Sara S. Jawdy, M.S.

Biosciences Technical Professional- Plant Systems Biology

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EDUCATION:

2006 **M.S.** Plant Sciences/Plant Biotechnology, University of Tennessee, Knoxville

2000 **B.S.** Horticulture, Plant Breeding Emphasis, The Pennsylvania State University, State College,

PA

PROFESSIONAL POSITIONS:

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| --- | --- |
| 2007-present | Technical Professional, Plant Systems biology group, Biosciences Division, ORNL |
| 2006-2007 | Post M.S. Intern, Plant Systems Biology Group, Biosciences Division, ORNL |
| 2003-2006 | M.S. Student, University of Tennessee, Knoxville/Plant Systems Biology group, ORNL |
| 2000-2003 | Post Bachelors Intern, Physiology Ecology Group, Environmental Sciences Division, ORNL |
| 1997-2000 | Student Intern, Plant Genetics and Breeding, Penn State University, State College, PA |
| 1999-2000 | Student Intern, The Penn State University Trial Gardens, Penn State University, State College, PA |

SKILLS AND QUALIFICATIONS:

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| --- | --- | --- |
| * Illumina technologies
* MiSeq operation
* Genomic fragment library synthesis
* Mate-pair library synthesis
* Small RNA library synthesis
* RNA library synthesis
* Roche 454 pyrosequencing
* ABI 3730 sequencing
* qPCR using ABI StepOnePlus and 7900HT
* Bio-Rad Experion automated electrophoresis
* Whole genome amplification
 | * Sterile tissue culture
* Shoot tip sterilization and sub-culture
* Protoplast assays
* Histochemical analysis of stem tissue
* Field sampling organization and execution
* Lab space management
* Standard cloning
* Standard and Tail-PCR
* Primer design
* Rolling circle amplification
* DNA and RNA extraction optimization
 | * Online functional annotation database queries (TAIR and Phytozome)
* Microsoft Office
* ABI qPCR analysis
* Agilent Bioanalyzer 2100
* Bio-Rad Experion
* Nucleic acid quantification using NanoDrop and Qubit
* Gel electrophoresis
* Confocal microscopy experience
* Plant care and maintenance in greenhouse and growth chambers
* LOSA training
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RESEARCH INTERESTS:

* RNA profiling for various projects and plant species
* Plant microbe interaction
* Plant improvement for bioenergy resources

SYNERGISTIC ACTIVITIES, SERVICE, AWARDS, AND HONORS:

* Oak Ridge National Lab Biosciences Division Distinguished Achievement Award in recognition of outstanding technical support. 2011

REFEREED PUBLICATIONS {**(h-index =17, i10-index = 27, total citations = 1081 [Google Scholar])}**:

