CURRICULUM VITAE

Lin Li, Ph.D

Vice Dean of College of Plant Science and Technology
Head of Dept. of Intelligent Agriculture
Dep. of Plant Genetics and Breeding
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Education

Sep 2005 – Jul 2010	**China Agricultural University** Ph. D, Plant Genetics Beijing, China
Sep 2001 – Jul 2005	**China Agricultural University** Bachelor, Plant Genetics and Agronomy (Major) and Computer Science (Minor) Beijing, China

Professional Experience

Aug 2010 – July 2013	**University of Minnesota, Twin Cities** Post-Doctor, Department of Agronomy and Plant Genetics MN, United States of America
July 2013 – 2016	**University of Minnesota, Twin Cities** Post-Doctor Research Associate, Department of Agronomy and Plant Genetics MN, United States of America

July 2016 – present **Huazhong Agricultural University**
Professor, Department of Agronomy and Plant Genetics
Wuhan, China

Research Interests

My interests are Biological Big-Data, Smart Breeding, and Smart Agriculture. Our research topic is centered on biological big data and systems biology in maize. Using biological big data and artificial intelligence technology, we are trying to unravel the molecular mechanism underlying maize plant architecture and the trade-off of silage maize biomass, resistance, and quality variation, which provide fundamental knowledge and germplasm resources for high-yield, high-resistance, and high-quality silage maize breeding.

Statistics of Peer-review Publications

H-Index: **30** *Publications:* **63** *Citations:* **5505 updated on Sep. 2025 by Scholar Google**

Awards

2023, The Youth Scientist Award of National Corn Seed Technology Innovation Center

2023, The Youth Innovation Award of Genetics Society of China.

2022, The First Prize of Teaching Achievement Award of Colleges and Universities in Hubei Province.

2022, Special Award for Teaching Achievement of Huazhong Agricultural University.

2022, Excellent Mentor Award of Huazhong Agricultural University.

2019, Outstanding Youth of National Natural Science Foundation of China.

2018, Overseas High-level Talents of Hubei Province.

2017, Chutian Scholar of Hubei Province.

2013, First Prize of Science and Technology Progress Award of the Ministry of Education.

2005, Merit undergraduate Student of China Agriculture University, and My graduate thesis was awarded as one of the top 100 merit graduate thesis of China Agriculture university (out of more than 2,000 students).

2002, 2003, 2004, The Second-class Scholarship of College of Agronomy and Biotechnology.

2002, 2003, 2004, Merit Student Awards of College of Agronomy and Biotechnology (This award is only given to students who perform well in study as well as in social activities).

Skills

Teaching Courses	**Bioinformatics**, **Techniques and applications of Biological Big-Data**, **Genetics**
Skills	Bioinformatics, Deep Learning, Machine Learning, Next Generation Sequencing, Quantitative & Qualitative Genetics Research, R Statistical Package, Computational Biology, Plant Genomics, Plant Biology, Programing (Java, Perl, Visual Basic, PHP), Database (sql-server, MySQL, access)
Languages	Chinese, English

Funding Projects

Lin Li (PI). RMB **25,000,000**, Big data-assisted design breeding of important agronomic traits in crop genomes. ***National Key R&D Program of China*** (2023-2028).

Lin Li (PI). RMB **630,000**, Cloning and functional validation of maize kernel mutant Sem1. Routine Project, ***National Natural Science Foundation of China*** (2018-2021).

Lin Li (PI). RMB **550,000**, Dissection of maize kernel mutant Sem1 governing the trade-off between grain yield and drought resistance. Routine Project, ***National Natural Science Foundation of China*** (2023-2026).

Lin Li (PI). RMB **1,300,000**, Molecular mechanisms underlying maize plant architecture. Outstanding Youth Project, ***National Natural Science Foundation of China*** (2020-2022).

Lin Li (PI). RMB **5,000,000**, Dissection of regulatory networks conferring maize plant architecture. Major Research Project, ***National Natural Science Foundation of China*** (2021-2022).

Lin Li (PI). RMB **2,000,000**, Identification and Utilization of Excellent Silage Biomass

Traits in 18 Teosinte Introgressed Populations. International (regional) Cooperation and Exchange Projects, ***National Natural Science Foundation of China*** (2023-2027).

Lin Li (PI). RMB **3,600,000**, **Outstanding Youth Cultivation Project of Central Universities** (2023-2025).

I have also anticipated several other projects as co-PI.

