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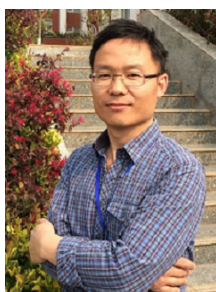
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生物化学与分子生物学专业



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简历:

毕业论文

(<http://www.kib.cas.cn/yjsjy/bylw/>)

1993.09—1997.07 山东师范大学学士

1997.07—2003.07 中国科学院昆明植物研究所博士

2003.09—2006.10 德国马普植物育种研究所博士后

2006.11—2014.08 德国马普植物育种研究所Full-time researcher

2014.08—至今 中国科学院昆明植物研究所，研究员，博士生导师

胡金勇，博士，研究员，博士生导师。1997年毕业于山东师范大学生物系；并于同年考入中国科学院昆明植物研究所跟随曾英研究员攻读硕士学位；于2000年直博，导师为李德铎研究员和曾英研究员；2003年7月获得植物学博士学位。2003年9月起在德国马普学会植物育种研究所先后跟随Heinz Saedler教授、Juliette de Meaux教授和Maarten Kornneef教授做博士后和full-time research scientist of MPI研究。2014年起就职于中国科学院昆明植物研究所中国科学院东亚植物多样性与生物地理学重点实验室，组建植物分子遗传与适应研究组。2016年获“云南省高端科技人才引进计划”支持。目前已经在Molecular Plant, The Plant Cell, Molecular Biology and Evolution, PNAS, Nature Communications, BMC Plant Biology, Scientific Reports等杂志发表论文30篇。国际分子进化生物学协会SMBE终身会员。

研究领域：

植物分子遗传与适应研究组 (PMGA) 依托中国科学院昆明植物研究所、中国科学院东亚植物多样性与生物地理学重点实验室，基于中国和西南地区丰富的生物多样性资源，以自然界存在的“野生突变体 (natural mutants)”十字花科和蔷薇科植物等为核心材料，以开花时间多样性等相关的基因调控网络 (Gene-Regulatory-Network, GRN) 为核心生物学问题和着眼点，综合利用基因组学、遗传学、分子生物学、生物化学、生物信息学、演化生物学等多种研究手段，解析植物开花习性多样性形成的分子遗传机制与演化趋势，发掘关键调控基因及机制，揭示多样性产生与维持的分子遗传基础和演化模式，为合理、有效利用与保护生物多样性资源奠定关键理论基础。主要包括：

1. 草本模式十字花科植物开花时间调控的分子遗传基础与自然变异；
2. 木本非模式蔷薇科植物开花习性多样性形成的分子遗传机制与变异；
3. 植物与环境互作的分子模式、机理与演化。

获奖及荣誉：

代表论著：

论文发表：

1. Cui W-H, Zhong M-C, Du X-Y, Qu X-J, Jiang X-D, Sun Y-B, Wang D, Chen S-Y, **Hu J-Y**[#]. The complete chloroplast genome sequence of a Rambler rose, *Rosa wichuraiana* (Rosaceae). *Mitochondrial DNA Part B*, 2020, 5:252-253. <http://dx.doi.org/10.1080/23802359.2019.1700198>.
2. Guo Z-H*, Ma P-F*, Yang G-Q*, **Hu J-Y***, Liu Y-L*, Xia E-H, Zhong M-C, Zhao L, Sun G-L, Xu Y-X, Zhao Y-J, Zhang Y-C, Zhang Y-X, Zhang X-M, Zhou M-Y, Guo Y, Guo C, Liu J-X, Ye X-Y, Chen Y-M, Yang Y, Han B, Lin C-S[#], Lu Y[#], Li D-Z[#] (*co-first authors; # co-corresponding authors). Genome sequences provide insights into the reticulate origin and unique traits of woody bamboos. *Molecular Plant*, 2019, 12:1353-1365. <https://doi.org/10.1016/j.molp.2019.05.009> (<https://doi.org/10.1016/j.molp.2019.05.009>).
3. Li S*, Yang G*, Yang S*, Just J, Yan H, Zhou N, Jian H, Wang Q, Chen M, Qiu X, Zhang H, Dong X, Jiang X, Sun Y, Zhong M, Bendahmane M, Ning G, Ge H[#], **Hu J-Y**[#], Tang K[#] (*co-first authors; # co-corresponding authors). The development of a high-density genetic map significantly improves the quality of reference genome assemblies for rose. *Scientific Reports*, 2019, 9:5985. DOI: 10.1038/s41598-019-42428-y.
4. Li S*, Qu X*, Zhong M, Jiang X, Dong X, Yi T, Tang K, Dai S[#], **Hu J-Y**[#]. Characterization of the complete chloroplast genome of *Rosa chinensis* 'Old Blush' (Rosaceae), an important cultivated Chinese rose. *Acta Horticulturae*, 2019, 1232:119-124. DOI: 10.17660/ActaHortic.2019.1232.19.
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6. Li S*, Zhong M*, Dong X*, Jiang X, Xu Y, Sun Y, Cheng F, Li D-Z, Tang K, Wang S[#], Dai S[#], **Hu J-Y**[#] (*co-first authors; # co-corresponding authors). Comparative transcriptomics identifies patterns of selection in roses. *BMC Plant Biology*, 2018, 18:371. <https://doi.org/10.1186/s12870-018-1585-x> (<https://doi.org/10.1186/s12870-018-1585-x>).
7. Guan Y, Liu L, Wang Q, Zhao J, Li P, **Hu J-Y**, Yang Z, Running MP, Sun H, Huang, J. Gene refashioning through innovative shifting of reading frames in mosses. *Nature Communications*, 2018, 9:1555. DOI:10.1038/s41467-018-04025-x.
8. **Hu J-Y***[#], Lei L*, de Meaux J[#] (*co-first authors; # co-corresponding authors). Temporal fitness fluctuations in experimental *Arabidopsis thaliana* populations. *PLOS ONE*, 2017, 12(6): e0178990. <https://doi.org/10.1371/journal.pone.0178990> (<https://doi.org/10.1371/journal.pone.0178990>).

