

Curriculum Vitae

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EDUCATIONAL BACKGROUND

1996 B.S. (Hons) in Agronomy and minor in computer science, Department of Horticulture, Huazhong Agricultural University (HZAU), China

1999 M.S. in Agronomy, Department of Horticulture, HZAU, China

2002 Ph.D. in Agronomy, Department of Horticulture, HZAU, China

ACADEMIC APPOINTMENTS

2007- Present Associate professor, College of Biological Sciences and Biotechnology, Beijing Forestry University, China

2006-2007 Lecturer, College of Biological Sciences and Biotechnology, Beijing Forestry University, China

2004-2006 JSPS postdoctoral fellow, Research Team for Global Warming on Fruit Tree, National Institute of fruit tree science (NIFTS), Tsukuba, Japan

2002-2004 Postdoctoral fellow, Institute of Genetics and developmental biology (IGDB), Chinese Academy of Science

RESEARCH INTERESTS

- ✧ Molecular regulation of fruit development and ripening
- ✧ Genetic diversity of horticultural crops
- ✧ Molecular regulation of plant cold tolerance
- ✧ QTL mapping of complex traits in plants

HONORS AND AWARDS

- ✧ 2004, JSPS Fellowship, Japan
- ✧ 2009, New Century Excellent Talent of the Ministry of Education, China

PROFESSIONAL ACTIVITIES

✧ **Editorial Service**

Recent Patents on Biotechnology, Editorial Editor (2014-)

Frontiers in Genetic Architecture, Review editor (2011-2013)

✧ **Journal Review Services**

PLoS ONE, Tree Genetics & Genomes, Trees - Structure and Function, Scientia Horticulturae, Acta Physiologiae Plantarum, Genetic and Molecular Biology, Journal

of Genetics and Genomic, and more than ten Journals on plant genetics and biotechnology in Chinese

◇ **Grant Reviewer**

National Natural Science Foundation of China

Key Projects of Ministry of Education, China

RECENT PUBLICATIONS (*Contributed equally; †Corresponding author)

1. Wang SQ, Liu Y, Ma LY, Liu HB, Tang Y, Wu LP, Wang Z, Li YY, Wu RL, **Pang XM**[†]. Isolation and Characterization of Microsatellite Markers and Analysis of Genetic Diversity in Chinese Jujube (*Ziziphus jujuba* Mill.). PLoS ONE, 2014, 9(6): e99842
2. Tong C, Shen L, Lv Y, Wang Z, Wang X, Feng S, Li X, Sui Y, **Pang XM**[†], Wu RL[†]. Structural mapping: how to study the genetic architecture of a phenotypic trait through its formation mechanism. Brief Bioinform, 2014,15(1):43-53
3. Zhai Y, Lv YF, Li X, Wu WM, Bo WH, Sheng DF, Xu F, **Pang XM**, Zheng BZ, Wu RL[†]. A synthetic framework for modeling the genetic basis of phenotypic plasticity and its costs. New Phytol, 2014, 20: 357-365
4. Wang Z, Kang M, Liu H, Gao J, Zhang Z, Li YY, Wu RL, **Pang XM**[†]. High-Level Genetic Diversity and Complex Population Structure of Siberian Apricot (*Prunus sibirica* L.) in China as Revealed by Nuclear SSR Markers. PLoS ONE, 2014, 9(2): e87381
5. Wang Z, Liu HB, Liu J, Li YY, Wu RL, **Pang XM**[†]. Mining new microsatellite markers for Siberian apricot (*Prunus sibirica* L.) from SSR-enriched genomic library. Scientia Horticulturae, 2014, 166:65–69
6. Liu J, Liu HB, Ma LY, Wang SQ, Gao J, Li YY, Wu RL, **Pang XM**[†]. A Chinese jujube (*Ziziphus jujuba* Mill.) fruit-expressed sequence tag (EST) library: Annotation and EST-SSR characterization. Scientia Horticulturae, 2014, 165: 99-105
7. Wang Z*, **Pang XM***, Wu WM, Wang JX, Wang ZH, Wu RL[†]. Modeling phenotypic plasticity in growth trajectories: A statistical framework. Evolution, 2014, 68: 81-91
8. Fu GF, Bo WB, **Pang XM**, Wang Z, Chen L, Song YP, Zhang ZY, Li J, Wu RL[†]. Mapping shape QTLs using a radius-entroid-contour model. Heredity,2013, 110(6):511-519
9. **Pang XM**, Wang Z, Yap JS, Bo WH, Lv YF, Xu F, Zhou T, Peng SF, Shen DF, Wu RL[†]. A statistical procedure to map high-order epistasis for complex traits. Briefings in Bioinformatics, 2013, 14 (3): 302-314
10. Liu HB, Liu J, Wang Z, Ma LY, Wang SQ, Lin XG, Wu RL, **Pang XM**[†]. Development and characterization of microsatellite markers in *Prunus Sibirica* (Rosaceae)," Applications in Plant Science,2013, 1(3):1200074
11. Lin XG, Yao LX, Li YY, Wu RL and **Pang XM**[†]. Identification of genes associated with fruit ripening in *Ziziphus jujuba* using suppression subtractive hybridization approach. Acta Physiologiae Plantarum, 2013, 35:1997–2008
12. Zhang ZY, **Pang XM**, Han JW, Wang Y and Li YY[†]. Conservation genetics of *Annamocarya sinensis* (Dode) Leroy, an endangered endemic species, Genetics and Molecular Research, 2013, 12(3), 3956-3974
13. Zhang ZY, Han JW, Jin Q, Wang Y, **Pang XM**, Li YY[†]. Development and