Publications

Representative Journal Publications (Corresponding author)

1. Li, Ruonan, et al. An epiallele of a gene encoding PfkB-type carbohydrate kinase affects plant architecture in maize. ***Plant Cell*** (2024) DOI: 10.1093/plcell/koaf017.
2. Luo, Zi, et al. A dynamic regulome of shoot-apical-meristem-related homeobox transcription factors modulates plant architecture in maize. ***Genome Biology*** (2024) 25: 245. ***Featured Article***
3. Han, Linqian, et al. A multi-omics integrative network map of maize. ***Nature Genetics*** (2023) 55.1: 144-153. ***Featured Article***
4. Sun, Xiaopeng, et al. The role of transposon inverted repeats in balancing drought tolerance and yield-related traits in maize. ***Nature Biotechnology*** (2023): 1-8.
5. Zhu, Wanchao, et al. A translatome-transcriptome multi-omics gene regulatory network reveals the complicated functional landscape of maize. ***Genome Biology*** (2023) 24.1: 1-26.
6. Wang, Xi, et al. QTG-Miner aids rapid dissection of the genetic base of tassel branch number in maize. ***Nature Communications*** 14 (1), 5232.
7. Li, Zhao, et al. DeepBSA: A deep-learning algorithm improves bulked segregant analysis for dissecting complex traits. ***Molecular Plant*** (2022) 15.9: 1418-1427.
8. Wu, Leiming, et al. Using interactome big data to crack genetic mysteries and enhance future crop breeding. ***Molecular plant*** (2021) 14.1: 77-94.
9. Zhang, Hongwei, et al. QTG-Seq accelerates QTL fine mapping through QTL partitioning and whole-genome sequencing of bulked segregant samples. ***Molecular plant*** (2019) 12.3: 426-437. ***Best Article of 2019 in Molecular Plant***

All Journal Publications

63. Wu, Hao, et al. AutoGP: An intelligent breeding platform for enhancing maize genomic selection. ***Plant Communications*** (2025) 6, 101240.

62. Li, Ruonan, et al. An epiallele of a gene encoding PfkB-type carbohydrate kinase affects plant architecture in maize. ***Plant Cell*** (2025) DOI: 10.1093/plcell/koaf017.

61. Zhu, Wanchao, et al. Big data and artificial intelligence-aided crop breeding: Progress and prospects. ***Journal of Integrative Plant Biology*** (2024) https://doi.org/10.1111/jipb.13791. ***Invited Expert Review***

60. Luo, Zi, et al. A dynamic regulome of shoot-apical-meristem-related homeobox transcription factors modulates plant architecture in maize. ***Genome Biology*** (2024) 25: 245. ***Featured Article***

59. Zhu, Wanchao, et al. The CropGPT project: A call for a global, coordinated effort in precision design breeding driven by AI using biological big-data. ***Molecular plant*** (2023) 10.1016/j.molp.2023.12.015.

58. Feng, Jiawu, et al. MaizeNetome: A multi-omics network database for functional genomics in maize. ***Molecular plant*** (2023) 16 (8), 1229-1231.

57. Wang, Xi, et al. QTG-Miner aids rapid dissection of the genetic base of tassel branch number in maize. ***Nature Communications*** (2023) 14 (1), 5232.

56. Wang, Xi, et al. Next-generation bulked segregant analysis for Breeding 4.0. ***Cell Reports*** (2023) 42 (9).

55. Li, Juan, et al. Genetic Mapping and Functional Analysis of a Classical Tassel Branch Number Mutant Tp2 in maize. ***Frontiers in Plant Science*** (2023) 14: 1868.

54. Zhu, Wanchao, et al. A translatome-transcriptome multi-omics gene regulatory network reveals the complicated functional landscape of maize. ***Genome Biology*** (2023) 24.1: 1-26.

53. Li, Juan, et al. iBP-seq: an efficient and low-cost multiplex targeted genotyping and epigenotyping system. ***The Crop Journal*** (2023).

52. Miao, Xinxin, et al. ZmHOX32 is related to photosynthesis and likely functions in plant architecture of maize. ***Frontiers in Plant Science*** 14 (2023).

51. Han, Linqian, et al. A multi-omics integrative network map of maize. ***Nature Genetics*** 55.1 (2023): 144-153.

50. Sun, Xiaopeng, et al. The role of transposon inverted repeats in balancing drought tolerance and yield-related traits in maize. ***Nature Biotechnology*** (2023): 1-8. F1000

49. Zhou, Tao, et al. Dominant complementation of biological pathways in maize hybrid lines is associated with heterosis. ***Planta*** (2022) 256.6: 111-111.

48. Xu, Qiang, et al. DNA demethylation affects imprinted gene expression in maize endosperm. ***Genome biology*** (2022) 23.1: 1-24.

