李梦

副教授

硕士生导师（欢迎报考）

南京市卫岗 1 号南京农业大学园艺学院　邮编：210095

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研究方向

1. 果树等园艺作物的基因组学和生物信息学大数据分析

2. 全基因组关联分析方法及生物统计学和相关应用研究

（总体上研究侧重于方法性研究和对于数据的深度挖掘，就业形势良好。）

教育经历

硕博连读：南京农业大学　　生物信息学，博士期间在康奈尔大学进修 18 个月

本科：南京农业大学　　统计学

主持或参与的科研项目

主持项目：

2017 年　江苏高校品牌专业建设工程资助项目

2014 年　中国博士后科学基金面上资助

2013 年　国家自然科学基金青年项目

2013 年　南京农业大学青年科技创新基金

同时，作为主要参加人，参与多个国家重大科技项目。

发表论文

1. Li M(李梦), Liu XL, Bradbury P, Yu JM, Zhang YM, Todhunter RJ, Buckler ES, Zhang ZW:

   Enrichment of statistical power for genome-wide association studies. BMC Biol 2014, 12.

（IF:7.98）

2. Li M(李梦), Li L, Dunwell J, Qiao X, Liu X, Zhang S: Characterization of the lipoxygenase (LOX) gene family in the Chinese white pear (Pyrus bretschneideri) and comparison with other members of the Rosaceae. BMC Genomics 2014, 15(1):444.（IF:3.99）

3. Li M(李梦), Dunwell JM, Zhang H, Wei S, Li Y, Wu J, Zhang S: Network analysis reveals the co-expression of sugar and aroma genes in the Chinese white pear (Pyrus bretschneideri). Gene 2018, 677:370-377. （IF:2.50）

4. Zhang W-J[#], Niu Y[#], Bu S-H[#], **Li M[#]**, Feng J-Y, Zhang J, Yang S-X, Odinga MM, Wei S-P, Liu X-F, Zhang Y-M: Epistatic Association Mapping for Alkaline and Salinity Tolerance Traits in the Soybean Germination Stage. *PLoS ONE* 2014, 9(1):e84750. （IF: 3.234, 2015）

5. Li C[#], **Li M[#]**, Dunwell JM, Zhang YM: Gene duplication and an accelerated evolutionary rate in 11S globulin genes are associated with higher protein synthesis in dicots as compared to monocots. *BMC Evol Biol* 2012, 12(1):1-9. （IF: 3.407, 2013）

6. Liu G[#], **Li M[#]**, Wen J, Du Y, Zhang YM: Functional mapping of quantitative trait loci associated with rice tillering. *Molecular Genetics and Genomics* 2010, 284(4):263-271. （IF: 2.635, 2011）

7. Wu J, Li L-T, **Li M**, Khan MA, Li X-G, Chen H, Yin H, Zhang S-L: High-density genetic linkage map construction and identification of fruit-related QTLs in pear using SNP and SSR markers. *Journal of Experimental Botany* 2014, 65(20):5771-5781. （IF: 5.526, 2015）

8. Yin H, Du J, Li L, Jin C, Fan L, **Li M**, Wu J, Zhang S: Comparative Genomic Analysis Reveals Multiple Long Terminal Repeats, Lineage-Specific Amplification, and Frequent Interelement Recombination for Cassandra Retrotransposon in Pear (Pyrus bretschneideri Rehd.). *Genome Biol Evol* 2014, 6(6):1423-1436. （IF: 4.229, 2015）

9. Chia J-M, Song C, Bradbury PJ, Costich D, de Leon N, Doebley J, Elshire RJ, Gaut B, Geller L, Glaubitz JC, Gore M, Guill KE, Holland J, Hufford MB, Lai J, **Li M**, Liu X, Lu Y, McCombie R, Nelson R, Poland J, Prasanna BM, Pyhajarvi T, Rong T, Sekhon RS, Sun Q, Tenaillon MI, Tian F, Wang J, Xu X, Zhang Z, Kaeppler SM, Ross-Ibarra J, McMullen MD, Buckler ES, Zhang G, Xu Y, Ware D: Maize HapMap2 identifies extant variation from a genome in flux. *Nat Genet* 2012, 44(7):803-807. （IF: 29.648, 2013）

10. Lipka AE, Tian F, Wang Q, Peiffer J, **Li M**, Bradbury PJ, Gore MA, Buckler ES, Zhang Z: GAPIT: genome association and prediction integrated tool. *Bioinformatics* 2012, 28(18):2397-2399. （IF: 4.621, 2013）

11. Huang X, Wei X, Sang T, Zhao Q, Feng Q, Zhao Y, Li C, Zhu C, Lu T, Zhang Z, **Li M**, Fan

D, Guo Y, Wang A, Wang L, Deng L, Li W, Lu Y, Weng Q, Liu K, Huang T, Zhou T, Jing Y, Li W, Lin Z, Buckler ES, Qian Q, Zhang Q-F, Li J, Han B: Genome-wide association studies of 14 agronomic traits in rice landraces. *Nat Genet* 2010, 42(11):961-967. （IF: 35.532, 2011）

12. Lu HY, **Li M**, Li GJ, Yao LL, Lin F, Zhang YM: Multiple loci in silico mapping in inbred lines. *Heredity* 2009, 103(4):346-354. （IF: 4.569, 2010）

13. Qiao X, **Li M**, Li LT, Yin H, Wu JY, Zhang SL: Genome-wide identification and comparative analysis of the heat shock transcription factor family in Chinese white pear (Pyrus bretschneideri) and five other Rosaceae species. *BMC Plant Biology* 2015, 15(1):1-16. （IF: 3.813, 2015）

14. Zhang QJ, Tao ST, **Li M**, Qi XX, Wu J, Yin H, Deng JL, Zhang SL: Identification of differentially expressed genes using digital gene expression profiles in Pyrus pyrifolia Nakai cv. Hosui bud release following early defoliation. *Tree Genetics & Genomes* 2015, 11(3):1-15. （IF: 2.451, 2015）

15. Tang Y, Liu XL, Wang JB, **Li M**, Wang QS, Tian F, Su ZB, Pan YC, Liu D, Lipka AE, Buckler ES, Zhang ZW: GAPIT Version 2: An Enhanced Integrated Tool for Genomic Association and Prediction. *Plant Genome-Us* 2016, 9(2).（IF: 2.923, 2017）

专利

2013 一个基于高分辨率溶解曲线鉴定梨果皮红/绿色泽的 SNP 标记及其应用　第 5 人

2014 一种梨果实横径主效 QTL 位点的 SNP 标记方法及其应用　第 3 人