WANG Qianwen

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Education

PHD | THE CHINESE UNIVERSITY OF HONG KONG | 2015.08 - 2021.02

· Major: Molecular Biotechnology

BACHELOR | NORTHEASTERN UNIVERSITY | 2010.09 - 2014.06

· Major: Computer Science

Research Experience

RESEARCH ASSOCIATE | THE CHINESE UNIVERSITY OF HONG KONG | 2021.04 - NOW

- · Bioinformatics and genomics analysis
- Investigated the effects of epigenetics including DNA methylation and small RNAs on salt priming stress response in soybean
- · Reanalyzed and deposited the published epigenetic data to our website

PHD | THE CHINESE UNIVERSITY OF HONG KONG | 2015.08 - 2021.02

- Studied the roles of histone deacetylase 6 (HDA6) in DNA methylation and histone modifications in Arabidopsis
- Investigated the effects of epigenetics including gene expression and histone modifications on salt priming stress response in soybean
- · Explored the genes that marked by H3K4me3 in soybean nodules
- · Helped with the fundamental experiments on molecular biotechnology

RESEARCH ASSISTANT | THE CHINESE UNIVERSITY OF HONG KONG (SHENZHEN RESEARCH INSTITUTE) | 2014.10 - 2015.05

· Helped with epigenetics data analysis

Teaching Experience

TEACHING ASSISTANT | THE CHINESE UNIVERSITY OF HONG KONG | 2015.08 – 2019.08

- Assisted lectures to prepare materials and teach in the undergraduate course
- Invigilated and graded examinations

GRADUATE RESEARCH CONSULTANTS (GRC) | UNITED COLLEGE, THE CHINESE UNIVERSITY OF HONG KONG | 2016.08 – 2017.08

- Assisted professor to discuss with undergraduate students
- · Provided group tutoring

Skills & Abilities

PROGRAMMING

· Bash/Shell, R, Python, MySQL, C, C++, HTML5, Java

ANALYSIS TECHNIQUES

· Support Vector Machines, K-means Clustering, Decision Trees

MUTIL-OMICS

• Bioinformatics and genomics analysis of plant epigenetics (including WGBS, ChIP-seq, smRNA-seq, ATAC-seq, Nanopore Direct RNA-seq and RNA-seq)

LANGUAGES

· Fluent in Chinese and English

Honors and Awards

Oral presentation | 2020-2021 Science Faculty Postgraduate Research Day, CUHK | Jan 2021 Best Presentation Award | SKLA/ IPMBAB Seminar Series 2020, CUHK | Nov 2020

Winner of The Young Scholar Competition | WUN Symposium cum Research Summit on Impacts of Grain Legume Research and Development in Developing Countries, CUHK | Jun 2017

Publications

Liu A, Xiao Z, Li M-W, Wong F-L, Yung W-S, Ku Y-S, <u>Wang Q</u>, Wang X, Xie M, Yim AK-Y, *et al.* 2019. Transcriptomic reprogramming in soybean seedlings under salt stress. *Plant, Cell & Environment* 42: 98–114.

<u>Wang Q*</u>, Yung W*, Wang Z, Lam H. 2020. The histone modification H3K4me3 marks functional genes in soybean nodules. *Genomics* 112: 5282–5294.

Huang M, Zhang L, Zhou L, Wang M, Yung WS, Wang Z, Duan S, Xiao Z, <u>Wang Q</u>, Wang X, et al. 2021. An expedient survey and characterization of the soybean JAGGED 1 (GmJAG1) transcription factor binding preference in the soybean genome by modified ChIPmentation on soybean protoplasts. *Genomics* 113: 344–355.

Yung W, Li M, Sze C, <u>Wang Q</u>, Lam H. 2021. Histone modifications and chromatin remodelling in plants in response to salt stress. *Physiologia Plantarum*: ppl.13467.

<u>Wang Q</u>*, Bao X*, Chen S*, Zhong H*, Liu Y, Zhang L, Xia Y, Kragler F, Luo M, Li XD, *et al.* 2021. AtHDA6 functions as an H3K18ac eraser to maintain pericentromeric CHG methylation in Arabidopsis thaliana. *Nucleic Acids Research*: 1–13.