47. Li, Zhao, et al. DeepBSA: A deep-learning algorithm improves bulked segregant analysis for dissecting complex traits. ***Molecular Plant*** (2022) 15.9: 1418-1427.

46. Haroon, Muhammad, et al. Ribonomics Approaches to Identify RBPome in Plants and Other Eukaryotes: Current Progress and Future Prospects. ***International Journal of Molecular Sciences*** (2022) 23.11: 5923.

45. Zhu, Wanchao, et al. Dynamic patterns of the translatome in a hybrid triplet show translational fractionation of the maize subgenomes. ***The Crop Journal*** (2022) 10.1: 36-46.

44. Wu, Leiming, et al. A cost-effective tsCUT&Tag method for profiling transcription factor binding landscape. ***Journal of Integrative Plant Biology*** (2022).

43. Wu, Xi, et al. Using high-throughput multiple optical phenotyping to decipher the genetic architecture of maize drought tolerance. ***Genome Biology*** (2021) 22.1: 1-26.

42. Huang, Yadong, et al. Genetic dissection of a pericentromeric region of barley chromosome 6H associated with Fusarium head blight resistance, grain protein content and agronomic traits. ***Theoretical and Applied Genetics*** (2021) 134.12: 3963-3981.

41. Wang, Hongze, et al. A teosinte-derived allele of a MYB transcription repressor confers multiple disease resistance in maize. ***Molecular plant*** (2021) 14.11: 1846-1863.

40. Zhu, Wanchao, et al. Large-scale translatome profiling annotates the functional genome and reveals the key role of genic 3′ untranslated regions in translatomic variation in plants. ***Plant communications*** (2021) 2.4: 100181.

39. Li, Zhao, et al. Single-molecule long-read sequencing reveals extensive genomic and transcriptomic variation between maize and its wild relative teosinte (*Zea mays* ssp. *parviglumis*). ***Molecular Ecology Resources*** (2022) 22.1: 272-282.

38. Liang, Yan, et al. Genome-wide identification and characterization of small peptides in maize. ***Frontiers in plant science*** (2021) 12: 1162.

37. Wu, Leiming, et al. Using interactome big data to crack genetic mysteries and enhance future crop breeding. ***Molecular plant*** (2021) 14.1: 77-94.

36. Luo, Zi, et al. Dynamic patterns of circular and linear RNAs in maize hybrid and parental lines. ***Theoretical and Applied Genetics*** (2020) 133.2: 593-604.

35. Xu, Jing, et al. Population-level analysis reveals the widespread occurrence and phenotypic consequence of DNA methylation variation not tagged by genetic variation in maize. ***Genome biology*** (2019) 20.1: 1-16.

34. Knauer, Steffen, et al. A high-resolution gene expression atlas links dedicated meristem genes

to key architectural traits. ***Genome research*** (2019) 29.12: 1962-1973.

33. Pan, Qingchun, et al. Trait ontology analysis based on association mapping studies bridges the gap between crop genomics and Phenomics. ***BMC genomics*** (2019) 20.1: 1-13.

32. Hemshrot, Alex, et al. Development of a multiparent population for genetic mapping and allele discovery in six-row barley. ***Genetics*** (2019) 213.2: 595-613.

31. Zhang, Pei, et al. A large-scale circular RNA profiling reveals universal molecular mechanisms responsive to drought stress in maize and Arabidopsis. ***The Plant Journal*** (2019) 98.4: 697-713.

30. Zhang, Lili, et al. SEED CAROTENOID DEFICIENT functions in isoprenoid biosynthesis via the plastid MEP pathway. ***Plant Physiology*** (2019) 179.4: 1723-1738.

28. Han, Linqian, et al. New lncRNA annotation reveals extensive functional divergence of the transcriptome in maize. ***Journal of Integrative Plant Biology*** (2019) 61.4: 394-405.

28. Luo, Zi, et al. Circular RNAs exhibit extensive intraspecific variation in maize. ***Planta*** (2019) 250.1: 69-78.

27. Zhang, Hongwei, et al. QTG-Seq accelerates QTL fine mapping through QTL partitioning and whole-genome sequencing of bulked segregant samples. ***Molecular plant*** (2019) 12.3: 426-437.

26. Han, Linqian, et al. RNA Isolation and analysis of LncRNAs from gametophytes of maize. ***Plant Long Non-Coding RNAs***. Humana Press, New York, NY, (2019). 67-86.

25. Chen, Lu, et al. Circular RNAs mediated by transposons are associated with transcriptomic and phenotypic variation in maize. ***New Phytologist*** (2018) 217.3: 1292-1306.

