# CURRICULUM VITAE

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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

Present Position

Research Assistant at Human Genetic Center, UTHealth, Houston, Texas

Experience

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

2012.12-2013.04, Visiting Student at the University of Texas Health Science Center at Houston, **Houston**, TX

2012.01-2013.12, Internship in the CAS-MPG Partner Institute for Computational Biology, **Shanghai**, China

2011.12-2014.09, Internship in the institute of Rheumatology, Immunology and Allergy, **Shanghai**, China

Professional activities

2013-present, International Association for the Study of Lung Cancer

2012-present, American Society of Human Genetics

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

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

Personal Statement

My research interests and activities mainly centered around the following areas: 1) Susceptibility or heritability components of Lung cancer derived from genetic (SNP, CNV) and epigenetic variation (DNA methylation). 2) Screening, early diagnosis and prognosis model for lung cancer identification or surveillance. 3) cancer biomarker research strategy leveraged by high dimensional genome-wide genetic or epigenetic dataset based on microarray or next generation sequencing. 4) Novel cancer related DNA methylation aberrant detection methods develop (bisulfite free detection) and analysis method (Functional based analysis method). 5) Relationship between elements of genome and epigenome and the interaction routine among environment factors with genetic and epigenetic variations in lung cancer.

References

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Abstract Published in Journals (Conference)

1. Guo S, Xiong M, Jin L, Wang J. (2014). Epigenetic Approaches for non-small cell lung cancer diagnosis based on DNA methylation, HGV2014, Sep 17- Sep 19, Belfast, Northern Ireland, UK (Full Scholarship)

2. Lin N, Jiang J, Guan X, Yu X, **Guo S** and Xiong MM. (2014). A novel method for ultrasound image analysis. NCI-NIBIB Point of Care Technologies for Cancer Conference. January 8-10, 2014, Natcher Center, NIH campus- Building 45, Bethesda, Maryland.

3. Lin N, Jiang J, **Guo S**, Yu X, Ma L and Xiong MM. (2014). Classification Analysis of Big Image Data. Statistical and Computational Theory and Methodology for Big Data Analysis. Feb 9-Feb 14, 2014, Calgary, AB Canada.

4. Yu J, Lin N, Ma L, **Guo S** and Xiong MM. (2014). Cloud computing for joint big genetic, epigentic and image data analysis. Keystone Symposia: Big Data in Biology, March 23—25, 2014. Fairmont San Francisco, San Francisco, California.

Seleted Publications ([1-19](#_ENREF_1))

1. Guo, S., Tan, L., Pu, W., Wu, J., Xu, K., Wu, J., Li, Q., Ma, Y., Xu, J. and Jin, L. (2014) Quantitative assessment of the diagnostic role of APC promoter methylation in non-small cell lung cancer. Clinical epigenetics, 6, 5.

2. Song, X., Guo, S., Chen, Y., Yang, C., Ji, H., Zhang, F., Jiang, Z., Ma, Y., Li, Y. and Jin L. (2014) Association between HLA-DQA1 gene copy number polymorphisms and susceptibility to rheumatoid arthritis in Chinese Han population. Journal of Genetics, 93.

3. Guo, S., Wang, Y., Li, Y., Jin, L., Xiong, M., Ji, Q.H. and Wang, J. (2014) Significant SNPs have limited prediction ability for thyroid cancer. Cancer Medicine.

4. Pan, L., Huang, Y., Wang, M., Zhuang, X., Luo, D., Guo, S., Zhang, Z., Huang, Q., Lin, S. and Wang, S. (2014) Positional cloning and next-generation sequencing identified a TGM6 mutation in a large Chinese pedigree with acute myeloid leukaemia. European Journal of Human Genetics.

5. Wu, L., Guo, S., Yang, D., Ma, Y., Ji, H., Chen, Y., Zhang, J., Wang, Y., Jin, L. and Wang, J. (2014) Copy number variations of HLA-DRB5 is associated with systemic lupus erythematosus risk in Chinese Han population. Acta biochimica et biophysica Sinica, 46, 155-160.

