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个人简介:

2005 年, 中国科学院遗传与发育生物学研究所, 博士。

2006.4-2008.12, 美国威斯康辛大学-麦迪逊分校园艺系 (Horticulture Department, University of Wisconsin-Madison), 博士后。

2009.1-2012.11, 美国威斯康辛大学-麦迪逊分校园艺系, Associate Scientist。

2012 年 12 月, 南京农业大学农学院作物遗传与种质创新国家重点实验室, 教授, 博士生导师。

2014 年, 美国威斯康辛大学-麦迪逊分校园艺系, “Honorary Associate/Fellow”。

2013 年, 美国威斯康辛大学农业与生命科学学院 2012-2013 年度 “杰出研究人员奖” (Academic Staff Excellence in Research Awards)。

2014 年, 江苏省双创人才。

主要研究方向: 植物表观调控基因组学

1. 植物R-loop、G4和i-Motif等non-B DNA生物学
2. 作物氮高效利用的表观分子基础。
3. 作物纳米表观基因组学

代表性论文:

1. Tao ST, Lin KD, Zhu QQ, **Zhang WL*** (*通讯). **2020**. MH-seq for functional characterization of open chromatin in plants. *Trends Plant Sci.*, **25**: 618-619.
2. Zhao HN[#], **Zhang WL^{#*}** (#共同第一, *共同通讯), Zhang T[#], Lin Y, Hu YD, Fang C, Jiang JM*. **2020**. Genome-wide MNase hypersensitivity assay unveils distinct classes of open chromatin associated with H3K27me3 and DNA methylation in *Arabidopsis thaliana*, *Genome Biol.*, **21**: 24.

3. Zhang PY[#], Feng YL[#] (#共同第一), Wei HY*, **Zhang WL*** (*共同通讯). **2019**. R-loop identification and profiling in plants. *Trends Plant Sci.*, **24**: 971-972.
4. Li ZJ[#], Wang MY[#], Lin KD[#], Xie YL[#] (#共同第一), Guo JY, Ye LH, Zhuang YL, Teng W, Ran XJ, Tong YP, Xue YB, **Zhang WL*** (*共同通讯), Zhang YJ*. **2019**. The bread wheat epigenome map reveals distinct chromatin architectural and evolutionary features of functional genetic elements. *Genome Biol.*, **20**: 139.
5. Fang Y[#], Chen LF[#] (#共同第一), Lin KD, Feng YL, Zhang PY, Pan XC, Sanders J, Wu YF, Wang XE, Su Z, Chen CY, Wei HY*, **Zhang WL*** (*共同通讯). **2019**. Characterization of functional relationships of R-loops with gene transcription and epigenetic modification in rice. *Genome Res.*, **29**: 1287-1297.
6. Zheng DY[#], Wang L[#], Chen LY[#], Pan XC[#] (#共同第一), Lin KD, Fang Y, Wang XE, **Zhang WL*** (通讯). **2019**. Salt-response genes are differentially regulated at the chromatin levels between seedlings and roots in rice. *Plant Cell Physiol.*, **60**: 1790-1803.
7. Chen LF[#], Wang XM[#], Wang L[#] (#共同第一), Fang Y, Pan XC, Gao XQ, **Zhang WL*** (通讯). **2019**. Functional characterization of chloroplast transit peptide in the small subunit of Rubisco in maize. *J. Plant Physiol.*, **237**: 12-20.
8. Zhao HN*, **Zhang WL*** ^{*,¶} (*共同第一; ¶共同通讯), Chen LF, Wang L, Marand AP, Wu YF, and Jiang JM^{*,¶}. 2018. Genome-wide mapping of open chromatin revealed proliferation of regulatory DNA elements derived from transposable elements in maize genome. *Plant Physiol* 176:2789-2803
9. Pan XC[#], Fang Y[#] (co-first author), Yang XM, Zheng DY, Chen LF, Wang L, Xiao J, Wang XE, Wang K, Cheng, ZK, Yu HX, and **Zhang WL** (通讯). 2017. Chromatin states responsible for the regulation of differentially expressed genes under 60Co- γ ray radiation in rice. *BMC Genomics* **18**:778
10. Liu Y[#], **Zhang WL*** (共同第一), Zhang K, Yiu Q, Yan HY, Jiao YN, Jiang JM, Xu WY, Su Z. 2017. Genome-wide mapping of DNase I hypersensitive sites reveals chromatin accessibility changes in Arabidopsis euchromatin and heterochromatin in regions under extended darkness. *Sci Rep* 7:4093

