Lu Zhang

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EDUCATION

2017.9 - 2024.6	**Master and PhD** (Animal Genetics, Breeding, and Reproduction) at Huazhong Agriculture University. Advisor: Professor Xinyun Li & Professor Shuhong Zhao
2023.11 - 2024.4	**Visiting Ph.D student** (Center for Quantitative Genetics and Genomics) at Aarhus University. Advisor: Professor Lingzhao Fang
2013.9 - 2017.6	**Bachelor's Degree** (Animal Science) at Shihezi University
2014.9 - 2016.6	**Exchange student** (Animal Science) at South China Agricultural University

SKILLS

NGS data processing	Hi-C, RNA-Seq, ChIP-Seq, ATAC-Seq, Single-cell data analysis
Programming	**Python, R, Linux,** Git, Nextflow, Snakemake, HTML
Languages	English, Mandarin

PROJECTS

Enhancer-Promoter Interaction Maps Unveil Skeletal Muscle Traits   Link to Paper

In 2022, our research team developed the BL-HiChIP technique. By applying this technology in conjunction with GRID-seq and GWAS data, we successfully identified functional genetic variants associated with key agricultural traits, such as KLF6 (related to days to 100 kg), MXRA8 (related to lean meat percentage), and TAF11 (related to loin muscle depth). In this project, I am mainly responsible for the development of supporting processes for BL-HiChIP technology and related data analysis.

Hi-Tag for Protein-Mediated Chromatin Interactions with Low Cell Number   Link to Paper

Building on the foundations of BL-HiChIP, in 2023, our team developed Hi-Tag, a new chromatin spatial conformation capture technology tailored for low-cell-number samples. This technology simplifies the experimental process and optimizes the data processing method. It only requires 100,000 cells and allows for the identification of high-confidence chromatin loops mediated by specific histones or transcription factors without the need for additional ChIP-Seq/CUT&Tag data. The Hi-Tag technology was presented through a poster at the 10th International Conference on 3D Genomics in Hangzhou, Zhejiang, where it received appreciation from many researchers. In this work, I am responsible for establishing the Hi-Tag analysis pipeline and conducting all data analysis. Link to Repo

Establishment and exploration of the pig pituitary single-cell atlas

Since the latter half of 2023, Combined with single-cell technology, my research focuses on the pituitary gland of pigs at various developmental stages, exploring cellular heterogeneity and its role in growth and functional regulation. By integrating Genome-Wide Association Study (GWAS) data, I have identified pituitary cell types that are closely linked to growth traits. These findings are crucial for understanding the molecular mechanisms behind the growth and developmental differences among pig breeds of varying body sizes and hold significant implications for future enhancements in pig production performance. In the project, I independently designed the analytical framework and conducted data analysis. The manuscript detailing these discoveries is currently being prepared for submission.

Additionally, throughout my Master's and doctoral programs, I have been actively involved in discussions and data analysis for some other research topics, aiding in the publication of several important findings.

PUBLICATIONS

1. Qi Xiaolong*,**Zhang Lu***, Zhao Qiulin, Zhou Peng, Zhang Saixian, Li Jingjin, Zheng Zhuqing, Xiang Yue, Dai Xueting, Jin Zhe, Jian Yaobang, Li Xinyun, Fu Liangliang, Zhao Shuhong, Hi-Tag: A Simple and Efficient Method for Identifying Protein-Mediated Long-Range Chromatin Interactions Using Low Cell Numbers, **SCIENCE CHINA Life Sciences**, 2023**(co-first author)**.

2. Jingjin Li*, Yue Xiang*, **Lu Zhang***, Xiaolong Qi, Zhuqing Zheng, Peng Zhou, Zhenshuang Tang, Yi Jin, Qiulin Zhao, Yuhua Fu, Yunxia Zhao, Xinyun Li, Liangliang Fu, Shuhong Zhao. Enhancer-promoter interaction maps provide insights into skeletal muscle-related traits in pig genome. ***BMC Biology***. 2022**(co-first author)**.

3. Luan Y., **Zhang L**., Hu M.,Xu Y., Hou Y., Li, X., Zhao S., Zhao Y., Li C. Identification and Conservation Analysis of Cis-Regulatory Elements in Pig Liver. ***Genes***. 2019, 10, 3484.

4. Zhang W, Xu Y, **Zhang L**, Wang S, Yin B, Zhao S, Li X. Synergistic effects of TGFβ2, WNT9a, and FGFR4 signals attenuate satellite cell differentiation during skeletal muscle development. ***Aging Cell***. 2018 Aug;17(4):e12788.

5. Weiya Zhang, Juan Ni, Jie Zhang, **Lu Zhang**, Huanhuan Zhou, Changzhi Zhao, Mengjin Zhu, Haiyan Wang, Jianlin Han, Xinyun Li & Shuhong Zhao. Three functional mutation sites affect the immune response of pigs through altering the expression pattern and IgV domain of the CD4 protein. ***BMC Mol and Cell Biol***. 21, 91 (2020).

6. Xiao C, Li J, Xie T, Chen J, Zhang S, Elaksher SH, Jiang F, Jiang Y, **Zhang L**, Zhang W, Xiang Y, Wu Z, Zhao S, Du X. The assembly of caprine Y chromosome sequence reveals a unique paternal phylogenetic pattern and improves our understanding of the origin of domestic goat. ***Ecol Evol***. 2021 May 4;11(12):7779-7795.

7. Zhang J, Hu S, Zhao C, Zhou Y, **Zhang L**, Liu H, Zhou P, Li S, Fu L, Zheng Z, et al. Genome-Scale CRISPR Knockout Screening Identifies BACH1 as a Key Regulator of Aflatoxin B1-Induced Oxidative Damage. ***Antioxidants*** 2022, 11, 1787. Antioxidants.