1. 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 SS, 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. Agave REVEILLE1 regulates the onset and release of seasonal dormancy in Populus. Plant Physiology (2022)
2. Hyden B, Feng K, Yates TB, Jawdy SS, Cereghino C, Smart LB, Muchero W. De Novo Assembly and Annotation of 11 Diverse Shrub Willow (Salix) Genomes Reveals Novel Gene Organization in Sex-Linked Regions. Preprints (2022)
3. Piatkowski BT, Carper DL, Carrell DL, Chen IMA, Clum A, Daum C, Eloe-Fadrosh EA, Gilbert D, Granath G, Huntemann M, Jawdy SS, Klarenberg IJ, Kostka JE, Kyrpides NC, Lawrence TJ, Mukherjee S, Nilsson MB, Palaniappan K, Pelletier DA, Pennacchio C, Reddy TBK, Roux S, Shaw AJ, Warshan D, Živković T, Weston DJ. Draft Metagenome Sequences of the Sphagnum (Peat Moss) Microbiome from Ambient and Warmed Environments across Europe. Microbiology resource announcements 11 (10), e00400-22 (2022)
4. Xie M, Chen JG, Gunter LE, Jawdy SS, Muchero W, Tuskan GA, Zhang J. Loss of function alleles of PtEPSP-TF and its regulatory targets in rice. US Patent 11,473,086 (2022)
5. Hu, R, Zhang J, Jawdy SS, Sreedasyam A, Lipzen A, Wang M, Ng V, Daum C, Keymanesh K, Liu D, Lu H, Ranjan P, Chen JG, Muchero W, Tschapslinski TJ, Tuskan GA, Schmutz J, Yang X. Comparative genomics analysis of drought response between obligate CAM and C3 photosynthesis plants. Journal of Plant Physiology 277, 153791 (2022)
6. Appidi MR, Bible AN, Carper DL, Jawdy SS, Giannone RJ, Hettich RL, Morrell-Falvey J, Abraham PE. Development of an Experimental Approach to Achieve Spatially Resolved Plant Root-Associated Metaproteomics Using an Agar-Plate System. Molecular Plant-Microbe Interactions 35 (8), 639-649.
7. Payyavula RS, Badmi R, Jawdy SS, Rodriguez Jr M, Gunter LE, Sykes RW, Winkeler KA, Collins CM, Rottmann WH, Chen JG, Biomass formation and sugar release efficiency of Populus modified by altered expression of a NAC transcription factor. Plant Direct 6 (8), e419 (2022)
8. Carrell AA, Veličković D, Lawrence TJ, Bowen BP, Louie KB, Carper DL, Chu RK, Mitchell HD, Orr G, Markillie LM, Jawdy SS, Grimwood J, Shaw AJ, Schmutz J, Northen TR, Anderton CR, Pelletier DA, Weston DJ. Novel metabolic interactions and environmental conditions mediate the boreal peat moss-cyanobacteria mutualism. The ISME Journal 16 (4), 1074-1085 (2022)
9. Carrell AA, Lawrence TJ, Cabugao KGM, Carper DL, Pelletier DA, Lee JH, Jawdy SS, Grimwood J, Schmutz J, Hanson PJ, Shaw AJ, Weston DJ. Habitat-adapted microbial communities mediate Sphagnum peatmoss resilience to warming. New Phytologist (2022)
10. Norby RJ, Warren JM, Iversen CM, Childs J, Jawdy SS, Walker AP. Forest stand and canopy development unaltered by 12 years of CO2 enrichment\* Tree physiology 42 (3), 428-440 (2022)
11. Kalluri U, McLennan M, Jawdy SS, Sparks S, Clark M, Martin S. Root image collection from genotype by environment (GxE) rood architecture study of the bioenergy species, Populus trichocarpa. Oak Ridge National Laboratory (ORNL), Oak Ridge, TN (United States) (2022)
12. Yuan G, Lu H, Weston DJ, Jawdy SS, Tschaplinski TJ, Tuskan GA, Yang X. Reporter genes confer new-to-nature ornamental traits in plants. Horticulture Research 9 (2022)
13. Sreedasyam A, Plott C, Hossain MS, Lovell JT, Grimwood J, Jenkins JW, Daum C, Barry K, Carlson J, Shu S, Phillips J, Amirebranhimi M, Zane M, Wang M, Goodstein D, Haas FB, Hiss M, Perroud PF, Jawdy SS, Hu R, Johnson J, Kropat J, Gallaher SD, Lipzen A, Tillman R, Shakirov EV, Weng X, Torres-Jerez I, Weers B, Conde D, Pappas MR, Liu L, Muchlinski A, Jiang H, Shyu C, Huang P, Sebastian J, Laiben C, Medlin A, Carey S, Carrell AA, Perales M, Swaminathan K, Allona I, Grattapaglia D, Cooper EA, Tholl D, Vogel JP, Weston DJ, Yang X, Brutnell TP, Kellogg EA, Baxter I, Udvardi M, Tang Y, Mockler TC, Juenger TE, Mullet J, Rensing SA, Tuskan GA, Merchant SS, Stacey G, Schmutz J. JGI Plant Gene Atlas: An updateable transcriptome resource to improve structural annotations and functional gene descriptions across the plant kingdom. bioRxiv (2022)
