

Zhuang Jing



Areas of Research

Tea Science.

Contact Information

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Research Interests

Tea plant evolutionary genomics; Tea plant domestication; Tea plant secondary metabolism; Tea plant abiotic stress

Education Background

Bachelor: Yangzhou University

Master: Yangzhou University

Doctor: Nanjing Agricultural University

Work experience

Associate Professor, Crop Breeding and Cultivation Research Institute, Shanghai Academy of Agricultural Sciences, 1999-2008

Researcher Scientist, Postdoctor, Life Science, Plant Biotech, Alberta Research Council, Canada, 2009-2011

Professor, Tea Science Research Institute, College of Horticulture, Nanjing Agricultural University, 2012-

Honors and Awards

Second class prize of Shanghai Advanced Science and Technology

Third class prize of Shanghai Advanced Science and Technology

Selected Publication

- (1) Book Chapter: Wang YX, Liu ZW, Li H, Wang WL, Cui X, **Zhuang J***. Understanding response of tea plants to heat stress and the mechanisms of adaptation. Chapter of “STRESS PHYSIOLOGY OF TEA IN THE FACE OF CLIMATE CHANGE”. Edit by Wenyan Han and Golam Jalal Ahammed. Springer Nature. 2018.
- (2) Liu ZW, Li H, Liu JX, Wang Y, **Zhuang J***. Integrative analysis of transcriptome, proteome, and microRNA reveals the effects of nitrogen sufficiency and deficiency conditions on theanine metabolism in tea plant (*Camellia sinensis*). Hort Res. 2020, 7:1-17.
- (3) Teng RM, Wu ZJ, Ma HY, Wang YX, **Zhuang J***. Differentially Expressed Protein Are Involved in Dynamic Changes of Catechins Contents in Postharvest Tea Leaves under Different Temperatures. J Agric Food Chem. 2019, 67(26):7547-7560. (封面论文)
- (4) Shen W, Li H, Teng R, Wang Y, Wang W, **Zhuang J***. Genomic and transcriptomic analyses of HD-Zip family transcription factors and their responses to abiotic stress in tea plant (*Camellia sinensis*). Genomics. 2019, 111(5):1142-1151.
- (5) Wu ZJ, Ma HY, **Zhuang J***. iTRAQ-based proteomics monitors the withering dynamics in postharvest leaves of tea plant (*Camellia sinensis*). Mol Genet Genomics. 2018, 293(1):45-59.
- (6) Cui X, Wang YX, Liu ZW, Wang WL, Li H, **Zhuang J***. Transcriptome-wide identification and expression profile analysis of the bHLH family genes in *Camellia sinensis*. Funct Integr Genomics. 2018, 18(5):489-503.
- (7) Li H, Liu ZW, Wu ZJ, Wang YX, Teng RM, **Zhuang J***. Differentially expressed protein and gene analysis revealed the effects of temperature on changes in ascorbic acid metabolism in harvested tea leaves. Hort Res. 2018, 5:65.
- (8) Wang WL, Wang YX, Li H, Liu ZW, Cui X, **Zhuang J***. Two MYB transcription factors (CsMYB2 and CsMYB26) are involved in flavonoid biosynthesis in tea plant [*Camellia sinensis* (L.) O. Kuntze]. BMC Plant Biol. 2018, 18(1):288.
- (9) Liu ZW, Li H, Wang WL, Wu ZJ, Cui X, **Zhuang J***. CsGOGAT Is Important in Dynamic Changes of Theanine Content in Postharvest Tea Plant Leaves under Different Temperature and Shading Spreadings. J Agric Food Chem. 2017, 65(44):9693-9702.
- (10) Liu ZW, Wu ZJ, Li H, Wang YX, **Zhuang J***. L-Theanine Content and Related Gene Expression: Novel Insights into Theanine Biosynthesis and Hydrolysis among Different Tea Plant (*Camellia sinensis* L.) Tissues and Cultivars. Front Plant Sci. 2017, 8:498.
- (11) Wu ZJ, Wang WL, **Zhuang J***. Developmental processes and responses to hormonal stimuli in tea plant (*Camellia sinensis*) leaves are controlled by GRF and GIF gene families. Funct Integr Genomics. 2017, 17(5):503-512.
- (12) Wu ZJ, Wang WL, **Zhuang J***. TCP family genes control leaf development and its responses to hormonal stimuli in tea plant [*Camellia sinensis* (L.) O. Kuntze]. Plant Growth Regul. (2017) 83:43–53
- (13) Liu ZW, Wu ZJ, Li XH, Huang Y, Li H, Wang YX, **Zhuang J***. Identification, classification, and expression profiles of heat shock transcription factors in tea plant (*Camellia sinensis*) under temperature stress. Gene. 2016, 576(1):52-59.
- (14) Wu ZJ, Li XH, Liu ZW, Li H, Wang YX, **Zhuang J***. Transcriptome-wide identification

