Curriculum Vitae

Wenfei JIN, PhD

Associate Professor (1000 Young Talent)
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Self-introduction

Dr. Wenfei Jin received his bachelor's degree from Zhengzhou University in 2006. He received his Ph.D. in Computational biology from Chinese Academy of Sciences and Max Planck Society Partner Institute for Computational Biology (PICB) with Prof. Li Jin (CAS member) and Prof. Shuhua Xu in 2012. Dr. Jin completed his Postdoc Fellow in systems biology at National Institutes of Health (NIH) with Dr. Keji Zhao in 2017. He was selected to "National 1000 young talents program of China" and joined in Southern University of Science and Technology (SUSTech) in 2017. Dr. Jin works on population genetics and precision medicine related field since his Ph.D. program. He has published >20 research articles and book chapters, including first/co-fist author articles on Nature, AJHG, Genome Res, Genome Biol and HMG. Dr. Jin and his colleagues developed single cell DNase-seq (scDNase-seq) that could provide key regulatory information for precision medicine (Jin, et.al, 2015 Nature). Dr. Jin is the recipient of many honors and awards including Springer Theses, CAS Excellent Doctoral Dissertation and NHLBI Orloff Award. Dr. Jin is especially interested in promoting the applications of single cell sequencing in clinical diagnosis and medical consultation.

Research interests

Dr. Jin's lab is interested in identifying genetic/epigenetic changes identifying genetic/epigenetic changes that drive oncogenesis, and developing disease risk prediction model for precision medicine. The long-term goal of the lab is to develop efficient personalized treatment for cancers based on patients' genetic background. In near future, the lab will focus on investigating genetic/epigenetic heterogeneity and micro-evolution of cancer cells using single cell sequencing related technologies.

Professional Experience

Mar.2017-present	Associate Professor, Southern University of Science and Technology
Jan.2013-Mar.2017	Postdoc fellow, National Institutes of Health (NIH) Mentor: Dr. Keji Zhao
Jan.2012-Dec.2012	Assistant researcher, Chinese Academy of Sciences and Max Planck Society Partner Institute for Computational Biology (PICB), SIBS, CAS

Education

Sept.2006-Dec.2011	Ph.D. in Computational Biology, PICB and University of Chinese Academies of Sciences
	Supervisors: Prof. Felix Li Jin (CAS member) and Dr. Shuhua Xu
Feb.2006-April.2006	Intern, Institute of Biochemistry and Cell Biology, SIBS, CAS Mentors: Prof. Mofang Liu and Prof. Enduo Wang (CAS member)

Sept.2001-July.2006   B.Sc. in Biotechnology, Zhengzhou University, China

Awards and Honors

2017   National 1000 Young Talents Program, China
2016   Orloff innovation Awards (Single cell DNase-seq), NHLBI, USA
2016   Fellows Award for Research Excellence (FARE), NIH, USA
2014   Springer Theses, Springer
2013   Excellent Doctoral Dissertation, Chinese Academy of Sciences
2012   First-author Awards, PICB
2012   Outstanding Graduate Award, University of Chinese Academy of Sciences
2012   SIBS-Eli Lilly Outstanding Ph.D. Thesis Awards, Eli Lilly
2011   Travel Awards, 12th International Congress of Human Genetics (ICHG)/61th ASHG
2011   Pfizer Awards, Shanghai Institutes for Biological Sciences
2010   Di'ao scholarship Awards, Chinese Academy of Sciences

Selected Publications

[1] **Jin W***, Tang Q*, Wan M, Cui K, Zhang Y, Ren G, Ni B, Sklar J, Przytycka T, Childs R, Levens D, Zhao K (*equal contribution). 2015. Genome-wide detection of DNase I hypersensitive sites in single cells and FFPE tissue samples. **Nature**. 528:142-146 (Highlighted by Nature Review Genetics)

[2] Kraushaar DC*, **Jin W***, Maunakea A, Abraham B, Ha M, Zhao K (*equal contribution). 2013. Genome-wide incorporation dynamics reveal distinct categories of turnover for the histone variant H3.3. **Genome Biol**. 14:R121.

