

一、教育经历

1. 2003. 09—2008. 07, 南京农业大学生命科学学院, 硕士, 博士
2. 1994. 09—1998. 07, 天津商业大学生物技术与食品科学学院, 学士。

二、工作经历

1. 2013. 01—至今, 南京农业大学, 资源与环境科学学院, 副教授
2. 2011. 11—2012. 12, 南京农业大学, 资源与环境科学学院, 讲师
3. 2008. 09—2011. 10, 南京农业大学, 农业资源与利用博士后流动站, 博士后
4. 1998. 09—2003. 08, 南京雨润集团, 技术员

三、教学情况

1. 本科生课程《植物生态学》
2. 研究生课程《非编码 RNA 研究进展》

四、主持项目

主要从事植物逆境生态和盐碱地开发利用。

1. 江苏省重点研发 (BE2017310-2), 骨干;
2. 江苏省科研院所农技推广试点项目 [TG(17)004], 骨干;
3. 国家自然科学基金 (31200204), 主持;
4. 中国博士后科学基金重点资助 (201003593), 主持;
5. 中国博士后科学基金 (20090451223), 主持。

五、发表论文

1. Xu ZK, Shao TY, Lv Z, Yue Y, Liu AH, Long XH*, **Zhou ZS**, Gao XM, Rengel Z. The mechanisms of improving coastal saline soils by planting rice. *Science of the Total Environment*. 2019 Nov 16:135529. doi: 10.1016/j.scitotenv.2019.135529.
2. Chen SJ, Zhu Y, Shao TY, Long XH*, Gao XM, **Zhou ZS**. Relationship between rhizosphere soil properties and disease severity in highbush blueberry (*Vaccinium corymbosum*). *Applied Soil Ecology*, 2019, 137: 187-194.
3. Xuan Y, **Zhou ZS***, Li HB, Yang ZM*. Identification of a group of XTHs genes responding to heavy metal mercury, salinity and drought stresses in *Medicago truncatula*. *Ecotoxicol Environmental Safety*, 2016, 132: 153-163.
4. Gao S, Yang L, Zeng HQ, **Zhou ZS**, Yang ZM, Li H, Sun D, Xie F, Zhang B. A cotton miRNA is involved in regulation of plant response to salt stress. *Scientific Reports*, 2016, 6:19736
5. Sun D, Chen J, **Zhou ZS**, Zhu CC, Hu LB, Wang L, Yang L, Yang ZM. Ectopic Expression of a Proteinase Inhibitor I4 (MtPiI4) Gene from *Medicago truncatula* Confers Plant Resistance to *Pseudomonas syringae* pv. Tomato DC3000. *Plant Molecular Biology Reporter*, 2015, 33:1686-96.
6. Song JB, Wang YX, Li HB, Li BW, **Zhou ZS***, Gao S, Yang ZM*. The F-box family genes as key elements in response to salt, heavy mental, and drought stresses in *Medicago truncatula*. *Functional & Integrative Genomics*. 2015, 15(4): 495-507.
7. **Zhou ZS**, Yang SN, Zhu CC, Liu ZP, Yang ZM. Molecular dissection of mercury-responsive transcriptome and sense/antisense genes in *Medicago truncatula* by high-throughput sequencing. *Journal of Hazardous Materials*. 2013, 252-253: 123-131.
8. **Zhou ZS**, Song JB, Yang ZM. Genome-wide identification of *Brassica napus* microRNAs and their targets in response to cadmium. *Journal of Experiment Botany*. 2012, 63(12): 4597-4613.

9. Zhang JJ, **Zhou ZS**, Song JB, Liu ZP, Yang H. Molecular dissection of atrazine-responsive transcriptome and gene networks in rice by high-throughput sequencing. *Journal of Hazardous Materials*. 2012, 219–220: 57–68.
10. **Zhou ZS**, Zeng HQ, Liu ZP, Yang ZM. Genome-wide identification of *Medicago truncatula* microRNAs and their targets reveals their differential regulation by heavy metal. *Plant, Cell and Environment*. 2012, 35: 86–99.
11. **Zhou ZS**, Guo K, Abdelrahman AE, Yang ZM. Salicylic acid alleviates mercury toxicity by preventing oxidative stress in roots of *Medicago sativa*. *Environmental & Experimental Botany*. 2009, 65(1): 27–34.
12. **Zhou ZS**, Wang SJ, Yang ZM. Biological detection and analysis of mercury toxicity to alfalfa (*Medicago sativa*) plants. *Chemosphere*. 2008, 70: 1500–1509.
13. **Zhou ZS**, Huang SQ, Yang ZM. Bioinformatic identification and expression analysis of new microRNAs from *Medicago truncatula*. *Biochemical and Biophysical Research Communications*. 2008, 374(3): 538–542.
14. **Zhou ZS**, Huang SQ, Guo K, Mehta SK, Zhang, PC, Yang ZM. Metabolic adaptations to mercury-induced oxidative stress in roots of *Medicago sativa* L. *Journal of Inorganic Biochemistry*. 2007, 101: 1–9.
15. 闻奋亮, 隆小华, 岳杨, 何腾飞, 高秀美, 周兆胜*. 菊芋蔗糖代谢相关产物与关键酶基因对高温的响应. *生态学杂志*, 2020, 39(1): 82–92.