姓　　名：	鲁非
职　　称：	研究员
职　　务：	中国科学院遗传与发育生物学研究所分子农业生物学中心副主任
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研究方向：	植物统计基因组学

简历介绍：

鲁非，博士，研究员，博士生导师，国家杰青。

　　1999年就读于西北农林科技大学生物技术学硕连读专业，期间从事生物信息、群体遗传及数量遗传学研究，2005年获得遗传学硕士学位。随后进入中国科学院遗传与发育学研究所攻读博士，期间从事水稻比较基因组学的研究，2010年获得遗传学博士学位以及中国科学院优秀毕业生称号，毕业论文入选中科院优秀博士毕业论文。2010年至2014年在康奈尔大学从事博士后研究，2014年至2017年在康奈尔大学任研究助理，进行玉米、木薯以及其他能源作物的数量遗传学及基因组学研究。2017年入选国家海外高层级人才引进计划，回国担任中国科学院遗传与发育生物学研究所研究员，主要围绕小麦进行包含数量遗传学、群体遗传学、以及基因组学等多学科交叉的植物统计基因组学研究。近年来在小麦基因组学以及适应性进化领域取得一系列重要进展，目前担任《遗传》、《植物学报》编委，中国遗传学会数量遗传学分会(筹)委员；2022年获得国家自然科学基金委"杰出青年科学基金"资助，以及获中国植物生理与植物分子生物学学会"卫志明青年创新奖"。

研究领域：

研究方向

　　人口增长、气候变化、以及环境冲击是当前农业发展所面对的三大挑战。鲁非博士领导的研究组致力于开发并应用最前沿的科学技术，提高主要农作物的育种速度，帮助实现高效、环境友好、并可持续的农业发展模式。小麦是世界三大粮食作物之一，也是目前所有作物中全球种植最为广泛的作物。在小麦中的研究创新将会产生大规模技术应用，从而创造巨大经济和社会价值；同时，小麦还是凝聚了驯化、选择、多倍化、远缘杂交、环境适应等自然或人工状态下品种改良技术的成功范例，具有极高的科学研究价值。因此，鲁非博士研究组以小麦为模式，利用遗传学、基因组学、进化生物学、统计学、计算机科学等手段在方法学上不断创新，解析小麦品种改良的基础遗传学规律，开发功能基因组预测技术并精细定位重要农艺性状的遗传控制位点，绘制"双轮驱动"的高精度育种设计蓝图，通过优化性状全基因组预测选择模型以及应用基因组工程技术(基因编辑和合成生物学)开发新一代植物育种体系。

　　实验室详细信息及代码托管请见
https://github.com/PlantGeneticsLab
https://plantgeneticslab.github.io/home/

奖励荣誉

2022 国家自然科学基金委"国家杰出青年科学基金"
2022中国植物生理与植物分子生物学学会"卫志明青年创新奖"
2021中国科学院遗传与发育生物学研究所"益海嘉里优秀导师奖"
2017 国家海外高层级人才引进计划（青年项目）
2012中国科学院"优秀博士论文奖"
2010中国科学院遗传与发育生物学研究所"益海嘉里优秀博士生奖"
2009中国中国科学院遗传与发育生物学研究所"振声奖"
2009中国科学院"中国科学院院长优秀奖"

教育招生

　　在鲁非博士研究组，研究生教育与科学研究同等重要。研究组致力于培养善于**独立思考、勇于探索、具有领导力**的青年科学家。研究组欢迎理想远大，聪明勤奋、品格坚韧、能够自我管理的青年学子积极申请报考博士研究生。

代表论著：

发表文章
(*Corresponding author; #Co-first author)

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22. Y. Zhou[#], X. Zhao[#], Y. Li, J. Xu, A. Bi, L. Kang, D. Xu, H. Chen, Y. Wang, Y. Wang, S. Liu, C. Jiao, H. Lu, J. Wang, C. Yin, Y. Jiao*, **F. Lu***. Triticum population sequencing provides insights into wheat adaptation. **Nature Genetics.** (2020). doi:10.1038/s41588-020-00722-w

21. Chunzhi Zhang, Pei Wang, Die Tang, Zhongmin Yang, **Fei Lu**, Jianjian Qi, Nilesh R. Tawari, Yi Shang, Canhui Li & Sanwen Huang. The genetic basis of inbreeding depression in potato. **Nature Genetics**. (2019). doi:10.1038/s41588-018-0319-1

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15. Candice N. Hirsch, Cory D. Hirsch, Alex B. Brohammer, Megan J. Bowman, Ilya Soifer, Omer Barad, Doron Shem-Tov, Kobi Baruch, **Fei Lu**, Alvaro G. Hernandez, Christopher J. Fields, Chris L. Wright, Klaus Koehler, Nathan Springer, Edward Buckler, C. Robin Buell, Natalia de Leon, Shawn M. Kaeppler, Kevin L. Childs, Mark Mikel. (2016). Draft Assembly of Elite Inbred Line PH207 Provides Insights into Genomic and Transcriptome Diversity in Maize. **The Plant Cell**. doi:10.1105/tpc.16.00353

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7. Abhijit Sanyal[#], Ammiraju S.S.Jetty[#], **Fei Lu**[#], Yeisoo Yu Teri Rambo, Jennifer Currie, Kristi Kollura, Hye-Ran Kim, Jinfeng Chen, Jianxin Ma, Phillip San Miguel, Mingsheng Chen, Rod A. Wing and Scott A. Jackson. (2010). Orthologous comparisons of the Hd1 region across genera reveal Hd1 gene lability within diploid Oryza species and disruptions to microsynteny in sorghum. **MOL BIOL EVOL**. DOI:10.1093/molbev/msq133

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