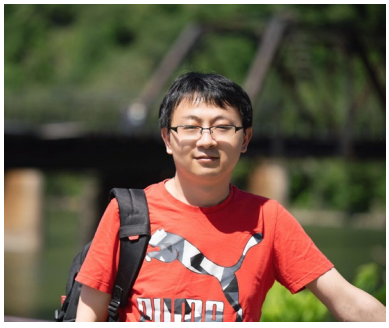
Curriculum Vitae

General information

Name	Hong Zhang	Gender	Male
Graduate school	Chinese Academy of Sciences	Degree	PhD
PhD Tutor	Prof. Guoping Zhao	Nationality	China
Present Address	4062 Campus Dr., Department of Cell Biology and Molecular Genetics, University of Maryland. hzhang21@umd.edu; hongzhang0188@gmail.com.		



Research experience

2019.03 – present: Post Doctoral Associate, the Department of Cell Biology and Molecular Genetics, University of Maryland, College Park, USA; Collaborator: Dr. Jiqiang Ling;
2018.02 – 2019.02: R&D scientist, Zhejiang Wolwo Biotechnology Co. Ltd., Shanghai Branch;
2014.09 – 2018.01: Ph.D. in Microbiology, Key Laboratory of Synthetic Biology, Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai, China; under the supervision of Prof. Guoping Zhao;
2013.06 – 2014.06: Research Assistant, Key Laboratory of Insect Developmental and Evolutionary Biology, Institute of Plant Physiology and Ecology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai, China; Collaborator: Dr. Erjun Ling;
2010.09 – 2013.06: M.S. in Genetics, Jiangsu Key Laboratory of Biodiversity and Biotechnology, School of Life Sciences, Nanjing Normal University, Nanjing, China;
2006.09 – 2010.07: B.S. in Biological Sciences, School of Biological Engineering, Huainan Normal University, Huainan, China.

Research fields

During the master's degree pursuing, the main research area is agricultural pest control, devoted to discovering pesticide-resistance related genes and proteins with all kinds of techniques. I led a graduate research project at province level before graduation.

After graduation, I worked with Dr. Erjun Ling in the institute of plant physiology and ecology, Chinese Academy of Sciences (Shanghai) for one year. Using Bombyx mori as a model, my main research area is insect development and immunity mainly using immunohistochemistry.

During the phD period in the Chinese Academy of Sciences (Shanghai), I worked in Professor Guoping Zhao' lab focusing on CRISPR/Cas9 technology development and innovation, and successfully applied for one patent about a novel and efficient method in genome editing; and another area is exploring the impact of post-translational regulation such as protein acetylation and succinylation. I have achieved original results in both fields and obtained an excellent students award in the University of Chinese Academy of Sciences.

Since 2019, I have been doing research as a postdoc with collaborator Dr. Jiqiang Ling in the University of Maryland to explore the impact of protein translation fidelity in bacteria and eukaryotes. Translational error through mutations in aminoacyl-tRNA synthetases and ribosomes result in many

diseases including neurological disorder, ageing, etc. I have already published some original results in bacteria and yeast.

Publications

1. **Zhang H**, Wu J, Lyu Z, Ling J. Impact of alanyl-tRNA synthetase editing deficiency in yeast. ***Nucleic Acids Res***. 2021, gkab766.
2. Yang YJ**, Zhang H**, Guo ZY, Zou SW, Long F, Wu JC, Li P, Zhao GP, Zhao W. Global insights into lysine acylomes reveal crosstalk between lysine acetylation and succinylation in *Streptomyces coelicolor* metabolic pathways. ***Mol. Cell. Proteomics***, 2021, 20: 100148.
3. **Zhang H**, Lyu Z, Fan Y, Evans CR, Barber KW, Banerjee K, Igoshin OA, Rinehart J, Ling J. Metabolic stress promotes stop-codon readthrough and phenotypic heterogeneity. ***Proc. Natl. Acad. Sci. USA***, 2020, 117(36): 22167-22172.
4. Li P, **Zhang H**, Zhao GP, Zhao W. Deacetylation enhances ParB-DNA interactions affecting chromosome segregation in *Streptomyces coelicolor*. ***Nucleic Acids Res***. 2020, gkaa245.
5. **Zhang H**, Li P, Ren SX, Cheng ZY, Zhao GP, Zhao W. *Sc*CobB2-mediated Lysine Desuccinylation Regulates Protein Biosynthesis and Carbon Metabolism in Streptomyces coelicolor. ***Mol. Cell. Proteomics***, 2019, 18(10): 2003-2017.
6. **Zhang H**, Cheng QX, Liu AM, Zhao GP, Wang J. A novel and efficient method for bacteria genome editing employing both CRISPR/Cas9 and an antibiotic resistance cassette. ***Front. Microbiol.***, 2017, 8: 812.
7. **Zhang H**, Li FL, Cheng C, Jiao DX, Zhou Z, Cheng LG. The identification and characterisation of a new deltamethrin resistance-associated gene, *UBL40*, in the diamondback moth, *Plutella xylostella* (L.). ***Gene***, 2013, 530(1): 51-56.
8. **Zhang H**, Cheng C, Li FL, Gu SY, Zhou Z, Cheng LG. Cloning and characterization of ubiquitin ribosome fusion gene *RpS27a*, a deltamethrin resistance associated gene from diamondback moth (*Plutella xylostella* L.). ***Turk. J. Zool.***, 2013, 37(4): 506-513.
9. **Zhang H**, Li FL, Cheng C, Liu BD, Cheng LG. cDNA representational difference analysis of deltamethrin-resistant and –susceptible strains in diamondback moth. ***Pak. J. Zool.***, 2013, 45(2): 511-519.
10. Zhang NN, **Zhang H**, Cheng C, Li FL, Gao SQ, Cheng LG. A comparative profiling of protein expression in the deltamethrin-sensitive and resistant strains of the diamondback moth (*Plutella xylostella*). ***Acta Entomologica Sinica***, 2013, 56(1): 1-8.

Patent:

One method for DNA editing, Jin Wang, Guoping Zhao, Hong Zhang. ZL201611022023.8.

Editorial board member

Frontiers in Microbiology.

Project

Graduate research and innovation projects in Jiangsu province, China (CXLX11_0884). 2011.06-2013.06, In charge.