



刘海军 (Ph.D)

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教育背景

遗传学博士(导师: 严建兵)
华中农业大学、
作物遗传改良国家重点实验室
[2012/07 - 2017/06]

理学学士

华中农业大学
生物科学(国家理科基地班)
[2007/09 - 2012/06]

工作经历

奥地利科学院孟德尔研究所
博士后
(合作导师: MAGNUS NORDBORG)
[2019/10 - 至今]

作物遗传改良国家重点实验室
博士后、科研助理
(合作导师: 严建兵)
[2017/07 - 2019/09]

项目资助

欧盟地平线 2020 及玛丽居里
基金联合资助博士后
(负责人: 金额: 10 万欧元)
[2021/01 - 2023/12]

国家自然科学基金青年项目
(负责人: 金额: 25 万元)
[2020/01 - 2022/12]

科技部重大科技专项
(参与人: 金额: 200 万元)
[2018/01 - 2019/12]

博士后创新人才计划
(负责人: 金额: 60 万元)
[2017/07 - 2019/07]

在研课题(主导)

- 拟南芥 1001 表型组计划
- 基于长读长 (long-reads) 及人工智能构建群体泛甲基化组
- 开发关联分析方法挖掘被广泛低估的遗传异质性

发表文章及获批专利

#: 共同第一作者; *: 通讯或共同通讯作者.

[此处只列举第一(含共同)及通讯(含共同)作者的工作, 详情请见 **ORCID**]

★ REVIEWS & COMMENTS ★

- Liang Y#, **Liu H-J**#, Yan J*, Tian F. Natural Variation in Crops: Realized Understanding, Continuing Promise. *Annu Rev Plant Biol*, 2021, 72:357-385.
- Liu H-J***, Yan J*. Crop genome-wide association study: A harvest of biological relevance. *Plant J*, 2019, 97: 8-18.
- Xiao Y#, **Liu H**#, Wu L#, Warburton M, Yan J*. Genome-wide Association Studies in Maize: Praise and Stargaze. *Mol Plant*, 2017, 10(3):359-374.
- Liu H***, Yan J*. Rice domestication: An imperfect African solution. *Nat Plants*, 2017, 3:17083. [Comment]

★ FUNCTIONAL GENOMICS & GENE CLONING ★

- Liu H-J**#, Wang X#, Xiao Y#, Luo J#, Qiao F#, Yang W#, Zhang R#, ..., Zhao J*, Yan J*. CUBIC: an atlas of genetic architecture promises directed maize improvement. *Genome Biol*, 2020, 21(1):20.

★ GENOME EDITING ★

- Liu H-J**#, Jian L#, Xu J#, ..., Yan J*. High-Throughput CRISPR/Cas9 Mutagenesis Streamlines Trait Gene Identification in Maize. *Plant Cell*, 2020, 32(5):1397-1413.
- Sun J#, Liu H#, ..., **Liu H-J***, Chen LL*. CRISPR-Local: a local single-guide RNA (sgRNA) design tool for non-reference plant genomes. *Bioinformatics*, 2019, 35(14):2501-2503.

★ OMICS ★

- Wang S#, Tian L#, **Liu H**#, ..., Yan J*, Wu L*. Large-Scale Discovery of Non-conventional Peptides in Maize and Arabidopsis through an Integrated Peptidogenomic Pipeline. *Mol Plant*, 2020, 13(7):1078-1093.
- Chen Q#, Han Y#, **Liu H**#, ..., Yang X*, Tian F*. Genome-Wide Association Analyses Reveal the Importance of Alternative Splicing in Diversifying Gene Function and Regulating Phenotypic Variation in Maize. *Plant Cell*, 2018, 30(7):1404-1423.
- Liu H**#, Luo X#, ..., Yan J*. Distant eQTLs and Non-coding Sequences Play Critical Roles in Regulating Gene Expression and Quantitative Trait Variation in Maize. *Mol Plant*, 2017, 10(3):414-426.
- Jin M#, **Liu H**#, He C#, Fu J*, ..., Yan J*. Maize pan-transcriptome provides novel insights into genome complexity and quantitative trait variation. *Sci Rep*, 2016, 6:18936.
- Liu H**#, Wang X#, ..., Yan J*. Genomic, Transcriptomic, and Phenomic Variation Reveals the Complex Adaptation of Modern Maize Breeding. *Mol Plant*, 2015, 8(6):871-84.

★ 获批专利 ★

- 刘海军, 许洁婷, 严建兵. 一种基因组特定区域的 DNA 测序方法: 中国, 201811606050.9. 2021-4-2.
- 金敏亮, 刘海军, 刘相国, 许洁婷, 严建兵. 降低玉米株高或延迟开花的方法: 中国, 202010109172.8. 2022-5-3.
- 金敏亮, 刘海军, 刘相国, 许洁婷, 严建兵. 控制玉米株高和花期的基因及其应用: 中国, 202010080086.9. 2020-2-4.