# Shicheng Guo

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Education

2009-2014 Ph.D Candidate School of life sciences, Fudan University, **Shanghai**, China

2005-2009 Bachelor of Science   School of life sciences, Northeast Agricultural University, **Harbin**, China

**Key Skills**

Programming Language: R, Perl, Linux

Software: Matlab, SPSS, Original, Ultraedit, Adobe photoshop and illustrator

Supercomputer Calculation: Ubuntu and Portable Batch System (torque)

Experience

2013.05-present, Research scholar at the University of Texas Health Science Center at Houston, **Houston**, TX

2012.12-2013.4, Visiting Student at the University of Texas Health Science Center at Houston, **Houston**, TX

2012.12-2013.6, Internship in the CAS-MPG Partner Institute for Computational Biology, **Shanghai**, China

2012.12-2013.6, Internship in the institute of Rheumatology, Immunology and Allergy, **Shanghai**, China

HONORS AND AWARDS

Molecular Biology Reports (MOLE-D-13-08360, 2014)

Cancer (CNCR-13-1244, 2013)

REVIEW ACTIVITIES

Participated Projects

*DNA methylation markers for the diagnosis and recurrence prediction of bladder cancer [data analysis and bioinformatic]*

*Relationship between hsa-miR-191 and Epithelial-to-Mesenchymal Transition in Hepatocellular Carcinoma[bioinformatic]*

*The DNA methylome of human peripheral blood mononuclear cells project [methylation validation]*

*The DNA methylome of silkworm project [methylation validation]*

*Pharmacogenomics in Non-small Cell Lung Cancer and lung cancer susceptibility [data analysis]*

*key molecular events in the pathogenesis and treatment of scleroderma-associated pulmonary fibrosis [data analysis]*

*Hypermethylation reduces expression of tumor-suppressor PLZF and regulates proliferation and apoptosis in NSCLC [data analysis and bioinformatic]*

Validation of the GWAS discovered thyroid cancer susceptibility loci in Chinese thyroid cancer population [data analysis and bioinformatics]

Title (Number) 2013-20

*International Association for the Study of Lung Cancer (IASLC), Fellow Member(ID: 415405)*

Patents

*Methods and kits for diagnosising of bladder cancer with urine exfoliated cell, China, authorized*

*Methods and kits for prognosising of bladder cancer after surgery with urine exfoliated cell, China, authorized*

Awards and Honors

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

2009-2013, Model Student of Academic Records (2009, 2012, 2013, Fudan University)

2007, Second prize of National Mathematical Modeling Contest in Heilongjiang provice

2007, Social practice scholarship (NEAU)

2006, National Encouragement Scholarship

2005-2007, Model Student of Academic Records (NEAU)

2005, National Scholarship

Data Submission

GSE54961 (2014): Epigenome analysis of serum cell-free circulating DNA in progression of HBV-related Hepatocellular carcinoma

GSE54854 (2014): Global Analysis of DNA Methylation by Methyl-Capture Sequencing Reveals Epigenetic change of pancreatic cancer

GSE33839 (2012): Identification of a novel set of DNA methylation markers in bladder cancer using MBD-methylCap/seq and urine DNA screening in a Chinese population

PUBLICATIONS[[1-11](#_ENREF_1)]

1. **S.-C. Guo**, Y.-L Wang, Y. Li. Li Jin, M.-M Xiong, J.-C Wang. Significant SNPs have limited prediction ability for thyroid cancer. Cancer Medicine, 2013. accept (first author)
2. Wang, Y.-L**\***., S.-H. Feng**\***, **S.-C. Guo\***, W.-J. Wei, D.-S. Li, Y. Wang, X. Wang, Z.-Y. Wang 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. (co-first author)
3. 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.
4. 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.
5. Zhao, Y., H. Zhou, K. Ma, J. Sun, X. Feng, J. Geng, J. Gu, W. Wang, H. Zhang, Y. He, **S. Guo**, X. Zhou, J. Yu, and Q. Lin, Abnormal methylation of seven genes and their associations with clinical characteristics in early stage non-small cell lung cancer. Oncol Lett, 2013. 5(4): p. 1211-1218.
6. 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.(co-first author)
7. 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. 18(14): p. 3972-3981.
8. 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.
9. 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 (New York, NY), 2011. 13(9): p. 841.
10. 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.
11. 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. Nat Biotechnol. 2010;28:516-20.
12. 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., Huang Y., 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., Zhang X. The DNA methylome of human peripheral blood mononuclear cells. PLoS biology. 2010;8:e1000533

Paper On the way

1. **S.-C. Guo**, LiXing Tan, Weilin Pu, Li Jin, Jiucun Wang, Diagnosis Role of APC Promoter Methylation in Non-Small Cell Lung Cancer: A Integrate-Analysis of Published Article and Microarray Data. Clinical Epigenetics, 2013 (submited)
2. **S.-C. Guo**, Weilin Pu, Li Jin, Jiucun Wang, DNA methylation microarray-based meta-analysis identifies a panel of epigenetic biomarkers for NSCLC cancer diagnosis, 2013. (submit soon)

References

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| Li Jin Dr. | Jiucun Wang Dr. | Momiao Xiong Dr. |
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1. Zhao, Y., H. Zhou, K. Ma, J. Sun, X. Feng, J. Geng, J. Gu, W. Wang, H. Zhang, Y. He, S. Guo, X. Zhou, J. Yu, and Q. Lin, *Abnormal methylation of seven genes and their associations with clinical characteristics in early stage non-small cell lung cancer.* Oncol Lett, 2013. **5**(4): p. 1211-1218.

2. 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.

3. 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.

4. 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.

5. 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.

6. 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. **18**(14): p. 3972-3981.

7. 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.

8. 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 (New York, NY), 2011. **13**(9): p. 841.

9. 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.

10. 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.* Nat Biotechnol, 2010. **28**(5): p. 516-520.

11. 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.