Curriculum Vitae

Wei-Chen Zhou, Ph.D.

Postdoctoral Research Fellow
Department of Computational Medicine & Bioinformatics,
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Education & Position

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

09/2009 - 07/2014 Ph.D. in Genetics, Fudan University, China;

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

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

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

Teaching Experience

09/2010 - 01/2011 Teaching Assistant. [Journal club for Human Evolution] for undergraduate & graduate students. School of Life Sciences, Fudan University.

02/2011 - 06/2011 Teaching Assistant. [Human Evolutionary Genetics] for undergraduate & graduate students. School of Life Sciences, Fudan University.

02/2012 - 06/2012 Teaching Assistant. [Human Evolutionary Genetics] for undergraduate & graduate students. School of Life Sciences, Fudan University.

09/2012 - 01/2013 Teaching Assistant. [Human Evolution] for undergraduate students. School of Life Sciences, Fudan University.

02/2013 - 06/2013 Teaching Assistant. [Human Evolutionary Genetics] for undergraduate & graduate students. School of Life Sciences, Fudan University.

Fellowship & Awards

2010 Academic Scholarships, 1st Class, Fudan University;

2011 Academic Scholarships, 2nd Class, Fudan University;

2012 Academic Scholarships, 2nd Class, Fudan University;

2013 **the 4th Research Funding of National Key Disciplines for Outstanding PhD Students**, Fudan university: Formation, mutation, and evolution of copy number variations in human genome.

2013 **Outstanding Graduate Students (2013),** Fudan University

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

Presentations & Posters

1. Weichen Zhou, Li Jin. 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.

2. Weichen Zhou, Li Jin, Feng Zhang. Increased genome instability in human DNA segments with closely spaced repeats. The Annual Meeting of Shanghai Genetics Society. 2012. POSTER. Poster Award 1st.

3. Weichen Zhou, Feng Zhang, Li Jin. Increased genome instability in human DNA segments with short low-copy repeats. The 13th International Meeting on Human Genome Variation and Complex Genome Analysis (HGV2012). Poster.

Publications

Peer-Reviewed Journals and Publications

1. **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. (*Co-first authors)

2. 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.*** pii: ddu572. (*Co-first authors)

3. 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.

4. 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.

5. Co-author. 2014. TBX6 Null Variants and a Common Hypomorphic Allele in Congenital Scoliosis. ***New England Journal of Medicine***. doi: 10.1056/NEJMoa1406829.

6. 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

7. 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.

8. 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.

9. 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.

10. Zhou W, Tan J. 2010. Dental Anthropology Suggests Southeast Asian Origins amongst the Jomon People of Japan. ***COM. on C.A.*** 4:e12, 2010

Non-Peer Reviewed Journals and Publications

11. **Zhou W***, Ma Y*, Zhang J, Pan Y, Liu J, Wang J, Jin L. Predictive model for inflammation grades of chronic hepatitis B: large-scaled analysis on clinical parameters and gene expressions. ***Under Review***.

12. **Zhou W***, Wang Y*, Wang J, Li X, Jin L. A novel standardized fold change method for microarray mRNA differential expression analysis. ***Under Review***.

13. Zhang L, Wang J, Zhang C, Li D, Xiao J, **Zhou W**, Carvalho CM, Liu C, Luo Y, Jin L, Lupski JR, Zhang F, Jiang Y. Comprehensive breakpoint analyses for genomic disorders reveal the correlation of CNV size and complexity with clinical severity at the PLP1 locus. ***Under Review***.

14. Chen Y, DongZ, Guan M, Zhang C, Li Y, Wang Y, Du A, Ma Y, **Zhou W**, Guo S, Jin L, Zou H, Zhang F, Wang J. Genome-wide CNV analysis identifies deletion polymorphisms upstream of autophagy gene IRGM as a risk factor for Gout. ***Under Review***.