24. Pan, Qingchun, et al. The genetic basis of plant architecture in 10 maize recombinant inbred line populations. ***Plant Physiology*** (2017) 175.2: 858-873.

23. Beier, Sebastian, et al. Construction of a map-based reference genome sequence for barley, Hordeum vulgare L. ***Scientific Data*** (2017) 4.1: 1-24.

22. Pan, Qingchun, et al. Complexity of genetic mechanisms conferring nonuniformity of recombination in maize. ***Scientific reports*** (2017) 7.1: 1-11.

21. Mascher, Martin, et al. A chromosome conformation capture ordered sequence of the barley genome. ***Nature*** (2017) 544.7651: 427-433.

20. Lin Li, Roman Briskine, Robert Schaefer, Patrick S. Schnable, Chad Myers, Nathan M. Springer and Gary Muehlbauer: Co-expression network analysis of duplicate genes in maize (*Zea mays* L.) reveals no subgenome bias. ***BMC Genomics***, (2016) 17:1.

19. Yadong Huang#, Lin Li#, Kevin P. Smith, Gary J. Muehlbauer. Differential transcriptomic

responses to Fusarium graminearum infection in two barley quantitative trait loci associated with Fusarium head blight resistance. ***BMC Genomics***, (2016) 17:387.

18. Qingchun Pan#, Lin Li#, Xiaohong Yang, Hao Tong, Shutu Xu, Zhigang Li, Weiya Li, Gary J. Muehlbauer, Jiansheng Li, Jianbing Yan. Genome-wide recombination dynamics are associated with phenotypic variation in maize. ***New Phytologist***, (2016) 210:1083-1094. ***Selected as an Editors' Choice by MaizeGDB, 02/16***

17. Yingni Xiao, Shawn Thatcher, Min Wang, Tingting Wang, Mary Beatty, Gina Zastrow-Hayes, Lin Li, Jiansheng Li, Bailin Li, Xiaohong Yang: Transcriptome analysis of near-isogenic lines provides molecular insights into starch biosynthesis in maize kernel. ***Journal of integrative plant biology*** (2015) DOI: 10.1111/jipb.12455.

16. Xiang Li, Lin Li, Jianbing Yan: Dissecting Meiotic Recombination based on Tetrad Analysis by Single Microspore Sequencing in Maize. ***Nature communications*** 2015:6.

15. Lin Li, Steven R Eichten, Rena Shimizu, Katherine Petsch, Cheng-Ting Yeh, Wei Wu, Antony M Chettoor, Scott A Givan, Rex A Cole, John E Fowler, Matthew Ms Evans, Michael J Scanlon, Jianming Yu, Patrick S Schnable, Marja C Timmermans, Nathan M Springer, Gary J Muehlbauer: *Genome-wide discovery and characterization of maize long non-coding RNAs*. ***Genome biology*** 02/2014; 15(2):R40. ***Selected as an Editors' Choice by MaizeGDB, 07/14***

14. Lin Li, Katherine Petsch, Rena Shimizu, Sanzhen Liu, Wayne Wenzhong Xu, Kai Ying, Jianming Yu, Michael J. Scanlon, Patrick S. Schnable, Marja C. P. Timmermans, Nathan M. Springer, Gary J. Muehlbauer: *Mendelian and Non-Mendelian Regulation of Gene Expression in Maize*. ***PLoS Genetics*** 01/2013; 9(1):e1003202. ***Selected as an Editors' Choice by MaizeGDB, 02/13***; ***Recommended by***

13. Qing Li, Xiaohong Yang, Shutu Xu, Ye Cai, Dalong Zhang, Yingjia Han, Lin Li, Zuxin Zhang, Shibin Gao, Jiansheng Li, Jianbing Yan: *Genome-wide association studies identified three independent polymorphisms associated with α-tocopherol content in maize kernels.* ***PLoS ONE*** 01/2012; 7(5):e36807.

12. Dianyi Shi, Lin Li, Jiewei Zhang, Panfeng Zhao, Lei Xing, Wenjun Xie, Jianbing Yan, Weiwei Jin: *Genome-wide examination of chlorophyll metabolic genes in maize and phylogenetic analysis among different photosynthetic organisms*. ***African Journal of Biotechnology***. 01/2011; 10:5559-5562.

11. Lin Li, Hui Li, Qing Li, Xiaohong Yang, Debo Zheng, Marilyn Warburton, Yuchao Chai, Pan

Zhang, Yuqiu Guo, Jianbing Yan, Jiansheng Li: *An 11-bp insertion in Zea mays fatb reduces the palmitic acid content of fatty acids in maize grain*. ***PLoS ONE*** 01/2011; 6(9):e24699.

