

Shicheng Guo

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Education

2009-2011 Ph.D School of life sciences, Fudan University, Shanghai, China
2005-2009 BS School of life sciences, Northeast Agricultural University, Harbin, China

Present Position

2017-now, Postdoc at Center for Human Genetics, Marshfield Clinic Research Institute, Marshfield, WI

Experience

2014-2017, Postdoc at Department of bioengineering, University of California, San Diego, CA
2013-2014, Research assistant at the University of Texas Health Science Center at Houston, TX
2012-2014, 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

Patents

Methods and kits for diagnosing of bladder cancer with urine exfoliated cell, China
Methods and kits for prognosing of bladder cancer after surgery with urine exfoliated cell, China
Methods for quantitative deconvolution and detection of heterogeneous nucleic acid sample, US(review).

Awards and Honors

2014, First Place Poster, 17th Annual Human and Molecular Genetics Program Symposium, GSBS, Houston, TX
2012, Silver award of "Cup of Challenge" for College Students' Innovative Undertaking Contest in Shanghai, China
2009-2013, Model Student of Academic Records (2009, 2012, 2013, Fudan University), Shanghai, China
2007, Second prize of National Mathematical Modeling Contest in Heilongjiang province, Harbin, China
2007, Social practice scholarship (NEAU), Harbin, China
2006, National Encouragement Scholarship, Harbin, China
2005-2007, Model Student of Academic Records (NEAU), Harbin, China
2005, National Scholarship (NEAU), Harbin, China

Conferences Reviewer

BIBM 2014: Bioinformatics and Biomedicine
ASHG 2017: Genetics and Epigenetics

Editorial Board Member

Journal of Clinical Epigenetics
Austin Journal of Lung Cancer Research
Jacobs Journal of Biomarkers
SM Journal of Pulmonary Medicine
SRL Oncology & Hematology

Publications

1. Pu, W., C. Wang, S. Chen, D. Zhao, Y. Zhou, Y. Ma, Y. Wang, C. Li, Z. Huang and L. Jin, Targeted bisulfite sequencing identified a panel of DNA methylation-based biomarkers for esophageal squamous cell carcinoma (ESCC). *Clinical Epigenetics*, 2017. 9(1): p. 129.
2. Lei, Y., L. Liu, S. Zhang, S. Guo, X. Li, J. Wang, B. Su, Y. Fang, X. Chen and H. Ke, Hdac7 promotes lung tumorigenesis by inhibiting Stat3 activation. *Molecular cancer*, 2017. 16(1): p. 170.
3. He, D., J. Liu, Y. Hai, Q. Zhu, Y. Shen, S. Guo, W. Zhang and X. Zhou, Increased DOT1L in synovial biopsies of patients with OA and RA. *Clinical rheumatology*, 2017: p. 1-6.

