

APPLICANT BIOGRAPHICAL SKETCHNAME OF APPLICANT: **Mei Zhang** 张梅DATE BIRTH: **Mar 18, 1984**eRA COMMONS USER NAME (credential, e.g., agency login): **ZHANG.MEI**POSITION TITLE: **Postdoctoral Scholar****EDUCATION/TRAINING**

INSTITUTION AND LOCATION	DEGREE (if applicable)	START DATE	END DATE	FIELD OF STUDY
China Agricultural University (CAU), Beijing	B.S	09/2004	07/2008	Plant Genetics and Breeding
CAU, Beijing	Ph.D.	09/2008	06/2013	Maize epigenetics and genomics
CAU, Beijing	Postdoc	06/2013	03/2015	Maize epigenetics and genomics
University of Minnesota, St. Paul MN	Visiting scholar	06/2014	12/2014	Maize epigenetics
Stanford University, Stanford CA	Postdoc	03/2015	Present	Maize anther development, epigenetics

A. Personal Statement

My long term research interests involve the development of maize male reproductive organs, particularly the anthers where meiosis occurs. I seek a comprehensive understanding of epigenetics status, and how alterations in chromatin modifications contribute to anther development. My academic training has prepared me in molecular biology, epigenetics, and bioinformatics. As an undergraduate researcher with Dr. Jinliang Yang, I analyzed maize bZIP transcription factors. As a pre-doctoral student plus 1.5 years as a postdoctoral scholar with Dr. Jinsheng Lai, I characterized imprinted maize genes (imprinting was discovered in maize and genetic analysis is very advanced), including regulation by allele-specific DNA methylation and histone modification on a genome-wide scale. I gained expertise in tissue collection and established DNA-seq, RNA-seq, and MethylC-seq library preparation for my projects and the lab. I am first author of two genome-wide studies, one on imprinted genes in maize and one on epigenetic regulation of imprinted genes in maize. I was also actively involved in a two other projects: analysis of genetic variation among inbred lines and assessing the translational landscape in maize seedlings by ribosome profiling. I received several academic awards during this time. For my postdoctoral training at Stanford University, I focus on maize anther development, in particular on the potential roles of long non-coding RNAs, in particular phased small RNA precursors and DNA methylation changes during development. My PI Dr. Walbot is an internationally recognized leader in maize anther development. The high regularity of maize anther development, large anthers, and a detailed staging system makes recovery of maize samples facile. Furthermore, I have mastered Laser Capture Microdissection for single pre-meiotic and meiotic cells.

B. Positions and Honors**Positions and Employment**

ACTIVITY/ OCCUPATION	START DATE	END DATE	FIELD	INSTITUTION/ COMPANY	SUPERVISOR/ EMPLOYER
Postdoc	06/2013	3/2015	Chromatin modification	CAU	Jinsheng Lai
Postdoc	03/2015	present	Maize anther development && Epigenetics	Stanford University	Virginia Walbot

Academic and Professional Honors

- 2014 The International Postdoc Exchange Fellowship Program (One year Chinese fellowship)
- 2013 Merit graduate student for research achievement at China Agriculture University
- 2013 Syngenta Laboratory Scholarship
- 2012 National Scholarship for Doctoral graduates
- 2012 President Scholarship of China Agricultural University
- 2012 Best Poster Award in the “Frontier of Life Science and Agricultural Biotechnology Innovation National Doctoral Forum”
- 2011 Scientific Research Achievement Award
- 2011 First-class Scholarship in the “Crop Genetics and Breeding the Second Doctoral Forum”
- 2010 Pioneer Scholarship of the National Maize Improvement Center
- 2008 Merit undergraduate Student of China Agricultural University
- 2005-2008 Merit undergraduate Student Scholarship

C. Contributions to Science

1. Graduate Career

I characterized genomic imprinting in maize. Imprinting was discovered in maize in 1970 using the R locus and its expression in maize endosperm. Prior work focused on individual genes, while I conducted a genome-wide analysis of all imprinted protein-coding and long non-coding RNAs in triploid endosperm; this tissue has two maternal and one paternal genome. My work permitted a global exploration of imprinted genes in seed development. We discovered that all differentially methylated regions (DMRs) in maize endosperm are uniformly hypomethylated in maternal alleles but hypermethylated in paternal alleles consistent with observations on individual genes in which only the maternal alleles are initially expressed. Additionally I collaborated on studies of genetic variation among elite maize inbred lines, which is expected to be a valuable resource for future genetic and molecular breeding of this important crop. I also identified novel maize miRNAs, which allows further study to address their functions.

