

## 教师信息



**张世华** Shihua Zhang

性 别: 男

单 位: 理学院

专业名称: 生物信息学

研究方向: 功能基因组学

技术职务: 副教授

办公电话: 0551-5786164

办公传真: 0551-5786164

E-mail: zhangshihua@ahau.edu.cn

通讯地址: 安徽省合肥市蜀山区长江西路130号

邮政编码: 230036

### 张世华 男, 博士, 硕士生导师

茶树生物学与资源利用国家重点实验室博士后, 美国佐治亚大学Jeffrey Bennetzen院士植物基因组组方向访问学者一年。主要从事茶树品质成分形成的功能基因组学和化学信息学课题研究, 近阶段尤其关注多层面组学数据的整合分析。迄今以第一作者(或通讯)在生命科学领域相关的期刊如《Briefings in Bioinformatics》、《BMC plant biology》、《Gene》和《FEBS letters》上发表SCI论文多篇。SM Journal of Bioinformatics and Proteomics期刊editor member, Nucleic Acids Research、Database、Scientific Reports等杂志referee。

Dr. Zhang is engaged in his scientific research as a post-doctor in State Key Laboratory of Tea Plant and Utilization in Anhui Agricultural University. He has worked as one-year-term visiting scholar in plant genomics field in The University of Georgia. His research interest is functional genomics and cheminformatics in the field of tea quality ingredient biosynthesis. He has first/corresponding authored a number of papers in refereed journals, including BMC Plant Biology, Gene, and FEBS Letters. He is a referee for several journals such as Nucleic Acids Research, Database and Scientific Reports.

主讲课程:

主要教学经历与成果:

- 1) 为本科生、研究生系统讲授《生物信息学》、《生物统计学》、《食品实验设计与数据分析》等课程;
- 2) 作为主要参与者, 参加全国农林院校“十二五”规划教材《生物信息学》的编写, 农业出版社

#### 科研情况:

##### 主持科研项目:

- 1) 基于网络建模解析水稻在不同非生物逆境下miRNA 的串扰调控关系 (国家自然科学基金青年基金, 31301248)
- 2) 植物非生物逆境下microRNA网络调控机制分析平台的构建 (中国博士后科学基金面上项目, 2013M531498)
- 3) 2014年安徽农业大学生物统计学学科点学科骨干培育项目 (2014XKPY-37)
- 4) 基于文本挖掘的人类遗传疾病的相关性研究 (11541298, 黑龙江省教育厅科学技术研究项目)

#### 论文论著:

##### First-author and corresponding papers:

- 1) **Shihua Zhang**, Liang Zhang, Yuling Tai, Xuewen Wang, Chi-Tang Ho and Xiaochun Wan\*, Gene Discovery of Characteristic Metabolic Pathways in the Tea Plant (*Camellia sinensis*) Using ‘Omics’-Based Network Approaches: A Future Perspective, *Front. Plant Sci.* 9:480. doi: 10.3389/fpls.2018.00480
- 2) **Shihua Zhang**†, Liang Zhang†, Yijun Wang†, Jian Yang, Mingzhi Liao, Shoudong Bi, Zhongwen Xie, Chi-Tang Ho and Xiaochun Wan\*, TBC2target: A Resource of Predicted Target Genes of Tea Bioactive Compounds *Front. Plant Sci.* 9:211. doi: 10.3389/fpls.2018.00211
- 3) **Shihua Zhang**\*, Hongdong Xuan\*, Liang Zhang, Sicong Fu, Yijun Wang, Hua Yang, Yuling Tai, Youhong Song, Jinsong Zhang, Chi-Tang Ho, Shaowen Li and Xiaochun Wan, TBC2health: a database of experimentally validated health-beneficial effects of tea bioactive compounds, *Briefings in Bioinformatics* 2016, doi: 10.1093/bib/bbw055
- 4) Linzhong Zhang, Hongdong Xuan, Yongchun Zuo, Gaojian XuPing Wang, Youhong Song, **Shihua Zhang**\*, Topological characteristics of target genes regulated by abiotic-stress-responsible miRNAs in a rice interactome network, *Functional & Integrative Genomics* 2016 16(3), 243-251 (通讯)
- 5) Hongdong Xuan, Linzhong Zhang, Xueshi Liu, Guomin Han, Juan Li, Xin Li, Aiguo Liu, Mingzhi Liao, **Shihua Zhang**\*, PLNlncRbase: a resource for experimentally identified lncRNAs in plants, *Gene* 2015, 573, 328-332 (通讯)
- 6) Leijie Li, Liangcai Zhang, Guiyou Liu, Rennan Feng, Lei Yang, **Shihua Zhang**\*, Mingzhi Liao\*, and Jinnlian Hua\*, Synergistic Transcriptional and Post-Transcriptional Regulation of ESC Characteristics by Core Pluripotency Transcription Factors in Protein-Protein Interaction Networks, *PLoS ONE* 2014 9(8): e105180. doi:10.1371/journal.pone.0105180 (通讯)
- 7) Hongdong Xuan, Xin Li, Shenrong Ren, **Shihua Zhang**\*, Modular organization of the human disease genes: a text-based network inference, *Bioinformatics* 2015, 11(9): 432-436 (通讯)
- 8) **Shihua Zhang**, Yi Yue, Liang Sheng, Yunzhi Wu, Guohua Fan, Ao Li, Xiaoyi Hu, Mingzhu ShangGuan and Chaoling Wei\*, PASmiR: a literature-curated database for miRNA molecular regulation in plant response to abiotic stress, *BMC plant biology* 2013, 13 (33), 1-8
- 9) **Shihua Zhang**, Jing Xu, Chaoling Wei\*, Sequence periodic pattern of HERV LTRs: A matrix simulation algorithm, *Journal of biosciences* 2012, 37(1), 1-6

