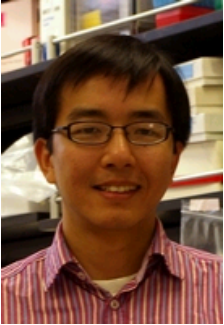


位置: [首页](#) > [研究队伍](#)
 [搜索](#)


焦雨铃

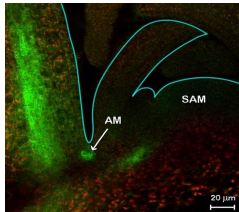
焦雨铃博士、研究员、博士生导师

2001年, 北京大学理学学士; 2003年, 耶鲁大学理学硕士; 2006年, 耶鲁大学哲学博士; 2006年-2010年, 加州理工学院从事博士后研究; 2010年至今, 遗传与发育生物学研究所任研究员。焦雨铃博士2005年获国家优秀自费留学生奖; 2006年获耶鲁大学John Spangler Nicholas杰出生物博士生奖; 2010年入选中国科学院百人计划。

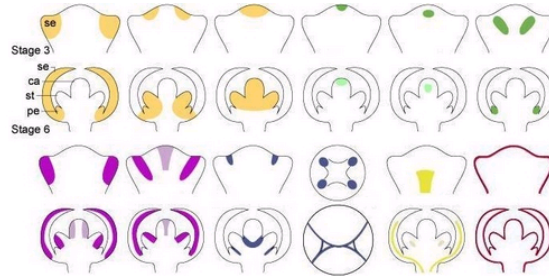
本实验室的研究紧密结合下一代DNA测序、基因芯片、信息学和遗传学方法, 运用系统生物学思想, 研究植物发育和转录组调控。

研究领域

1. 植物侧芽发生和株型研究: 植物的株型在很大程度上取决于侧芽 (axillary meristem, AM) 的发生和生长。对于作物, 株型进而影响产量。侧芽发生于从顶端分生组织 (shoot apical meristem, SAM) 分化出的叶子基部具有分化潜能的干细胞, 能够形成新的顶端分生组织。本实验室通过遗传分析、转录谱分析、以及活体成像研究侧芽发生的机制和相关激素的作用。对于侧芽发生的研究也有助于对植物干细胞的维持和分化这一基本生物学问题的了解。



2. 细胞特异转录谱的绘制和研究: 细胞是生物的基本单位, 不同细胞的转录谱亦不尽相同。但是, 单类的细胞通常难于分离, 而研究单类细胞的转录谱就更加困难。本实验室发展了高通量分析单类细胞转录谱的技术, 并以花发育过程为例研究各个细胞类群的时空转录谱。以大量细胞特异转录谱为基础, 本实验室重建花发育过程的转录调控网络以发现未知基因和调控过程。



论文

原始论文

- Jiao, Y. and Meyerowitz, E.M. (2010). Cell-type specific analysis of translating RNAs in developing flowers reveals new levels of control. *Mol. Syst. Biol.* 6: 419.
- Sugimoto, K., Jiao, Y. and Meyerowitz, E.M. (2010). *Arabidopsis* regeneration from multiple tissues occurs via a root development pathway. *Dev. Cell* 18: 463-471. [Faculty of 1000 Biology 选评](#)
- Jiao, Y., Tausta, S.L., Gandotra, N., Sun, N., Liu, T., Clay, N.K., Ceserani, T., Chen, M., Ma, L., Holford, M., Zhang, H.-y., Zhao, H., Deng, X.-W. and Nelson, T. (2009). A transcriptome atlas of rice cell types uncovers cellular, functional and developmental hierarchies. *Nat. Genet.* 41: 258-263. [Faculty of 1000 Biology 选评](#)
- Jiao, Y., Riechmann, J.L. and Meyerowitz, E.M. (2008). Transcriptome-wide analysis of uncapped mRNAs in *Arabidopsis* reveals regulation of mRNA degradation. *Plant Cell* 20: 2571-2585. [编辑选评: Plant Cell 20: 2545](#) [Faculty of 1000 Biology 选评](#)

5. Zhou, J., Wang, X., Jiao, Y., Qin, Y., Liu, X., He, K., Chen, C., Ma, L., Wang, J., Xiong, L., Zhang, Q., Fan, L. and Deng, X.W. (2007). Global genome expression analysis of rice in response to drought and high-salinity stresses in shoot, flag leaf, and panicle. *Plant Mol. Biol.* 63: 591-608.

