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Education and Employment

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

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

09/2009 - 07/2014 Ph.D., Genetics, Supervisor: Prof. Li (Felix) Jin, Fudan University, Shanghai, PRC; Thesis: Mutation, function, and evolution of structural variations in human genome.

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

Grants

Current Grants

5 U01 MH106892-05: 2/3 Schizophrenia Genetics and Brain Somatic Mosaicism NIH-DHHS-US- 14-PAF07285
Key Personnel with Effort (Principal Investigator: Moran, John V)
05/2015-01/2020. $3,860,653 ($736,465)

1 U41 HG007497-01: Comprehensive Detection of Haplotype-Resolved Structural Variation in Human Genomes NIH-DHHS-US through a consortium with Jackson Laboratory- 18-PAF07010
Key Personnel with Effort (PI-on-Sub: Mills, Ryan Edward)
04/2019-03/2023. $635,600

Submitted Grants

Chan-Zuckerberg Initiative, Essential Open Source Software for Science: Applications for genome processing and analysis of long-read sequence data
Key Personnel with Effort (Principal Investigator: Mills, Ryan Edward)
08/2019-07/2020. $95,021 (turned down)

Past Grants

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.
08/2013-08/2014. $8,000

Teaching Activity

07/2019 - 08/2019 Mentoring high school student (Thomas Chang) in Mills Lab.

02/2013 - 06/2013 Human Evolutionary Genetics. Teaching Assistant. Fudan University.

09/2012 - 01/2013 Human Evolution. Teaching Assistant. Fudan University.

02/2012 - 06/2012 Human Evolutionary Genetics. Teaching Assistant. Fudan University.

02/2011 - 06/2011 Human Evolutionary Genetics. Teaching Assistant. Fudan University.

09/2010 - 01/2011 Journal club of Human Evolution. Teaching Assistant. Fudan University.

Honors and Awards

2019 *Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research*, semifinalist, the 69th Annual Meeting of the American Society of Human Genetics.

OGPS Postdoctoral Travel Award, University of Michigan Medical School.

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

2014 *Shanghai Outstanding Graduates*, Shanghai Municipal Education Commission.

2013 *National Scholarship for Graduate Students*, Ministry of Education of the People's Republic of China.

Outstanding Graduate Students, Fudan University.

2012 Academic Scholarships, 2nd Class, Fudan University.

2011 Academic Scholarships, 2nd Class, Fudan University.

2010 Academic Scholarships, 1st Class, Fudan University.

Journal Reviews

12/2019 Nucleic Acid Research

05/2018 Genome Research

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

Presentations & Posters

1. Zhou W, Mills RE. Refining polymorphic retrotransposon insertions in human genomes. *The American Society of Human Genetics*, 2019. Platform Presentation.

2. 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.

3. Zhou W, Chapman MR, Yeh G. Stress-induced Alzheimer's disease. *The 16th Annual Pathology Research Symposium*, 2017.

4. 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.

5. 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.

6. 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. Presentation.

7. 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.

8. 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. Zhou W, Emery SB, Flasch DA, Wang Y, Kwan KY, Kidd JM, Moran JV, and Mills RE: Identification and characterization of occult human-specific LINE-1 insertions using long-read sequencing technology. Accepted, *Nucleic Acid Research*.

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

3. Zhou W*, Wang Y*, Fujino M, Shi L, Jin L, Li X, Wang J: 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.* 2018. doi: 10.1002/2211-5463.12343.

4. McConnell MJ*, Moran JV*, Abyzov A, Akbarian S, Bae T, Cortes-Ciriano I, Erwin JA, Fasching L, Flasch DA, Freed D, Ganz J Jaffe AE, Kwan KY, Kwon M, Lodato MA, Mills RE, Paquola ACM, Rodin RE, Rosenbluh C, Sestan N, Sherman MA, Shin JH, Song S, Straub RE, Thorpe J, Weinberger DR, Urban AE, Zhou B, Gage FH, Lehner T, Senthil G, Walsh CA, Chess A, Courchesne E, Gleeson JG, Kidd JM, Park PJ, Pevsner J, Vaccarino FM, and Brain Somatic Mosaicism Nework: Intersection of diverse neuronal genomes and neuropsychiatric disease: The Brain Somatic Mosaicism Network. *Science*. 2017. doi: 10.1126/science.aal1641.

5. 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: Predictive model for inflammation grades of chronic hepatitis B: Large-scale analysis of clinical parameters and gene expressions. *Liver International*. 2017. doi: 10.1111/liv.13427.