10. Xiaohong Yang, bullet Shibin, Gao , Shutu Xu, bullet Zuxin, Zhang , Boddupalli M Prasanna, Lin Li, bullet Jiansheng, Li , Jianbing Yan: *Characterization of a global germplasm collection and its potential utilization for analysis of complex quantitative traits in maize*. ***Molecular Breeding*** 28/2011; 4: 511-526.

9. Lin Li, Hui Li, JiYing Li, ShuTu Xu, XiaoHong Yang, JianSheng Li, JianBing Yan: *A genome-wide survey of maize lipid-related genes: candidate genes mining, digital gene expression profiling and co-location with QTL for maize kernel oil.* ***Science China Life sciences*** 06/2010; 53(6):690-700.

8. Xiaohong Yang, Jianbing Yan, Trushar Shah, Marilyn L Warburton, Qing Li, Lin Li, Yufeng Gao, Yuchao Chai, Zhiyuan Fu, Yi Zhou, Shutu Xu, Guanghong Bai, Yijiang Meng, Yanping Zheng, Jiansheng Li: *Genetic analysis and characterization of a new maize association mapping panel for quantitative trait loci dissection*. ***Theoretical and Applied Genetics*** 03/2010; 121(3):417-31.

7. Qing Li, Lin Li, Xiaohong Yang, Marilyn L Warburton, Guanghong Bai, Jingrui Dai, Jiansheng Li, Jianbing Yan: *Relationship, evolutionary fate and function of two maize co-orthologs of rice GW2 associated with kernel size and weight.* ***BMC Plant Biology*** 01/2010; 10:143.

6. Lin Li, Qing Li, Libo Wang, Zuxin Zhang, Jiansheng Li, Jianbing Yan: *Genetic analysis of QTL affecting recombination frequency in whole genome of maize and rice*. ***Scientia Agricultura Sinica***. 01/2009; 42:2262-2270.

5. Qing Li, Lin Li, JingRui Dai, JianSheng Li, JianBing Yan: *Identification and characterization of CACTA transposable elements capturing gene fragments in maize*. **Chinese Science Bulletin** 01/2009; 54:642-651.

4. Hailin, Ma; Xiaohong, Yang; Yuqiu, Guo; Lin, Li, Guanghong, Bai; Jiansheng, Li: Correlation Analysis of Kernel Traits and Oil Concentration in Maize. ***Crops*** 2009; 1:11.

3. Wenkai Xiao, Jing Zhao, Shengci Fan, Lin Li, Jinrui Dai, Mingliang Xu: *Mapping of genome-wide resistance gene analogs (RGAs) in maize (Zea mays L.)*. ***Theoretical and Applied Genetics*** 09/2007; 115(4):501-8.

2. Gui-Xiang Wang, Yu Chen, Jiu-Ran Zhao, Lin Li, Schuyler S. Korban, Feng-Ge Wang, Jian-Sheng Li, Jin-Rui Dai, Ming-Liang Xu: *Mapping of defense response gene homologs and their association with resistance loci in maize*. ***Journal of Integrative Plant Biology*** 01/2007;

11:1580-1598.

1. Jian-Bing Yan, Ji-Hua Tang, Yi-Jiang Meng, Xi-Qing Ma, Wen-Tao Teng, Subhash Chander, Lin Li, Jian-Sheng Li: *Improving QTL mapping resolution based on genotypic sampling--a case using a RIL population.* ***Acta Genetica Sinica*** 08/2006; 33(7):617-24.

Patents

China Patent ZL 2020-1-0523088.0 – An efficient and low-cost multiplex targeted genotyping and epigenotyping system

China Patent ZL 2022-1-0095668.3 – Functional validation of *Zea mays Zm00001d045529* gene in regulation of the maize seed development and its application

China Patent ZL 2010-1-0285616.X – Functional validation of *Zea mays fatb* gene in regulation of the ratio of saturated to unsaturated fatty acids in maize kernels and its application

Editor Experience and Journal Reviews

Associate Editor for ***the Plant Genome, Journal of Integrative Plant Biology***

Junior Editor for ***Journal of Genetics and Genomics***

Served as peer reviewer for tens of manuscripts at ***Nature Genetics***, ***Plant Cell***, ***Trends in Genetics***, ***Advanced Science***, ***Science Advance***, ***Genome Biology***, ***Genome Research, Cell Reports, Nature Plants, Nature Communications, Molecular Biology and Evolution, Molecular Plant, Journal of Integrative Plant Biology, Plant Biotechnology Journal, New Phytologists, Plant Communications, Plant Physiology, Theoretical and Applied Genetics, Crop Science, Crop Journal et al.***