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BIOGRAPHICAL SKETCH

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NAME: Shicheng Guo, PhD

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POSITION TITLE: Postdoctoral Fellow–Human Genetics

EDUCATION/TRAINING

| INSTITUTION AND LOCATION | DEGREE  (if applicable) | Completion Date  MM/YYYY | FIELD OF STUDY |
| --- | --- | --- | --- |
| Northeast Agriculture University | B.S. | 06/2009 | Biology |
| Fudan University | Ph.D. | 01/2015 | Human Genetics |
| University of Texas Health Science Center at Houston | Postdoc | 04/2015 | Genetic [Epidemiology](https://en.wikipedia.org/wiki/Epidemiology) |
| University of California, San Diego | Postdoc | 10/2017 | Human Genetics |

# A. Personal Statement

1. My research has focused on the epigenome architecture assembly (Human and other important model organisms), genetics (SNPs, CNVs) and epigenetics (DNA methylation and miRNA) variation screening and validation to discover disease-related susceptibility factors. These disease-susceptibility factors can then be used as diagnostic and prognostic biomarkers for clinical research to human complex disease, such as lung cancers, thyroid cancer, bladder cancer, liver cancer, ankylosing spondylitis (AS), [gout](https://scholar.google.com/citations?view_op=view_citation&hl=ru&user=4tIViCAAAAAJ&citation_for_view=4tIViCAAAAAJ:QUX0mv85b1cC), and systemic sclerosis (SSc). My previous work includes (i) the identification of SSc and RA-predisposing SNPs and CNVs using case-control approaches, (ii) identification of diagnostic biomarkers for human cancer with solid tissue, and (iii) origin-tissue mapping for cell-free DNA based on tissue-specific methylation panel. Current areas of investigation include disease susceptibility screening applying GWAS and PheWAS approaches and genetic-epigenetic interactions in the etiology and application to the disease subtype screening, diagnosis and prognosis. The ultimate goals of my research are to develop widely-applicable methods/markers for disease diagnosis, subtype identification or prognosis. I have experience on different bioinformatics analysis for genetic variation,, epigenetic data (methylation sequencing, ChIP-seq data), text-mining and machine learning analysis based on Perl, R and Python.

B. Positions and Honors

## Positions and Employment

2015-2015 Postdoctoral Fellow, University of Texas Health Science Center at Houston, TX

2015-2017 Postdoctoral Fellow, University of California, San Diego, CA

2017-Pres Postdoctoral Fellow, Center for Human Genetics, Marshfield Clinic, WI

## Other Experience and Professional Memberships

2013-2015 Research Assistant, University of Texas Health Science Center at Houston, Houston, TX

2012-2013 Visiting Scholar, University of Texas Health Science Center at Houston, Houston, TX

2012-2013 Internship in the CAS-MPG Partner Institute for Computational Biology, Shanghai, China

2011-2014 Internship in the institute of Rheumatology, Immunology and Allergy, Shanghai, China

## Honors

2014 First Place Poster, 17th Annual Human and Molecular Genetics Program Symposium, GSBS, TX

2012 Silver award of “Cup of Challenge” for College Students’ Innovative Undertaking Contest in Shanghai

2007 Second prize of National Mathematical Modeling Contest in Heilongjiang province, Harbin, China

# C. Contribution to Science

1. **Autoimmune Disease Susceptibility Variation Identification.**

Earlier in my career, I investigated the genetic variation (SNP and CNV screens) involved in systemic sclerosis and rheumatoid arthritis within Chinese Han population. Applying a multiple candidate pre-selection method, I identified susceptibility genes, such as an important CNV within *HLA-DQA1* and *APOBEC3A/3B* for SSc, *CFH* for age-related macular degeneration, and *FOXE1* for thyroid cancer. I also conducted a large association study interrogating genetic variations in miRNA for human cancer and identified miR-4293 for non-small cell lung cancer, and[miR-196a2/miR-499](javascript:void(0)) for [esophageal squamous cell carcinoma](javascript:void(0)). These findings have provided much needed molecular insight into the role of regulation and genetic variants in the etiologies of these cancers.

