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Education & Employment

09/2005 - 07/2009 B.S.E., Bioinformatics, Huazhong University of Science and Technology, Hubei, PRC;

09/2009 - 07/2014 Ph.D., Genetics, Fudan University, Shanghai, PRC;

Thesis: Mutation, function, and evolution of structural variation in human genome. Supervisor: Prof. Li (Felix) Jin;

07/2014 - 10/2015 Research associate, Ministry of Education Key Laboratory of Contemporary Anthropologyb, Jin Lab, Fudan University, PRC;

11/2015 - present Postdoctoral fellowship, Department of Computational Medicine and Bioinformatics, Ryan E. Mills Lab, University of Michigan, Ann Arbor, MI, USA.

Honors & Awards

2010 Academic Scholarships, 1st Class, Fudan University, Shanghai;
2011 Academic Scholarships, 2nd Class, Fudan University, Shanghai;
2012 Academic Scholarships, 2nd Class, Fudan University, Shanghai;
2013 **The 4th Research Funding of National Key Disciplines for Outstanding PhD Students**: Formation, mutation, and evolution of copy number variations in human genome. Ministry of Education of the People's Republic of China;
2013 **Outstanding Graduate Students (2013),** Fudan University, Shanghai;
2013 **National Scholarship for Graduate Students (2013),** Ministry of Education of the People's Republic of China;
2014 **Shanghai Outstanding Graduates (2014),** Shanghai Municipal Education

Commission;

2016 **Shanghai Outstanding Dissertation of Ph.D. (2015),** Shanghai Municipal Education Commission.

Teaching

09/2010 - 01/2011 Journal club for Human Evolution. Teaching Assistant. School of Life Sciences, Fudan University.

02/2011 - 06/2011 Human Evolutionary Genetics. Teaching Assistant. School of Life Sciences, Fudan University.

02/2012 - 06/2012 Human Evolutionary Genetics. Teaching Assistant. School of Life Sciences, Fudan University.

09/2012 - 01/2013 Human Evolution. Teaching Assistant. School of Life Sciences, Fudan University.

02/2013 - 06/2013 Human Evolutionary Genetics. Teaching Assistant. School of Life Sciences, Fudan University.

Journal Reviews

03/2018 5th International Conference on Algorithms for Computational Biology
05/2018 Genome Research

Presentations & Posters

1. Zhou W, Emery SB, Flasch DA, Wang Y, Kwan KY, Moran JV, Kidd JM, Mills RE. Refining the ability to detect human-specific LINE-1 insertions using long-read sequencing technology. *The American Society of Human Genetics*, 2018.
2. Zhou W, Chapman MR, Yeh G. Stress-induced Alzheimer's disease. *The 16th Annual Pathology Research Symposium*, 2017.
3. Zhou W, Emery SB, Flasch DA, Wang Y, Kwan KY, Moran JV, Kidd JM, Mills RE. PALMER: A novel pre-masking method for detecting mobile element insertions using long-read sequencing technology. *The American Society of Human Genetics*, 2017. **Reviewers' Choice Abstract**.
4. Zhou W. Predictive model for inflammation grades of chronic hepatitis B: large-scaled analysis on clinical parameters and gene expressions. *The 26th Conference of The Asian Pacific Association for The Study Of The Liver (APASL)*, 2017.

5. Zhou W, Jin L. Whole genome functional traits and evolutionary clues between Copy Number Variations and Segmental Duplications in human genome. *The Annual Meeting of Shanghai Genetics Society*, 2013. **Speaker**.
6. Zhou W, Jin L, Zhang F. Increased genome instability in human DNA segments with closely spaced repeats. *The Annual Meeting of Shanghai Genetics Society*, 2012. **1st Poster Award**.
7. Zhou W, Zhang F, Jin L. Increased genome instability in human DNA segments with short low-copy repeats. *The 13th International Meeting on Human Genome Variation and Complex Genome Analysis*, 2012.

Peer-Reviewed Journals and Publications

1. Li Y, Liu X, Ma Y, Wang Y, **Zhou W**, Hao M, Yuan Z, Liu J, Xiong M, Shugart YY, Wang J, Jin L. 2018. knnAUC: an open-source R package for detecting nonlinear dependence between one continuous variable and one binary variable. ***BMC Bioinformatics.*** http://doi.org/10.1186/s12859-018-2427-4.

