

BIOGRAPHICAL SKETCH

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NAME Guo, Shicheng	POSITION TITLE Predoctoral Fellow University of Texas Health Science Center at Houston
eRA COMMONS USER NAME (agency login) N/A	

EDUCATION/TRAINING

(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)

INSTITUTION AND LOCATION	DEGREE (if applicable)	MM/YYYY	FIELD OF STUDY
Northeast Agricultural University, Harbin, Heilongjiang	BS	06/2009	Biology
Fudan University, Shanghai, Shanghai	DSC	12/2014	Genetics
CAS-MPG Partner Institute for Computational Biology, Shanghai, Shanghai	Graduate Student	12/2013	Human Population Genetics
Institute of Rheumatology, Immunology and Allergy, Fudan University, Shanghai, Shanghai	Graduate Student	12/2014	Immunology and Genetics
University of Texas Health Science Center at Houston, Houston, Texas	Graduate Student	09/2014	Biostatistic

A. PERSONAL STATEMENT

Statement of Research Interests and Goals Shicheng Guo Ministry of Education Key Laboratory of Contemporary Anthropology School of Life Sciences Fudan University May 2014

My research interests and activities over the past five years have mainly centered around three areas: 1) Disease susceptibility derived from DNA methylation, 2) population epigenetics (DNA methylation), 3) DNA Methylation based biomarker identification leverage high dimensional dataset, 4) Interaction between DNA methylation and genetic variations (SNP), 5) Novel DNA methylation detection (bisulfite free detection) and analysis method (Functional based analysis method). 6) Relationship between elements of epigenome (5m, 5mc, 5hmc, histone modifications) and the application on human disease.

Human genome project, 1000 genome project and Human cancer project have been completed one by one. More and more evidences show that the contribution from the epigenetic variation is more important than genetic variations. Actually, I think it suggest the environment plays the most part of the role on the pathological or etiological of the majority complex disease, such as cancer, coronary artery disease, autoimmune diseases and so on.

Statement of Research Interests and Goals My future professional research interests and activities will concentrate in the following areas: 1) Disease susceptibility/heritability derived from DNA methylation, 2) population epigenetics (DNA methylation), 3) DNA Methylation based biomarker identification leverage high dimensional dataset, 4) Interaction between DNA methylation and genetic variations (SNP), 5) Novel DNA methylation detection (bisulfite free detection) and analysis method (Functional based analysis method). 6) Relationship between elements of epigenome (5m, 5mc, 5hmc, histone modifications) and the application on human disease. Human genome project, 1000 genome project and Human cancer project have been completed one by one. More and more evidences show that the contribution from the epigenetic variation is more important than genetic variations. Actually, I think it suggest that the environment plays the most part of the role on the pathological or etiological of the majority complex disease, such as cancer, coronary artery disease, autoimmune diseases and so on.

Methylation and SNP Double Model in Next Generation eQTL Research

A fundamental challenge in the post-genome era is to understand and annotate the consequences of genetic variation, particularly within the context of human tissues, for example, annotation to expression quantitative trait loci (eQTL). eQTL are most important genomic variations which have great biological regulation power. However, traditional research usually just focuses on SNP variations in human genome. CpG methylation derived expression quantitative trait loci are another important source of the gene expression variation. Genome variation, DNA

methylation and gene expression have complicated relationship. Both DNA methylation and DNA methylation could cause high or low gene expression for specific gene, also, they might bring alternative splicing so that give complex biological phenotypes or traits. TCGA has provided large number DNA methylation, SNPs, CNVs and gene expression for same individual, which means, we can conducted our above analysis right now. Association between SNP and DNA methylation, DNA methylation and gene expression, SNP and gene expression can be easily validated by current molecular biological technique. The identification of such relationship would provide valuable information for pharmaceutical drug design, personalized medicine and fundamental of molecular/cellular biology.

