucc.) flowers and fruits and development of simple sequence repeat markers. ***BMC Genetics***, 11: 66. (参与作者)
50. Song C, Jia Q, Fang J, Li F, **Wang Chen**, Zhang Z. 2010. Computational identification of citrus microRNAs and target analysis in citrus expressed sequence tags. ***Plant Biology***, 12: 927–934. (参与作者)
51. Dong Q, Cao X, Yang G, Yu H, Nicholas K, **Wang Chen**, Fang J. 2010. Discovery and characterization of SNPs in Vitisvinifera and genetic assessment of some grapevine cultivars. ***Scientia Horticulturae***, 125: 233-238. (参与作者)
52. Fang JG, **Wang Chen**, Yu Hua Ping, Zheng Y, Li Xiao Ying, Song Chang Nian, Chen Jin Feng. 2009. Identification of 57 navel sweet orange cultivars with AFLP markers. ***The Journal of Horticultural Sciences & Biotechnology***, 84: 585-590. (参与作者)
53. 宣旭娴,盛子璐,解振强,黄雨晴,巩培杰,张川,郑婷,**王晨***.vvi-miR172s 及其靶基因响应赤霉素调控葡萄果实发育的作用分析,***中国农业科学***,2021,54(6):1199-1217(通讯作者)
54. 王文然,解振强,诸葛雅贤,白云赫,管乐,吴伟民,张培安,郑婷,房经贵,**王晨***.GA3 介导 miR171s 及其靶基因 VvSCLs 调控葡萄种子发育的作用分析,中国农业科学,2021,54(2):357-369(通讯作者)
55. 张文颖，韩旭，朱旭东，解振强，纠松涛，黄雨晴，贾海锋，房经贵，**王晨***. 葡萄 miR159s 靶基因的鉴定及其应答 GA 在果实不同组织的调控作用[J]. ***中国农业科学***, 2019, 52(16) (通讯作者).
56. 张文颖, 朱旭东, 崔腾飞, 贾海峰, 房经贵, **王晨***. 葡萄 VvRGL 基因应答 GA 调控无核果实发育的研究. ***西北植物学报***, 2019, 3:381-390. (通讯作者)
57. 崔梦杰, 郭凤菲, **王晨***, 纠松涛, 朱旭东, 房经贵. 葡萄 AGL11、AGL15 基因克隆及在赤霉素诱导葡萄无核果实发育过程中的作用[J]. ***南京农业大学学报*** 2019, 42(02): 261-269. (通讯作者)
58. 汤崴, 白云赫, 胡雨晴, **王晨***, 崔梦杰, 张文颖, 房经贵. 葡萄木质素相关基因 PAL、4CL、CAD 特征鉴定及其应答赤霉素在果实发育过程中的作用.[J]. ***南京农业大学学报***, 2019, 42(03):48-57. (通讯作者)
59. 王文然, 樊秀彩, **王晨***, 刘崇怀, 房经贵. 2019. 果树雄性不育的研究进展. **分子植物育种**, 1-10. (通讯作者)
60. 王文然, **王晨*,** 解振强, 贾海锋, 汤崴, 崔梦杰, 房经贵. 2018. VvmiR397a 及其靶基因 VvLACs 在葡萄果实发育中的作用分析. ***园艺学报***, 45(08):1441-1455(通讯作者).
