

Jihua Ouyang

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🌐 <https://github.com/Learnerhua> 🏠 <https://learnerhua.github.io/Home>

Seeking bioinformatics-related job

EDUCATION

Sun Yat-sen University, Guangzhou, China

Sep 2021 - Jun 2024

MPhil in Bioinformatics, School of Life Science

- **GPA:** 3.60/5.00
- **Major courses:** Molecular Systems Biology(3.8), Marine Biomedical Immunology(3.6), Experimental Design and Statistical Analysis(4.0)
- **Honor:** The First Prize Scholarship
- **Acquired skills:** Skilled in the data analysis of **Comparative Genomics** and **Microbiomics**; Familiar with several programming languages like **Python, R, Shell** and **Perl**; proficient in the use of **Linux** operation system.

Southern Medical University, Guangzhou, China

Sep 2015 - Jun 2020

BSc in Biotechnology, School of Laboratory Medicine and Biotechnology

- **GPA:** 3.51/5.00 (top 5%)
- **Major courses:** Bioinformatics(4.2), Advanced Mathematics(4.5), Molecular Biology (3.8), Medical Statistics (3.8), Cell Engineering (4.1), Genetic Engineering (3.8), Microbial Engineering (3.9), Biopharmaceuticals (4.1)
- **Honor:** National Encouragement scholarship, The Third Prize Scholarship
- **Certificates:** CET6(573), National Computer Grade II Certificate(MS Office)
- **Acquired skills:** Basic laboratory skills in biology including but not limited to **WB, ELISA, plasmid extraction, bacterial transformation and culture, protein purification, cell culture, production of monoclonal antibodies**; Familiar with animal experimental techniques as well as some chemistry experimental techniques.

RESEARCH EXPERIENCE

1. Exploring proteins contain multiple concatenated ApeC domain in Platyhelminthes

2021 - Present

The apextrin C-terminal (ApeC) domain is a category of brand-new protein domain which was defined within last decade. Cutting-edge research highlights that the wide distribution of ApeC-containing proteins (ACPs) span across non-vertebrate Eumetazoa and its evolutionary origins can even be traced back to prokaryotic organisms such as Eubacteria. An intriguing phenomenon in Platyhelminthes, a venerable Bilateria renowned for its unparalleled regenerative abilities, is that the ACPs seem to be restricted to two of the three classes within obligate parasitic group Neodermata, including Trematoda and Cestoda but mysteriously disappear in another significant ectoparasitic class—Monogenea—as well as in those free-living species among Platyhelminthes. Given the fact that immense damage caused by parasitic Platyhelminthes to aquaculture and ACPs may play a crucial role in the parasite-host interactions as important components of fish's immune system, our team decide to clarify the taxonomic distribution, sequence diversification, fundamental biological structure and potential functions of ACPs in Platyhelminthes.

As the backbone of the project, I have taken on the majority of the work so far, including searching for ACPs from public databases and the Monogenea transcriptome data we have measured, applying the principles of comparative genomics to uncover and summarize the structural attributes of protein sequences, building a new model with higher sensitivity for identifying ACPs in massive sequences data and so on.

Achievement: Up until now, the major portion of the project has been finished and some novel features of ACPs have been detected in Platyhelminthes, I am currently in the process of drafting a paper and have aspirations to publish it in the near future. In addition, I was listed as the sixth author of a ApeC-related paper:

Jin Li, Shumin Liu, Yang Zhang, Qiuyun Huang, Hao Zhang, **Jihua OuYang**, Fan Mao, Huiping Fan, Wenjie Yi, Meiling Dong, Anlong Xu* and Shengfeng Huang*. Two Novel Mollusk Short-form ApeC-containing Proteins Act as Pattern Recognition Proteins for Peptidoglycan. *Frontiers in Immunology*. 2022 Oct 7; 13:971883. <https://doi.org/10.3389/fimmu.2022.971883>

2. The changes in the fish's intestinal microbiota environment caused by the absence of CM **2021 - Present**

Chitin-based peritrophic matrix (PM) plays a critical role in the invertebrate immunity and digestion, but the functions of its counterpart in vertebrate – PM-like chitinous membrane (CM) are largely remain elusive. Under the circumstances, our team created a zebrafish model genetically devoid of the CM and used it to study short-term and long-term CM functions in fish of which the impact on the intestinal microbiota is also an important component.

So, my job in this project is to assist in developing a pipeline that is capable of analyzing microbial 16S amplicon sequencing data which enables us to find the similarities and disparities between the treatment groups and control groups properly and promptly. As of now, I have completed the first phase of the work and have preliminarily established a pipeline which is named “LuckyMicrobe” based on several major platforms such as QIIME2 and USEARCH and can be accessed on my Github homepage <https://github.com/Learnerhua/LuckyMicrobe-testing->. With the support of this pipeline, we have found that CM-less fish could not maintain a normal gut microbiota.

Achievement: Being listed as the seventh author of the related article:

Zirui Yue, Zhaoyu Fan, Hao Zhang, Buhan Feng, Chengyi Wu, Shenghui Chen, **Jihua Ouyang**, Huiping Fan, Panwei Weng, Huixiong Feng, Shangwu Chen, Meiling Dong, Anlong Xu* and Shengfeng Huang*. Differential roles of the fish chitinous membrane in gut barrier immunity and digestive compartments. EMBO Reports. 2023. <https://doi.org/10.15252/embr.202256645>

3. Recombinant Expression, Isolation and Purification of Perfringolysin O **2019 - 2020**

Produced by Clostridium perfringens, the pore-forming toxin perfringolysin O(PFO) is one of the cholesterol-dependent cytolysins(CDCs) and able to interact with cholesterol in mammalian cell membrane surface to form a bilayer-spanning pore, it plays an important role in the occurrence of diseases development and is widely applied in all kinds of cell biology experiment as a kind of perforin. The expression, isolation and purification of PFO is the basis for studying or using its biological activity.

I dedicated myself completely to the acquisition of PFO during my senior year. Finally , the target protein was induced to be expressed in large quantities, reaching a certain purity and concentration through separation, purification and concentration. Meanwhile, a series of optimal experimental conditions for the expression of PFO were explored, which laid a solid foundation for the follow-up experiments.

Achivement: I completed my **undergraduate thesis** based on this research.

4.The synthesis of bio-nano material: MOFs(Metal-Organic Frameworks) **2018 - 2019**

In my junior year, I participated in a National Innovation and entrepreneurship training program for college students, my supervisor was a professor from the school of pharmaceutical who specializes in synthesizing new types of MOFs(Metal-Organic Frameworks), a highly ordered crystalline materials with fascinating structures, flexible porosity, high surface area and uniform open cavities. MOFs have been explored for gas storage, separations, catalysis, nanoscale reactors, bioimaging as well as drug delivery.

At that time, I took responsibility for assisting graduate students to synthesize new MOFs, a flow work including materials weighing, dissolving, adjusting pH, stirring, filtering, drying, grinding, products packaging and marking.

Achievement: Being listed as the fourth author of the article:

Xie, B. P., Chai, J. W., Fan, C.,**Ouyang, J. H.**, Duan, W. J., Sun, B., ... & Chen, J. X. (2020). Water-Stable Silver-Based Metal–Organic Frameworks of Quaternized Carboxylates and Their Antimicrobial Activity. ACS Applied Bio Materials, 3(12), 8525-8531. <https://pubs.acs.org/doi/10.1021/acsabm.0c00896>