

Haikuo Li

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Education

Washington University in St. Louis

8/2019 – 2024 (expected)

Ph.D. Training Program, Division of Biology and Biomedical Sciences

- Thesis Mentor: **Benjamin D. Humphreys**, M.D., Ph.D.
- Program in Molecular Genetics and Genomics, which ranked #1 in graduate programs

Shanghai Jiao Tong University

9/2015 – 6/2019

Bachelor of Science, Bioscience (Zhiyuan Honors Program)

- 2019 Top 0.2% Bachelor Thesis: #1 in Bioscience
- 2019 Outstanding Graduate in Bachelor Degree, Shanghai

Research Interests

Single-cell technologies; Proteomics; Fibrotic diseases; Tissue regeneration; Cancer biology

Research Experiences

Humphreys Lab, Washington University in St. Louis

4/2020 – 2024 (expected)

Ph.D. thesis Lab, advised by Benjamin D. Humphreys

- Studying tissue fibrosis and regeneration leveraging single-cell technologies

Rotations, Washington University in St. Louis

8/2019 – 4/2020

First-year rotation researches, advised by Tim R. Peterson, Sidharth V. Puram, Benjamin D. Humphreys

- Peterson Lab: Understanding the intracellular effects of Cationic Amphipathic Drugs on organelles

Cationic Amphipathic Drugs are utilized in various clinical applications, but their underlying intracellular mechanisms are largely unknown. We hypothesized that due to different drug treatments, cell organelles would exhibit different morphology and changes of their abundance, ultimately contributing to distinct mechanisms of cell death. In this rotation, I successfully completed the imaging tests to investigate the intracellular drug effects.

- Puram Lab: Studying the tumor heterogeneity of head and neck cancer by single-cell sequencing

Cell hashing is a single-cell RNA sequencing (scRNA-seq) method multiplexing different cell lines with unique antibody barcodes. It enables us to reduce the routine cost of scRNA-seq and decrease the technology-dependent batch effects. In this rotation, I successfully performed cell hashing on head and neck squamous cell carcinoma (HNSCC) cell lines which generated a series of datasets with promising data quality.

- Humphreys Lab: Studying transcriptomic variations in kidney diseases

RNAscope, a nucleic acid in situ hybridization assay, allows characterization and validation of RNA markers with high sensitivity and specificity. In this rotation, I pioneered the RNAscope assay in the lab on multiple kidney models and successfully identified novel molecular heterogeneity in kidney, as well as transcriptomic variations in certain kidney diseases.

Ring Lab, Department of Immunobiology, Yale University

7/2018 – 4/2019

Visiting undergraduate intern, advised by Aaron M. Ring

- Modulating immune cytokines by protein engineering

Yan Lab, Shanghai Center for Systems Biomedicine, Shanghai Jiao Tong University

9/2016 – 7/2018

Undergraduate Researcher, advised by Wei Yan

- Discovery of lymphoma classifiers via mass spectrometry; clinic proteomics

Undergraduate Research Description

Ring Lab, Department of Immunobiology, Yale University

7/2018 – 4/2019

At Ring Lab, we concentrated on enhancing the immunotherapeutic efficacy of interleukin-18 (IL-18) by protein engineering. Previous clinical trials showed that IL-18 immunotherapy was not fully effective in the phase 2 clinical trial. The upregulation of IL-18-binding protein (IL-18BP) should be responsible for this restraint. Here, our lab leveraged protein engineering approaches to develop a “super-agonist” “Decoy-Resistant” IL-18 (DR-18) to unlock a potent immunotherapeutic cytokine pathway. Besides, I conducted my thesis research independently (2019 Top 0.2% Bachelor Thesis ([PDF](#)) of Shanghai Jiao Tong University): we aimed to further improve the tumor-targeting specificity of DR-18, balancing its therapeutic efficacy and potential toxicity. Here, we proposed two assays, pro-peptide assay and pH-sensitive assay: the former assay leveraged the unique property of IL-18 that precursor peptide processing is required for its maturation. The latter assay harnessed the extracellular acidity of tumor and aimed to construct a low-pH favorable variant. Both assays were developed and evaluated in vitro, ex vivo, and in vivo.