- of *Camellia sinensis* WRKY transcription factors in response to temperature stress. Mol Genet Genomics. 2016, 291(1):255-269.
- (15) Wu ZJ, Li XH, Liu ZW, Li H, Wang YX, **Zhuang J***. Transcriptome-based discovery of AP2/ERF transcription factors related to temperature stress in tea plant (*Camellia sinensis*). Funct Integr Genomics. 2015, 15(6):741-752.
 - (16) Wu ZJ, Li XH, Liu ZW, Xu ZS, **Zhuang J***. De novo assembly and transcriptome characterization: novel insights into catechins biosynthesis in *Camellia sinensis*. BMC Plant Biol. 2014, 14:277.
 - (17) **Zhuang J**, Li MY, Wu B, Liu YJ, Xiong AS. Arg156 in the AP2-Domain Exhibits the Highest Binding Activity among the 20 Individuals to the GCC Box in BnaERF-B3-hy15, a Mutant ERF Transcription Factor from *Brassica napus*. Front Plant Sci. 2016, 7:1603.
 - (18) **Zhuang J**, Wang F, Xu ZS, Xiong AS. Microarray analysis of different expression profiles between wild-type and transgenic rice seedlings overexpression *OsDREB1B1* gene. Biologia. 2015, 70(6): 760-770.
 - (19) **Zhuang J***, Zhu B. Analysis of *Brassica napus* ESTs: gene discovery and expression patterns of AP2/ERF-family transcription factors. Mol Biol Rep. 2014, 41(1): 45-56.
 - (20) **Zhuang J**, Zhang J, Hou XL, Wang F, Xiong AS. Transcriptomic, Proteomic and Functional Genomic Approaches for the Study of Abiotic Stress in Vegetable Crops. Crit Rev Plant Sci. 2014, 33:225-237.
 - (21) **Zhuang J**, Jiang HH, Wang F, Peng RH, Yao QH, Xiong AS. A Rice OsAP23, Functioning as an AP2/ERF Transcription Factor, Reduces Salt Tolerance in Transgenic Arabidopsis. Plant Mol Biol Rep. 2013 31:1-10.
 - (22) **Zhuang J**, Yao QH, Xiong AS, Zhang J. Isolation, phylogeny and expression patterns of AP2-like genes in apple (*Malus x domestica* Borkh). Plant Mol Biol Rep. 2011 29: 209-216.
 - (23) **Zhuang J**, Chen JM, Yao QH, Xiong F, Sun CC, Zhou XR, Zhang J, Xiong AS. Discovery and expression profile analysis of AP2/ERF family genes from *Triticum aestivum*. Mol Biol Rep. 2011, 38: 745-753.
 - (24) **Zhuang J**, Anyia A, Vidmar J, Xiong AS, Zhang J. Discovery and expression assessment of the AP2-like genes in *Hordeum vulgare*. Acta Physiol Plant. 2011, 33, 1639-1649.
 - (25) **Zhuang J**, Deng DX, Yao QH, Zhang J, Xiong F, Chen JM, Xiong AS. Discovery, phylogeny and expression patterns of AP2-like genes in maize. Plant Grow Regul. 2010, 62:51-58.
 - (26) **Zhuang J**, Xiong AS, Peng RH, Gao F, Zhu B, Zhang J, Fu XY, Jin XF, Chen JM, Zhang Z, Qiao YS, Yao QH. Analysis of *Brassica rapa* ESTs: gene discovery and expression patterns of AP2/ERF family genes. Mol Biol Rep. 2010, 37:2485-2492.
 - (27) **Zhuang J**, Sun CC, Zhou XR, Xiong AS, Zhang J. Isolation and characterization of an AP2/ERF-RAV transcription factor BnaRAV-1-HY15 in *Brassica napus* L. HuYou15. Mol Biol Rep. 2011, 38:3921-3928.
 - (28) **Zhuang J**, Peng RH, Max Cheng, Zhang J, Cai B, Zhang Z, Gao F, Zhu B, Fu XY, Jin XF, Chen JM, Qiao YS, Xiong AS, Yao Q. Genome-wide analysis of the putative AP2/ERF family genes in *Vitis vinifera*. Sci Hort. 2009, 123: 73-81.
 - (29) **Zhuang J**, Cai B, Peng RH, Zhu B, Jin XF, Xue Y, Gao F, Fu XY, Tian YS, Zhao W, Qiao YS, Zhang Z, Xiong AS, Yao QH. Genome-wide analysis of the AP2/ERF gene family in *Populus trichocarpa*. Biochem Biophys Res Comm. 2008, 371(3): 468-474.
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