14. Shrestha HK, Solis MIV, Jawdy SS, Tuskan GA, Yang X, Abraham PE. Temporal dynamics of protein and post-translational modification abundances in Populus leaf across a diurnal period. Proteomics 21 (20), e01306-20 (2021)
15. Yates TB, Feng K, Zhang J, Singan V, Jawdy SS, Ranjan P, Abraham PE, Barry K, Lipzen A, Pan C, Schmutz J, Chen JG, Tuskan GA, Muchero W. The Ancient Salicoid Genome Duplication Event: A Platform for Reconstruction of De Novo Gene Evolution in Populus trichocarpa. Genomoe biology and evolution 13 (9), evab198. (2021)
16. Carper DL, Weston DJ, Barde A, Timm CM, Lu TY, Burdick LH, Jawdy SS, Klingeman DM, Robeson MS, Veach AM, Cregger MA, Kalluri UC, Schadt CW, Podar M, Doktycz MJ, Pelletier DA. Culitvating the Bacterial Microbiota of Populus Roots. Msystems 6 (3), e01306-20. (2021)
17. Muchero W, Labbe JL, Gunter LE, Chen JG, Jawdy SS, Yang X, Tuskan GA, Wang J, Czamecki O, Ranjan P. Methods of improving mycorrhization in plants and genetically modified plants with improved mycorrhization. US Patent 11,028,404, 2021 (2021)
18. Lu TY, Barde A, Weston DJ, Pelletier DA, Klingeman DM, Kalluri UC, Burdick LH, Podar M, Schadt CW, Jawdy SS, Veach AM, Cregger MA, Doktycz MJ, Timm CM, Robeson MS, Carper DL. Cultivating the Bacterial Microbiota ofPopulusRoots. mSystems (2021)
19. Zhang J, Xie M, Li M, Ding J, Pu Y, Bryan AC, Rottmann W, Winkeler KA, Collins CM, Singan V, Lindquist EA, Jawdy SS, Gunter LE, Engle NL, Yang X, Barry K, Tschaplinski TJ, Schmutz J, Tuskan GA, Muchero W, Chen JG. Overexpression of a Prefoldin β subunit gene reduces biomass recalcintrance in the bioenergy crop Populus. Plant biotechnology journal 18 (3), 859-871 (2020)
20. Hu R, Zhang J, Haiwei L, Jawdy SS, Lipzen A, Wang M, Ng V, Sreedasyam A, Schmutz J, Liu D, Ranjan P, Chen J, Tschaplinski TJ, Tuskan GA, Yang X. Comparative Genomics Analysis of Drought Response between CAM and C3 Photosynthesis Plants Plant and Animal Genome XXVII Conference (January 11-15, 2020)
21. Carrell AA, Lawrence TJ, Cabugao KGM, Carper DL, Pelletier DA, Jawdy SS, Grimwood J, Schmutz J, Hanson PJ, Shaw AJ, Weston DJ. Sphagnum peat moss thermotolorance is modulated by the microbiome. bioRxiv (2020)
22. Xie M, Zhang J, Singan VR, McGranahan MJ, LaFayette PR, Jawdy SS, Engle N, Doeppke C, Tschaplinski TJ, Davis MF, Lindquist E, Barry K, Schmutz J, Parrott WA, Chen F, Tuskan GA, Chen JG, Muchero W. Identification of functional single nucleotide polymorphism of Populus trichocarpa PtrEPSP-TF and determination of its transcriptional effect. Plant Direct 4 (1), 1-12 (2020)
23. Yang Y, Yoo CG, Rottmann W, Winkeler KA, Collins CM, Gunter LE, Jawdy SS, Yang X, Pu Y, Ragauskas AJ, Tuskan GA, Chen JG. PdWND3A, a wood-associated NAC domain-containing protein, affects lignin biosynthesis and composition in Populus. BMC plant biology 19 (1), 1-1 (2019)
24. Yin H, Guo HB, Weston DJ, Borland AM, Ranjan P, Abraham PE, Jawdy SS, Wachira J, Tuskan GA, Tschaplinski TJ, Wullschleger SD, Guo H, Hettich RL, Gross SM, Wang Z, Visel A, Yang X. Correction to: Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in Agave. BMC Genomics 20 (1), 1-1 (2019)
