Curriculum Vitae

Fudan University

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**Objective**

Apply for exchange visiting in 2012-2013

**Introduction**

My name is Shicheng Guo, a Ph.D. candidate studying at Ministry of Education Key Laboratory of Contemporary Anthropology, School of Life Sciences, Fudan University, Shanghai, China and will be graduated at 2014. What I am researching now is computational epigenetics, including investigation on the role of DNA and miRNA methylation in the cancer pathogenesis, development, and the clinical value in cancer therapy and prognosis with bioinformatic and computational methods and tools. Cancer is a complex disease with great heterogeneous but with a common DNA methylation alternative ( genome-wide hypomethylation and local hypermathylation ) which can be used to be as excellent dignosis and prognosis biomarker. In the past three years, I had participated in series of important research(see below), participated in publishing several important papers(Nature Biotechnology, Plos Biology et al) and two chinese patents.

**Key Skills**

Programming Language: R, Perl, Matlab

Specific Software: Matlab, SPSS, Original, Ultraedit, Emacs, Adobe photoshop, Adobe illustrator

OS: Ubuntu and Portable Batch System(torque)

**Languages**

English, Chinese.

**Education and internship**

2009-2014 PH.D candidate Fudan University,shanghai,china

2005-2009 Bachelor of Science   Northeast Agricultural University, Harbin,china

**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-smallCcell Lung Cancer and lung cancer susceptibility [data analysis]*

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

**Patents**

*Methods and kits for diagnosising of bladder cancer with urine exfoliated cell 201110287529.2*

*Methods and kits for prognosising of bladder cancer after surgery with urine exfoliated cell  201110430858.8*

**Main Publishment(no including chinese articles)**

*1. Zhao Y,* ***Guo S****, Sun J, Huang Z, Zhu T, Zhang H, Gu J, He Y, Wang W, Ma K et al: 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):e35175(co-fisrt author).*

2. 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. 841-53.

3. Zhou, X.Y., J.F. Sun, Y.H. He, H.Y. Zhang, J. Yu, **S.C. Guo**, Y. Cai, X.C. Hu, and J.D. 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, 2010. **32**(5): p. 328-33.

4. Xiang, H., J. Zhu, Q. Chen, F. Dai, X. Li, M. Li, H. Zhang, G. Zhang, D. Li, Y. Dong, L. Zhao, Y. Lin, D. Cheng, J. Yu, J. Sun, X. Zhou, K. Ma, Y. He, Y. Zhao, **S. Guo**, M. Ye, G. Guo, Y. Li, R. Li, X. Zhang, L. Ma, K. Kristiansen, Q. Guo, J. Jiang, S. Beck, Q. Xia, W. Wang, and J. Wang, *Single base-resolution methylome of the silkworm reveals a sparse epigenomic map.* Nature Biotechnology, 2010. **28**(5): p. 516-20.

5. Li, Y., J. Zhu, G. Tian, N. Li, Q. Li, M. Ye, H. Zheng, J. Yu, H. Wu, J. Sun, H. Zhang, Q. Chen, R. Luo, M. Chen, Y. He, X. Jin, Q. Zhang, C. Yu, G. Zhou, Y. Huang, H. Cao, X. Zhou, **S. Guo**, X. Hu, X. Li, K. Kristiansen, L. Bolund, J. Xu, W. Wang, H. Yang, J. Wang, R. Li, S. Beck, and X. Zhang, *The DNA methylome of human peripheral blood mononuclear cells.* Plos Biology, 2010. **8**(11): p. e1000533.