Xiangjie Zhao

Ph.D. in Bioinformactics

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Living place: Beijing

Education

Institute of Genetics and Developmental Biology, Chinese Academy of Sciences   *Sep 2017 - Jun 2024*
Ph.D. in Bioinformatics

College of Biological Sciences and Engineering, Fuzhou University   *Sep 2013 - Jun 2017*
B.S. in Bioengineering

Skills

Omics data analysis
- RNA-seq, CUT&Tag-seq, ChIP-seq, Single-cell omics, Spatial transcriptomics

Programming
- Python, R, Shell, Web development

Experiment
- Mouse behavioral experiment, Mouse tissue dissection (especially brain), Immunofluorescence

Language
- Chinese, English

Research Interests

- Multi-omics data integration analysis
- Animal behavior and neurological disease
- Cancer heterogeneity

Recent Works

Clinical big data analysis of hypertensive patients
Hypertension is a disease in which arterial blood pressure remains at an excessively high level, and its incidence has shown a blowout growth in the past decade, and gradually tends to be younger. Long-term high blood pressure can cause a series of cardiovascular diseases. Both genetic and environmental influences are risk factors for high blood pressure. This project is based on large-scale clinical data of hypertensive patients. In this project, I participated in the design of the subject, established data analysis methods, cleaned clinical data, and explored the risk factors related to hypertension and their associated diseases as well as the population differences in drug efficacy, etc. The project is expected to provide beneficial references for the precision medicine of hypertension.

Single-cell transcriptome analysis of the microenvironment in multiple myeloma
Multiple myeloma is a cancer of plasma cells. Studies have shown that the bone marrow microenvironment can affect the proliferation, metastasis and drug resistance of multiple myeloma, but the mechanism is not clear. In this project, I participated in the project design and completed the analysis of single-cell transcriptome. We have identified a new multiple myeloma cell type that arises after interaction with bone marrow mesenchymal stem cells, which have a stronger protein translation ability and similar properties to cancer stem cells. Through single-cell communication analysis, we found that bone marrow mesenchymal stem cells may induce the proliferation of multiple myeloma through the cytokine IL6. In addition, we found that the transcriptome of myeloma cells cocultured with bone marrow mesenchymal stem cells had more drug resistance characteristics than myeloma cells cultured alone.

Systematic analysis of human hormone receptors
Hormones act on hormone receptors (HRs) to exert their functions of remote regulation and multi-organ coordination. Therefore, HR has a very wide range of important physiological functions and has been the focus of basic research and a common target for drug development. However, the current research on HR is often limited to a limited category of HR or a special disease state, and there is a lack of systematic analysis of all HRs in various tissues and cells of the human body. In this project, I participated in the design of the project and completed the data collection and analysis. We conducted a systematic collection and comprehensive bioinformatics analysis of human HRs. Systematic analyses of HR provide researchers with a panoramic picture of hormonal regulation in the human body.

Function of glucagon receptor in mouse cerebellum
The regulation of energy metabolism-related hormones on the central nervous system has been reported, but the research is still insufficient. When analyzing the expression of HRs related to energy metabolism in the brain, we found that glucagon receptor (GCGR) was specifically expressed in the cerebellum of mice. At present, there are no reports that GCGR regulates cerebellar function. Therefore, we constructed a mouse model of brain-specific *Gcgr* knockout and analyzed the role of GCGR in the central nervous system with this model. In this project, I participated in the design of the subject, and completed mouse behavioral experiments, cerebellar morphological analysis, cerebellar single cell data analysis, etc. The study of cerebellar GCGR reveals a new mechanism by which the brain senses and responds to changes in peripheral energy reserves through HR to regulate its own behavior.

Publications

Papers
- <u>Zhao X</u>, Wang XJ. A systematic expression analysis of human hormone receptors. 2024. (In submission)
- <u>Zhao X</u>, Zhang Z, Xie D, Wang XJ. Glucagon receptor in cerebellar neurons regulates body weight and locomotor activity. 2024. (In preparation)
- Zhang Z, Wu C, Dai C, Shi Q, Fang G, Xie D, <u>Zhao X</u>, Liu YJ, Wang CCL, Wang XJ. A multi-axis robot-based bioprinting system supporting natural cell function preservation and cardiac tissue fabrication. Bioact Mater. 2022:18:138-150.

Website
An interactive analysis web app of human tissue hormonal communications (HTHC)
https://hthc-123456789.shinyapps.io/HTHC/

Talks

International Student Workshop 2020
Organizer: IGDB, NAIST and UC Davis
Topic: Analysis of drug resistance in multiple myeloma and the interaction with mesenchymal stem cells by scRNA-seq

Future Science Salon
Organizer: Key Laboratory of Genetic Network Biology, IGDB
Topic: Phthalates ---- the sword of Damocles hanging over everyone's head

Technical Forum
Organizer: Prof. Xiu-Jie Wang's lab, Key Laboratory of Genetic Network Biology, IGDB
Topic: Born for interactive computing ---- Project Jupyter

Journal Club
Organizer: Prof. Xiu-Jie Wang's lab, Key Laboratory of Genetic Network Biology, IGDB
Topic: Diverse topics such as neurology, immunity, cancer and metabolism. Details and related slides/posters can be found in my personal GitHub page.