* 1. **Guo, S**., Y. Li, Y. Wang, H. Chu, Y. Chen, Q. Liu, G. Guo, W. Tu, W. Wu, H. Zou, L. Yang, R. Xiao, Y. Ma, F. Zhang, M. Xiong, L. Jin, X. Zhou, and J. Wang, Copy Number Variation of HLA-DQA1 and APOBEC3A/3B Contribute to the Susceptibility of Systemic Sclerosis in the Chinese Han Population. *J Rheumatol*, 2016. 43(5): p. 880-6.
  2. Wang, Y.L**ǂ**., S.H. Feng**ǂ**, **S. Guoǂ**, W.J. Wei, D.S. Li, Y. Wang, X. Wang, Z.Y. Wang, Y.Y. Ma, L. Jin, Q.H. Ji, and J.C. Wang, Confirmation of papillary thyroid cancer susceptibility loci identified by genome-wide association studies of chromosomes 14q13, 9q22, 2q35 and 8p12 in a Chinese population. *J Med Genet*, 2013. 50(10): p. 689-95. (ǂContributed equally)
  3. Huang, L**ǂ**, Y. Li**ǂ**, **S. Guoǂ**, Y. Sun, C. Zhang, Y. Bai, S. Li, F. Yang, M. Zhao, B. Wang, W. Yu, C.C. Khor, and X. Li, Different hereditary contribution of the CFH gene between polypoidal choroidal vasculopathy and age-related macular degeneration in Chinese Han people. *Invest Ophthalmol Vis Sci*, 2014. 55(4): p. 2534-8. (ǂContributed equally)
  4. L., L. Chen, X. Ni, **S. Guo**, Y. Zhou, C. Wang, Y. Zheng, F. Shen, V.K. Kolluri, M. Muktiali, Z. Zhao, J. Wu, D. Zhao, Z. He, X. Feng, Z. Yuan, J. Zhang, L. Jin, J. Wang, and M. Wang, Genetic variant of miR-4293 rs12220909 is associated with susceptibility to non-small cell lung cancer in a Chinese Han population. *PloS one*, 2017. 12(4): p. e0175666.
  5. Shen, F., J. Chen, **S. Guo**, Y. Zhou, Y. Zheng, Y. Yang, J. Zhang, X. Wang, C. Wang, D. Zhao, M. Wang, M. Zhu, L. Fan, J. Xiang, Y. Xia, Q. Wei, L. Jin, and J. Wang, Genetic variants in miR-196a2 and miR-499 are associated with susceptibility to esophageal squamous cell carcinoma in Chinese Han population. *Tumour Biol*, 2016. 37(4): p. 4777-84.

1. **Epigenome architecture assembly to normal and disease tissues**

Starting in 2015, I investigated the epigenetic variation in human disease, particularly focusing on DNA methylation. I participated several large projects to build the epigenome architecture for human normal and disease cells or tissues. This work evaluated genomic methylation profile (methylome) for normal human blood cells, the methylome of animal model ‘silk’, the methylome of CD4+ T-cells of [rheumatoid arthritis](javascript:void(0)), the methylome of pancreatic cancer and hepatocellular carcinoma with different methylation methods, such as BS-seq and MBD-seq.

