



**Chao Zhang**  
Research Associate

## Research interests

My long-term research interests involve understanding fundamental questions about human evolution, integrating multi-omic data to investigate the impact of human evolution on patterns of genetic variation and how this contributes to variable phenotypes and disease risk, and eventually advancing precision medicine of global populations in the light of human evolution.

## Education and work experience

- March 2024 – Present      Research Associate, University of Pennsylvania, US. Sarah Tishkoff Lab.
- Feb. 2019 – March 2024.    Postdoc. University of Pennsylvania, US. Sarah Tishkoff Lab.
- July 2012 - July 2018.    Ph.D. Max-Planck Independent Research Group on Population Genomics, CAS-MPG Partner Institute for Computational Biology, Chinese Academy of Sciences (CAS), China.
- July 2008–July 2012.    B.S. Yangzhou University, China.

## Honors

2018 **Lindau program Awardee**, Sino-German Science Center  
2018 **Presidential Scholarship**, UCAS, Chinese Academy of Sciences  
2018 Outstanding Graduates of Shanghai, China  
2016 PhD National Scholarship, UCAS, Chinese Academy of Sciences  
2015 and 2017 Merit Student, UCAS, Chinese Academy of Sciences

## Personal statement

My academic training and research experience have provided me with a solid background in computational biology and population genetics, and excellent skills in driving and solving scientific questions. In 2012, I started my Ph.D program and majored in computational biology. I conducted research with Dr. Shuhua Xu at PICB, Chinese Academy of Sciences, on human population genomics focusing on ethnically diverse Asian populations. With six years of training, I gained expertise in statistical programming, genomic data (mainly whole-genome sequencing data) analysis and human evolution. I conducted several projects which were published in high-profile journals. I contributed to the construction of the evolutionary history and identification of the adaptive variants for the Tibetan highlander populations including the Tibetan and Sherpa people, by using deep WGS data for the first time (Zhang et al., *Genome Biology* 2017, Lu et al., *AJHG* 2016, and Deng and Zhang et al., *National Science Review* 2019). I was involved in the construction of the first human genetic variant database in China, which was awarded as the top ten bioinformatics advances, and among the top ten bioinformatics databases in 2019 in China (Zhang et al., *Genome Biology* 2019, Zhang et al., *NAR* 2017, and Gao and Zhang et al., *NAR* 2019). I also contributed to the genomic diversity and post-admixture adaptation in the Uyghurs (Pan and Zhang et al., *National Science Review* 2021). In addition, I contributed to the identifying causal variants in a 7-generation Pakistan dwarf family by using WGS data (Zhang et al., *Heredity* 2018), and collaborating with lab members on other projects.

In 2019, I worked as a predoctoral researcher with Dr. Sarah Tishkoff at the University of Pennsylvania. Dr. Tishkoff is a member of the National Academy of Sciences and the National Academy of Medicine. At her lab, I have unprecedented opportunities to get access multi-omics data including genomic, transcriptomic, metabolic, phenotypic data, etc. This provides me with new conceptual and technical training in integrative genomic analyses based on which I highlighted the importance of African integrative genomics in studying precision medicine in indigenous African populations (Zhang et al., *Trends in Genetics* 2022). During the COVID pandemic, I conducted a study of global patterns of genetic variation at genes

involved in SARS- CoV-2 infection aiming to understand the genetic basis of population susceptibility to COVID from the evolutionary aspect. The project was published in the PNAS in May of 2022 (Zhang et al., PNAS 2022). I am now working on a large-scale project involving multi-omics data from diverse indigenous African populations.

I have published more than 10 scientific papers as the first or co-first author in high-profile journals including PNAS, Trends in Genetics, Genome Biology (2017/2019), National Science Review (2019/2021), Nucleic Acids Research (2018/2019), AJHG, and Nature Communications.