61. 崔梦杰, **王晨***, 冷翔鹏, 汤崴, 张文颖, 朱旭东, 贾海锋, 沈文彪, 房经贵. 2018. 葡萄 SBP-box 转录因子家族的生物信息学分析及其应答激素调控葡萄果实成熟的作用分析. ***南京农业大学学报***, 41(3): 429-439. (通讯作者)
62. 张培安 ,王壮伟, 蔡斌华, 文习成, 田亮, **王晨**, 贾海锋, 房经贵. 2018. ABA 对‘巨峰’葡萄采后成熟关键基因表达的影响. 园艺学报,45(06):1067-1080. (参与作者)
63. 张文颖, **王晨*,** 朱旭东, 马超, 王文然, 冷翔鹏, 郑婷, 房经贵. 2018. 葡萄全基因组 DELLA 蛋白基因家族鉴定及其应答外源赤霉素调控葡萄果实发育的特征. 中国农业科学, 51(16):3130-3146. (通讯作者)
64. 张文颖, **王晨***, 汤崴, 崔梦杰, 朱旭东, 李晓鹏, 房经贵. 2018. 果树果实胚败育研究进展. 分子植物育种, 16(12):4043-4054. (通讯作者)

65. 汤崴, 王洁, 张文颖, 崔梦杰, 朱旭东, 纠松涛, 房经贵, **王晨***. 2018. 木质素在果树果核退化中的作用. 分子植物育种, 16(11):3752-3762. (通讯作者)
66. 李傲, 崔梦杰,王梦琦, 刘众杰, 陈立德, **王晨***, 房经贵*. 2018.叶面喷施 NaH2PO4, K2SO4 以及 KH2PO4 对葡萄磷钾吸收相关基因表达的影响.分子植物育种,16(16):5415-5426. (通讯作者)
67. 崔腾飞, **王晨***, 吴伟民, 纠松涛, 项殿芳, 汤崴, 房经贵. 2018. 近10年来中国葡萄新品种概况及其育种发展趋势分析. 江西农业学报, 30(03):41-48+53. (通讯作者)
68. 房经贵*, 朱旭东, 贾海锋, 王晨. 2017. 植物蔗糖合酶生理功能研究进展. 南京农业大学学报,40(05):759-768.
69. 王梦琦, 解振强, 孙欣, 李晓鹏, 朱旭东, **王晨**, 房经贵. 2017. 葡萄 miR159 及其靶基因 VvGAMYB 在花发育过程中的作用分析. 园艺学报, 44(06):1061-1072.
70. 崔梦杰, **王晨***, 张文颖, 汤威, 朱旭东, 李晓鹏, 房经贵. 2017. 无核葡萄研究进展. ***植物生理学报***, 53(03):317-330. (通讯作者)
71. 王文然, 樊秀彩, 张文颖, 刘崇怀, 房经贵, **王晨***. 2017. 果树赤霉素代谢与信号途径研究进展. ***生物技术通报***, 33(11):1-7. (通讯作者)
72. 崔梦杰, **王晨***, 吴伟民, 王洁, 汤崴, 张文颖. 2017. 葡萄转录因子数据库中 17 个 MADS-box 成员在果实发育成熟过程中的表达特征分析. ***果树学报***, 34(12):1497-1508. (通讯作者)
73. 张超博, 纠松涛, 王梦琪, **王晨***. 2016. 夏黑葡萄功能叶的留叶数对果实品质和产量的影响. ***中外葡萄与葡萄酒***, (05):46-47+53(通讯作者)
74. 张演义, 张全军, 徐颖洁, 钟必凤, 任国慧, **王晨***. 2014. 10 个农家品种梨花粉形态扫描电镜观察. ***西南农业学报***, 27(05):2119-2123.
75. 朱旭东, 上官凌飞, 孙欣, **王晨**, 房经贵. 2014. DNA 标记在植物品种鉴定上的应用现状. ***中国农学通报***, 30(30):234-240. (参与作者)
76. 彭永彬, 李玉, 徐鹏程, 王晨*, 上官凌飞. 2014. 葡萄果实硬度及影响硬度的主要因素. ***浙江农业学报***, 26(05):1227-1234.
77. 李玉, **王晨***, 夏如兵, 曹尚银. 2014.中国石榴栽培史.***中国农史***, 33(01):30-37+20. (通讯作者)
78. 王西成, **王晨**, 房经贵*, 孙欣, 冷翔鹏. 2013. 葡萄 VvGA2ox1 基因克隆、亚细胞定位及时空表达分析. ***南京农业大学学报***, 36(1): 29-34. (参与作者)
79. 任国慧, 陶然, **王晨**, 孙欣, 房经贵*. 2013. 葡萄浆果着色与 UFGT 和 MYBA 基因表达量的关系研究. ***南京农业大学学报***, 36(4): 30-36. (参与作者)
80. 王西成, 吴伟民, 房经贵*, 钱亚明, **王晨**, 宋长年, 赵密珍. 2013. 葡萄赤霉素受体基因 VvGID1A 的分离、亚细胞定位及表达分析. ***园艺学报***, 40(5): 839-848. (参与作者)