9. Dong X, Jiang X, Kuang G, Wang Q, Zhong M, Jin D, **Hu J-Y**[#]. Genetic control of flowering time in woody plants: roses as an emerging model. *Plant Diversity*, 2017, 39: 104-110. doi: 10.1016/j.pld.2017.01.004.
10. **Hu J-Y**^{*#}, Zhou Y, He F, Liu L-Y, Turck F, Coupland G, de Meaux J[#] (*co-first authors; [#] co-corresponding author). MiR824-modulated *AGAMOUS-LIKE-16* module participates in repressor complexes to control flowering in *Arabidopsis thaliana*. *The Plant Cell*, 2014, 26:2024-2037.
11. Luo Y, **Hu J-Y**, Li L, Luo Y-L, Wang P-F, Song B-H. Genome-wide analysis of gene expression reveals gene regulatory networks that regulate chasmogamous and cleistogamous flowering in *Pseudostellaria heterophylla* (Caryophyllaceae). *BMC Genomics*, 2016, 17:382.
12. Liu L, Adrian J, Pankin A, **Hu J-Y**, Dong X, von Korff M, Turck F. Induced and natural variation of promoter length modulates the photoperiodic response of *FLOWERING LOCUS T*. *Nature communications*, 2014, 5, doi:10.1038/ncomms5558.
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14. He F, Zhang X, **Hu J-Y**, Turck F, Dong X, Goebel U, Borevitz J, de Meaux J. Genome-wide analysis of cis-regulatory divergence between species in the Arabidopsis genus. *Mol Biol Evol*, 2012, 29: 3385-3395.
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21. **Hu J-Y**, Saedler H. Evolution of Inflated-Calyx-Syndrome (ICS) in Solanaceae. *Mol. Biol. Evol.*, 2007, 24: 2443-2453.
22. Zhao Y-H, Wang G-Y, Zhang J-P, Yang J-B, Peng S, Gao L-M, **Hu J-Y**, Li D-Z, Gao L-Z. 2006. Isolation and identification of florally expression-related genes in a paleoherb species, *Asarum caudigerum* by suppression subtractive hybridization and phylogenetic analysis. *Annals of Botany*, 2006, 98: 157-163.
23. Zhang X-Q, **Hu J-Y**, Zeng Y, Liu X-Z. Identification of proteins from *Gastrodia elata* by two-dimensional electrophoresis and peptide mass fingerprinting. *Acta Botanica Yunnanica* 2004, 26: 89-95.
24. Dong X, **Hu J-Y**, Xie T-H, Sun M-S, Dai C-B, Ma Y-B. Construction of a recombinant human adenovirus expressing the ORF2 antigen of HEV and immunization of mice by mucosal system. *Zhongguo Yi Xue Ke Xue Yuan Xue Bao*, 2003, 25:324-328.
25. **Hu J-Y**, Zeng Y, Sang Y-Y. Two-dimensional polyacrylamide gel electrophoresis analysis of proteins from albino-green chimeric leaves of *Iris japonica*. *Acta Botanica Yunnanica*, 2002, 24: 387-391.
26. Zeng Y, Sang Y-Y, **Hu J-Y**, Li Z-J. Purification and characterization of a trypsin inhibitor from *Tinospora crispa*. *Acta Botanica Yunnanica*, 2002, 24: 103-108.
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28. Zeng Y, **Hu J-Y**, Li Z-J. MADS-box genes in the evolutionary development of plant reproductive structures. *Plant Physiology Communications*, 2001, 37: 281-287.
29. **Hu J-Y**, Sang Y-Y, Zeng Y. Progress in the research of plasminogen activator inhibitor type-2. *Acta Biochemica Biophysica Sinica*, 2000, 32: 206-210.
30. **Hu J-Y**, Zeng Y, Sang Y-Y, Wang D. Recent advances of the UPA study. *Chin J Cell Biol.* 2001, 23: 67-71.

