

姓名：蔡彩平 博士，副教授，硕士生导师

性别：女

毕业院校：南京农业大学

办公地址：理科楼 A418

办公电话：025-84395311

电子邮箱：cpcai@njau.edu.cn

研究方向：棉花基因组研究与分子育种

研究内容：构建了富含功能标记的四倍体栽培棉种遗传图谱，开发了 10,180 对 A/D 基因组同源基因间内含子长度多态的 ILPs 标记，开发了 8 万点的陆地棉全基因组覆盖的 CottonSNP80K 芯片。基于这些不同类型的标记开展以下两方面研究：1. 全基因组水平开展纤维品质及耐盐相关性状分析，挖掘出一批优异种质资源及优质耐盐基因/QTLs，进一步对这些候选基因/QTLs 开展功能解析，创造目标性状改良的遗传材料；2. 利用突变体材料开展棉花表皮毛、叶型、叶色等重要性状关键基因的发掘及功能分析。

以第一作者发表 SCI 论文 9 篇，参编《Transgenic Cotton》本科教材的一章，主持国家自然科学基金等国家、省部级项目 6 项。博士研究生论文获 2010 年江苏省优秀博士学位论文。2012 年入选南京农业大学首批“钟山学术新秀”。

教育经历：

2005.9-2009.6，南京农业大学，农学院，作物遗传育种，博士

2002.9-2005.6，山西农业大学，农学院，硕士

1998.9-2002.6，山西农业大学，农学院，学士

工作经历：

2017.3-2018.12, East Carolina University, Department of Biology, Visiting Scholar

2014/12-至今，南京农业大学，农学院，副教授

2009/7-2014/11，南京农业大学，农学院，讲师

代表性论文：(#为同等贡献作者，*为通讯作者)

1. **Cai C**, Wang X, Zhang B, Guo W*. Tobacco Rattle Virus-Induced Gene Silencing in Cotton. *Methods Mol Biol.* 2019,1902:105-119.
2. **Cai C**#, Guo W, Zhang B*. Genome-wide identification and characterization of SPL transcription factor family and their evolution and expression profiling analysis in cotton. *Sci Rep.* 2018, 8(1):762.
3. **Cai C**#, Zhu G#, Zhang T, Guo W*. High-density 80 K SNP array is a powerful tool for genotyping *G. hirsutum* accessions and genome analysis. *BMC Genomics.* 2017, 18(1):654.
4. **Cai C**#, Wu S#, Niu E, Cheng C, Guo W*. Identification of genes related to salt stress tolerance using intron-length polymorphic markers, association mapping and virus-induced gene silencing in cotton. *Sci Rep.* 2017, 7(1):528.
5. **Cai C**, Zhang X, Niu E, Zhao L, Li N, Wang L, Ding L, Guo W*. *GhPSY*, a phytoene synthase gene, is related to the red plant phenotype in upland cotton (*Gossypium hirsutum* L.). *Mol Biol Rep.* 2014, 41(8):4941-52.
6. **Cai C**, Ye W, Zhang T, Guo W*. Association analysis of fiber quality traits and exploration of elite alleles in Upland cotton cultivars/accessions (*Gossypium hirsutum* L.). *J Integr Plant Biol.* 2014, 56(1):51-62.
7. **Cai C**, Tong X, Liu F, Lv F, Wang H, Zhang T, Guo W*. Discovery and identification of a novel Ligon lintless-like mutant (Lix) similar to the Ligon lintless (Li1) in allotetraploid cotton. *Theor Appl Genet.* 2013, 126(4):963-70.
8. **Cai C**, Niu E, Du H, Zhao L, Feng Y, Guo W*. Genome-wide analysis of the WRKY transcription factor gene family in *Gossypium raimondii* and the expression of orthologs in cultivated tetraploid cotton. *The Crop J*, 2014, 2:4941-52.
9. Guo W#, **Cai C**#, Wang C, Zhao L, Wang L, Zhang T*. A preliminary analysis of genome structure and composition in *Gossypium hirsutum*. *BMC Genomics.* 2008, 9:314.
10. Guo W#, **Cai C**#, Wang C, Han Z, Song X, Wang K, Niu X, Wang C, Lu K, Shi B, Zhang T*. A microsatellite-based, gene-rich linkage map reveals genome structure, function and evolution in *Gossypium*. *Genetics.* 2007, 176(1):527-41.