4. Guo, S., Q. Zhu, T. Jiang, R. Wang, Y. Shen, X. Zhu, Y. Wang, F. Bai, Q. Ding and X. Zhou, Genome-wide DNA methylation patterns in CD4+ T cells from Chinese Han patients with rheumatoid arthritis. *Modern rheumatology*, 2017. 27(3): p. 441-447.
5. Guo, S., R. Wang, T. Jiang, F. Bai, Q. Ding, Y. Ma, Y. Wang, Y. Yang, X. Wang and L. Tan, Alterations and diagnosis potential of serum lipid profiles in rheumatoid arthritis patients. *INTERNATIONAL JOURNAL OF CLINICAL AND EXPERIMENTAL PATHOLOGY*, 2017. 10(3): p. 3503-3509.
6. Guo, S., D. Diep, N. Plongthongkum, H.-L. Fung, K. Zhang and K. Zhang, Identification of methylation haplotype blocks aids in deconvolution of heterogeneous tissue samples and tumor tissue-of-origin mapping from plasma DNA. *Nature Genetics*, 2017. 49(4): p. 635-642.
7. 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.
8. Fan, L., L. Chen, X. Ni, S. Guo, Y. Zhou, C. Wang, Y. Zheng, F. Shen, V.K. Kolluri and M. Muktiali, 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.
9. Ding, W., W. Pu, L. Wang, S. Jiang, X. Zhou, W. Tu, L. Yu, J. Zhang, S. Guo and Q. Liu, Genome-wide DNA methylation analysis in systemic sclerosis reveals hypomethylation of interferon-associated genes in CD4+ and CD8+ T cells. *Journal of Investigative Dermatology*, 2017.
10. Zhang, X., J. Zhang, R. Wang, S. Guo, H. Zhang, Y. Ma, Q. Liu, H. Chu, X. Xu and Y. Zhang, Hypermethylation reduces the expression of PNPLA7 in hepatocellular carcinoma. *Oncology letters*, 2016. 12(1): p. 670-674.
11. Suzuki, K., Y. Tsunekawa, R. Hernandez-Benitez, J. Wu, J. Zhu, E.J. Kim, F. Hatanaka, M. Yamamoto, T. Araoka and Z. Li, In vivo genome editing via CRISPR/Cas9 mediated homology-independent targeted integration. *Nature*, 2016. 540(7631): p. 144-149.
12. Shen, F., J. Chen, S. Guo, Y. Zhou, Y. Zheng, Y. Yang, J. Zhang, X. Wang, C. Wang and D. Zhao, Genetic variants in miR-196a2 and miR-499 are associated with susceptibility to esophageal squamous cell carcinoma in Chinese Han population. *Tumor Biology*, 2016. 37(4): p. 4777-4784.
13. 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. *Journal of Cancer*, 2016. 7(15): p. 2280.
14. Guo, S., Y. Li, Y. Wang, H. Chu, Y. Chen, Q. Liu, G. Guo, W. Tu, W. Wu and H. Zou, Copy Number Variation of HLA-DQA1 and APOBEC3A/3B Contribute to the Susceptibility of Systemic Sclerosis in the Chinese Han Population. *The Journal of rheumatology*, 2016. 43(5): p. 880-886.
15. Zhang, P., J. Wang, T. Lu, X. Wang, Y. Zheng, S. Guo, Y. Yang, M. Wang, V.K. Kolluri and L. Qiu, miR-449b rs10061133 and miR-4293 rs12220909 polymorphisms are associated with decreased esophageal squamous cell carcinoma in a Chinese population. *Tumor Biology*, 2015. 36(11): p. 8789-8795.
16. Wang, J., J. Li, J. Gu, J. Yu, S. Guo, Y. Zhu and D. Ye, Abnormal methylation status of FBXW10 and SMPD3, and associations with clinical characteristics in clear cell renal cell carcinoma. *Oncology letters*, 2015. 10(5): p. 3073-3080.
17. Pan, L.-l., Y.-m. Huang, M. Wang, X.-e. Zhuang, D.-f. Luo, S.-c. Guo, Z.-s. Zhang, Q. Huang, S.-l. Lin and S.-y. Wang, Positional cloning and next-generation sequencing identified a TGM6 mutation in a large Chinese pedigree with acute myeloid leukaemia. *European Journal of Human Genetics*, 2015. 23(2): p. 218-223.
18. Lin, N., J. Jiang, S. Guo and M. Xiong, Functional Principal Component Analysis and Randomized Sparse Clustering Algorithm for Medical Image Analysis. *PloS one*, 2015. 10(7): p. e0132945.
19. Jiang, J., N. Lin, S. Guo, J. Chen and M. Xiong, Multiple functional linear model for association analysis of RNA-seq with imaging. *Quantitative biology (Beijing, China)*, 2015. 3(2): p. 90.
20. Guo, S., F. Yan, J. Xu, Y. Bao, J. Zhu, X. Wang, J. Wu, Y. Li, W. Pu and Y. Liu, Identification and validation of the methylation biomarkers of non-small cell lung cancer (NSCLC). *Clinical epigenetics*, 2015. 7(1): p. 3.
21. Guo, S., T. Jiang, R. Wang, Y. Shen, X. Zhu, F. Bai, Q. Ding, G. Chen and D. He, Genome-wide Dna Methylation Patterns in Cd4+ T Reveal Significant Contribution of Dna Methylation to Rheumatoid Arthritis. *Arthritis & Rheumatology*, 2015. 67: p. 1596-1597.