- characterization of new microsatellites for walnut (*Juglans regia*), *Genetics and Molecular Research*, 12(4), 4723-4734, 2013
14. Yang XX, Lv YF, **Pang XM**, Tong CF, Wang Z, Li X, Feng SS, Tobias CM, Wu RL[†]. A unifying framework for bivalent multilocus linkage analysis of allotetraploids. *Briefings in Bioinformatics*, 2013, 14: 96–108
 15. Wang Z, **Pang XM**, Lv YF, Xu F, Zhou T, Li X, Feng SS, Li JH, Li ZK, Wu RL[†]. A dynamic framework for quantifying the genetic architecture of phenotypic plasticity. *Briefings in Bioinformatics*, 2013, 14: 82–95
 16. Zhao XY, Tong CF, **Pang XM**, Wang Z, Guo YQ, Du F, Wu RL[†]. Functional mapping of ontogeny in flowering plants. *Briefings in Bioinformatics*. *Briefings in Bioinformatics*, 2012, 13: 317–328
 17. Wang JX, Dong XL, **Pang XM**, Lv YF, Yi HL, Yang XX, Wang Z, Wu S, Wu RL[†]. Simultaneous estimation of genetic linkage and preferential pairing factor for a triploid population with unphased markers. *Chinese Science Bulletin*, 2012, 57: 2711-2720
 18. Yang XX*, Lv YF*, **Pang XM***, Tong CF, Wang Z, Li X, Feng SS, Tobias CM, Wu RL*. A unifying framework for bivalent multilocus linkage analysis of allotetraploids. *Brief Bioinform* , 2013, 14: 96–108
 19. Wang Z*, **Pang XM ***, Lv YF, Xu F, Zhou T, Li X, Feng SS, Li JH, Li ZK, Wu RL[†]. A dynamic framework for quantifying the genetic architecture of phenotypic plasticity. *Brief Bioinform* , 2013, 14: 82–95
 20. Zhao XY*, Tong CF*, **Pang XM ***, Wang Z, Guo YQ, Du F, Wu RL[†]. Functional mapping of ontogeny in flowering plants. *Briefings in Bioinformatics*. *Brief Bioinform* 2012, 13: 317–328,
 21. Hou W, Lin S, Li Y, **Pang XM**, Zeng Y, Wu R[†]. A model for linkage analysis with apomixis. *Theor Appl Genet.*, 2011, 123(5):681-691
 22. Tong C, Zhang B, Wang Z, Xu M, **Pang XM**, Si J, Huang M, Wu R[†]. Multiallelic epistatic model for an out-bred cross and mapping algorithm of interactive quantitative trait loci. *BMC Plant Biol.* 11:148,2011
 23. Li Q, Huang Z, Xu M, Wang C, Gai J, Huang Y, **Pang XM**, Wu R[†]. Functional mapping of genotype-environment interactions for soybean growth by a semiparametric approach. *Plant Methods.*, 6:13, 2010
 24. **Pang XM**, Nada K, Kurosawa T, Ban Y and Moriguchi T[†]. Effect of methylglyoxal bis-(guanylhydrazone) on polyamine and ethylene biosynthesis of apple fruit after harvest. *Acta Physiologiae Plantarum.* 32(5), 1005-1010, 2010
 25. Wen XP*, **Pang XM*** Liu JH, Kitashiba H, Honda C and Moriguchi T[†]. Overexpression of SPDS1 gene in transgenic pear shows high tolerance to stresses with the altered polyamine titers. 2008, 17(2):251-263
 26. Liu JH, Nada K, **Pang XM**, Honda C, Kitashiba H and Moriguch T[†]. Role of polyamines in peach fruit development and storage. *Tree physiology.* 2006, 26: 791-798.
 27. Li YH, Qian Q, Zhou YH, Yan MX, Sun L, Zhang M, Fu ZM, Wang YH, Han B, **Pang XM**, Chen MS, Li JY[†]. BRITTLE CULM 1, Which Encodes a COBRA-Like protein, affects the mechanical properties of rice plants. *The Plant Cell*, 2003; 15 (9): 2020-2031
 28. **Pang XM**, Wen XP, Hu CG, Deng XX[†]. Genetic diversity of Poncirus accessions as revealed by amplified fragment length polymorphism (AFLP). *Journal of Horticultural Science & Biotechnology.* 2006, 81: 269 - 275