6. Zhao, Y., Zhou, H., Ma, K., Sun, J., Feng, X., Geng, J., Gu, J., Wang, W., Zhang, H. Guo, S., and He, Y. (2013) Abnormal methylation of seven genes and their associations with clinical characteristics in early stage non-small cell lung cancer. Oncology letters, 5, 1211-1218.

7. Wang, Y., Feng, S., Guo, S., Wei, W., Li, D., Wang, Y., Wang, X., Wang, Z.-Y., Ma, Y.-Y. and Jin, L. (2013) 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, 50, 689-695.

8. Wang, X., Wang, L., Guo, S., Bao, Y., Ma, Y., Yan, F., Xu, K., Xu, Z., Jin, L. and Lu, D. (2013) Hypermethylation reduces expression of tumor-suppressor PLZF and regulates proliferation and apoptosis in non-small-cell lung cancers. The FASEB Journal, 27, 4194-4203.

9. Wang, J., Yang, Y., Guo, S., Chen, Y., Yang, C., Ji, H., Song, X., Zhang, F., Jiang, Z. and Ma, Y. (2013) Association between copy number variations of HLA-DQA1 and ankylosing spondylitis in the Chinese Han population. Genes and immunity.

10. Lin, S., Pan, L., Guo, S., Wu, J., Jin, L., Wang, J.-C. and Wang, S. (2013) Prognostic role of microRNA-181a/b in hematological malignancies: a meta-analysis. PloS one, 8, e59532.

11. Zhao, Y., Guo, S., Sun, J., Huang, Z., Zhu, T., Zhang, H., Gu, J., He, Y., Wang, W. and Ma, K. (2012) Methylcap-seq reveals novel DNA methylation markers for the diagnosis and recurrence prediction of bladder cancer in a Chinese population. PloS one, 7, e35175.

12. Wu, J., Liu, J., Zhou, Y., Ying, J., Zou, H., Guo, S., Wang, L., Zhao, N., Hu, J. and Lu, D. (2012) 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, 18, 3972-3981.

13. Wu, J., Wu, J., Zhou, Y., Zou, H., Guo, S., Liu, J., Lu, L. and Xu, H. (2011) Quantitative assessment of the variation in IGF2BP2 gene and type 2 diabetes risk. Acta Diabetologica, 1-11.

14. He, Y., Cui, Y., Wang, W., Gu, J., Guo, S., Ma, K. and Luo, X. (2011) 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), 13, 841.

15. Zhou, X., Sun, J., He, Y., Zhang, H., Yu, J., Guo, S., Cai, Y., Hu, X. and Zhu, J. (2010) 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, 32, 328.

16. Xiang, H., Zhu, J., Chen, Q., Dai, F., Li, X., Li, M., Zhang, H., Zhang, G., Guo, S., Li, D. and Dong, Y. (2010) Single base-resolution methylome of the silkworm reveals a sparse epigenomic map. Nature biotechnology, 28, 516-520.

17. Li, Y., Zhu, J., Tian, G., Li, N., Li, Q., Ye, M., Zheng, H., Yu, J., Guo, S., Wu, H. and Sun, J. (2010) The DNA methylome of human peripheral blood mononuclear cells. PLoS biology, 8, e1000533.

18. AO, J., GAO, X., QIU, Y. and Guo, S. (2009) Real-time quantitative PCR and the application in the detection of genetically modified plants [J]. Journal of Northeast Agricultural University, 6, 033.

19. AO, J.-x., GAO, X.-j., QU, B., YUAN, X.-h., LIU, Y., QIU, Y.-w. and Guo, S. (2008) Construction of a standard reference plasmid for detecting exogenous genes in transgenic soybean, maize and rice [J]. Journal of China Agricultural University, 6, 005.