

Liang Xu



Areas of Research

Vegetable genetics, breeding & biotechnology;
Bioinformatics and comparative genomics.

Contact Information

Office location: Room B6014 Life Sci. Build.,
Nanjing Agricultural University, Nanjing, Jiangsu
Province, P. R. China

Office phone: 086-25-84395563

Email address: naxuliang@njau.edu.cn

Research Interests

Root vegetable genetics & breeding; Root vegetable biotechnology & comparative genomics

By integrating the molecular biology experiments, bioinformatics, genetic transformation and data-mining approaches, our team are interested in elucidating the molecular genetic mechanism underlying several important horticulture traits (e.g. bolting and flowering, taproot formation, quality traits and biotic/abiotic stress response) in root vegetable crops such as radish, aiming to establishing optional strategies for high-efficient genetically engineering desirable and high-quality root vegetable cultivars in plant breeding programs.

Education Background

09/2008-06/2013, Ph.D (Agriculture Sci.), College of Horticulture, Nanjing Agricultural University, P. R. China.

09/2004-06/2008, B.S. (Agriculture Sci.), College of Horticulture, Qingdao Agricultural University, P. R. China.

Work experience

01/2017-present, Associate professor, National Key Laboratory of Crop Genetics and Germplasm Enhancement, College of Horticulture, Nanjing Agricultural University, P. R. China.

11/2017-09/2019, Postdoc, Department of Plant Biology, Michigan State University, USA.

09/2013-12/2016, Lecturer, National Key Laboratory of Crop Genetics and Germplasm Enhancement, College of Horticulture, Nanjing Agricultural University, P. R. China.

Honors and Awards

1. Yong Academic Scientist of Zhongshan Scholars, 2019.1-2022.12, Nanjing Agricultural University, P. R. China.
 2. 2nd Class of the Sci. & Technol. Progress Award, 2016, Ministry of Education, P. R. China.
 3. Excellent Doctoral Dissertation Award of Jiangsu Province, 2014, P. R. China.
-

Selected Publication

(#): Co-first author; (*): Corresponding author.

1. **Xu L**, Zhang F, Tang MJ, Wang Y, Dong JH, Ying JL, Chen YL, Hu B, Li C, Liu LW^(*). Melatonin confers cadmium tolerance by modulating critical heavy metal chelators and transporters in radish plants. *J Pineal Res*, 2020, 69: e12659.
2. Luo XB^(#), **Xu L**^(#), Wang Y, Dong JH, Chen YL, Tang MJ, Fan LX, Zhu YL, Liu LW^(*). An ultra-high density genetic map provides insights into genome synteny, recombination landscape and taproot skin color in radish (*Raphanus sativus* L.). *Plant Biotechnol J*, 2020, 18: 274–286.
3. Karanja KB^(#), **Xu L**^(#), Wang Y, Tang MJ, Muleke ME, Dong JH, Liu LW^(*). Genome-wide characterization of the AP2/ERF gene family in radish (*Raphanus sativus* L.): Unveiling evolution and patterns in response to abiotic stresses. *Gene*, 2019, 718: 144048.
4. Chen W^(#), Wang Y^(#), **Xu L**^(#), Dong JH, Zhu XW, Ying JL, Wang QJ, Fan LX, Li C, Liu LW^(*). Methyl jasmonate, salicylic acid and abscisic acid enhance the accumulation of glucosinolates and sulforaphane in radish (*Raphanus sativus* L.) taproot. *Sci Horti*, 2019, 250: 159–167.
5. **Xu L**^(#), Wang Y^(#), Zhang F, Tang MJ, Chen YL, Wang J, Karanja KB, Luo XB, Zhang W, Liu LW^(*). Dissecting root proteome changes reveals new insight into cadmium stress response in radish (*Raphanus sativus* L.). *Plant Cell Physiol*, 2017, 58: 1901–1913.
6. Feng HY^(#), **Xu L**^(#), Wang Y, Tang MJ, Zhu XW, Zhang W, Sun XC, Nie SS, Muleke EM, Liu LW^(*). Identification of critical genes associated with lignin biosynthesis in radish

(*Raphanus sativus* L.) by *de novo* transcriptome sequencing. *Mol Genet Genomics*, 2017, 292:1151–1163.

7. Wang YY^(#), Liu W^(#), **Xu L**^(#), Wang Y, Chen YL, Luo XB, Tang MJ, Liu LW^(*). Development of SNP markers based on transcriptome sequences and their application in germplasm identification in radish (*Raphanus sativus* L.). *Mol Breeding*, 2017, 37: 26.

8. Wang Y^(#), **Xu L**^(#), Tang MJ, Jiang HY, Chen W, Zhang W, Wang RH, Liu LW^(*). Functional and integrative analysis of the proteomic profile of radish root under Pb exposure. *Front Plant Sci*, 2016, 7: 1871.

9. **Xu L**, Wang Y, Liu W, Wang J, Zhu XW, Zhang KY, Yu RG, Wang RH, Xie Y, Zhang Wei, Gong YQ, Liu LW^(*). *De novo* sequencing of root transcriptome reveals complex cadmium-responsive regulatory networks in radish (*Raphanus sativus* L.). *Plant Sci*, 2015, 236: 313–323.

10. Wang Y^(#), Shen H^(#), **Xu L**^(#), Zhu XW, Li C, Zhang W, Xie Y, Gong YQ, Liu LW^(*). Transport, ultrastructural localization and distribution of chemical forms of lead in radish (*Raphanus sativus* L.). *Front Plant Sci*, 2015, 6: 293.

11. **Xu L**^(#), Jiang QW^(#), Wu J, Wang Y, Gong YQ, Wang XL, Limer C, Liu LW^(*). Identification and molecular mapping of the *RsDmR* locus conferring resistance to downy mildew at seedling stage in radish. *J Integr Agr*, 2014, 13: 2362–2369.

12. Wang XL^(#), **Xu L**^(#), Song ZH, Zhu XW, Wang Y, Wang RH, Gong YQ, Limer C, Liu LW^(*). Resistance gene analogue isolation and RGA-based marker development for identifying downy mildew resistance in radish (*Raphanus sativus* L.). *Euphytica*, 2014, 198: 289–303.

13. **Xu L**, Wang Y, Zhai LL, Xu YY, Wang LJ, Gong YQ, Yu RG, Limer C, Liu LW^(*). Genome-wide identification and characterization of cadmium-responsive microRNAs and their target genes in radish (*Raphanus sativus* L.) roots. *J Exp Bot*, 2013, 64: 4271–4287.

14. **Xu L**, Wang Y, Xu YY, Wang LJ, Zhai LL, Zhu XW, Gong YQ, Ye S, Liu LW^(*). Identification and characterization of novel and conserved microRNAs in radish (*Raphanus sativus* L.) using high-throughput sequencing. *Plant Sci*, 2013, 201–202: 108–114.

15. **Xu L**, Wang LJ, Gong YQ, Dai WH, Wang Y, Zhu XW, Wen TC, Liu LW^(*). Genetic linkage map construction and QTL mapping of cadmium accumulation in radish (*Raphanus sativus* L.). *Theor Appl Genet*, 2012, 125: 659–670.

16. Zhang YY^(#), **Xu L**^(#), Zhu XW, Gong YQ, Xiang F, Sun XC, Liu LW^(*). Proteomic analysis of heat stress response in leaves of radish (*Raphanus sativus* L.). *Plant Mol Biol Rep*, 2012, 31: 195–203.