

Shuaiqi Liu

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EDUCATION

Hong Kong University of Science and Technology, Guangzhou, China

PhD candidate of Bioscience and Biomedical Engineering

Sep 2023-Now

Zhejiang University, Hangzhou, China

Master of Applied Biology

Sep 2020-Jun 2023

Northeast Forestry University, Harbin, China

Bachelor of Animal Science

Sep 2016-Jun 2020

PUBLICATION

1. **Shuaiqi Liu**, Huan Tian, Yusong Xu, Huabing Wang. Juvenile hormone regulates silk gene expression by m6A RNA methylation. *Cellular and Molecular Life Sciences*.
2. **Shuaiqi Liu**, Shunze Jia, Huan Tian, Yinghui Li, Kaiwen Hu, Yicheng Lu, Jianguo Tao, Yusong Xu, Huabing Wang. Evolution of m6A related genes in insects and function of METTL3 in embryonic development of silkworm. *Insect Molecular Biology*.
3. Huan Tian, **Shuaiqi Liu**, Wenhui Jing, Zhihua Hao, Yinghui Li, Zhehao Lu, Zekai Ding, Yusong Xu, Huabing Wang. Imaginal disc growth factor mediates melanin synthesis and energy metabolism in *Bombyx mori*. *Archives of Insect Biochemistry and Physiology*.
4. Zhou Yanyan, Jin Yue, **Liu Shuaiqi**, Xu Shiliang, Huang Yuxin, Xu Yusong, Shi Liangen, Wang Huabing. Genome-wide identification and comparative analysis of lipocalin families in lepidoptera with an emphasis on *Bombyx mori*. *Insect Science*.
5. Qin Ti, Wang Dongquan, Qu Ningxin, **Liu Shuaiqi**, Li Bo, Chai Hongliang. Bird species identification using faecal DNA analysis. *Chinese Journal of Wildlife*. (Chinese)

PATENTS

1. **Shuaiqi Liu**, A feed pulverizer shell is convenient to observe and connect to the feeder. 201820780179.0 [P]. 2018-05-24.

RESEARCH EXPERIENCE

Master Student in College of Animal Sciences

Zhejiang University, Hangzhou, China

Sep 2020-Sep 2023

- Project 1: Exploring the evolutionary relationship of m6A related genes in insects and the molecular biological functions during embryonic development. To do this, I adopted evolutionary analysis, CRISPR-Cas9 gene editing, embryonic RNAi technology, and transcriptome sequencing. I found that m6A related genes are highly conserved in 206 species of insects and play an important role in regulating Wnt and Toll / Imd signaling pathways during embryonic development of silkworm.
- Project 2: To investigate the regulation relationship between the Juvenile hormone (JH) and m6A related genes with conjoint analysis of MeRIP sequencing and transcriptome sequencing data. I performed RNAi, gene overexpression and point mutation of m6A sites to identify the mechanism of JH regulates the expression of silk-associated genes expression via m6A.

Undergraduate Researcher in National Forestry and Grassland Administration Detecting Center of Wildlife

Northeast Forestry University, Harbin, China

Jan 2017-Jan 2018

- Developed a system of species identification based on bird fecal DNA and the system incorporated complete sequence analysis and clear standards.

Resident Ecologist Intern in Shanghai Zoo

Shanghai Zoo, Shanghai, China

Jan 2018

- Investigated community ecology and wildlife management in Shanghai Zoo through the Shanghai Research Experience for Students Program.
- Performed independent research project on *Anthracoceros coronatus* habits within *A. coronatus* Park of Shanghai Zoo. I discovered that during the breeding period of *A. coronatus*, the food provided by the male *A. coronatus* to the female *A. coronatus* has distinct structural features and is different from the usual ones.

TEACHING EXPERIENCE

- Winter 2022 – Teaching Assistant for Laboratory of Animal Molecular Cell Biology at Zhejiang University
- Autumn 2021 – Teaching Assistant for Modern Applied Animal Experimental Technique at Zhejiang University

VOLUNTEER WORK AND OUTREACH

- The 19th Asian Games Hangzhou 2022, 2022, volunteer candidate
- The University Science Camp in Zhejiang University, 2022, volunteer
- The 37th "bird-loving week" in Heilongjiang Province, 2018, volunteer
- The 36th "bird-loving week" in Heilongjiang Province, 2017, volunteer
- Shanghai Zoo, 2018, volunteer

SKILLS

Lab Skills: Molecular biology techniques (PCR, qPCR, RT-PCR, DNA/RNA extraction, CRISPR-Cas9 gene editing system, and molecular cloning), protein analysis (immunoblotting) and protein expression and purification (*E. coli* and insect cell expression system), Dot-blot, high throughput sequencing techniques (RIP-seq, RNA-Seq) analysis, cell culture, and flow cytometry.

Languages: R, Python, Shell