25. Henning JA, Weston DJ, Pelletier DA, Timm CM, Jawdy SS, Classen AT. Relatively rare root endophytic bacteria drive plant resource allocation patterns and tissue nutrient concentration in unpredictable ways. American Journal of Botony 106 (11), 1423-1434. (2019)
26. Cope KR, Bascaules A, Irving TB, Venkateshwaran M, Maeda J, Garcia K, Rush TA, Ma C, Labbé J, Jawdy S, Steigerwald E, Setzke J, Fung E, Schnell KG, Wang Y, Schlief N, Bücking H, Strauss SH, Maillet F, Jargeat P, Bécard G, Puech-Pagès V, Ané JM. The Ectomycorrhizal Fungus Laccaria bicolor Produces Lipochitooligosaccharides and Uses the Common Symbiosis Pathway to Colonize Populus Roots. The Plant Cell. 31:2386-2410 (2019)
27. Zhang J, Li M, Bryan AC, Yoo CG, Rottmann W, Winkeler KA, Collins CM, Singan V, Lindquist EA, Jawdy SS, Gunter LE, Engle NL, Yang X, Barry K, Tschaplinski TJ, Schmutz J, Pu Y, Ragauskas AJ, Tuskan GA, Muchero W, Chen JG. Overexpression of a serine hydroxymethyltransferase increases biomass production and reduces recalcitrance in the bioenergy crop Populus. Sustainable Energy and Fuels 3: 195 (2019)
28. Tschaplinski TJ, Abraham PE, Jawdy SS, Gunter LE, Martin MZ, Engle NL, Yang X, Tuskan GA. The nature of the progression of drought stress drives differential metabolomic responses in Populus deltoides. Annals of Botany doi: 10.1093/aob/mcz002. [Epub ahead of print] (2019)
29. Zhang J, Xie M, Li M, Ding J, Pu Y, Bryan AC, Rottmann W, Winkeler KA, Collins CM, Singan V, Lindquist EA, Jawdy SS, Gunter LE, Engle NL, Yang X, Barry K, Tschaplinski TJ, Schmutz J, Tuskan GA, Muchero W, Chen JG. Overexpression of a Prefoldin β subunit gene reduces biomass recalcitrance in the bioenergy crop Populus. Plant Biotechnology Journal doi: 10.1111/pbi.13254. [Epub ahead of print] (2019)
30. Mewalal R, Yin H, Hu R, Jawdy S, Vion P, Tuskan GA, Le Tacon F, Labbé JL, Yang X. Identification of Populus Small RNAs Responsive to Mutualistic Interactions with Mycorrhizal Fungi, Laccaria bicolor and Rhizophagus irregularis. Frontiers in Microbiology 10:515 (2019)
31. Labbé J, Muchero W, Czarnecki O, Wang J, Wang X, Bryan AC, Zheng K, Yang Y, Xie M, Zhang J, Wang D, Meidl P, Wang H, Morrell-Falvey JL, Cope KR, Maia LGS, Ané JM, Mewalal R, Jawdy SS, Gunter LE, Schackwitz W, Martin J, Le Tacon F, Li T, Zhang Z, Ranjan P, Lindquist E, Yang X, Jacobson DA, Tschaplinski TJ, Barry K, Schmutz J, Chen JG, Tuskan GA. Mediation of Plant-Mycorrhizal Interaction by a Lectin Receptor-Like Kinase. Nature Plants 5:676-680 (2019)
32. Muchero W, Sondreli KL, Chen JG, Urbanowicz BR, Zhang J, Singan V, Yang Y, Brueggeman RS, Franco-Coronado J, Abraham N, Yang JY, Moremen KW, Weisberg AJ, Chang JH, Lindquist E, Barry K, Ranjan P, Jawdy S, Schmutz J, Tuskan GA, LeBoldus JM. Association mapping, transcriptomics, and transient expression identify candidate genes mediating plant–pathogen interactions in a tree. PNAS 115:11573-11578 (2018)
33. Garcia B, Labbe J, Jones P, Abraham P, Hodge I, Climer S, Jawdy S, Gunter L, Tuskan G, Yang X, Tschaplinski T, Jacobson D. Phytobiome and Transcriptional Adaptation of Populus deltoides to Acute Progressive Drought and Cyclic Drought. Phytobiomes Journal 2:249-260 (2018)
34. Badmi R, Payyavula RS, Bali G, Guo HB, Jawdy SS, Gunter LE, Yang X, Winkeler KA, Collins C, Rottmann WH, Yee K, Rodriguez M Jr, Sykes RW, Decker SR, Davis MF, Ragauskas AJ, Tuskan GA, Kalluri UC. A New Calmodulin-Binding Protein Expresses in the Context of Secondary Cell Wall Biosynthesis and Impacts Biomass Properties in Populus. Frontiers in Plant Science 9:1669 (2018)
35. Timm CM, Carter KR, Carrell AA, Jun SR, Jawdy SS, Vélez JM, Gunter LE, Yang Z, Nookaew I, Engle NL, Lu TS, Schadt CW, Tschaplinski TJ, Doktycz MJ, Tuskan GA, Pelletier DA, Weston DJ. Abiotic Stresses Shift Belowground Populus-Associated Bacteria Toward a Core Stress Microbiome. mSystems 3: e00070-17 (2018)
