CURRICULUM VITAE

Personal Information				
Name	Nian Wang	Gender	Male	
Position Title		Associate Professor		
Working Department		College of Horticulture and Forestry		
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Research Interest

- Dissecting plant traits by Bioinformatics, Large Data Based Genomics, Population Genetics and Molecular Biology.
- Plant-Pathogen interaction in woody species.
- Tree molecular breeding.

Professional Memberships

No

Other Roles

No

Education & Working Experience

Education

- Ph.D. in Developmental Biology, 2004-2009, National Key Laboratory of Crop Genetic Improvement, Huazhong Agricultural University, Wuhan, China.
- B.S. in Forestry, 2000-2004, Forestry Department, Huazhong Agricultural University, Wuhan, China.

Working Experience

- 2009.6-2010.10 Postdoc, Plant Breeding Institute, Kiel University, Germany.
- 2010.11-2013.7, Associate Professor, Chinese Academy of Sciences.
- 2013.8-2014.8, Associate Professor, Chinese Academy of Agricultural Sciences.

- 2014.9-2015.8, Visiting Research Scientist, USDA/Cornell University, USA.
- 2015.9-present, Associate Professor, Huazhong Agricultural University.

Publications

1. **Wang N**, Wang Y, Tian F, King GJ, Zhang C, Long Y, Shi L, Meng J*. A functional genomics resource for Brassica napus: development of an EMS mutagenized population and discovery of FAE1 point mutations by TILLING. New Phytologist 2008 (180): 751-765

2. **Wang N**, Shi L, Tian F, Ning H, Wu X, Long Y, Meng J, Meng J*. Assessment of FAE1 diversity in three Brassica species and their association to seed erucic acid content with EcoTILLING. BMC Plant Biology. 2010 (10):137

3. **Wang N**, Qian W, Suppanz I, Wei L, Mao B, Long Y, Meng J, Müller AE*, Jung C. Flowering time variation in oilseed rape (Brassica napus L.) is associated with allelic variation in the FRIGIDA homologue BnaA.FRI.a. Journal of Experimental Botany. 2011 (15):5641-58

4. **Wang N**, Fang Linchuan, Xin Haiping, Wang Lijun, Li Shaohua*. Construction of a high-density genetic map for grape using next generation restriction-site associated DNA sequencing. BMC Plant Biology. 2012, 12:148

5. **Wang N***, Zheng Yu, Fang Linchuan, Xin Haiping, Li Shaohua*. Comprehensive analysis of NAC domain transcription factor gene family in Vitisvinifera. Plant Cell Reports. 32(1):61-75

6. **Wang N***, Xiang Yue, Fang Linchuan, Xin Haiping, Li Shaohua*. Patterns of gene duplication and their contribution to expansion of large gene families in grapevine. Plant Molecular Biology Reporter 31(4):852-856

7. **Wang N**, Li F, Chen BY, Xu K, Yan GX, Qiao JW, Li J, Gao GZ, Bancroft I, King GJ, Meng JL, Wu XM*. Genome-wide investigation of genetic changes during modern breeding of Brassica napus. Theoretical and Applied Genetics. 2014 (127): 8.

8. Fang LC, Hou YL, Wang LJ, Xin HP, **Wang N***, Li SH*. Myb14, a direct activator of STS, is associated of resveratrol content variation in berry skin in two grape cultivars. Plant Cell Reports. 2014, 33(10):1629-40 (**Co-corresponding author**).

9. Chen J, **Wang N**, Fang LC, Liang ZC, Li SH *, Wu BH*. Construction of a high-density genetic map and QTLs mapping for sugars and acids in grape berries. BMC Plant Biol. 2015; 15: 28 (Co-first authors;**IF: 3.813**).

10. **Wang N** and Shi L. Screening of mutations by TILLING in plants. Methods Mol Biol. 2015; 1245:193-203.

11.**Wang N**, Chen B, Xu K, Gao G, Li F, Qiao J, Yan G, Li J, Li H, Wu X.Association Mapping of Flowering Time QTLs and Insight into Their Contributions to Rapeseed Growth Habits. Front Plant Sci. 2016; 24;7:338.

Additional Information
No