81. 慕茜, 刘更森, 孙欣, 李玉, 陶然, **王晨**, 房经贵* . 2013. ‘藤稔’葡萄冬季休眠后期花芽发育相关基因表达的分析. ***园艺学报***, 40(5): 828-838. (参与作者)
82. 张彦苹, 慕茜, 李晓鹏, **王晨**, 宋长年, 房经贵*. 2013. 葡萄卷须及其相关研究. ***植物生理学报***, 49 (3): 234-240. (参与作者)
83. 任国慧, 陶然, 文习成, 李玉, **王晨,** 房经贵*. 2013. 重要果树果实裂果现象及防治措施的研究进展. ***植物生理学报***, 49(4): 324-330. (参与作者)
84. **王晨，**张演义，房经贵，宋长年，刘洪，王西成．2012．葡萄重要花发育调控因子 microR156、mcromiR172 及其靶基因在冬芽二次成花过程中的表达特性及作用机制研究. ***南京农业大学学报***, 35, (4): 59- 64. (第 1 作者)
85. 陶然, **王晨**, 房经贵*, 上官凌飞, 冷翔鹏, 张彦苹. 2012. 我国葡萄育种研究概况. ***江西***

农业学报, 24(6), 24-30　(参与作者)

86. **王晨**, 孙欣, 房经贵. 冷翔鹏, 李晓颖, 慕茜. 2011. 葡萄重要 microRNAs 及其靶基因在冬芽二次成花过程中的表达特性分析. ***西北植物学报***, 31(12): 2429-2436. (第 1 作者)
87. 曹雪, **王晨**, 房经贵, 杨光, 于华平, 宋长年. 2011. 葡萄 SPL9 和 SPL10 基因全长 cDNA 克隆、亚细胞定位和表达分析. ***园艺学报***, 38(2): 240- 250. (参与作者)
88. 上官凌飞, **王晨,** 房经贵, 李晓颖, 王西成, 宋长年. 2011. 利用 GenBank 中大量葡萄 EST 序列分离有效基因的电子表达分析平台方法初探. ***中国农业科学***, 44(13): 2748-2755. (参与作者)
89. 郭磊, **王晨**, 曹雪, 杨光, 慕茜, 房经贵. 2011. 葡萄夏芽成花过程中相关基因的 cDNA-RAPD 分析. ***华北农学报***, 2011, 26(2): 43-48. (参与作者)
90. 王玉娟, **王晨**, 房经贵*, 宋长年, 上官凌飞. 2011. 葡萄浆果的生长发育及相关组学研究概况. ***中外葡萄与葡萄酒***, 176: 65-70. (参与作者)
91. **王晨**, 刘洪, 房经贵, 宋长年, 李晓颖, 章镇. 2010. 基于 EST 库的葡萄(Vitisvinifera) APETAAL2 基因 cDNA 克隆及其表达分析. ***果树学报***, 27 (2): 207-212. (第 1 作者)
92. **王晨**, 王文艳, 初建青, 杨光, 郭磊, 房经贵. 2010. 夏黑葡萄花及果实全长 cDNA 文库的构建及鉴定. ***华北农学报***, 25(4): 30-34. (第 1 作者)
93. 张彦苹, **王晨**, 于华平, 蔡斌华, 房经贵. 2010. 适于葡萄不同组织 RNA 提取方法的筛选. ***西北农学报***, 19(11): 135- 140. (参与作者)
94. 曹雪, 上官凌飞, 于华平, 杨光, **王晨,** 谭洪花, 房经贵*. 2010. 葡萄 SBP 基因家族生物信息学分析. ***基因组学与应用生物学***, 29(4), 791-798. (参与作者)
95. **王晨**, 房经贵, 王涛, 谭洪花. 2009. 果树果实中的糖代谢. ***浙江农业学报***, 21(5): 529-534. (第 1 作者)
96. **王晨**, 王涛, 房经贵, 章镇, 蔡斌华. 2009. 果树设施栽培研究进展. ***江苏农业科学***, (1): 197-200. (第 1 作者)
97. **王晨**, 房经贵, 曹雪, 杨光. 2009. 葡萄中原花青素的代谢. ***中国农学通报***, 25(9): 169-173. (第 1 作者)
98. **王晨**, 房经贵, 章镇, 曹尚银, 张美勇. 2009. 浅谈中国果树品种权益保护及其现状. ***中国农学通报***, 25(24): 298-302. (第 1 作者)
99. **王晨**, 房经贵, 刘洪, 谭洪花. 2009. 葡萄与葡萄酒的营养成分. ***江苏林业科技***, 36(4): 38-40. (第 1 作者)
100. 房经贵, **王晨**, 王涛, 蔡斌华. 2009. 梨花芽高接栽培技术. ***中国南方果树***, 38(4): 58-59. (参与作者)