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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），Research Associate。

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。

目前在《Plant Physiology》、《Plant Cell》、《Genome Research》和《PNAS》等杂志上发表第一或通讯作者论文 18 篇。参编学术专著 3 篇，受邀国际会议（PAG，Plant & Animal Genomic Conference）报告 3 次。

主要研究方向：植物表观基因组学

1. 植物 R-loop 生物学
2. 作物氮高效利用的表观分子基础。

发表论文：

1. Zhao HN[*], **Zhang WL**[*,¶] ([*]co-first author; [¶] co-correspondence author), 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

2. 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** (correspondence author). 2017. Chromatin states responsible for the regulation of differentially expressed genes under 60Co~γ ray radiation in rice. BMC genomics **18**:778
3. Liu Y[#], **Zhang WL**[#] (co-first author), 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. Scientific reports 7:4093
4. Zhang K, Xu WY, Wang CC, Yi X, **Zhang WL**[#] ([#]co-correspondence author), 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
5. Fang Y, Wang L,Wang XM,You Q, Pan XC, Xiao J, Wang XE, Wu YF, Su Z[#], **Zhang WL**[#] ([#] co-correspondence author).2016. Histone modifications facilitate the coexpression of bidirectional promoters in rice. BMC genomics 17:768
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8. 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 (*Co-first author)
9. **Zhang WL**, Zhang T, Wu YF, Jiang JM (2014). Open chromatin in plant genomes. Cytogenetic and Genome Research. 143:18-27.
10. 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 (*Co-first author).

11. Yi CD, **Zhang WL***, Dai XB, Li X, Gong ZY, Zhou Y, Liang GH, Gu MH. **2013**. Identification and diversity of functional centromere satellite in the wild rice species *Oryza brachyantha*. Chromosome Res. 21:725-737. (*Co-first author)
12. **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.
13. **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.
14. **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.
15. **Zhang WL**, Wai C, Ming R, Yu Q, and Jiang J. **2010**. Integration of genetic and cytological maps and development of a pachytene chromosome-based karyotype in papaya. Tropical Plant Biology 3: 166-70.
16. Lu JY*, **Zhang WL***, Xue H, Pan Y, Zhang CH, He XH, and Liu M. **2010.** Changes in AFLP and SSR DNA polymorphisms induced by short-term space flight of rice seeds. Biol. Plantarum 54: 112-116. (*Co-first author)
17. **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.
18. **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.
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书本章节：

1. **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.
2. **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.
3. **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)** Open chromatin associated with plant genome. National Congress of Plant Biology. Oct.9-11, 2013. Zhongshan Hotel, Nanjing, China.
2. **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.
3. **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：

欢迎对植物表观基因组学和生物信息研究方向感兴趣，具有生物信息、或生理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。