29. **Pang XM**, Hu CG, Deng XX[†]. Phylogenetic relationships within Citrus and its related genera as inferred from AFLP markers. *Genetic Resources and Crop Evolution*. 2007, 54(2): 429-436
30. **Pang XM**, Hu CG, Deng XX[†]. Phylogenetic relationships among Citrus and its relatives as revealed by SSR markers. *Acta Genetica Sinica*. 2003, 30(01): 81-87
31. Wen XP, **Pang XM**, and Deng XX[†]. Characterization of genetic relationships of *Rosa roxburghii* Tratt and its relatives using morphological traits and RAPD and AFLP markers. *Journal of Horticultural Science & Biotechnology*. 2004, 79: 189 - 196
32. Liu JH, **Pang XM**, ChenYJ, Meng HJ, Deng XX[†]. Molecular characterization of the nuclear and cytoplasmic genomes of intergeneric diploid plants from cell fusion between *Microcitrus papuana* and rough lemon. *Plant Cell Reporter*, 2002, 21: 327 – 332

GRANT SUPPORT

Number	Funding Period	Funding Agency	Title	Role
BLX2007015	2009-2009	MOE, China	Fingerprinting of Chinese jujube cultivars	PI
JD-201005	2010-2010	MOE, China	Collection, characterization and utilization of Chinese jujube germplasm	PI
30800883	2009-2011	NSF, China	Mining DEGs relating to fruit ripening of Chinese jujube	PI
NCET-10-0223	2010-2012	MOE, China	Genetic diversity and population of Siberian Apricot (<i>Prunus sibirica</i> L.) in China	PI
31372019	2013-2016	NSF, China	High density of RAD genetic map and QTL mapping of cold tolerance in Chinese jujube	PI
201004017	2010-2014	MOST, China	Key technology of enhancing Chinese jujube industry	PI
2013BAD14B03	2013-2017	MOST, China	Key technology of producing fresh and dried Chinese jujube	Co-PI