Genome-wide Epigenetic Association Study between Methylation and Middle Heritability Disease

In the past decades, population genetics has been unprecedentedly developed, especially, in complex disease. Hundreds of susceptibility genes were identified by genome-wide association study. However, my previous study showed the prediction ability was severely limited with significant SNPs identified by GWAS study even for some high familial risk disease. Missing heritability mainly derived from epigenetic variations, has been proposed by large number of genetic epidemiologists. Genome-wide epigenetic association study (eGWAS) or genome-wide DNA methylation association study provided powerful ability to discover disease association epigenetic pathological or etiological factor for middle or low heritability disease. Current DNA methylation high throughput technology, such as MBD-seq, Methylation microarray, has equipped such ability to apply eGWAS or mGWAS on the 1000-2000 population size with case-control design or cohort study (Samples could be obtained from our cohort population in Taizhou, Jiangsu). Some interesting binary outcome disease such as cancer/normal, or quantitative trait, such as body-mass index (BMI), relative lymphocyte proportions (RLP), blood pressure (RP), intelligence quotient (IQ) can be considered in our future research proposal in China or U.S or as the International collaboration project.

Eventually, because my skilled statistic and bioinformatics training, I can complete majority analysis work in current biological lab, that means, I would provide enough collaboration with colleagues to push our project going on with higher efficiency.

B. POSITIONS AND HONORS

Positions and Employment

2013 - 2014 Predoctoral Fellow, University of Texas Health Science Center at Houston, Houston, TX

Other Experience and Professional Memberships

Honors

2014 First Place Poster, GSBS human and molecular genetics symposium at University of Texas
2012 Silver award, Cup of Challenge for College Students' Innovative Undertaking Contest in Shanghai
2007 Second prize, National Mathematical Modeling Contest in Heilongjiang province

C. SELECTED PEER-REVIEWED PUBLICATIONS

- Xiao Q, Gao S, Luo H, Fan W, Guo S, Yao H, Leng S, Xu Z, Tao T, Liu X, Jingfang Z, Zhang M, Li D, Xiao Q. 9q33.3, a stress-related chromosome region, contributes to reducing lung squamous cell carcinoma risk. *Journal of thoracic oncology : official publication of the International Association for the Study of Lung Cancer*. 2014; 9(7):1041-7. PubMed PMID: 24926550.
- Guo S, Wang YL, Li Y, Jin L, Xiong M, Ji QH, Wang J. Significant SNPs have limited prediction ability for thyroid cancer. *Cancer medicine*. 2014; 3(3):731-5. PubMed PMID: 24591304.
- Huang L, Li Y, Guo S, Sun Y, Zhang C, Bai Y, Li S, Yang F, Zhao M, Wang B, Yu W, Zhao M, Khor CC, Li X. Different hereditary contribution of the CFH gene between polypoidal choroidal vasculopathy and age-related macular degeneration in Chinese Han people. *Investigative ophthalmology & visual science*. 2014; 55(4):2534-8. PubMed PMID: 24692129.
- Song X, Guo S, Chen Y, Yang C, Ji H, Zhang F, Jiang Z, Ma Y, Li Y, Jin L, Zou H, Zhou X, Wang J. Association between HLA-DQA1 gene copy number polymorphisms and susceptibility to rheumatoid arthritis in Chinese Han population. *Journal of genetics*. 2014; 93(1):215-8. PubMed PMID: 24840843.
- Guo S, Tan L, Pu W, Wu J, Xu K, Wu J, Li Q, Ma Y, Xu J, Jin L, Wang J. Quantitative assessment of the diagnostic role of APC promoter methylation in non-small cell lung cancer. *Clinical epigenetics*. 2014; 6(1):5. PubMed PMID: 24661338; PubMed Central PMCID: PMC3997934.