6. **Jiao, Y.** and Deng, X.W. (2007). A genome-wide transcriptional activity survey of rice transposable element-related genes. *Genome Biol.* 8: R28.
7. Su, N., He, K., **Jiao, Y.**, Chen, C., Zhou, J., Li, L., Bai, S., Li, X. and Deng, X.W. (2007). Distinct reorganization of the genome transcription associates with organogenesis of somatic embryo, shoots, and roots in rice. *Plant Mol. Biol.* 63: 337-349.
8. **Jiao, Y.**, Ma, L., Strickland, E. and Deng X.W. (2005). Conservation and divergence of light-regulated genome expression patterns during seedling development in rice and *Arabidopsis*. *Plant Cell* 17: 3239-3256.
9. Ma, L., Chen, C., Liu, X., **Jiao, Y.**, Su, N., Li, L., Wang, X., Cao, M., Sun, N., Zhang, X., Bao, J., Li, J., Pedersen, S., Bolund, L., Zhao, H., Yuan, L., Wong, G.K.-S., Wang, J., Deng, X.W. and Wang, J. (2005). A microarray analysis of the rice transcriptome and its comparison to *Arabidopsis*. *Genome Res.* 15: 1274-1283.
[Faculty of 1000 Biology 选评](#)
10. **Jiao, Y.**, Jia, P., Wang, X., Su, N., Yu, S., Zhang, D., Ma, L., Feng, Q., Jin, Z., Li, L., Xue, Y., Cheng, Z., Zhao, H., Han, B. and Deng, X.W. (2005). A tiling microarray expression analysis of rice chromosome 4 suggests a chromosome-level regulation of transcription. *Plant Cell* 17: 1641-1657.
[封面文章](#)
11. Ma, L., Sun, N., Liu, X., **Jiao, Y.**, Zhao, H. and Deng, X.W. (2005). Organ-specific expression of *Arabidopsis* genome during development. *Plant Physiol.* 138: 80-91.
12. **Jiao, Y.**, Yang, H., Ma, L., Sun, N., Yu, H., Liu, T., Gao, Y., Gu, H., Chen, Z. Wada, M., Gerstein, M., Zhao, H., Qu, L.-J. and Deng X.W. (2003). A genome-wide analysis of blue-light regulation of *Arabidopsis* transcription factor gene expression during seedling development. *Plant Physiol.* 133: 1480-1493.
- [综述](#)
1. **Jiao, Y.** and Riechmann, J.L. (2011). Transcriptome-wide analysis of uncapped mRNAs. *Methods Mol. Biol.* Invited review in preparation.
2. Nelson, T., Tausta, S.L., Gandotra, N., Liu, T., Ceserani, T., Chen, M., **Jiao, Y.**, Ma, L., Deng, X.-W., Sun, N., Holfold, M., Li, N. and Zhao, H. (2008). The promise of systems biology for deciphering the control of C4 leaf development: transcriptome profiling of leaf cell types. In: *Charting New Pathways To C4 Rice*, J.E. Sheehy, P.L. Mitchell and B. Hardy, eds., World Scientific, pp. 317-332.
3. **Jiao, Y.**, Lau, O.S. and Deng, X.W. (2007). Light-regulated transcriptional networks in higher plants. *Nat. Rev. Genet.* 8: 217-230.



©2008-2009 中国科学院遗传与发育生物学研究所 版权所有 京ICP备09063187号

地址: 北京市朝阳区北辰西路1号院2号, 遗传与发育生物学研究所

邮编: 100101 邮件: genetics@genetics.ac.cn