22. Dong, Z., S. Guo, Y. Yang, J. Wu, M. Guan, H. Zou, L. Jin and J. Wang, Association between ABCG2 Q141K polymorphism and gout risk affected by ethnicity and gender: a systematic review and meta - analysis. *International journal of rheumatic diseases*, 2015. 18(4): p. 382-391.
23. Zhao, Y., F. Xue, J. Sun, S. Guo, H. Zhang, B. Qiu, J. Geng, J. Gu, X. Zhou and W. Wang, 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. *Clinical epigenetics*, 2014. 6(1): p. 30.
24. Zhao, Y., J. Sun, H. Zhang, S. Guo, 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. *Clinical epigenetics*, 2014. 6(1): p. 18.
25. Xiao, Q., S. Gao, H. Luo, W. Fan, S. Guo, H. Yao, S. Leng, Z. Xu, T. Tao and X. Liu, 9q33. 3, a stress-related chromosome region, contributes to reducing lung squamous cell carcinoma risk. *Journal of Thoracic Oncology*, 2014. 9(7): p. 1041-1047.
26. Wang, R., J. Zhang, Y. Ma, L. Chen, S. Guo, X. Zhang, Y. Ma, L. Wu, X. Pei and S. Liu, Association study of miR- 149 rs2292832 and miR- 608 rs4919510 and the risk of hepatocellular carcinoma in a large- scale population. *Molecular medicine reports*, 2014. 10(5): p. 2736-2744.
27. Song, X., S. Guo, Y. Chen, C. Yang, H. Ji, F. Zhang, Z. Jiang, Y. Ma, Y. Li and L. Jin, Association between HLA-DQA1 gene copy number polymorphisms and susceptibility to rheumatoid arthritis in Chinese Han population. *Journal of genetics*, 2014. 93(1): p. 215-218.
28. Huang, L., Y. Li, S. Guo, Y. Sun, C. Zhang, Y. Bai, S. Li, F. Yang, M. Zhao and B. Wang, Different Hereditary Contribution of the CFH Gene Between Polypoidal Choroidal Vasculopathy and Age-Related Macular Degeneration in Chinese Han PeopleHereditary Contribution of CFH in PCV and AMD. *Investigative ophthalmology & visual science*, 2014. 55(4): p. 2534-2538.
29. He, D., J. Wang, L. Yi, X. Guo, S. Guo, G. Guo, W. Tu, W. Wu, L. Yang and R. Xiao, Association of the HLA-DRB1 with Scleroderma in Chinese Population. *PloS one*, 2014. 9(9): p. e106939.
30. 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 medicine*, 2014. 3(3): p. 731-735.
31. Guo, S., L. Tan, W. Pu, J. Wu, K. Xu, J. Wu, Q. Li, Y. Ma, J. Xu and L. Jin, Quantitative assessment of the diagnostic role of APC promoter methylation in non-small cell lung cancer. *Clinical epigenetics*, 2014. 6(1): p. 5.
32. Zhao, Y., H. Zhou, K. Ma, J. Sun, X. Feng, J. Geng, J. Gu, W. Wang, H. Zhang and Y. He, Abnormal methylation of seven genes and their associations with clinical characteristics in early stage non-small cell lung cancer. *Oncology letters*, 2013. 5(4): p. 1211-1218.
33. Wu, L., S. Guo, D. Yang, Y. Ma, H. Ji, Y. Chen, J. Zhang, Y. Wang, L. Jin and J. Wang, Copy number variations of HLA-DRB5 is associated with systemic lupus erythematosus risk in Chinese Han population. *Acta Biochim Biophys Sin*, 2013. 46(2): p. 155-160.
34. Wang, Y.-L., S.-H. Feng, S.-C. Guo, W.-J. Wei, D.-S. Li, Y. Wang, X. Wang, Z.-Y. Wang, Y.-Y. Ma and L. Jin, Confirmation of papillary thyroid cancer susceptibility loci identified by genome-wide association studies of chromosomes 14q13, 9q22, 2q35 and 8p12 in a Chinese population. *Journal of medical genetics*, 2013: p. jmedgenet-2013-101687.
35. Wang, X., L. Wang, S. Guo, Y. Bao, Y. Ma, F. Yan, K. Xu, Z. Xu, L. Jin and D. Lu, Hypermethylation reduces expression of tumor-suppressor PLZF and regulates proliferation and apoptosis in non-small-cell lung cancers. *The FASEB Journal*, 2013. 27(10): p. 4194-4203.
36. Wang, J., Y. Yang, S. Guo, Y. Chen, C. Yang, H. Ji, X. Song, F. Zhang, Z. Jiang and Y. Ma, Association between copy number variations of HLA-DQA1 and ankylosing spondylitis in the Chinese Han population. *Genes and immunity*, 2013. 14(8): p. 500-503.
37. Lin, S., L. Pan, S. Guo, J. Wu, L. Jin, J.-C. Wang and S. Wang, Prognostic role of microRNA-181a/b in hematological malignancies: a meta-analysis. *PloS one*, 2013. 8(3): p. e59532.
38. Zhao, Y., S. Guo, J. Sun, Z. Huang, T. Zhu, H. Zhang, J. Gu, Y. He, W. Wang and K. Ma, 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.
39. Wu, J., J. Liu, Y. Zhou, J. Ying, H. Zou, S. Guo, L. Wang, N. Zhao, J. Hu and D. Lu, 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*, 2012.
40. Wu, J., J. Wu, Y. Zhou, H. Zou, S. Guo, J. Liu, L. Lu and H. Xu, Quantitative assessment of the variation in IGF2BP2 gene and type 2 diabetes risk. *Acta Diabetologica*, 2011: p. 1-11.

