

Liwang Liu



Areas of Research

Genetic Breeding and Biotechnology of Vegetable Crops; Applied Genomics; Radish Germplasm Enhancement and Utilization.

Contact Information

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Research Interests

Genetic Breeding; Applied Genomics; Radish Germplasm Enhancement and Utilization; Biotechnology of Vegetable Crops.

We employ genomic approaches, molecular biology technology and traditional breeding methods to dissect the genetic mechanism and facilitate genetic improvement of horticultural traits in radish. The main works focus on investigation of genetic regulatory network in response to heavy metal stresses in radish; dissection of molecular mechanism underlying key horticultural traits including heat, salt and bolting tolerance; identification and utilization of germplasm resources, and molecular design breeding in radish; development of elite cultivars and germplasm enhancement.

Education Background

Bachelor: Anhui Normal University (China) , 1994

Master: Nanjing Agricultural University (China) , 1997

Ph.D: Nanjing Agricultural University (China) , 2002

Post-Doc: North Dakota State University (USA) , 2005-2007

Senior Visiting Scholar: Michigan State University (USA) , 2016-2017

Work Experience

Assistant/ Associate Professor, Nanjing Agricultural University, 2003-2008

Professor, Nanjing Agricultural University, 2008-

Chief Professor, Nanjing Agricultural University, 2019-

Honors and Awards

Leading talent of National Ten Thousand Talent Program of China

Editorial board member, *Front Plant Sci* (2016-2020) and *J Nanjing Agricultural University*(2018-)

Chief scientist, Radish Industry Chain Project of Jiangsu Province

New Century Excellent Talents of the Ministry of Education of China

Youth Science and Technology Award of Jiangsu Province, 2012

Second prize for Science and Technology Progress Award, Ministry of Education of China (2016, **PI**)

Second prize of Science and Technology Progress Award of Jiangsu province (2011, **PI**)

Second prize of Science and Technology Progress Award, Ministry of Agriculture and Rural Affairs of China (2019, **PI**)

Selected Publication

Recent Peer-Reviewed Publications (* Corresponding author)

Luo X.[#], Xu L.[#], Wang Y, Dong J., Chen Y., Tang M., Fan L., Zhu Y., Liu L.*. 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, doi: 10.1111/pbi.13195.

Xu L, Zhang F, Tang M., Wang Y, Dong J., Ying J., Chen Y., Hu B., Li C, Liu L. Melatonin confers cadmium tolerance by modulating critical heavy metal chelators and transporters in radish plants. *J Pineal Res.* 2020, 69: e12659. <https://doi.org/10.1111/jpi.12659>

Xie Y, Ying J., Xu L, Wang Y, Dong J., Chen Y., Tang M., Li C, Muleke M E, Liu L. Genome-wide sRNA and mRNA transcriptomic profiling insights into dynamic regulation of taproot thickening in radish (*Raphanus sativus* L.). *BMC Plant Biol* 2020, 20: 373. <https://doi.org/10.1186/s12870-020-02585-z>

Xu L, Wang Y, Zhang F, Tang M., Chen Y., Wang J, Bernard K., Luo X., Zhang W, Liu L.*. Dissecting the root proteome changes reveals new insight into Cadmium stress response in radish (*Raphanus sativus* L.). *Plant and Cell Physiology.* 2017, 58(11):1901-1913. doi: 10.1093/pcp/pcx131.

Fan L., Wang Y, Xu L., Tang M., Zhang X., Ying J., Li C., Dong J., Liu L.*. A genome-wide association study uncovers a critical role of the RsPAP2 gene in red-skinned *Raphanus sativus* L. *Hortic Res*, 2020, 7: 164, doi: 10.1038/hortres.2020.164