Representative publications:

1. Jiao Y[#], Song W[#], **Zhang M[#]**, Lai J. 2011. Identification of novel maize miRNAs by measuring the precision of precursor processing. *BMC Plant Biol.* 11: 141. ([#Co-First Authors](#))
2. **Zhang M[#]**, Zhao H[#], Xie S[#], Chen J, Xu Y, Wang K, Zhao H, Guan H, Hu X, Jiao Y, Song W, Lai J. 2011. Extensive, clustered parental imprinting of protein-coding and noncoding RNAs in developing maize endosperm. *Proc Natl Acad Sci U S A.* 108: 20042-7.
3. Lai J, Li R, Xu X, Jin W, Xu M, Zhao H, Xiang Z, Song W, Ying K, **Zhang M**, Jiao Y, Ni P, Zhang J, Li D, Guo X, Ye K, Jian M, Wang B, Zheng H, Liang H, Zhang X, Wang S, Chen S, Li J, Fu Y, Springer NM, Yang H, Wang J, Dai J, Schnable PS, Wang J. 2010. Genome-wide patterns of genetic variation among elite maize inbred lines. *Nat Genet.* 42(11):1027-30.
4. Jiang Y, Zeng B, Zhao H, **Zhang M**, Xie S, Lai J. 2012. Genome-wide transcription factor gene prediction and their expressional tissue-specificities in maize. *J Integr Plant Biol.* 54(9):616-30.

2. Postdoctoral Career

1: As a postdoctoral fellow in China (06/2013 ~ 03/2015) I studied the epigenetic regulation of genomic imprinting. I found that the endosperm maternal alleles exhibit all allele-specific H3K27me3 peaks. Based on this, we proposed a model for how DNA methylation and Histone modification of H3K27me3 up-regulate Maternally Expressed Genes (MEGs) and down-regulate Paternally Expressed Genes (PEGs). I also characterized the dynamic transcriptomes of embryo and endosperm, which provides a valuable resource for understanding the genetic control of seed development of monocotyledonous plants. Furthermore, we also analyzed the translational landscape in maize seedlings under drought stress: we showed that maize responds to drought stress through a highly dynamic translational mechanism.

2: As a postdoctoral scholar at Stanford University (03/2015 ~ present), my research focus is on long non-coding RNAs and on differential methylation of *PHAS* loci. PhasiRNAs are short, phased RNAs highly enriched in anthers; this class of small RNA was discovered in the Walbot lab and shares many properties with piRNAs from animal testes (more recently shown to be diced in phase from long precursors like the maize phasiRNAs). Using mutants depleted for 24-nt phasiRNAs, I discovered a link to DNA methylation maintenance and hypothesize that these small RNAs participate in an RNA-directed DNA methylation pathway in anthers. With regard to lncRNAs, I found that nearly all contain short open reading frames and hence may encode peptides; the lncRNAs show discrete, stage-specific expression supporting the idea that they encode developmental regulators. Strikingly, I found all *PHAS*, as a special type of lncRNAs, are ribosome-protected just immediately 5' of the miRNA cleavage site. And these ribosome-protected regions correspond to short ORFs. These results indicates ribosomes or small peptide potentially play important roles in the phasiRNA biogenesis pathway.

5. **Zhang M[#]**, Xie S[#], Dong X[#], Zhao X, Zeng B, Chen J, Li H, Yang W, Zhao H, Wang G, Chen Z, Sun S, Hauck A, Jin W, Lai J. 2014. Genome-wide high resolution parental-specific DNA and histone methylation maps uncover patterns of imprinting regulation in maize. **Genome Res.** 24(1):167-76.
6. Dong X[#], **Zhang M[#]**, Chen J[#], Peng L, Zhang N, Wang X, Lai J. 2017. Dynamic and Antagonistic Allele-Specific Epigenetic Modifications Controlling the Expression of Imprinted Genes in Maize Endosperm. **Mol Plant.** 6;10(3):442-455
7. Chen J, Zeng B, **Zhang M**, Xie S, Wang G, Hauck A, Lai J. 2014. Dynamic transcriptome landscape of maize embryo and endosperm development. **Plant Physiol.** 166(1):252-64.
8. Lei L, Shi J, Chen J, **Zhang M**, Sun S, Xie S, Li X, Zeng B, Peng L, Hauck A, Zhao H, Song W, Fan Z, Lai J. 2015. Ribosome profiling reveals dynamic translational landscape in maize seedlings under drought stress. **Plant J.** 84(6):1206-18.
9. **Zhang M. et al.**, (2018) The long non-coding RNA precursors of male reproductive phasiRNAs in maize anthers are loaded on ribosomes. **Submitted.**
10. **Zhang M. et al.**, (2018) Maize anther long non-coding RNAs. **Invited article for a special issue of Molecular Plant. Manuscript in preparation.**
11. **Zhang M. et al.**, (2018) DNA methylomes of male sterile mutants *dcl5* and *ms23* unveils 24-nt phasiRNAs roles during anther development. **Manuscript in preparation.**

Complete List of Published Work in My Bibliography:

<http://www.ncbi.nlm.nih.gov/sites/myncbi/12GRz3eMvsAf/bibliography/50504531/public/?sort=date&direction=ascending>.