41. He, Y., Y. Cui, W. Wang, J. Gu, S. Guo, K. Ma and X. Luo, 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*, 2011. 13(9): p. 841IN23-853.
42. Zhou, X., J. Sun, Y. He, H. Zhang, J. Yu, S. Guo, Y. Cai, X. Hu and J. Zhu, Correlation of the methylation status of CpG islands in the promoter region of 10 genes with the 5-Fu chemosensitivity in 3 breast cancer cell lines]. *Zhonghua zhong liu za zhi [Chinese journal of oncology]*, 2010. 32(5): p. 328.
43. Xiang, H., J. Zhu, Q. Chen, F. Dai, X. Li, M. Li, H. Zhang, G. Zhang, D. Li and Y. Dong, Single base-resolution methylome of the silkworm reveals a sparse epigenomic map. *Nature biotechnology*, 2010. 28(5): p. 516-520.
44. Li, Y., J. Zhu, G. Tian, N. Li, Q. Li, M. Ye, H. Zheng, J. Yu, H. Wu and J. Sun, The DNA methylome of human peripheral blood mononuclear cells. *PLoS biology*, 2010. 8(11): p. e1000533.
45. Ao, J.-X., X.-J. Gao, Y.-B. Yu, B. Qu, X.-H. Yuan, Y. Liu and S.-C. Guo, Construction of a General Standard Molecule for the Qualitative Detection in Different Transgenic Foodcrops. *Journal of Northeast Agricultural University (English Edition)*, 2009. 16(2): p. 37-41.
46. AO, J., X. GAO, Y. QIU and S. GUO, Real-time quantitative PCR and the application in the detection of genetically modified plants [J]. *Journal of Northeast Agricultural University*, 2009. 6: p. 033.
47. AO, J.-x., X.-j. GAO, B. QU, X.-h. YUAN, Y. LIU, Y.-w. QIU and S.-c. GUO, Construction of a standard reference plasmid for detecting exogenous genes in transgenic soybean, maize and rice [J]. *Journal of China Agricultural University*, 2008. 6: p. 005.