- 10) **Shihua Zhang**, Chunyu Wang, Bo Xi, Xia Li\*, Association between tumor necrosis factor- $\alpha$ -308G/A polymorphism and chronic obstructive pulmonary disease: An update, *Respirology* 2011, 16, 107-115
- 11) **Shihua Zhang**, Chao Wu, Xia Li\*, Xi Chen, Wei Jiang, Binsheng Gong, Jiang Li, Yuqing Yan, From phenotype to gene: detecting disease-specific gene functional modules via a text-based disease phenotype network construction, *FEBS letters* 2010, 584, 3635-3643
- 12) **Shihua Zhang** and Yi Xiao\*, Quasiperiodic property in Alu repeats, *Physical Review E* 2006, 74, 022901-4

**Co-author papers:**

- 11) Yuan Yang, Wenjing Wang, Liangcai Zhang, **Shihua Zhang**, Guiyou Liu, Yingcui Yu, Mingzhi Liao, Association of single nucleotide polymorphism rs6983267 with the risk of prostate cancer, *Oncotarget*. 2016 Mar 18. doi: 10.18632/oncotarget.8186.
- 12) Yongchun Zuo, Wenxia Su, **Shihua Zhang**, Shanshan Wang, Chengyan Wu, Lei Yang, Guangpeng Li, Discrimination of membrane transporter protein types using K-nearest neighbor method derived from similarity distance of total diversity measure, *Molecular BioSystems* 2015 11(3):950-7.
- 13) Wei Liu, Xuefeng Bai, Yuejuan Liu, Wei Wang, Junwei Han, Qiuyu Wang, Yanjun Xu, Chunlong Zhang, **Shihua Zhang**, Xuecang Li, Zhonggui Ren, Jian Zhang, Chunquan Li, Topologically inferring pathway activity toward precise cancer classification via integrating genomic and metabolomic data: prostate cancer as a case, *Scientific Reports*, 2015, 5:1-15
- 14) Liang Zhang, Yuhui Han, Jinjun Shan, Yuhong Liang, Liwei Xu, **Shihua Zhang**, JunSong Li, Xiaochun Wan, Simultaneous determination of seven catechins in rat plasma by ultra-high performance liquid chromatography tandem mass spectrometry and its application to a pharmacokinetics study, *Analytical Methods* 2015, 7(22), 9415-9420
- 15) Chao Wu, Fan Zhang, Xia Li, **Shihua Zhang**, Jiang Li, Fei Su, Kongning Li, Yuqing Yan, Composite functional module inference: detecting cooperation between transcriptional regulation and protein interaction by mantel test, *BMC Systems Biology* 2010, 4:82

**Conference papers:**

- 16) **Shihua Zhang**, Mingzhi Liao, Xia Li\*, The modular property implied in the human disease gene network, *The 5th International Conference on Frontier of Computer Science and Technology - Workshop on Bioinformatics and System Biology*, Start Page 58, Wuhan, June 4-6, 2010
- 17) **Shihua Zhang**, Chao Wu, Xia Li\*, Mingzhi Liao, Yuqing Yan, Sequence periodicity of human endogenous retroviruses, *The 5th International Conference on Frontier of Computer Science and Technology - Workshop on Bioinformatics and System Biology*, Start Page 47, Wuhan, June 4-6, 2010

