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Education

2009 – 2014 China Agricultural University, China. Ph.D., Plant Genetics & Breeding
2005 – 2009 Shandong Agricultural University, China. B.S., Biotechnology

Professional Experience

2023 – present Assistant Professor, Texas Tech University
2021 – 2023 Researcher 5, The University of Minnesota, Twin Cities
2019 – 2021 Postdoctoral Research Associate, The University of Minnesota, Twin Cities
2018 – 2019 Postdoctoral Research Associate, The University of Tennessee, Knoxville
2015 – 2018 Postdoctoral Research Associate, Oak Ridge National Laboratory
2014 – 2015 Lecturer, Shandong Agricultural University, China.

Editorial Position

Associate Editor, Plant Cell, Tissue and Organ Culture (PCTOC)
Co-editor, Special Issue entitled "Genome Editing and New Plant Breeding Technologies", PCTOC

Patents

1. Yang, X., **Liu, D**., Hu, R., Tuskan, GA., Genes for enhancing salt and drought tolerance in plants and methods of use. US11535860B2
2. Yang, X., Tuskan, GA., **Liu, D**., Hu, R., Chen, JG., Xie, M., Genes for enhancing drought and heat tolerance in plants, and methods of use. US11041164B2
3. Liu, Q., Zhai, H., He, S., Wang, L., **Liu, D**., A salt tolerance-related protein IbEST from sweetpotato and its encoding gene and application, CN103204915B
4. Liu, Q., Zhai, H., He, S., **Liu, D**., Plant salt tolerance-related protein IbERD3 and encoding gene and application. CN104004071B
5. Shi, C., Liu, H., **Liu, D**., Sun, Z., Guo, F., A cultivation method for improving the storage root quality of edible sweetpotato. CN104303779B

Publications

1. **Liu, D.,** Ellison, EE., Myers, EA., Donahue, LI., Xuan, S., Swanson, R., Qi, S., Prichard, LE., Starker, CG., Voytas, DF., 2024. Heritable gene editing in tomato through viral delivery of isopentenyl transferase and single-guide RNAs to latent axillary meristematic cells. *PNAS*, 121 (39), e2406486121
2. **Liu, D.,** Myers, EA., Xuan, S., Prichard, LE., Donahue, LI., Ellison, EE., Starker, CG., Voytas, DF., 2024. Heritable, multinucleotide deletions in plants using viral delivery of a repair exonuclease and guide RNAs. *Plant Physiology*, kiae015.
3. Hu, R., Zhang, J., Jawdy, S., Sreedasyam, A., Lipzen, A., Wang, M., Ng, V., Daum, C., Keymanesh, K., **Liu, D.,** Hu, A., Chen, JG., Tuskan, GA., Schmutz, J., Yang, X., 2024. Transcriptomic analysis of the CAM species *Kalanchoë fedtschenkoi* under low-and high-temperature regimes. *Plants*, 13(23), p.3444.

