

THE GIS SPEAKER SERIES

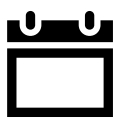


Genetic Diversity and a Pangenome Reference of Chinese Populations

Dr. Shuhua Xu

School of Life Sciences, Fudan University

Host: LIU Jianjun



Friday 23 August 2024
9.30am – 10.00am



GIS Seminar Room (Level 2)
60 Biopolis Street, Genome, Singapore 138672

About The Speaker

Dr. Shuhua Xu is a professor of human population genetics and a Distinguished Professor of Fudan University. He received his PhD at Fudan University, China. From 2012 to 2018, he held the position of Max-Planck Independent Research Group Leader at PICB. In 2013, he was appointed as Distinguished Adjunct Professor at ShanghaiTech University. Since 2015, he has been appointed a Distinguished Chinese Academy of Sciences Professor. He is the Award holder of The Royal Society Newton Advanced Fellowships (UK), Distinguished Young Scholars of the National Science Fund (China), and Prize of Natural Science Award (China). His scientific research has focused on population genomics research of human admixture history and biological adaptation to the local environment. His research aims to understand microevolution mechanisms in humans, while genetic admixture was taken as a cut-in point to pursue this ambition. The Population Genomics Group led by Dr. Xu is using computational approaches and developing new methods to dissect the genetic architecture of human populations, quantitatively characterize their admixture features, and reveal their migration history and adaptive divergence. Dr. Xu has authored many scientific papers published in *Science*, *Nature*, *Cell*, *PNAS*, *Nature Genetics*, *Nature Communications*, *Genome Biology*, *The American Journal of Human Genetics*, *Nucleic Acids Research*, *Genome Research*, *Molecular Biology and Evolution*, *the PLoS* and the *BMC* series. Dr. Xu serves as Editorial Board member of several international peer-reviewed journals such as *JGG*, *Hereditas*, *Human Genomics*, *Molecular Genetics and Genomics* (co-Editor-in-Chief), *Frontier in Genetics*, *Scientific Reports*, *BMC Genetics* (Section Editor), *BMC Genomic Data* (Senior Editor).

About The Seminar

On behalf of the Chinese Pangenome Consortium (CPC)

China is populated by 1.4 billion people of multiple ethnic groups with high cultural and language diversities. The Chinese Pangenome Consortium (CPC) aims to produce high-quality genomic sequences from people representative of the majority ethnic group (Han) and the 55 other defined ethnic groups of China, as well as of multiple unrecognized ethnic groups not yet characterized genetically. In the first phase of the CPC's pangenome project, the CPC produced a collection of 116 high-quality genome assemblies from 58 core individuals (one assembly for each of the two sets of chromosomes each person carries) representing 36 non-Han Chinese ethnic groups. At the stage of Phase II, apart from the initial 58 core samples, CPC aims to produce high-quality, phased, chromosome-level haplotype sequences of 500 individuals, which will cover the 56 ethnic groups as officially defined as well as many unidentified ethnic groups that have never been well-covered by any previous work. A more ambitious endeavor of the CPC, most likely at Phase III or partly at Phase II, is to generate telomere-to-telomere (T2T) chromosome sequence assemblies with both HiFi reads and nanopore ultra-long reads data. I will give a brief overview of these efforts in a 20-minute talk.