11. Zhang K, Xu WY, Wang CC, Yi X, **Zhang WL**[#] (#共同通讯), Su Z[#]. 2017. Differential deposition of H2A.Z in combination with histone modifications within related genes in rice callus and seedling. *Plant J*,89:264-277
12. Fang Y, Wang L, Wang XM, You Q, Pan XC, Xiao J, Wang XE, Wu YF, Su Z[#], **Zhang WL**[#] (# 共同通讯).2016. Histone modifications facilitate the coexpression of bidirectional promoters in rice. *BMC Genomics* 17:768
13. Fang Y, Wang XM, Wang L, Pan XC, Xiao J, Wang XE, Wu YF, **Zhang WL** (通讯).2016. Functional characterization of open chromatin in bidirectional promoters of rice. *Sc Rep* 6:32088
14. Zhu B*, **Zhang WL***, Zhang T*, Liu B, Jiang JM. 2015. Open Chromatin Signature-based Enhancer Prediction and Validation in *Arabidopsis thaliana*. *Plant Cell*, 27:2415-2426 (*共同第一)
15. Zhang T*, **Zhang WL***, Jiang JM. 2015. Genome-Wide Nucleosome Occupancy and Positioning and Their Impact on Gene Expression and Genome Evolution in Plants. *Plant Physiol.* 168:1406-1416 (*共同第一)
16. **Zhang WL**, Zhang T, Wu YF, Jiang JM (2014). Open chromatin in plant genomes. *Cytogenetic and Genome Res.* 143:18-27.
17. Zhang T*, Talbert PB*, **Zhang WL***, Wu YF, Yang ZJ, Henikoff J, Henikoff S, Jiang JM. **2013**. The CentO satellites confers translational and rotational phasing on cenH3 nucleosomes in rice centromeres. *Proc. Natl. Acad. Sci. USA.* 110: E4875-E4883 (*共同第一).
18. **Zhang WL**, Zhang T, Wu YF, and Jiang JM. **2012**. Mapping regulatory DNA elements and protein-binding footprints using signatures of open chromatin in *Arabidopsis thaliana*. *Plant Cell*, 24:2719-2731.
19. **Zhang WL**, Wu YF, Schnable JC, Zeng ZX, Freeling M, Crawford GE, and Jiang JM. **2012**. High-resolution mapping of open chromatin in the rice genome. *Genome Res.* 22: 151-162.
20. **Zhang WL**, Friebe B, Gill BS, and Jiang JM. **2010**. Centromere inactivation and epigenetic modifications of a plant chromosome with three functional centromeres. *Chromosoma* 119: 553-63.

21. **Zhang WL**, Wang XE, Yu QY, Ming R, and Jiang JM. **2008**. DNA methylation and heterochromatinization in the male-specific region of the primitive Y chromosome of papaya. *Genome Res.* 18: 1938-1943.
22. **Zhang WL**, Lee H-R, Koo D-K, Jiang JM. 2008. Epigenetic modification of centromeric chromatin: Hypomethylation of DNA sequences in the CENH3-associated chromatin in *Arabidopsis thaliana* and maize. *Plant Cell* 20: 25-34.
23. **Zhang WL**, Yi CD, Bao WD, Liu B, Cui JJ, Yu HX, Cao XF, Gu MH, Min Liu, and Cheng ZK. **2005**. The Transcribed 165-bp CentO is the major functional centromeric element in the wild rice species *Oryza punctata*. *Plant Physiol.* 139: 306-315.

书本章节：

1. Zhang AC, Li XX, Zhao HN, Jiang JM, **Zhang WL** (correspondence author). (2021). Genome-wide identification of open chromatin in plants using MH-seq. *Methods in Molecular Biology* (in press).
2. **Zhang WL** (correspondence author) and Jiang JM (2018). Application of MNase-seq in the global mapping of nucleosome positioning in plants. In: *Methods in Molecular Biology: Plant Transcription Factor*. 1830:353-366.
3. **Zhang WL** and Jiang JM (2015). Genome-wide mapping of DNaseI hypersensitive sites in plants. In: *Methods in Molecular Biology: Plant Functional Genomics*.1284:71-89.
4. **Zhang WL** and Jiang JM (2014) *Molecular Cytogenetics of Papaya*. In: *Genetics and Genomics of Papaya*. Ray M and Moore P (ed.) Springer p157-167, ISBN: 978-1-4614-8086-0 (Print) 978-1-4614-8087-7

会议报告：

1. **Wenli Zhang** (报告人) Functional Characterization of non-B DNA Structures in Plants. National Congress of Crop Science. Oct. 27-30, 2019. Blossom Water

Museum Hotel, Hangzhou, China.

2. **Wenli Zhang (报告人)** Open chromatin associated with plant genome. National Congress of Plant Biology. Oct.9-11, 2013. Zhongshan Hotel, Nanjing, China.
3. **Wenli Zhang (报告人)**, Chingman Wai, Qingyi Yu, Ray Ming, and Jiming Jiang. Cytological characterization of the papaya genome. In: Abstract of Plant &Animal Genomics **XX** Conference. Jan. 14-18, 2012. Town & Country Convention Center, San Diego, CA.USA. P: W310.
4. **Wenli Zhang (报告人)**, Xiue Wang, Qingyi Yu, Ray Ming, and Jiming Jiang. Epigenetic modifications in the male-specific region of the primitive Y chromosome of papaya. In: Abstract of Plant &Animal Genomics **XVII** Conference. Jan. 10-14, 2009. Town & Country Convention Center, San Diego, CA.USA. P: W355.

招生招聘:

欢迎对植物表观遗传学，生物信息和表观基因组学研究方向感兴趣，具有生物信息，生化和分子生物学等研究背景的优秀毕业生加入；同时热忱欢迎对本实验室研究方向感兴趣的学生前来攻读硕、博士学位。