

+86 172 0031 5641
Thuwal, Saudi Arabia
xinglin.qian@kaust.edu.sa

Xinglin (Jerome) Qian

Prospective Ph.D. Student

github.com/JeromeeX
linkedin.com/in/jeromexqian

A master student with extensive experience in biochemistry and molecular genetics, currently focusing on synthetic biology and genomics in *C. elegans*.

EDUCATION

MSc., Bioscience, King Abdullah University of Science and Technology

08/2022 - Now

GPA: 3.93/4.00

Supervisor: *Christian Frøkjær-Jensen*

- *Genomics (A), Introduction to Nanopore Sequencing (Ph.D. course, A), Fundamentals of Neuroscience (Ph.D. course, A-, exams >90%)*

BSc., Biological Science of Honors Program, China Agricultural University

09/2018 - 07/2022

GPA: 3.51/4.00

Supervisor: *Huiqiang Lou*

- *Inorganic and Analytical Chemistry (A-), Biochemistry I, II (A, A-), Physical Chemistry (A+), Molecular Biology (A), Genetics (A), Cell Biology (A), Microbial Physiology (A), Plant Physiology (A-), Probability and Statistics (A), Bioinformatics (A), Biostatistics (A-)*

EXPERIENCE

Internship

09/2021 - 05/2022

Rao lab, IDG/McGovern Institute, Peking University

Beijing, China

- Focusing on Prime Editing modification and adapting it in *Drosophila melanogaster* neurons.
- With extensive experience in molecular cloning, immunochemical, and *Drosophila* behavioral assays.

Internship

09/2020 - 08/2021

Rao lab, Chinese Institute for Brain Research (CIBR)

Beijing, China

- Focusing on genes with potential influence on sleep homeostasis in *Drosophila melanogaster*.
- With experience in molecular cloning, contributed to the establishment of a primer auto-design platform for high-throughput gene screening.

Internship

07/2019 - 08/2019

*Institute of Zoology, Chinese Academy of Sciences
Ludong University*

*Beijing, China
Shandong, China*

- Focusing on taxonomy revision for *Pinus* genus in Mount Dongling, Beijing and *Gaetice* genus in Yantai, Shandong.
- With extensive experience in lepidoptera and herbaceous specimen making.

RESEARCH PROJECTS

A novel target-enrichment sequencing strategy in *C. elegans*

Undergoing

- Created *WormDigester*, an *in silico* tool to simulate *C. elegans* genome digestion by common endonucleases and to illustrate the length distribution of digested fragment.
- Created *genomedigester*, of which the input is a genome FASTA file and the output is the simulated DNA gel electrophoresis and Bioanalyser results of the digested input by certain endonuclease(s).
- Created a transgenic strain carrying designed extrachromosomal array for target enrichment and sequenced it with nanopore flow cells. Conducted sequencing analyses including basecalling, alignment, array assembly, and other customized assays.

Characterization of a standardized neuron-specific promoter biological parts for *C. elegans*

In draft

- Designed and characterized two 296-bp constructs as standardized *C. elegans* neuron-specific (BAG and ASER, respectively) promoters, which are incorporated into *WormBuilder* promoter pool.
- Created plasmids suitable for *MosTI* single-copy insertion, with which the expression of interchangeable reporter genes are driven by the characterized promoters.

Modification of Prime Editing towards a higher efficiency in *Drosophila* neurons

Unpublished

- Replaced the reverse transcriptase (RT) used in Prime Editing with HIV-1 RT, and separated HIV-1 RT and Cas9n (D10A) into different open reading frames.
- Determined its efficiency in HEK293T cell line and *Drosophila in vivo* neurons.

SKILLS

Tools and Languages

Python, \LaTeX , Markdown

Wet Lab Techniques

Molecular cloning (e.g., Gibson Assembly, Golden-Gate Assembly, RT-qPCR), nanopore sequencing, cell culture and transient transfection, Western Blot

Communication

Mandarin, English (IELTS: C1), French (TCF: B2), Shanghaiese, Cantonese