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BIOGRAPHICAL SKETCH

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NAME: Shicheng Guo, PhD

eRA COMMONS USER NAME (credential, e.g., agency login): SHICHENGGUO

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 (SNP, CNV) and epigenetics (DNA methylation and miRNA) variation screening and validation to discover disease related susceptibility factors to provided 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 works include the identification of SSc and RA related SNP, CNV variations with case-control study, diagnostic biomarker for human cancer with solid tissue and origin-tissue mapping for cell-free DNA based on tissue-specific methylation panel. Current areas of investigation include disease related susceptibility screening applying GWAS and pheWAS approach and genetic-epigenetic interaction in the etiology and application on 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.[1-14]

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. (\*Co-Corresponding Author)

2. **Guo, Sǂ**., Q. Zhuǂ, T. Jiangǂ, 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)

3. **Guo, Sǂ**., D. Diepǂ, 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)

4. 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. (\*Co-Corresponding Author)

5. Pu, W., X. Geng, S. Chen, L. Tan, Y. Tan, A. Wang, Z. Lu, **S. Guo,** X. Chen, and J. Wang, Aberrant methylation of CDH13 can be a diagnostic biomarker for lung adenocarcinoma. J Cancer, 2016. 7(15): p. 2280-2289. (\*Co-Corresponding Author)

6. **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. (First Author)

7. **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. (First Author)

8. Zhao, Yǂ., F. Xueǂ, J. Sunǂ, **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)

9. Zhao, Yǂ., J. Sunǂ, H. Zhangǂ, **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)

10. Huang, L. ǂ, Y. Liǂ, **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)

11. **Guo, S.,** Y.L. Wang, Y. Li, L. Jin, M. Xiong, Q.H. Ji, and J. Wang, Significant SNPs have limited prediction ability for thyroid cancer. Cancer Med, 2014. 3(3): p. 731-5. (First Author)

12. **Guo, S.,** L. Tan, W. Pu, 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. (First Author)

13. Wang, Y.L. ǂ, S.H. Fengǂ, **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)

14. Zhao, Y. ǂ, **S. Guoǂ**, J. Sunǂ, 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)

B. Positions and Honors

## Positions and Employment

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

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

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

## Other Experience and Professional Memberships

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

2012-2013 Visiting Scholar at the 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.**

Early in my career, I investigated serials of genetic variation (SNP and CNV) in systemic sclerosis and rheumatoid arthritis within Chinese Han population. Apply multiple candidate pre-selection method, I identified some interesting complex disease associated Susceptibility genes, such as CNV of HLA-DQA1 and APOBEC3A/3B for SSc, CFH gene for age-related macular degeneration, FOXE1 for thyroid cancer. I also conducted widely study on association between genetic variations in miRNA and human cancer and identified miR-4293 for non-small cell lung cancer, [miR-196a2/miR-499](javascript:void(0)) for [esophageal squamous cell carcinoma](javascript:void(0)).

* 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., S.H. Feng,* ***S. Guo****, 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.*
  3. *Huang, L., Y. Li,* ***S. Guo****, 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.*
  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 and epigenetic variations in human complex diseases.**

From 2015, I have been made some investigation on the epigenetic variation in human disease, especially in DNA methylation. I participated several project to build the epigenome architecture for human normal and disease cell or tissues, such as genomic methylation profile (methylome) for normal human blood cells, methylome of animal model ‘silk’, methylome of CD4+ T-cells of [rheumatoid arthritis](javascript:void(0)), methylome of pancreatic cancer and hepatocellular carcinoma with different methylation method, such as BS-seq and MBD-seq. DNA methylation was demonstrated to be aberrant in the early stage of cancers and therefore, 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 mapping the origin of the cell-free DNA fragment based on tissue-specific methylation signals which provided an approach for the non-invasive cancer diagnosis. In our current works, we will integrate human genetic and epigenetic variations and investigate the interaction effect/application on disease precision diagnosis or 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.*
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  5. *Pu, W., X. Geng, S. Chen, L. Tan, Y. Tan, A. Wang, Z. Lu,* ***S. Guo****, X. Chen, and J. Wang, Aberrant methylation of CDH13 can be a diagnostic biomarker for lung adenocarcinoma. J Cancer, 2016. 7(15): p. 2280-2289.*
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  7. *Zhao, Y., F. Xue, J. Sun,* ***S. Guo****, 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.*
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  10. *Zhao, Y.,* ***S. Guo****, J. Sun, 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.*

**Complete List of Published Work:**

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