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Areas of Research

Genetics, Genomics and Breeding of Strawberry and Pear

Contact Information

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We are committed to developing new technologies and methods that can improve the planting level and better products of strawberry and pear. We combine comparative genomics and functional genomics to study the phenotype of important traits, and to understand their genetic and molecular basis, and ultimately serve the cultivation and breeding of strawberry and pear.

Specific Research Interests

1. Imprinted Genes in Strawberry

The ploidy levels of genus *Fragaria* are diverse, interspecific and interploidy hybridization barriers occur generally in the genus. Genomic imprinting is an inheritance process independent of the classical Mendelian inheritance. Sexual reproductive isolation in flowering plants is closely related to the genomic imprinting mechanism. Our interest is to identify the imprinted genes and their regulatory small RNA (sRNA) molecules in strawberry for providing a basis of epigenetics in interspecific and interploidy hybridization barriers of *Fragaria* spp.

2. Self-incompatibility in genus *Fragaria*

The mechanism of gametophytic self-incompatibility (GSI) in genus *Fragaria* is complex. My lab. has exploiting this by various ways: including identifying the style-specific S-RNase genes and the modifiers involved in S-RNase-based GSI process of diploid *Fragaria viridis*, analyzing the function of cis-acting elements by point mutation and combination mutation, screening candidate transcription factor genes from cDNA library by yeast one-hybrid system, and using transcription factor RNA co-

immunoprecipitation (RIP) and locating lncRNAs expressed by the non-coding sequence of S-RNase.

3. Soil Treatment Technologies on Strawberry Planting

The main production form of strawberry is facility forcing cultivation. Continuous cropping obstacles are important in strawberry production. We are committed to finding environmentally friendly, safe and effective soil treatment technologies, with emphasis on appropriate rotation, crop selection and returning techniques.

4. Mechanism of Russeting of Pear Fruit Skin

Based on transcriptome data, we obtained genes with significant difference between brown and green pericarp. In order to analyze the molecular mechanism of GDSL genes in russet pericarp, we have collaborated with the lab (Jocelyn Rose) in Cornell University on functional analysis of GDSL gene involved in suberin assembly. On this basis, we plan to further explore the genes related to russet peel of pear, and provide new theoretical basis and gene resources for genetic improvement on peel color of pear.

Education Background

Bachelor, Nanjing Agricultural University, 1989.09-1993.07

Master, Nanjing Agricultural University, 1999.09-2003.07

Doctor, Nanjing Agricultural University, 2005.09-2009.12

Work experience

Lecturer, Nanjing Agricultural University, 1994-1998

Assistant Professor, Nanjing Agricultural University, 1998-2004

Associate Professor, Nanjing Agricultural University, 2004-2010

Visiting Professor, Chiba University, 2011

Professor, Nanjing Agricultural University, 2010-present

Selected Publication

1. Zhang Hong, Jing XT, Chen Y, Liu Z, Xin YT, **Qiao YS**. The genome-wide analysis of RALF-like genes in strawberry (wild and cultivated) and five other plant species (Rosaceae). *Genes* 2020, 11: 174
2. Du Jianke, Lv Y, Xiong JS, Ge CF, Iqbal S, **Qiao YS**. Identifying genome-wide sequence variations and candidate genes implicated in self-incompatibility by resequencing *Fragaria viridis*. *International Journal of Molecular Sciences* 2019, 20: 1039
3. Xue Huabai, Zhang PJ, Shi T, Yang J, Wang L, Wang SK, Su YL, Zhang HR, **Qiao YS**, Li XG. Genome-wide characterization of simple sequence repeats in *Pyrus bretschneideri*

and their application in an analysis of genetic diversity in pear. *BMC Genomics* 2018, 19: 473