- Wu L, Guo S, Yang D, Ma Y, Ji H, Chen Y, Zhang J, Wang Y, Jin L, Wang J, Liu J. Copy number variations of HLA-DRB5 is associated with systemic lupus erythematosus risk in Chinese Han population. *Acta biochimica et biophysica Sinica*. 2014; 46(2):155-60. PubMed PMID: 24366815.
- Wang X, Wang L, Guo S, Bao Y, Ma Y, Yan F, Xu K, Xu Z, Jin L, Lu D, Xu J, Wang JC. Hypermethylation reduces expression of tumor-suppressor PLZF and regulates proliferation and apoptosis in non-small-cell lung cancers. *FASEB journal : official publication of the Federation of American Societies for Experimental Biology*. 2013; 27(10):4194-203. PubMed PMID: 23804241.
- Zhao Y, Zhou H, Ma K, Sun J, Feng X, Geng J, Gu J, Wang W, Zhang H, He Y, Guo S, Zhou X, Yu J, Lin Q. Abnormal methylation of seven genes and their associations with clinical characteristics in early stage non-small cell lung cancer. *Oncology letters*. 2013; 5(4):1211-1218. PubMed PMID: 23599765; PubMed Central PMCID: PMC3629069.
- Lin S, Pan L, Guo S, Wu J, Jin L, Wang JC, Wang S. Prognostic role of microRNA-181a/b in hematological malignancies: a meta-analysis. *PloS one*. 2013; 8(3):e59532. PubMed PMID: 23533632; PubMed Central PMCID: PMC3606212.
- Wu J, Wu J, Zhou Y, Zou H, Guo S, Liu J, Lu L, Xu H. Quantitative assessment of the variation in IGF2BP2 gene and type 2 diabetes risk. *Acta diabetologica*. 2012; 49 Suppl 1:S87-97. PubMed PMID: 22015911.
- Wu J, Liu J, Zhou Y, Ying J, Zou H, Guo S, Wang L, Zhao N, Hu J, Lu D, Jin L, Li Q, Wang JC. Predictive value of XRCC1 gene polymorphisms on platinum-based chemotherapy in advanced non-small cell lung cancer patients: a systematic review and meta-analysis. *Clinical cancer research : an official journal of the American Association for Cancer Research*. 2012; 18(14):3972-81. PubMed PMID: 22705987.
- Zhao Y, Guo S, Sun J, Huang Z, Zhu T, Zhang H, Gu J, He Y, Wang W, Ma K, Wang J, Yu J. Methylcap-seq reveals novel DNA methylation markers for the diagnosis and recurrence prediction of bladder cancer in a Chinese population. *PloS one*. 2012; 7(4):e35175. PubMed PMID: 22529986; PubMed Central PMCID: PMC3328468.
- He Y, Cui Y, Wang W, Gu J, Guo S, Ma K, Luo X. Hypomethylation of the hsa-miR-191 locus causes high expression of hsa-mir-191 and promotes the epithelial-to-mesenchymal transition in hepatocellular carcinoma. *Neoplasia (New York, N.Y.)*. 2011; 13(9):841-53. PubMed PMID: 21969817; PubMed Central PMCID: PMC3182276.
- Li Y, Zhu J, Tian G, Li N, Li Q, Ye M, Zheng H, Yu J, Wu H, Sun J, Zhang H, Chen Q, Luo R, Chen M, He Y, Jin X, Zhang Q, Yu C, Zhou G, Sun J, Huang Y, Zheng H, Cao H, Zhou X, Guo S, Hu X, Li X, Kristiansen K, Bolund L, Xu J, Wang W, Yang H, Wang J, Li R, Beck S, Wang J, Zhang X. The DNA methylome of human peripheral blood mononuclear cells. *PLoS biology*. 2010; 8(11):e1000533. PubMed PMID: 21085693; PubMed Central PMCID: PMC2976721.
- Xiang H, Zhu J, Chen Q, Dai F, Li X, Li M, Zhang H, Zhang G, Li D, Dong Y, Zhao L, Lin Y, Cheng D, Yu J, Sun J, Zhou X, Ma K, He Y, Zhao Y, Guo S, Ye M, Guo G, Li Y, Li R, Zhang X, Ma L, Kristiansen K, Guo Q, Jiang J, Beck S, Xia Q, Wang W, Wang J. Single base-resolution methylome of the silkworm reveals a sparse epigenomic map. *Nature biotechnology*. 2010; 28(5):516-20. PubMed PMID: 20436463.

D. RESEARCH SUPPORT