会议报告及墙报:

1. Genomic dissection of regulatory mechanisms of floral transition in roses and *Arabidopsis*. "Flower Development Workshop", Presqu'île de Giens, France, 18-22 June, 2019.

2. The miR824-AGL16 module regulates the timing of floral transition and the adaptive potential of *Arabidopsis thaliana*. CSH-Asia conference on “Frontiers of Plant Biology: Epigenetics and Development”, Suzhou, China, 08-12, June, 2015.
3. Natural variation at ath-miR824 modulates the adaptive potential of *Arabidopsis thaliana*. 云南省植物学会“第十二届会员代表大会暨61周年学术年会”, Kunming, 5-6 Feb, 2015.
4. Adaptive values of non-coding RNAs in *Arabidopsis thaliana*. Invited talk at the Institute of Biochemistry and Biophysics, PAS (Warsaw, Poland). 28 July 2011.
5. Natural variation of the precursor’s structure of ath-miR824 fine-tunes the adaptation of *Arabidopsis thaliana*. CSHLAsia RNA Biology, Suzhou, China. 1-5 November 2010.
6. A locus harboring the *ath-miR824* affects seeds germination and adaptability of *Arabidopsis* in field. 3rd Workshop on the Molecular Aspects of Seed Dormancy and Germination. York, UK. 18-21, July 2010.
7. Functional analyses of the natural variation of one microRNA in *Arabidopsis thaliana*. XVII Congress of the Federation of European Societies of Plant Biology, Valencia, Spain. 4-9 July 2010.
8. Structural variation of *ath-miR824* precursors fine-tunes life cycle traits and contributes to the adaptive evolution of *Arabidopsis thaliana*. ESEB 12th Congress (12th Congress of the European Society for Evolutionary Biology), Turino, Italy, 24-29 August 2009.
9. Molecular evolutionary study suggests the plesiomorphic nature of the inflated calyx syndrome, a calyx morphological novelty, in Solanaceae. The 5th Solanaceae Genome Workshop (SOL 2008). Cologne, Germany, 12-16 October 2008.
10. Phenotypic consequences of allelic variation at *pre-miR824* in *Arabidopsis thaliana*. Annual day of the Max-Planck-Institute for Plant Breeding research. Cologne, Germany, 4 November 2008.
11. Molecular evolution of the inflated calyx syndrome (ICS) in Solanaceae. XVI Congress of the Federation of European Societies of Plant Biology. Tampere, Finland, 17-22 August 2008.
12. Comparative transcriptomic analysis of the flowering diversity in roses. VII international symposium on rose research and cultivation. 2-7, July, 2017, Angers, France . (Poster)

13. Adaptive significance of ath-miR824 natural variation in Arabidopsis thaliana. 23rd International Conference on Arabidopsis Research (ICAR). 3-7, July, 2012, Vienna, Austria. (Poster)
14. Adaptive significance of ath-miR824 natural variation in Arabidopsis thaliana. Plant RNA meeting. 8-9, July, 2012, Vienna, Austria. (Poster)
15. A new layer of epigenetic variation mediates the life history of Arabidopsis thaliana. ESF-EMBO Conference on Epigenetics in Context, Sant Feliu, Spain. 18-23 Sept. 2011. (Poster)
16. Is the structurally differentiated ath_miR824 one of the key players in the environmental adaptation of Arabidopsis thaliana? XX International Congress of Genetics, Berlin, Germany, 12-17 July 2008. (Poster)


承担科研项目情况:

1. 中国科学院昆明植物研究所引进“海外杰出人才”：“植物适应的分子机理和进化” (2014-2019) ；
2. 国家自然科学基金面上项目(31570311)：“植物开花时间基因参与气孔运动调节的分子机制研究” (2016-2019) ；
3. 云南省高端科技人才引进计划“月季开花适应的分子机理研究” (2016-2018) 。



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