[3] Hu H, Liu X, **Jin W**, Ropers HH, Wienker TF. 2015. Evaluating information content of SNPs for sample-tagging in re-sequencing projects. **Sci Rep**. 5:10247.

[4] **Jin W***, Li R*, Zhou Y, Xu S. (* equal contribution) 2014. Distribution of ancestral chromosomal segments in admixed genomes and its implications for inferring population history and admixture mapping. **Euro J Hum Genet**. 22:930-937.

[5] Qin P, Li Z, **Jin W**, Lu D, Lou H, Shen J, Jin L, Shi Y, Xu S. 2014. A panel of ancestry informative markers to estimate and correct potential effects of population stratification in Han Chinese. **Euro J Hum Genet**. 22:248-253.

[6] Wang E*, **Jin W***, Duan W*, Qiao B, Sun S, Huang G, Shi K, Jin L, Wang H (*equal contribution). 2013. Association of two variants in SMAD7 with the risk of congenital heart disease in the Han Chinese population. **PloS ONE**. 8:e72423.

[7] **Jin W**, Xu S, Wang H, Yu Y, Shen Y, Wu B, Jin L. 2012. Genome-wide detection of natural selection in African Americans pre- and post-admixture. **Genome Res**. 22:519-527.

[8] **Jin W**, Wang S, Wang H, Jin L, Xu S. 2012. Exploring population admixture dynamics via empirical and simulated genome-wide distribution of ancestral chromosomal segments. **Am J Hum Genet**. 91:849-862.

[9] **Jin W**, Qin P, Lou H, Jin L, Xu S. 2012. A systematic characterization of genes underlying both complex and Mendelian diseases. **Hum Mol Genet**. 21: 1611-1624. (F1000 highlighted)

[10] Xu S, Li S, Yang Y, Tan J, Lou H, **Jin W**, Yang L, Pan X, Wang J, Shen Y, Wu B, Wang H, Jin L. 2011. A genome-wide search for signals of high altitude adaptation in Tibetans. Mol Biol Evol. 28: 1003-1011.

[11] Lou H, Li S, Yang Y, Kang L, Zhang X, **Jin W**, Wu B, Jin L, Xu S. 2011.A map of copy number variations in Chinese populations. **PloS ONE**. 6:e27341.

[12] Hatin WI, Etemad A, **Jin W**, Qin P, Xu S, Jin L, Tan S-G, Limprasert P, Feisal MA, Rizman-Idid M. 2014. A genome wide pattern of population structure and admixture in peninsular Malaysia Malays. **HUGO J**. 8:1-18.

[13] Lou H, Li S, **Jin W**, Fu R, Lu D, Pan X, Zhou H, Ping Y, Jin L, Xu S. 2015. Copy number variations and genetic admixtures in three Xinjiang ethnic minority groups. **Euro J Hum Genet**. 23:536-542.

[14] Yan S, Wang CC, Zheng HX, Wang W, Qin ZD, Wei LH, Wang Y, Pan XD, Fu WQ, He YG, Xiong LJ, **Jin W**, Li SL, An Y, Li H, Jin L. 2014. Y chromosomes of 40% Chinese descend from three neolithic super-grandfathers. **PloS ONE**. 9:e105691.

[15] Xu S, Yin X, Li S, **Jin W**, *et al*. 2009. Genomic dissection of population substructure of Han Chinese and its implication in association studies. **Am J Hum Genet**. 85: 762-774.

[16] Xu S, **Jin W**, Jin L. 2009. Haplotype sharing analysis showing Uyghurs are unlikely genetic donors. **Mol Biol Evol**. 26: 2197-2206.

Books and Book Chapters

[1] **Jin W**. 2015. Admixture Dynamics, Natural Selection and Diseases in Admixed Populations. ISBN 978-94-017-7406-2. 114 Pages. **Springer**

[2] Xu S, **Jin W**. 2012. Population Genetics in the Genomic Era. Studies in Population Genetics, M. Carmen Fusté (Ed.). ISBN 978-953-51-0588-6. **Intech**.