## Publication

1. **Chao Zhang**, Anurag Verma, Yuanqing Feng, Marcelo C. R. Melo, Michael McQuillan, Anastasia Lucas, Joseph Park, Alessia Ranciaro, Simon Thompson, William Beggs, Jibril Hirbo, Sununguko Wata Mpoloka, Gaonyadiwe George Mokone, Regeneron Genetic Center, Thomas Nyambo, Dawit Wolde Meskel, Gurja Belay, Charles Fokunang, Alfred K. Njamnshi, Sabah A. Omar, Scott M. Williams, Daniel Rader, Marylyn D. Ritchie, Cesar de la Fuente Nunez, Giorgio Sirugo, Sarah Tishkoff. Impact of natural selection on global patterns of genetic variation, and association with clinical phenotypes, at genes involved in SARS-CoV-2 infection, *PNAS*, 2022.
2. **Chao Zhang**, Mathew Hansen, Sarah Tishkoff. Advances in integrative African genomics. *Trends in Genetics*, 2021. (Feature review, Series: Celebrating the Human Genome Project and its outcomes)
3. Yuanqing Feng, Ning Xie, Fumitaka Inoue, Shaohua Fan, Joshua Saskin, **Chao Zhang**, Fang Zhang, Matthew EB Hansen, Thomas Nyambo, Sununguko Wata Mpoloka, Gaonyadiwe George Mokone, Charles Fokunang, Gurja Belay, Alfred K Njamnshi, Michael S Marks, Elena Oancea, Nadav Ahituv, Sarah A Tishkoff. Integrative functional genomic analyses identify genetic variants influencing skin pigmentation in Africans. *Nature Genetics* 2024
4. Yuwen Pan, **Chao Zhang\*(Contributed equally)**, Yan Lu, Zhilin Ning, Dongsheng Lu, Yang Gao, Yajun Yang, Yaqun Guan, Dolikun Mamatysupu, AAGC Consortium, Shuhua Xu. Genomic diversity and post-admixture adaptation in the Uyghurs. *National Science Review*, 2021.
5. **Chao Zhang**, Yan Lu, Qidi Feng, Xiaoji Wang, Haiyi Lou, Jiaojiao Liu, Zhilin Ning, Kai Yuan, Yuchen Wang, Ying Zhou, Lian Deng, Lijun Liu, Yajun Yang, Shilin Li, Lifeng Ma, Zhiying Zhang, Li Jin, Bing Su, Longli Kang and Shuhua Xu. Differentiated demographic histories and local adaptations between Sherpas and Tibetans. *Genome Biology*, 2017, 18, 115.
6. **Chao Zhang**; Yang Gao; Zhilin Ning; Yan Lu; Xiaoxi Zhang; Jiaojiao Liu; Bo Xie; Zhe Xue; Xiaoji Wang; Kai Yuan; Xueling Ge; Yuwen Pan; Chang Liu; Lei Tian; Yuchen Wang; Dongsheng Lu; Boon-Peng Hoh; Shuhua Xu. PGG.SNV: Understanding the evolutionary and medical implications of human single nucleotide variation in diverse populations. *Genome Biology*, 2019, 20, 215.
7. **Chao Zhang**, Yang Gao, Jiaojiao Liu, Zhe Xue, Yan Lu, Lian Deng, Lei Tian, Qidi Feng, Shuhua Xu. PGG.Population: A database for understanding the genomic diversity and genetic ancestry of human populations. *Nucleic Acids Research*, 2018, 46(D1):D984- D993.
8. Lian Deng, **Chao Zhang\*(Contributed equally)**, Kai Yuan, Yang Gao, Yuwen Pan, Xueling Ge, Yaoxi He, Yuan Yuan, Yan Lu, Xiaoxi Zhang, Hao Chen, Haiyi Lou, Xiaoji Wang, Dongsheng Lu, Jiaojiao Liu, Lei Tian, Qidi Feng, Asifullah Khan, Yajun Yang, Zi-Bing Jin, Jian Yang, Fan Lu, Jia Qu, Longli Kang, Bing Su, Shuhua Xu. Prioritizing adaptive variants by analyzing deep-sequenced genomes and quantitative traits of Tibetan highlanders. *National Science Review*, 2019.
9. Yang Gao, **Chao Zhang (Contributed equally)**, Liyun Yuan et al., PGG.Han: the Han Chinese genome database and analysis platform. *Nucleic Acids Research*, 2019.
10. Xin Luo, Yaoxi He, **Chao Zhang (Contributed equally)**, Xiechao He, Lanzhen Yan, Min Li, Ting Hu, Yan Hu, Jin Jiang, Xiaoyu Meng, Weizhi Ji, Xudong Zhao, Ping Zheng, Shuhua Xu & Bing Su Trio sequencing does not reveal unexpected mutations in Cas9-edited monkeys. *Nature Communication*, 2019.
11. Dongsheng Lu, Haiyi Lou, Kai Yuan, Xiaoji Wang, Yuchen Wang, **Chao Zhang\*(Contributed equally)**, Yan Lu, Xiong Yang, Lian Deng, Ying Zhou, Qidi Feng, Ya Hu, Qiliang Ding, Yajun Yang, Shilin Li, Li Jin, Yaqun Guan, Bing Su, Longli Kang, Shuhua Xu. Ancestral Origins and Genetic History of Tibetan Highlanders. *The American Journal of Human Genetics*, 2016, 3, 580-594.
12. **Chao Zhang**, Jiaojiao Liu, Furhan Iqbal, Yan Lu, Saima Mustafa, Firdous Bukhari, Haiyi Lou, Ruiqing Fu, Zhendong Wu, Xiong Yang, Ihtisham Bukhari, Muhammad Aslam, Shuhua Xu. A missense point mutation in COL10A1 identified with whole-genome deep sequencing in a 7-generation Pakistan dwarf family. *Heredity*, 2018, 120(1):83-89.
13. **Chao Zhang**, Jing Li, Tei Tian, Dongsheng Lu, Kai Yuan, Yuan Yuan, Shuhua Xu. Differential Natural Selection of Human Zinc Transporter Genes between African and Non-African Populations. *Scientific Reports*, 2015, 5, 9658.

