

Shangguan Lingfei



Areas of Research

Grape Physiology and Molecular Biology; Grape Functional Genomics

Contact Information

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Research Interests

Dr. Shangguan integrates the bioinformatics, molecular biology, genomics, field trials and other technical methods to investigate the grape biological and industrial issues, especially the responsive mechanism of copper stress, bud dormancy, and precise cultivation. Moreover, I do much technical service to grape and wine industries.

Education Background

Doctor: Nanjing Agricultural University

Postdoctoral: Beltsville Agricultural Research Center: USDA ARS

Work experience

Lecturer, Nanjing Agricultural University, 2013.09-2015.12

Associate Professor, Nanjing Agricultural University, 2016.01-now

Development Center for Science and Technology, MARA, program executive, 2017.04-2019.04

Honors and Awards

College of Horticulture Teaching Excellence Award, 2016

College of Horticulture Outstanding Communist Party Member, 2016

Selected Publication

Shangguan LF*, Chen MX, Fang X, Xie ZQ, Gong PJ, Huang YX, Wang ZC, Fang JG. 2000. Comparative transcriptome analysis provides insight into regulation pathways and temporal and spatial expression characteristics of grapevine (*Vitis vinifera*) dormant buds in different nodes. *BMC Plant Biology*, 20:390.

Shangguan LF*, Fang X, Jia HF, Chen MX, Zhang KK, Fang JG. 2020. Characterization of DNA methylation variations during fruit development and ripening of *Vitis vinifera* (cv.'Fujiminori'). *Physiology and Molecular Biology of Plants*, 26(4):617–637.

Shangguan LF[#], Chen MX[#], Fang X, Xie ZQ, Zhang KK, Zheng T, Pu YF, Fang JG. 2020. Comparative study of *DAM*, *Dof*, and *WRKY* gene families in fourteen species and their expression in *Vitis vinifera*. *3 Biotech*, 10(2): 72.

Shangguan LF, Fang X, Chen LD, Cui LW, Fang JG*. 2018. Genome-wide analysis of *autophagy-related genes* (*ARGs*) in grapevine and plant tolerance to copper stress. *Planta*, 247(6): 1449-1463.

Shangguan LF, Mu Q, Fang X, Zhang KK, Jia HF, Li XY, Bao YQ, Fang JG*. 2017. RNA-sequencing reveals biological networks during table grapevine ('Fujiminori') fruit development. *PLoS ONE*, 12(1): e0170571.

Leng XP[#], Wang PP[#], Zhu XD, Li XP, Zheng T, Shangguan LF*, Fang JG*. 2017. Ectopic expression of *CSD1* and *CSD2* targeting genes of miR398 in grapevine is associated with oxidative stress tolerance. *Functional & Integrative Genomics*, 17(6): 697-710.

Wang MQ[#], Sun X[#], Wang C*, Cui LW, Chen LD, Zhang CB, Shangguan LF*, Fang JG. 2017. Characterization of miR061 and its target genes in grapevine responding to exogenous gibberellic acid. *Functional & Integrative Genomics*, 17(5): 537-549.

Leng XP[#], Wang PP[#], Zhao PC, Wang MQ, Cui LW, Wang C*, Shangguan LF*. 2017. Conservation of microRNA-mediated regulatory networks in response to copper stress in grapevine. *Plant Growth Regulation*, 82: 293.

Shangguan LF, Sun X, Zhang CQ, Mu Q, Leng XP, Fang JG*. 2015. Genome identification and analysis of genes encoding the key enzymes involved in organic acid biosynthesis pathway in apple, grape, and sweet orange. *Scientia Horticulturae*, 185, 22-28.

Leng XP, Mu Q, Wang XM, Li XP, Zhu XD, Shangguan LF*, Fang JG*. 2015. Transporters, chaperones, and P-type ATPases controlling grapevine copper homeostasis. *Functional & Integrative Genomics*, 15(6): 673-684.
