

Dr. Huanwei Wang

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Brisbane, Queensland, Australia

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Work Experience

QIMR Berghofer Medical Research Institute, Australia Aug/2024-present

Research Officer

Supervised by A/Prof. Matthew Law and Prof. Stuart Macgregor

University of Queensland, Australia

Adjunct Associate Lecturer/Fellow Aug/2024-present

Postdoctoral Research Fellow Mar/2021-July/2024

Supervised by A/Prof. Loic Yengo and Prof. Peter Visscher

GeneDock Inc., China Apr/2016-Mar/2017

Bioinformatics engineer

Education

University of Queensland, Australia Apr/2017-July/2021

Ph.D., Quantitative Genetics

Supervised by Prof. Jian Yang and A/Prof. 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. **Huanwei Wang**, Pierrick Wainschtein, Julia Sidorenko, Mulusew Wli, Yuanxiang Zhang, Kathryn E. Kemper, Zhili Zheng, Valentin Hivert, Jian Zeng, Michael E. Goddard, Peter Visscher, Loic Yengo. Pitfalls in estimating the contribution of ultra-rare genetic variants to the heritability of complex traits. Under preparation. 2024.

2. Kathryn E. Kemper, Julia Sidorenko, **Huanwei Wang**, Ben J. Hayes, Naomi R. Wray, Loic Yengo, Matthew C. Keller, Mike E. Goddard, Peter M. Visscher. Genetic

influence on within-person longitudinal change in anthropometric traits in the UK Biobank. *Nature Communications*, 2024, 15(1), p1-11.

3. Angli Xue, Zhihong Zhu, **Huanwei Wang**, Longda Jiang, Peter M. Visscher, Jian Zeng, Jian Yang. Unravelling the complex causal effects of substance use behaviours on common diseases. *Communications Medicine*, 2024, 4 (1), 43.
4. 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, 55 (10), 1769-1776.
5. 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.
6. 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.
7. 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.
8. 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.
9. 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.

10. **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)

11. 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).

12. 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. Pitfalls in estimating SNP-based heritability for singleton genetic variants, Cold Spring Harbor Laboratory – “Biology of Genomes” meeting 2024, New York, USA.
2. Quantification of the contribution of ultra-rare coding variants to trait heritability (oral presentation), UQ Centre for Genetic and Genomics Symposium 2022, Brisbane, Australia.
3. Quantification of the contribution of ultra-rare coding variants to trait heritability (oral presentation) , UQ Early Career Researcher Symposium 2022, Brisbane, Australia.
4. 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.
5. 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.
6. 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.

7. 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

For Nature Genetics (1 manuscript), Nature Communications (4), Science Advances (1), American Journal of Human Genetics (1), BMC Medicine (1), G3: Genes, Genomes, Genetics (1), and Bioinformatics (1).

Teaching

1. Navigating the UK Biobank Research Analysis Platform, 1st Australian UK Biobank Symposium, 2024, Brisbane, Australia.
2. Prediction accuracy and pitfall, UQ Genetic and Genomics Winter School, 2022 and 2023, Brisbane, Australia.

Supervision

1. Literature review course for a master student, BIOX7100 2024, UQ
2. Research project course for an undergraduate student, SCIE3220 2018, UQ

Service

1. UQ IMB Early-Mid Career Researcher Association (EMCRA) committee member, 2023 and 2024
2. UQ IMB Centre for Population and Disease Genomics (CPDG) teaching workshop coordinator, 2024