14. Qidi Feng, Yan Lu, Xumin Ni, Kai Yuan, Yajun Yang, Xiong Yang, Chang Liu, Haiyi Lou, Zhilin Ning, Yuchen Wang, Dongsheng Lu, **Chao Zhang**, Ying Zhou, Meng Shi, Lei Tian, Xiaoji Wang, Xi Zhang, Jing Li, Asifullah Khan, Yaqun Guan, Kun Tang, Sijia Wang, Shuhua Xu. Genetic History of Xinjiang's Uyghurs Suggests Bronze Age Multiple-Way Contacts in Eurasia. *Molecular Biology and Evolution*, 2017, 34, 2572- 2582.
15. Ling-Xiang Wang, Yan Lu, **Chao Zhang (Contributed equally)**, Lan-Hai Wei, Yan S, Huang YZ, Wang CC, Mallick S, Wen SQ, Jin L, Xu SH, Li H, Reconstruction of Y-chromosome phylogeny reveals two neolithic expansions of Tibeto-Burman populations, *Molecular Genetics and Genomics*, 2018.
16. Lei Tian, Asifullah Khan, Zhilin Ning, Kai Yuan, **Chao Zhang**, Haiyi Lou, Yuan Yuan, Shuhua Xu. Genome-wide comparison of allele-specific gene expression between African and European populations. *Human Molecular Genetics*, 2018, 27, 1067-1077.
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18. MA McQuillan, **C Zhang**, SA Tishkoff, A Platt. The importance of including ethnically diverse populations in studies of quantitative trait evolution. *Current Opinion in Genetics & Development*, 2021
19. Genomics Data Center Members National, Database Resources of the National Genomics Data Center in 2020. *Nucleic acids research*, 2019.
20. Yun-Zhi Huang, Lan-Hai Wei, Shi Yan, Shao-Qing Wen, Chuan-Chao Wang, Ya-Jun Yang, Ling-Xiang Wang, Yan Lu, **Chao Zhang**, Shu-Hua Xu, Da-Li Yao, Li Jin, Hui Li. Whole sequence analysis indicates a recent southern origin of Mongolian Y-chromosome C2c1a1a1-M407. *Molecular genetics and genomics*, 2018.
21. Lan-Hai Wei, Shi Yan, Yik-Ying Teo, Yun-Zhi Huang, Ling-Xiang Wang, Ge Yu, Woei-Yuh Saw, Rick Tzee-Hee Ong, Yan Lu, **Chao Zhang**, Shu-Hua Xu, Li Jin, Hui Li. Phylogeography of Y-chromosome haplogroup O3a2b2-N6 reveals patrilineal traces of Austronesian populations on the eastern coastal regions of Asia. *PloS ONE*, 2017.
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25. Jin Sun, Lan-Hai Wei, Ling-Xiang Wang, Yun-Zhi Huang, Shi Yan, Hui-Zhen Cheng, Rick Tzee-Hee Ong, Woei-Yuh Saw, Zhi-Quan Fan, Xiao-Hua Deng, Yan Lu, **Chao Zhang**, Shu-Hua Xu, Li Jin, Yik-Ying Teo, Hui Li. Paternal gene pool of Malays in Southeast Asia and its applications for the early expansion of Austronesians. *American Journal of Human Biology*, 2021.
26. Zhaohui Yang, Caijuan Bai, Youwei Pu, Qinghong Kong, Yongbo Guo, Ouzhuluobu, Gengdeng, Xuyang Liu, Qi Zhao, Zhichao Qiu, Wangshan Zheng, Yaoxi He, Yihan Lin, Lian Deng, **Chao Zhang**, Shuhua Xu, Yi Peng, Kun Xiang, Xiaoming Zhang, Baimayangji, Cirenyangji, Chaoying Cui, Baimakangzhuo, Gonggalanzi, Bianba, Yongyue Pan, Jingxue Xin, Yong Wang, Shiming Liu, Liangbang Wang, Hengliang Guo, Zhenzhen Feng, Shaobo Wang, Hong Shi, Binghua Jiang, Tianyi Wu, Xuebin Qi, Bing Su. Genetic adaptation of skin pigmentation in highland Tibetans. *PNAS*, 2022