4. Wang Tao, Huang DY, Chen BY, Mao NN, **Qiao YS**, Ji MX. Differential expression of photosynthesis-related genes in pentaploid interspecific hybrid and its decaploid of *Fragaria* spp. *Genes & Genomics* 2018, 40: 321-331
5. Jia Xiaodong, Li MZ, Luo HT, Zhai M, Guo ZR, Li YR, **Qiao YS**, Wang LJ. Transcriptome survey reveals candidate genes involved in lipid metabolism of *Carya illinoensis*. *International Journal of Agriculture and Biology* 2018, 20: 991-1004
6. Jia Xiaodong, Luo HT, Xu MY, Zhai M, Guo ZR, **Qiao YS**, Wang LJ. Dynamic changes in phenolics and antioxidant capacity during pecan (*Carya illinoensis*) kernel ripening and its phenolics profiles. *Molecules* 2018, 23: 435
7. Xue Huabai, Shi T, Wang FF, Zhou HK, Yang J, Wang L, Wang S, Su YL, Zhang Z, **Qiao YS**, Li XG. Interval mapping for red/green skin color in Asian pears using a modified QTL-seq method. *Horticulture Research* 2017, 4: 17053
8. Cheng Hui, Li JF, Zhang H, Cai BH, Gao ZH, **Qiao YS**, Mi L. The complete chloroplast genome sequence of strawberry (*Fragaria X ananassa Duch.*) and comparison with related species of Rosaceae. *PeerJ* 2017, 5: e3919
9. Gu Xianbin, Gao ZH, Yan YC, Wang XY, **Qiao YS**, Chen YH. RdreB1BI enhances drought tolerance by activating AQP-related genes in transgenic strawberry. *Plant Physiology and Biochemistry* 2017, 119: 33-42
10. Ge Chunfeng, Chen BY, Liu L, Gao ZH, **Qiao YS**, Mi L. Identification and chromosome doubling of interspecific hybrids from *Fragaria viridis* x *F. mandshurica*. *Scientia Horticulturae* 2016, 212: 210-219
11. Wang Tao, Liu L, Ning CL, Lu ZQ, Jia XD, Gao ZH, **Qiao YS**. Alterations of DNA methylation and gene expression during hybridization and polyploidization in *Fragaria* spp.. *Scientia Horticulturae* 2016, 201: 218-224
12. Zhou He, Cai BH, Lü ZQ, Gao ZH, **Qiao YS**. Development, characterization, and annotation of potential simple sequence repeats by transcriptome sequencing in pears (*Pyrus pyrifolia* Nakai). *Genetics and Molecular Research* 2016, 15: gmr.15038683
13. Gu Xianbin, Chen YH, Gao ZH, **Qiao YS**, Wang XY. Transcription factors and anthocyanin genes related to low-temperature tolerance in rd29ARdreB1BI transgenic strawberry. *Plant Physiology and Biochemistry* 2015, 89: 31-43
14. Zhang Jiyu, Qu SC, **Qiao YS**, Zhang Z, Guo ZR. Overexpression of the *Malus hupehensis MhNPR1* gene increased tolerance to salt and osmotic stress in transgenic tobacco. *Molecular Biology Reports* 2014, 41: 1553-1561
15. Guan Lin, Huang JF, Feng GQ, Wang XW, Wang Y, Chen BY, **Qiao YS**. Survey of simple sequence repeats in woodland strawberry (*Fragaria vesca*). *Genetics and Molecular Research* 2013, 12: 2637-2651

16. Gu Xianbin, Gao Z, Zhuang W, **Qiao YS**, Wang X, Mi L, Zhang Z, Lin Z. Comparative proteomic analysis of rd29A RdreB1BI transgenic and non-transgenic strawberries exposed to low temperature. *Journal of Plant Physiology* 2013, 170: 696-706
17. Zhang Jiyu, **Qiao YS**, Lv D, Gao ZH, Qu SC, Zhang Z. *Malus hupehensis* NPR1 induces pathogenesis-related protein gene expression in transgenic tobacco. *Plant Biology* 2012, 14(S1): 46-56
18. Zhang Jiyu, Gao ZH, Guo ZR, Zhou J, **Qiao YS**, Qu SC, Zhang Z. Characterization and expression of β -1 3- glucanase gene cloned from *Malus hupehensis*. *Afr J Agr Res* 2012, 7: 597-606
19. Xi Li, Xu KY, **Qiao YS**, Qu SC, Zhang Z, Dai WH. Differential expression of ferritin genes in response to abiotic stresses and hormones in pear (*Pyrus pyrifolia*). *Molecular Biology Reports* 2011, 38: 4405-4413
20. Wang Qingju, Xu KY, Tong ZG, Wang SH, Gao ZH, Zhang JY, Zong CW, **Qiao YS**, Zhang Z. Characterization of a new dehydration responsive element binding factor in central arctic cowberry. *Plant Cell Tiss Organ Cult* 2010, 101: 211-219
21. Wang Xinwei, Xiong AS, Yao QH, Zhang Z, **Qiao YS**. Direct isolation of high-quality low molecular weight RNA of pear peel from the extraction mixture containing nucleic acid. *Mol Biotechnol* 2010, 44: 61-65.
22. Li Zhiqiang, **Qiao YS**, Tong ZG, Zhou J, Zhang Z. Effect of ethylene and 1-MCP on post-harvest physiology and on expression of the ethylene receptor genes *PpETR3* and *PpERS2* in pear (*Pyrus pyrifolia* Nakai 'Kikusui') fruit. *The Journal of Horticultural Science & Biotechnology* 2010, 85: 71-77