* 1. **Guo, Sǂ**., Q. Zhu**ǂ**, T. Jiang, R. Wang, Y. Shen, X. Zhu, Y. Wang, F. Bai, Q. Ding, X. Zhou, G. Chen, and D.Y. He, Genome-wide DNA methylation patterns in CD4+ T cells from Chinese Han patients with rheumatoid arthritis. *Mod Rheumatol*, 2017. 27(3): p. 441-447. (ǂContributed equally)
  2. Zhao, Y**ǂ**., F. Xue**ǂ**, J. Sun**ǂ**, **S. Guoǂ**, H. Zhang, B. Qiu, J. Geng, J. Gu, X. Zhou, W. Wang, Z. Zhang, N. Tang, Y. He, J. Yu, and Q. Xia, Genome-wide methylation profiling of the different stages of hepatitis B virus-related hepatocellular carcinoma development in plasma cell-free DNA reveals potential biomarkers for early detection and high-risk monitoring of hepatocellular carcinoma. *Clin Epigenetics*, 2014. 6(1): p. 30. (ǂContributed equally)
  3. Zhao, Y**ǂ**., J. Sun**ǂ**, H. Zhang**ǂ**, **S. Guoǂ**, J. Gu, W. Wang, N. Tang, X. Zhou and J. Yu, High-frequency aberrantly methylated targets in pancreatic adenocarcinoma identified via global DNA methylation analysis using methylCap-seq. *Clin Epigenetics*, 2014. 6(1): p. 18. (ǂContributed equally)
  4. Zhao, Y**ǂ**., **S. Guoǂ**, J. Sun**ǂ**, Z. Huang, T. Zhu, H. Zhang, J. Gu, Y. He, W. Wang, K. Ma, J. Wang, and J. Yu, 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): p. e35175. (ǂContributed equally)

1. **Epigenetic variations and diagnosis or prognosis biomarkers for human complex diseases.**

DNA methylation was demonstrated to be aberrant in the early stage of cancers. We identified large number of methylation-based diagnosis and prognosis markers for non-small cell lung cancer, bladder cancer and pancreatic cancers. Since the DNA methylation has different patterns for different tissue types, we proposed a prediction model to map the origin of the cell-free DNA fragments based on tissue-specific methylation signals which provided a useful approach for diagnosing non-invasive cancer. In my current investigations, I am integrating human genetic and epigenetic variation to investigate interaction effects and apply those findings to disease diagnosis and disease subtype identification.

* 1. Pu, W., C. Wang, S. Chen, D. Zhao, Y. Zhou, Y. Ma, Y. Wang, C. Li, Z. Huang, L. Jin, **S. Guo**, J. Wang, and M. Wang, Targeted bisulfite sequencing identified a panel of DNA methylation-based biomarkers for esophageal squamous cell carcinoma (ESCC). *Clin Epigenetics*, 2017. 9: p. 129.
  2. **Guo, S**., D. Diep, N. Plongthongkum, H.L. Fung, and K. Zhang, Identification of methylation haplotype blocks aids in deconvolution of heterogeneous tissue samples and tumor tissue-of-origin mapping from plasma DNA. *Nat Genet*, 2017. 49(4): p. 635-642. . (ǂContributed equally)
  3. Geng, X., W. Pu, Y. Tan, Z. Lu, A. Wang, L. Tan, S. Chen, **S. Guo**, J. Wang, and X. Chen, Quantitative assessment of the diagnostic role of FHIT promoter methylation in non-small cell lung cancer. *Oncotarget*, 2017. 8(4): p. 6845-6856.
  4. **Guo, S**., F. Yan, J. Xu, Y. Bao, J. Zhu, X. Wang, J. Wu, Y. Li, W. Pu, Y. Liu, Z. Jiang, Y. Ma, X. Chen, M. Xiong, L. Jin, and J. Wang, Identification and validation of the methylation biomarkers of non-small cell lung cancer (NSCLC). *Clin Epigenetics*, 2015. 7: p. 3.
  5. **Guo, Sǂ**., L. Tan**ǂ**, W. Pu**ǂ**, J. Wu, K. Xu, Q. Li, Y. Ma, J. Xu, L. Jin, and J. Wang, Quantitative assessment of the diagnostic role of APC promoter methylation in non-small cell lung cancer. *Clin Epigenetics*, 2014. 6(1): p. 5. (ǂContributed equally)

**Complete List of Published Work:**

# https://www.ncbi.nlm.nih.gov/myncbi/browse/collection/45297273/?sort=date&direction=descending