Yan Lab, Shanghai Center for Systems Biomedicine, Shanghai Jiao Tong University

9/2016 – 7/2018

At Yan Lab, I completed a proteomic study as the first author. Development of molecular classifiers of lymphoma for precision medicine practice, in together with the traditional lymphoma classification, has been highly demanded. In this study, we leveraged Data Independent Acquisition (DIA) mass spectrometry method on 109 lymph node samples from clinical patients, covering a comprehensive suite of lymphoma subtypes including B-NHL, T-NHL, HL, Lymphadenitis, Tumor metastatic lymph

node, and Non-neoplastic lymph node. We generated a lymphoma-associated proteomic profiling data resource, quantified and validated significant classifiers of different disease subgroups, and provided classifiers correlating with the aggressive and prognostic characteristics of lymphoma.

Long Lab, Department of Ecology and Evolution, The University of Chicago

6/2017 – 8/2017

My summer research at UChicago (advised by [Manyuan Long](#)) focused on evolutionary biology. The birth of new novel genes plays an essential role in understanding and elaborating the evolution of genetic systems. Here, we used phylogenetic analysis to discover positively selected genes among mammalian species.

Publications

Surveying the Human Single Cell Landscape

Kidney International 2020

Haikuo Li, Benjamin D. Humphreys

Clinical Proteomics Analysis using Data Independent Acquisition-Mass Spectrometry (DIA-MS) Identified Classifiers for Molecular Characterization of Lymphoma

Pending

Haikuo Li, Jinghan Wang, Wenjuan Yu, Fang Yu, Zhongqi Li, Xin Ku, Jie Jin, Wei Yan

Posters

Clinical Proteomics Analysis using Data Independent Acquisition-Mass Spectrometry (DIA-MS) Identified Classifiers for Molecular Characterization of Lymphoma ([PDF](#))

Human Proteome Organization World Congress 2018

Haikuo Li, Jinghan Wang, Wenjuan Yu, Fang Yu, Zhongqi Li, Xin Ku, Jie Jin, Wei Yan

Modulating the Tumor-Targeting Specificity of “Decoy-Resistant” Interleukin-18 by Protein Engineering ([PDF](#))

SJTU Academic Festival 2019

Haikuo Li, Ting Zhou*, Aaron M. Ring*

Detecting Positively Selected Genes among Mammalian Species Using Phylogenetic Analysis of Maximum Likelihood ([PDF](#))

SJTU Academic Festival 2017

Haikuo Li, Jianhai Chen*, Manyuan Long*

Academic Honors

Top 0.2% Bachelor Thesis of Shanghai Jiao Tong University (PDF)	2019
Outstanding Graduate in Bachelor Degree, Shanghai	2019
The Best Design Prize, 2nd SJTU Academic Festival, Shanghai	2019
Academic Excellence Scholarship (First-class), Shanghai Jiao Tong University	2016,2017,2018
#1 Student Presentation, National Biology Education Conference of Chinese Ministry of Education, Guangdong	2018
The Best Talent Prize, 1st SJTU Academic Festival, Shanghai	2017
Enrolled in Bioscience Honors Program of Shanghai Jiao Tong University	2015
Top 0.1% in Chinese University Entrance Examination	2015
Bronze medal, Chinese Mathematical Olympiad (CMO), Chongqing	2014
Enrolled in the Province’s Mathematical Olympiad Team	2014

Other Activities

Teaching Assistant, College Genetics Course, Shanghai Jiao Tong University	2/2019 – 6/2019
Speaker, National Biology Education Conference of Chinese Ministry of Education, Guangdong	5/2018
Teaching Assistant, College Macrobiology Course, Shanghai Jiao Tong University	2/2018 – 6/2018
Presidium, Students’ Union of Zhiyuan Honors Program, Shanghai Jiao Tong University	6/2017 – 3/2018
Teaching Assistant, College Biochemistry Course, Shanghai Jiao Tong University	9/2017 – 1/2018