2. **Zhou W***, Wang Y*, Fujino M, Shi L, Jin L, Li X, Wang J. 2017. A standardized fold change (SFC) method for microarray differential expression analysis used to reveal genes involved in acute rejection in murine allograft models. ***FEBS Open Bio.*** doi: 10.1002/2211-5463.12343.

3. McConnell MJ*, Moran JV*, et al. Brain Somatic Mosaicism Nework. 2017. Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. ***Science***. doi: 10.1126/science.aal1641

4. **Zhou W***, Ma Y*, Zhang J, Hu J, Zhang M, Wang Y, Li Y, Wu L, Pan Y, Zhang Y, Zhang X, Zhang X, Zhang Z, Zhang J, Li H, Lu L, Jin L, Wang J, Yuan Z, Liu J. 2017. Predictive model for inflammation grades of chronic hepatitis B: Large-scale analysis of clinical parameters and gene expressions. ***Liver International***. doi: 10.1111/liv.13427.

5. Zhang L, Wang J, Zhang C, Li D, Carvalho C, Ji H, Xiao J, Wu Y, **Zhou W**, Wang H, Jin L, Luo Y, Wu X, Lupski JR, Zhang F, Jiang Y. 2017. Efficient CNV breakpoint analysis reveals unexpected structural complexity and correlation of dosage-sensitive genes with clinical severity in genomic disorders. ***Human Molecular Genetics***. doi: 10.1093/hmg/ddx102.

6. Wu N*, Ming X*, Xiao J*, et al. 2015. TBX6 Null Variants and a Common Hypomorphic Allele in Congenital Scoliosis. ***New England Journal of Medicine***. doi: 10.1056/NEJMoa1406829.

7. Chen L, **Zhou W**, Zhang L, Zhang F. 2014. Genome architecture and its roles in human copy number variation. ***Genomics & Informatics***. 2014, 12(4):136-144.

8. Chen L*, **Zhou W***, Zhang C, Lupski JR, Jin L, Zhang F. 2014. CNV instability associated with DNA replication dynamics: evidence for replicative mechanisms in CNV mutagenesis. ***Human Molecular Genetics***. doi: 10.1093/hmg/ddu572. (*Co-first authors)

9. Peng Z, **Zhou W**, Fu W, Du R, Jin L, Zhang F. 2014. Correlation between frequency of non-allelic homologous recombination and homology properties: evidence from homology-mediated CNV mutations in the human genome. ***Human Molecular Genetics***. doi: 10.1093/hmg/ddu533.

10. Chen Y, Guo L, Chen J, Zhao X, **Zhou W**, Zhang C, Wang J, Jin L, Pei D, Zhang F. 2014 Genome-wide CNV analysis in mouse induced pluripotent stem cells reveals dosage effect of pluripotent factors on genome integrity. ***BMC Genomics***. doi:10.1186/1471-2164-15-79

11. **Zhou W***, Zhang F*, Chen X, Shen Y, Lupski JR, Jin L. 2013. Increased genome instability in human DNA segments with self-chains: homology-induced structural variations via replicative mechanisms. ***Human Molecular Genetics***. doi: 10.1093/hmg/ddt113.

12. Lin R, Wang X, **Zhou W**, Fu W, Wang Y, Huang W, Jin L. 2011. Association of Polymorphisms in the Solute Carrier Organic Anion Transporter Family Memb er 1B1 Gene with Essential Hypertension in the Uyghur Population. ***Annals of human Genetics***. doi: 10.1111/j.1469-1809.2010.00622.x.

13. Lin R, Fu W, **Zhou W**, Wang Y, Wang X, Huang W, Jin L. 2011. Association of Heme Oxygenase-1 Gene Polymorphisms with Essential Hypertension and Blood Pressure in the Chinese Han Population. ***Genetic Testing and Molecular Biomarkers***. doi: 10.1089/gtmb.2010.0103.

14. Lin R, Wang X, **Zhou W**, Fu W, Wang Y, Huang W, Jin L. 2011. Association of a BLVRA Common Polymorphism with Essential Hypertension and Blood Pressure

in Kazaks. ***Clinical and Experimental Hypertension***. doi: 10.3109/10641963.2010.531854.

15. **Zhou W**, Tan J. 2010. Dental Anthropology Suggests Southeast Asian Origins amongst the Jomon People of Japan. ***COM. on C.A***. doi: 10.4236/coca.2010.41012.

16. **Zhou W**. 2010. Genetic and environmental factors of pathogeny: a population genetics view. ***COM. on C.A***. doi: 10.4236/coca.2010.41021.