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Education and Research Experience

2019-2024: **Post Doc** in **Institute of Genetics and Developmental Biology** (Prof. Falong Lu lab) joint with **Institute of Zoology** (Prof. Hongmei Wang lab), Chinese Academy of Sciences
2016-2019: Research assistant in Institute of Genetics and Developmental. Biology
2010-2016: **Ph.D. in Genetics** (*Bioinformatics direction*, Supervisor: Prof. Mingsheng Chen, Thesis title: Comparative study of heterochromatin and heterochromatic genes), **Institute of Genetics and Developmental Biology,** Chinese Academy of Sciences
2008-2010: Research assistant in Chinese Academy of Agricultural Sciences
2006-2008**: M.S. in Crop Genetics, Jilin University, China**
2002-2006: **B.S. in Biotechnology, Hunan University, China**

Selected publications (# first/co-first author, * corresponding author)

1. **Wang M#**, Liu Y#, Sun R#, Liu F#, Li J, Yan L, Zhang J, Xie X, Li D, Wang Y, Li S, Zhu X, Li R*, Lu F*, Xiao Z*, Wang H*. Single-nucleus multi-omic profiling of human placental syncytiotrophoblasts identifies cellular trajectories during pregnancy. **Nat Genet** (2024) 56, 294-305. (Article)

Syncytiotrophoblast (STB) differentiation study.
Abstract: The human placenta has a vital role in ensuring a successful pregnancy. Despite the growing body of knowledge about its cellular compositions and functions, there has been limited research on the heterogeneity of the billions of nuclei within the syncytiotrophoblast (STB), a multinucleated entity primarily responsible for placental function. Here we conducted integrated single–nucleus RNA sequencing and single–nucleus ATAC sequencing analyses of human placentas from early and late pregnancy. Our findings demonstrate the dynamic heterogeneity and developmental trajectories of STB nuclei and their correspondence with human trophoblast stem cell (hTSC)–derived STB. Furthermore, we identified transcription factors associated with diverse STB nuclear lineages through their gene regulatory networks and experimentally confirmed their function in hTSC and trophoblast organoid–derived STBs. Together, our data provide insights into the heterogeneity of human STB and represent a valuable resource for interpreting associated pregnancy complications.
PMID: 3826760

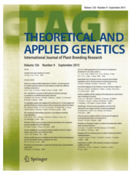
2. Quan Y#, **Wang M#**, Xu C, Wang X, Qin D, Lin Y, Lu X, Lu F*, Li L*. Cnot8 eliminates naive regulation networks and is essential for naive-to-formative pluripotency transition. **Nucleic Acids Res** (2022) 50(8):4414-4435.

Cnot8 driven embryonic pluripotency transition.

Abstract: Mammalian early epiblasts at different phases are characterized by naïve, formative, and primed pluripotency states, involving extensive transcriptome changes. Here, we report that deadenylase Cnot8 of Ccr4–Not complex plays essential roles during the transition from naïve to formative state. Knock out (KO) Cnot8 resulted in early embryonic lethality in mice, but Cnot8 KO embryonic stem cells (ESCs) could be established. Compared with the cells differentiated from normal ESCs, Cnot8 KO cells highly expressed a great many genes during their differentiation into the formative state, including several hundred naïve–like genes enriched in lipid metabolic process and gene expression regulation that may form the naïve regulation networks. Knockdown expression of the selected genes of naïve regulation networks partially rescued the differentiation defects of Cnot8 KO ESCs. Cnot8 depletion led to the deadenylation defects of its targets, increasing their poly(A) tail lengths and half–life, eventually elevating their expression levels. We further found that Cnot8 was involved in the clearance of targets through its deadenylase activity and the binding of Ccr4–Not complex, as well as the interacting with Tob1 and Pabpc1. Our results suggest that Cnot8 eliminates naïve regulation networks through mRNA clearance, and is essential for naïve–to–formative pluripotency transition.

PMID: 35390160

3. **Wang M#**, Zhang Y#, Lin ZS*, Ye XG, Yuan YP, Ma W, Xin ZY*. Development of EST-PCR markers for *Thinopyrum intermedium* chromosome 2Ai#2 and their application in characterization of novel wheat-grass recombinants. **Theor Appl Genet** (2010) 121(7): 1369-1380.



A comparative genomics study in earlier year.

PMID: 20585749

Contributed publications

4. Wang Y#, Wu H#, Jiang X#, Jia L#, **Wang M**, Rong Y, Chen S, Wang Y, Xiao Z*, Liang X*, Wang H*. LMNA Determines Nuclear Morphology During Syncytialization of Human Trophoblast Stem Cells. **Front Cell Dev Biol.** (2022) 10:836390.

5. Jiang X#, Zhai J#, Xiao Z#, Wu X#, Zhang D#, Wan H, Xu Y, Qi L, **Wang M**, Yu D, Liu Y, Wu H, Sun R, Xia S, Yu K, Guo J, Wang H*. Identifying a dynamic transcriptomic landscape of the *cynomolgus macaque* placenta spanning during pregnancy at single-cell resolution. **Dev Cell.** (2023) 58:806-821.

6. Wu X#, Zhao W, Wu H, Zhang Q, Wang Y, Yu K, Zhai J, Mo F, **Wang M**, Li S, Zhu X, Liang X, Hu B, Liu G, Wu J, Wang H, Guo F, Yu L. An aggregation of human embryonic and trophoblast stem cells reveals the role of trophectoderm on epiblast differentiation. **Cell Prolif.** (2023) 56, e13492.

7. Chen J, Huang Q, Gao D, Wang J, Lang Y, Liu T, Li B, Bai Z, Luis Goicoechea J, Liang C.. **Wang M**,.. Wing RA, Chen M. Whole-genome sequencing of *Oryza brachyantha* reveals mechanisms underlying *Oryza* genome evolution. **Nature communications** (2013) 4: 1595.

8. Bai Z, Chen J, Liao Y, **Wang M**, Liu R, Ge S, Wing RA, Chen M. The impact and origin of copy number variations in the *Oryza* species. **BMC genomics** (2016)17: 261.

9. Wei G, Tian P, Zhang F, Qin H, Miao H, Chen Q, Hu Z, Cao L,**Wang M**, Gu X et al. Integrative Analyses of Nontargeted Volatile Profiling and Transcriptome Data Provide Molecular Insight into VOC Diversity in Cucumber Plants (*Cucumis sativus*). **Plant physiology** (2016) 172(1): 603-618.

10. Liao Y, Zhang X, Li B, Liu T, Chen J, Bai Z, **Wang M**, Shi J, Walling JG, Wing RA et al. Comparison of *Oryza sativa* and *Oryza brachyantha* Genomes Reveals Selection-Driven Gene Escape from the Centromeric Regions. **The Plant cell** (2018) 30(8): 1729-1744.

11. Tian P, Zhang X, Xia R, Liu Y, **Wang M**, Li B, Liu T, Shi J, Wing R, Meyers B, Chen M. Evolution and diversification of reproductive phased small interfering RNAs in *Oryza* species. **NEW PHYTOLOGIST** (2021) 229(5): 2970-2983

12. **Wang M#**, Zou H#, Lin Z, Wu Y, Chen X, Yuan Y. Expressed sequence tag-PCR markers for identification of alien barley chromosome 2H in wheat. **Genetics and molecular research** (2012) 11(3): 3452-3463.

Referees

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