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赵涵

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主要从事玉米功能基因组和生物信息学研究。主要承担国家自然科学基金，转基因专项和国家重点研发项目等。目前的研究方向为玉米氮高效利用的遗传解析和玉米杂种优势群专化分子标记开发并用于辅助育种研究，构建了玉米氮响应的遗传调控网络，确定了部分关键的节点转录因子，通过生物信息学手段和大数据分析获得的分子标记已筛选出2000余份背景明确的优良自交系。近五年来发表论文30余篇，其中SCI 12篇，专利10余项。 *Genetics*, *Plant Breeding*, *MGG*, *JGG*, *Crop Science*, *Molecular*, *Plant Cell Reports*, *Scientific Reports*, *Plos One*等期刊的审稿人和教育部、农业部等部委项目评审验收专家。

- F Lin, L Jiang, Y Liu, Y Lv, H Dai, **H. Zhao**. Genome-wide identification of housekeeping genes in maize. *Plant Molecular Biology* 2014, 86, 543-554
- Lucas, C.J., **Zhao, H.**, Schneerman, M. and Moose, S.P. 2012. Genomic changes in response to 110 cycles of selection for seed protein and oil concentration in maize. Book chapter in *Seed Genomics*. P. Becraft ed., Wiley
- Feng Lin, Huabing Bao, Yuhe Liu, Jun Yang, Huixue Dai, and **Han Zhao**. Genome-wide discovery of maize tissue-specific genes in maize. *Plant Molecular Biology Reports*. 2016.
- Lv Y, Liang Z, Ge M, Qi WC, Zhang TF, Lin F, Peng Z, **Zhao H**. Genome-wide identification and functional prediction of nitrogen-

responsive intergenic and intronic long non-coding RNAs in maize (*Zea mays* L.). *BMC Genomics*, 2016, 17:350

- Lv Y, Liu Y, **Zhao H**. mInDel: a high-throughput and efficient pipeline for genome-wide InDel marker development. *BMC Genomics*, 2016, 17:290
- Qi WC, Lin F, Liu Y, Huang B, Cheng J, Zhang W, **Zhao H**. High-throughput development of simple sequence repeat markers for genetic diversity research in *Crambe abyssinica*. *BMC Plant Biology* 2016, 16:139
- Jiang L, Ge M, **Zhao H**, Zhang T. Analysis of heterosis and quantitative trait loci for kernel shape related traits using triple testcross population in maize. *PLoS One*. 2015;10(4), e0124779
- Pei du, Lifang Zhuang, Yanzhi Wang, Li Yuan, Qing Wang, Danrui Wang, dawadondup Dawadondup, Lijun Tan, Jan Shen, Haibin Xu, **Han Zhao**, Chenggen Chu, Zengjun Qi . Development of oligonucleotides and multiplex probes for quick and accurate identification of wheat and *Thinopyrum bessarabicum* chromosomes Genome. Published on the web 14 September 2016, 10.1139/gen-2016-0095
- Li, C., Qiao, Z., Qi, W., Wang, Q., Yuan, Y., Yang, X., Tang, Y., Mei, B., Lv, Y., **Zhao, H.**, Xiao, H., Song, R.(2015). Genome-wide characterization of cis-acting DNA targets reveals the transcriptional regulatory framework of Opaque2 in maize. *Plant Cell* 27: 532–545
- Wei Zhang, Nelson Garcia, Yaping Feng, **Han Zhao**, Joachim Messing, Genome-wide histone acetylation correlates with active transcription in maize, *Genomics*, Volume 106, Issue 4, October 2015, Pages 214-220
- Zhang TF, Ge M, Ye X, Bughrara SS, **Zhao H**. Construction of a linkage map for quantitative trait loci associated with economically important traits in creeping bentgrass (*Agrostis stolonifera* L.). *Euphytica* 2012 188: 347-360
- **Zhao H.**, S.S. Bughrara, and Jose Alberto Oliveira 2009. Genetic relationships in snow mold resistant clones of creeping bentgrass.

Plant Breeding, DOI: 10.1111/j.1439-0523.2009.01690.x.

地址: 江苏省南京市钟灵街50号 **电话:** 025-84390297 苏ICP备10002657号-6 赵涵 - 研究员 - 江苏省农业科学院种质资源与生物技术研究所 Copyright © 2003-2015, All Rights Reserved