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- Xu L, Wang Y, Zhai L., Xu Y., Wang L., Zhu X., Gong Y., Yu R., Limera C., Liu L.*. Genome-wide identification and characterization of cadmium-responsive microRNAs and their targets in radish (*Raphanus sativus* L.) roots. *J Exp Bot*, 2013, 64(14):4271-4287.
- Xu L, Wang L, Gong Y., Dai W., Wang Y, Zhu X., Wen T., Liu L.*. Genetic linkage map construction and QTL mapping of cadmium accumulation in radish. *Theor Appl Genet*, 2012, 125(4):659-670, doi: 10.1007/s00122-012-1858-y .
- Xu L, Wang Y, Xu Y., Wang L., Zhai L., Zhu X., Gong Y., Ye S, Liu L.*. Identification and characterization of novel and conserved microRNAs in radish (*Raphanus sativus* L.) using high-throughput sequencing. *Plant Science*, 2013, 201-202: 108-114.
- Liu L., Guo W., Zhu X., Zhang T.*. Inheritance and fine mapping of fertility restoring gene for cytoplasmic male sterility in *Gossypium*. *Theor Appl Genet*, 2003, 106:461-469
- Wang Y#, Pan Y#, Liu Z., Zhu X., Zhai L., Xu L., Yu R., Gong Y., Liu L.*. De novo transcriptome sequencing of radish (*Raphanus sativus* L.) and analysis of major genes involved in glucosinolate metabolism. *BMC genomics*, 2013, 14: 836. doi: 10.1186/1471-2164-14-836.
- Xie Y., Xu L., Wang Y., Fan L., Chen Y., Tang M., Luo X., Liu L.*. Comparative proteomic analysis provides insight into a complex regulatory network of taproot formation in radish (*Raphanus sativus* L.). *Hortic Res*, 2018, 5:51. DOI 10.1038/s41438-018-0057-7
- Cheng W.#, Tang M.#, Xie Y, Xu L, Wang Y, Luo X., Fan L., Liu L.*. Transcriptome-based gene expression profiling of diploid radish (*Raphanus sativus* L.) and the corresponding autotetraploid. *Mol. Biol. Rep*, 2019, 46(1): 933-945. doi: 10.1007/s11033-018-4549-1.
- Wang Y#, Liu W#, Xu L#, Wang Y, Chen Y., Luo X., Tang M., Liu L*. Development of SNP markers based on transcriptome sequences and their application in germplasm identification in radish (*Raphanus sativus* L.). *Mol. Breed*, 2017, 37:26, DOI: 10.1007/s11032-017-0632-x.
- Luo X., Xu L, Liang D., Wang Y, Zhang W, Zhu X., Zhu Y., Jiang H., Tang M., Liu L. *. Comparative transcriptomics uncovers alternative splicing and molecular marker development in radish (*Raphanus sativus* L.), *BMC Genomics*, 2017, 18: 505. doi: 10.1186/s12864-017-3874-4.
- Sun X., Liu Y., Wang L., Zhu X., Gong Y., Liu L.*. Molecular characterization of the *Rs-Rfl* gene and molecular marker-assisted development of elite radish (*Raphanus sativus* L.) CMS lines with a functional marker for fertility restoration. *Mol. Breed*, 2012, 30:1727-1736. doi: 10.1007/s11032-012-9756-1
- Nie S., Li C, Xu L, Wang Y, Huang D., Muleke M., Sun X., Xie Y., Liu L.*. De novo transcriptome analysis in radish (*Raphanus sativus* L.) and identification of critical genes involved in bolting and flowering. *BMC Genomics*, 2016, 17: 389. doi: 10.1186/s12864-016-2633-2.
- Yu R., Wang Y, Xu L, Zhu X., Zhang W, Wang R., Gong Y., Limera C., Liu L.*. Transcriptome profiling of root microRNAs reveals novel insights into taproot thickening in radish (*Raphanus sativus* L.). *BMC Plant Biol*, 2015, 15:30. doi: 10.1186/s12870-015-0427-3
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- Sun X.(#), Wang Y(#), Xu L, Li C, Zhang W, Luo X., Jiang H., Liu L. *. Unraveling the root proteome changes and its relationship to molecular mechanism underlying salt stress response in radish (*Raphanus sativus* L.). *Front. Plant Sci*. 2017, 8: 1192. doi: 10.3389/fpls.2017.01192.

- Feng H. (#), Xu L. (#), Wang Y, Tang M., Zhu X., Zhang W., Sun X., Nie S., Muleke M., Liu L.*. Identification of critical genes associated with lignin biosynthesis in radish (*Raphanus sativus* L.) by de novo transcriptome sequencing. *Mol. Genet. Genomics*, 2017, 292(5):1151-1163. DOI: 10.1007/s00438-017-1338-9.
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- Wang Y.(#), Liu W.(#), Shen H., Chen Y., Zhai L, Xu L, Wang R., Gong Y., Cecilia L., Liu L.*. Identification of radish (*Raphanus sativus* L.) miRNAs and their target genes to explore miRNA-mediated regulatory networks in lead (Pb) stress responses by high-throughput sequencing and degradome analysis. *Plant Mol Biol Rep*, 2015, 33(3):358-376, DOI: 10.1007/s11105-014-0752-y.
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Reference

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