6. 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: Efficient CNV breakpoint analysis reveals unexpected structural complexity and correlation of dosage-sensitive genes with clinical severity in genomic disorders. *Human Molecular Genetics*. 2017. doi: 10.1093/hmg/ddx102.

7. Wu N*, Ming X*, Xiao J*, Wu Z, Chen X, Shinawi M, Shen Y, Yu G, Liu J, Xie H, Gucev ZS, Liu S, Yang N, Al-Kateb H, Chen J, Zhang J, Hauser N, Zhang T, Tasic V, Liu P, Su X, Pan X, Liu C, Wang L, Shen J, Shen J, Chen Y, Zhang T, Zhang J, Choy KW, Wang J, Wang Q, Li S, Zhou W, Guo J, Wang Y, Zhang C, Zhao H, An Y, Zhao Y, Wang J, Liu Z, Zuo Y, Tian Y, Weng X, Sutton VR, Wang H, Ming Y, Kulkarni S, Zhong TP, Giampietro PF, Dunwoodie SL, Cheung SW, Zhang X, Jin L, Lupski JR, Qiu G, Zhang F: TBX6 Null Variants and a Common Hypomorphic Allele in Congenital Scoliosis. *New England Journal of Medicine*. 2015. doi: 10.1056/NEJMoa1406829.

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

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

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

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

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

13. Lin R, Wang X, Zhou W, Fu W, Wang Y, Huang W, Jin L: Association of polymorphisms in the solute carrier organic anion transporter family member 1B1 gene with essential hypertension in the Uyghur Population. *Annals of human Genetics*. 2011. doi: 10.1111/j.1469-1809.2010.00622.x.

14. Lin R, Fu W, Zhou W, Wang Y, Wang X, Huang W, Jin L: Association of heme oxygenase-1 gene polymorphisms with essential hypertension and blood pressure in the Chinese Han population. *Genetic Testing and Molecular Biomarkers*. 2011. doi: 10.1089/gtmb.2010.0103.

15. Lin R, Wang X, Zhou W, Fu W, Wang Y, Huang W, Jin L: Association of a BLVRA common polymorphism with essential hypertension and blood pressure in Kazaks. *Clinical and Experimental Hypertension*. 2011. doi: 10.3109/10641963.2010.531854.

16. Zhou W, Tan J: Dental anthropology suggests southeast Asian origins amongst the Jomon people of Japan. *Communication on Contemporary Anthropology*. 2010. doi: 10.4236/coca.2010.41012.

17. Zhou W, Genetic and environmental factors of pathogeny: a population genetics view. *Communication on Contemporary Anthropology*. 2010. doi: 10.4236/coca.2010.41021.

Non-Peer-Reviewed Journals and Publications

1. Zook JM, Hansen NF, Olson ND, Chapman LM, Mullikin JC, Xiao C, Sherry S, Koren S, Phillippy AM, Boutros PC, Sahraeian SME, Huang V, Rouette A, Alexander N, Mason CC, Hajirasouliha IC, Ricketts CC, Lee J, Tearle R, Fiddes IT, Barrio AM, Wala J, Carroll A, Ghaffari N, Rodriguez OL, Bashir A, Jackman S, Farrell JJ, Wenger AM, Alkan C, Soylev A, Schatz MC, Garg S, Church G, Marschall T, Chen K, Fan X, English AC, Rosenfeld JD, Zhou W, Mills RE, Sage JM, Davis JR, Kaiser MD, Oliver JS, Catalano AP, Spies N, Chaisson MJP, Sedlazeck FJ, Salit M, and Genome in a Bottle Consortium: A robust benchmark for germline structural variant detection. *BioRxiv*. 2019. doi.org/10.1101/664623. In revision, *Nature Biotechnology*.

2. Zhou W, Boyle A and Mills RE: Refining polymorphic retrotransposon insertions in human genomes. In preparation.

3. Dayama G, Zhou W, Prado J, Marques-Bonet T, Mills RE: Evolution of nuclear mitochondrial insertions in the whole genomes of primates. In preparation.

4. Li Y, Liu X, Ma Y, Liang M, Wang Y, Hao M, Zhang H, Zhou W, Yuan Z, Liu J, Xiong M, Shugart YY, Wang J, Jin L: Nonlinear Prediction Distance Independence Test: an efficient method for nonlinear dependence of two continuous variables. In preparation.