

Dr. Huanwei Wang

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Work Experience

University of Queensland, Australia Mar/2021-present
Postdoctoral Research Fellow
Supervised by Dr. Loic Yengo with Prof. Peter Visscher
GeneDock Inc., China Apr/2016-Mar/2017
Bioinformatics engineer

Education

University of Queensland, Australia Apr/2017-July/2022
Ph.D., Quantitative Genetics
Supervised by Prof. Jian Yang and Dr. Allan McRae
Shanghai Jiao Tong University, China Sep/2012-Dec/2015
M.S., Biochemistry and Molecular Biology
Supervised by Prof. Kankan Wang
Zhejiang University, China Sep/2008-Jun/2012
B.S., Pharmaceutical Sciences

Publications

1. Adrian I. Campos, Shinichi Namba, Shu-Chin Lin, Kisung Nam, Julia Sidorenko, **Huanwei Wang**, Yoichiro Kamatani, The Biobank Japan Project, Ling-Hua Wang, Seunggeun Lee, Yen-Feng Lin, Yen-Chen Anne Feng, Yukinori Okada, Peter Visscher, Loic Yengo.. Boosting the power of genome-wide association studies within and across ancestries by using polygenic scores. *Nature Genetics*, 2023.
2. Gibran Hemani, Joseph E Powell, **Huanwei Wang**, Konstantin Shakhbazov, Harm-Jan Westra, Tonu Esko, Anjali K Henders, Allan F McRae, Nicholas G Martin, Andres Metspalu, Lude Franke, Grant W Montgomery, Michael E Goddard, Greg Gibson, Jian Yang, Peter M Visscher. Phantom epistasis between unlinked loci. *Nature*, 2021, 596 (7871), E1-E3.

Update: 27/Sep/2023

3. Jian Zeng, Angli Xue, Longda Jiang, Luke R Lloyd-Jones, Yang Wu, **Huanwei Wang**, Zhili Zheng, Loic Yengo, Kathryn E Kemper, Michael E Goddard, Naomi R Wray, Peter M Visscher, Jian Yang. Widespread signatures of natural selection across human complex traits and functional genomic categories. *Nature communications*, 2021, 12 (1), 1-12.
4. Joana A. Revez, Tian Lin, Zhen Qiao, Angli Xue, Yan Holtz, Zhihong Zhu, Jian Zeng, **Huanwei Wang**, Julia Sidorenko, Kathryn E. Kemper, Anna A. E. Vinkhuyzen, Julanne Frater, Darryl Eyles, Thomas H. J. Burne, Brittany Mitchell, Nicholas G. Martin, Gu Zhu, Peter M. Visscher, Jian Yang, Naomi R. Wray, John J. McGrath. Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. *Nature communications*, 2020, 11(1), p. 1647.
5. Yang Wu, Ting Qi, **Huanwei Wang**, Futao Zhang, Zhili Zheng, Jennifer E. Phillips-Cremins, Ian J. Deary, Allan F. McRae, Naomi R. Wray, Jian Zeng, Jian Yang. Promoter-anchored chromatin interactions predicted from genetic analysis of epigenomic data. *Nature communications*, 2020. 11(1): p. 2061.
6. Luke R. Lloyd-Jones, Jian Zeng, Julia Sidorenko, Loic Yengo, Gerhard Moser, Kathryn E. Kemper, **Huanwei Wang**, Zhili Zheng, Reedik Magi, Tonu Esko, Andres Metspalu, Naomi R. Wray, Michael E. Goddard, Jian Yang, Peter M. Visscher. Improved polygenic prediction by Bayesian multiple regression on summary statistics. *Nature communications*, 2019, 10(1), p. 5086.
7. **Huanwei Wang**, Futao Zhang, Jian Zeng, Yang Wu, Kathryn E. Kemper, Angli Xue, Min Zhang, Joseph E. Powell, Michael E. Goddard, Naomi R. Wray, Peter M. Visscher, Allan F. McRae, Jian Yang. Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank. *Science Advances*, 2019, 5(8), p.eaaw3538. (first author)
8. Yizhen Li, **Huanwei Wang**, Xiaoling Wang, Wen Jin, Yun Tan, Hai Fang, Saijuan Chen, Zhu Chen, and Kankan Wang. Genome-wide studies identify a novel interplay between AML1 and AML1/ETO in t(8;21) acute myeloid leukemia. *Blood*, 2015; 127(2): 233-242. (co-first author).
9. Hui Zhang, Jianqing Mi, Hai Fang, Zhao Wang, Chun Wang, Lin Wu, Bin Zhang, Mark Minden, Wentao Yang, **Huanwei Wang**, Junmin Li, Xiaodong Xi, Saijuan Chen, Ji Zhang, Zhu Chen, and Kankan Wang. Preferential eradication of acute myelogenous leukemia stem cells by fenretinide. *Proc. Natl. Acad. Sci. U. S. A.*, 2013; 110: 5606-5611.

Google scholar: <https://scholar.google.com/citations?user=B8z18fgAAAAJ&hl=en>

Conferences

1. Quantification of the contribution of ultra-rare coding variants to trait heritability (oral presentation). UQ Centre for Genetic and Genomics Symposium 2022. Brisbane, Australia.
2. Quantification of the contribution of ultra-rare coding variants to trait heritability (oral presentation). UQ Early Career Researcher Symposium 2022. Brisbane, Australia.
3. Quantification of the contribution of ultra-rare coding variants to trait heritability (oral presentation and runner-up award for oral presentation <5 years post PhD). GeneMappers Conference Virtual 2021.
4. Integrating the genetic and environmental information to improve the phenotype prediction for body mass index (Poster presentation). The 6th International Conference of Quantitative Genetics Virtual 2020.
5. Genotype-by-environment interactions inferred from genetic effects on phenotypic variability in the UK Biobank (Poster presentation). Gordon Research Conference Quantitative Genetics and Genomics 2019. Tuscany, Italy.
6. Quantifying the inflation in test-statistics for epistasis due to imperfect tagging using whole-genome sequence data (lightning talk). GeneMappers Conference 2018. Queensland, Australia.

Peer review

One manuscripts for Nature Genetics, two manuscripts for Nature Communications, one manuscript for American Journal of Human Genetics, one for BMC Medicine, and one for G3: Genes, Genomes, Genetics.

Teaching

1. Prediction accuracy and pitfall (teaching instructor). UQ Genetic and Genomics Winter School 2022. Queensland, Australia.
2. Prediction accuracy and pitfall (teaching instructor). UQ Genetic and Genomics Winter School 2023. Queensland, Australia.

Supervision

- Research project course for an undergraduate student, SCIE3220 2018, UQ
- Literature review course for a master student, BIOX7100 2023, UQ

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