4. **Liu, D.,** Tang, D, Xie, M., Zhang, J., Zhai, L., Mao, J., Luo, C., Lipzen, A., Zhang, Y., Savage, E., Yuan, G., Guo, HB., Tadesse, D., Hu, R., Jawdy, S., Cheng, H., Li, L., Yer, H., Clark, MM., Sun, H., Shi, J., Budhathoki, R., Kumar, R., Kamuda, T., Li, Y., Pennacchio, C., Barry, K., Schmutz, J., Berry, R., Muchero, W., Chen, JG., Li, Y., Tuskan, GA., Yang, X., 2023. *Agave REVEILLE1* regulates the onset and release of seasonal dormancy in *Populus*. *Plant Physiology*, 191(3), 1492-1504.
5. **Liu, D.,** Xuan, S., Prichard, LE., Donahue, LI., Pan, C., Nagalakshmi, U., Ellison, EE., Starker, CG., Dinesh-Kumar, SP., Qi, Y., Voytas, DF., 2022. Heritable base-editing in *Arabidopsis* using RNA viral vectors. *Plant Physiology*, 189(4), 1920-1924.
6. Hu, R., Zhang, J., Jawdy, S., Sreedasyam, A., Lipzen, A., Wang, M., Ng, V., Daum, C., Keymanesh, K., **Liu, D.,** Lu, H., Ranjan, P., Chen, JG., Muchero, W., Tschaplinski, TJ., Tuskan, GA., Schmutz, J., Yang, X., 2022. Comparative genomics analysis of drought response between obligate CAM and C_3 photosynthesis plants. *Journal of Plant Physiology*, 277, 153791.
7. **Liu, D.,** Hu, R., Zhang, J., Guo, HB., Cheng, H., Li, L., Borland, AM., Qin, H., Chen, JG., Muchero W., Tuskan, GA., and Yang X., 2021. Overexpression of an *Agave* phospho*enol*pyruvate carboxylase improves plant growth and stress tolerance. *Cells*, 10(3), 582.
8. Yang, X., **Liu, D.,** Lu, H., Weston, D.J., Chen, J.G., Muchero, W., Martin, S., Liu, Y., Hassan, M.M., Yuan, G. and Kalluri, U.C., 2021. Biological Parts for Plant Biodesign to Enhance Land-Based Carbon Dioxide Removal. *BioDesign Research,* Article ID 9798714.
9. Yang, X., Medford, JI., Markel, K., Shih, P., De Paoli, HC., Trinh, CT., McCormick, AJ., Ployet, R., Hussey, SG., Myburg, AA., Jensen, PE., Hassan, MM., Zhang, J., Muchero1, W., Kalluri, U.C., Yin, H., Zhuo, R, Abraham, P., Chen, JG, Weston, D., Yang, Y, **Liu, D.,** Li, Y., Labbe, J., Yang, B., Lee, J., Cottingham, RW., Martin, S., Lu, M., Tschaplinski, TJ., Yuan, G., Lu, H., Ranjan, P., Mitchell, J., Wullschleger, S.D., Tuskan, GA., 2020. Plant Biosystems Design Research Roadmap 1.0. *BioDesign Research,* Article ID 8051764.
10. Yuan, G., Hassan, MM., **Liu, D.,** Lim, SD., Yim, WC., Cushman, JC., Markel, K., Shih, PM., Lu, H., Weston, DJ., Chen, JG., Tschaplinski, TJ., Tuskan, GA., Yang, X., 2020. Biosystems Design to Accelerate C_3-to-CAM Progression. *BioDesign Research*, Article ID 3686791.
11. Zhang, J., Hu, R., Sreedasyam, A., Lipzen, A., Wang, M., Garcia, T., Yerramsetty, P., **Liu, D.,** Ng, V., Schmutz, J., Cushman, J., Borland, AM., Pasha, A., Provart, N., Chen, JG., Muchero, W., Tuskan, GA., Yang, X., 2020. Expression atlas and co-expression network reveal effects of light quality and intensity in *Kalanchoë fedtschenkoi*, a plant with crassulacean acid metabolism. *GigaScience*, 9(3), giaa018.
12. **Liu, D.,** Chen, M., Mendoza, B., Cheng, H., Hu, R., Li, L., Trinh. CT., Tuskan, GA., and Yang X., 2019. CRISPR/Cas9-mediated targeted mutagenesis for functional genomics research of crassulacean acid metabolism plants. *Journal of Experimental Botany*, 70, 6621-6629.
13. Yang, X., **Liu, D.**, Tschaplinski, TJ., Tuskan, GA., 2019. Comparative genomics provides new insights into the evolutionary mechanism and gene function in CAM plants. *Journal of Experimental Botany*, 70, 6539-6547.
14. **Liu, D.,** Palla, K., Hu, R., Moseley, R., Mendoza, C., Chen, M., Abraham, P., Labbé, J., Kalluri, U., Tschaplinski, TJ., Cushman, J., Borland, AM., Tuskan, GA., Yang, X., 2018. Perspectives on the basic and applied aspects of crassulacean acid metabolism (CAM) research. *Plant Science*, 274, 394-401.
15. Lim, S., Yim, W., **Liu, D**., Hu, R., Yang, X., Cushman, J., 2018 A *Vitis vinifera* basic helix-loop-helix transcription factor enhances plant cell size, vegetative biomass, and reproductive yield. *Plant Biotechnology Journal*, 16, 1595-1615.
16. Yang, X., Hu, R., Yin, H., Jenkins, J., Shu, S., Tang, H., **Liu, D.,** Weighill, DA., Yim, WC., Ha, J., Heyduk, K., Goodstein, DM., Guo, HB., Moseley, RC., Fitzek, E., Jawdy, S., Zhang, Z., Xie, M., Hartwell, J., Grimwood, J., Abraham, PE., Mewalal, R., Beltrán, JD., Boxall, SF., Dever, LV., Palla, KJ., Albion, R., Garcia, T., Mayer, J., Lim, SD., Wai, CM., Peluso, P., Van Buren, R., De Paoli, HC., Borland, AM., Guo, H., Chen, JG., Muchero, W., Yin, Y., Jacobson, DA., Tschaplinski, TJ.,

Hettich, RL., Ming, R., Winter, K., Leebens-Mack, JH., Smith, JAC., Cushman, J., Schmutz, J., Tuskan, GA., 2017. The *Kalanchoë* genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. *Nature Communications*, 8, 1899.

