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Shicheng Guo, Ph.D. – Personal Statement

I was born in Shandong, China in 1986 and completed my bachelor training at Northeast Agriculture University, Harbin in 2009. In my bachelor's training, I am interested and focus on identifying novel viral pathologies for human diseases. In 2009 and then I received a reward to join the Ph.D. degree School of Medicine Fudan at University. My supervisor is Dr. Li Jin who graduated from the School of Public Health at the University of Texas while committee numbers included Dr. Momiao Xiong, Dr. Jiucun Wang, and Dr. Jingde Zhu. It is a high diversity committee from different research fields. Dr. Jin is the vice president of Fudan University. He is quite busy and usually does not have enough time to meet him. He is famous in the population genetics field. Dr. Xiong focuses on genetic epidemiology and statistical genetics. Dr. Wang focuses on human immunology and autoimmune diseases while Dr. Zhu focuses on epigenetics and DNA methylation research. Especially in Dr. Zhu's lab, I accepted a comprehensive training in DNA methylation research from wet lab to computational training. I conducted almost all kinds of methylation assay including methylation-specific PCR (MSP), bisulfite methylation PCR (BSP), methylation-binding domain-based next-generation sequencing (MBD-seq). With these admixtures, my scientific research was tuned as genetics and epigenetics research at a population level. I am interested in identifying associated variants and genes with the genome-wide association study (GWAS) and epigenome-wide association study (EWAS). I am interested in novel methods to identify new genetic signals for human complex diseases. I am also interested in apply genetic and DNA methylation variations to define new subgroup for human diseases, identify diagnostic and prognostic biomarkers.

From 2013 to 2015, I received a reward to join a Fudan-UThealth exchanging program to be a visiting student in Dr. Momiao Xiong's lab in Houston, Texas. In Dr. Xiong's lab, I try to propose a new computational tool that is based on functional principal components analysis (FPCA) to analyze RNA-seq data in which RNA-seq reads will be taken as longitudinal data by genomic position. Meanwhile, I also tried to use this method to analyze image data. In the middle of 2015, I find a postdoc opportunity at UCSD and try to extend my methylation research in cell-free DNA methylation and try to map the methylation signal to the origin of the tissue. In this study, we proposed a new measurement called methylation haplotype and methylation haplotype load to measure the complexity and methylation level at the same time. We found the novel measurement could be powerfully used in cancer prediction and tissue-of-origin mapping. As I mentioned, I am quite interested in DNA methylation research in the large population size and conducted genetic-epigenetics research. In 2017, I received an offer in the Center for Precision Medicine at Marshfield Clinic Research Institute (MCRI). MCRI has a large cohort (PMRP) containing 20,000 samples and genotyping data have been completed with exome-array. It is exactly a nice sample to conducted methylation research and then genetic-epigenetics interaction could be conducted. Working together with Steven Schordi, I proposed an approach to conducted the compound heterozygote analysis to identify novel disease genes. We applied this method in the PMRP hemochromatosis dataset and identified a significant signal located in FGF6 genes and finally, we demonstrated it is a novel iron metabolism gene with the molecular and cellular approach. At the end of 2018, I received an NLM fellowship offer to investigate "Phenome-wide Association Study of Genetic Variation in Epigenetic Factors to Test the Role of Epigenetics in Human Complex Disease". What a pity, the fellowship can only be started when I receive the green card which maybe comes out in December, 2020.

This is all journey I have made in the academic path. Along with the research, I have traveled different cites in the US and I hope to have another experience with different working and living environments and friends.

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