17. **Liu, D.,** Mewalal, R., Hu, R., Tuskan, GA., Yang, X., 2017. New technologies accelerate the exploration of non-coding RNAs in horticultural plants. *Horticulture Research*, 4, 17031.
18. Li, R., Kang, C., Song, X., Yu, L., **Liu, D.,** He, S., Zhai, H., Liu, Q., 2017. A ζ-carotene desaturase gene, *IbZDS*, increases β-carotene and lutein contents and enhances salt tolerance in transgenic sweetpotato. *Plant Science*, 262, 39-51.
19. **Liu, D.,** Hu, R., Palla, K.J., Tuskan, GA., Yang, X., 2016. Advances and perspectives on the use of CRISPR/Cas9 systems in plant genomics research. *Current Opinion in Plant Biology*, 30,70-77.
20. Li, R., Zhai, H., Kang, C., **Liu, D.,** He, S., Liu, Q., 2015. *De Novo* transcriptome sequencing of the orange-fleshed sweet potato and analysis of differentially expressed genes related to carotenoid biosynthesis. *International Journal of Genomics*, 43802.
21. **Liu, D.,** He, S., Song, X., Zhai, H., Liu, N., Zhang, D., Ren, Z., Liu, Q., 2015. *IbSIMT1*, a novel salt-induced methyltransferase gene from *Ipomoea batatas*, is involved in salt tolerance. *Plant Cell, Tissue and Organ Culture (PCTOC)*, 120, 701-715.
22. Chen, W., He, S., **Liu, D.,** Patil, GB., Zhai, H., Wang, F., Stephenson, TJ., Wang, Y., Wang, B., Valliyodan, B., Nguyen, HT., 2015. A sweetpotato geranylgeranyl pyrophosphate synthase gene, *IbGGPS*, increases carotenoid content and enhances osmotic stress tolerance in *Arabidopsis thali*ana. *PloS One*, 10, p.e0137623.
23. **Liu, D.,** He, S., Zhai, H., Wang, L., Zhao, Y., Wang, B., Li, R., Liu, Q., 2014. Overexpression of *IbP5CR* enhances salt tolerance in transgenic sweetpotato. *Plant Cell, Tissue and Organ Culture (PCTOC)*, 117, 1-16.
24. **Liu, D.,** Wang, L., Liu, C., Song, X., He, S., Zhai, H., Liu, Q., 2014. An *Ipomoea batatas* iron-sulfur cluster scaffold protein gene, *IbNFU1*, is involved in salt tolerance. *PloS One*, 9, e93935.
25. **Liu, D.,** Wang, L., Zhai, H., Song, X., He, S., Liu, Q., 2014. A novel α/β-hydrolase gene *IbMas* enhances salt tolerance in transgenic sweetpotato. *PloS One*, 9, e115128.
26. Wang, L.., He, S., Zhai, H., **Liu, D.,** Wang, Y., Liu, Q., 2013. Molecular cloning and functional characterization of a salt tolerance-associated gene *IbNFU1* from sweetpotato. *Journal of Integrative Agriculture*, 12, 27-35.
27. Chen, W., Zhai H., Yang, Y., He, S., **Liu, D.**, Liu, Q., 2013. Identification of differentially expressed genes in sweetpotato storage roots between Kokei No. 14 and its mutant Nongdafu 14 using PCR-based cDNA subtraction. *Journal of Integrative Agriculture*, 12, 589-595.
28. Wang, L., Dai, C., **Liu, D.,** Liu, Q., 2012. Identification of a male-specific amplified fragment length polymorphism (AFLP) marker in *Broussonetia papyrifera*. *African Journal of Biotechnology*, 1, 8196-8201.
29. **Liu, D.,** Zhao, N., Zhai, H., Yu, X., Jie, Q., Wang, L., He, S., Liu, Q., 2012. AFLP fingerprinting and genetic diversity of main sweetpotato varieties in China. *Journal of Integrative Agriculture*, 11, 424-1433.