36. Zhang J, Yang Y, Zheng K, Xie M, Feng K, Jawdy SS, Gunter LE, Ranjan P, Singan VR, Engle N, Lindquist E, Barry K, Schmutz J, Zhao N, Tschaplinski TJ, LeBoldus J, Tuskan GA, Chen JG, Muchero W. Genome‐wide association studies and expression‐based quantitative trait loci analyses reveal roles of HCT2 in caffeoylquinic acid biosynthesis and its regulation by defense‐responsive transcription factors in Populus. New Phytologist 220:502-516 (2018)
37. Abraham PE, Garcia BJ, Gunter LE, Jawdy SS, Engle N, Yang X, Jacobson DA, Hettich RL, Tuskan GA, Tschaplinski TJ. Quantitative proteome profile of water deficit stress responses in eastern cottonwood (Populus deltoides) leaves. PLoS ONE 13:e0190019 (2018)
38. Yin H, Guo HB, Weston DJ, Borland AM, Ranjan P, Abraham PE, Jawdy SS, Wachira J, Tuskan GA, Tschaplinski TJ, Wullschleger SD, Guo H, Hettich RL, Gross SM, Wang Z, Visel A, Yang X. Diel rewiring and positive selection of ancient plant proteins enabled evolution of CAM photosynthesis in Agave. BMC Genomics 19:588 (2018)
39. Bryan AC, Zhang J, Guo J, Ranjan P, Singan V, Barry K, Schmutz J, Weighill D, Jacobson D, Jawdy S, Tuskan GA, Chen JG, Muchero W. A variable polyglutamine repeat affect subcellular localization and regulatory activity of a Populus ANGUSTIFOLIA. Genes Genomes Genetics 8:2631-2641 (2018)
40. Xie M, Muchero W, Bryan AC, Yee K, Guo HB, Zhang J, Tschaplinski TJ, Singan VR, Lindquist E, Payyavula RS, Barros-Rios J, Dixon R, Engle N, Sykes RW, Davis M, Jawdy SS, Gunter LE, Thompson O, DiFazio SP, Evans LM, Winkeler K, Collins C, Schmutz J, Guo H, Kalluri U, Rodriguez M, Feng K, Chen JG, Tuskan GA. A 5-enolpyruvylshikimate-3-phosphate synthase-like gene is a transcriptional regulator of Phenylpropanoid and Flavonoid Pathways. The Plant Cell 30:1645-1660 (2018)
41. Yang X, Hu R, Yin H, Jenkins J, Shu S, Tang H, Liu D, Weighill DA, Cheol Yim W, 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 JA, Don Lim S, Man Wai C, 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 JC, Schmutz J, Tuskan GA. The Kalanchoë genome provides insights into convergent evolution and building blocks of crassulacean acid metabolism. Nature Communications 8:1899 (2017)
42. Yang Y, Yoo CG, Winkeler KA, Collins CM, Hinchee MAW, Jawdy SS, Gunter LE, Engle NL, Pu Y, Yang X, Tschaplinski TJ, Ragauskas AJ, Tuskan GA, Chen JG. Overexpression of a Domain of Unknown Function 231-containing protein increases O-xylan acetylation and cellulose biosynthesis in Populus. Biotechnology for Biofuels 10:311 (2017)
43. Plett JM, Yin H, Mewalal R, Hu R, Li T, Ranjan P, Jawdy S, De Paoli HC, Butler G, Burch-Smith TM, Guo HB, Ju Chen C, Kohler A, Anderson IC, Labbé JL, Martin F, Tuskan GA, Yang X. Populus trichocarpa encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis. Scientific Reports 7:382 (2017)
44. Yang Y, Yoo CG, Guo HB, Rottmann W, Winkeler KA, Collins CM, Gunter LE, Jawdy SS, Yang X, Guo H, Pu Y, Ragauskas AJ, Tuskan GA, Chen JG. Overexpression of a domain of unknown function 266-containing protein results in high cellulose content, reduced recalcitrance, and enhanced plant growth in the bioenergy crop Populus. Biotechnology for Biofuels 10:74 (2017)
45. Henning JA, Weston DJ, Pelletier DA, Timm CM, Jawdy SS, Classen AT. Root bacterial endophytes alter plant phenotype but not physiology. PeerJ 4:e2606 (2016)
46. Yang Y, Labbé J, Muchero W, Yang X, Jawdy SS, Kennedy M, Johnson J, Sreedasyam A, Schmutz J, Tuskan GA, Chen JG. Genome-wide analysis of lectin receptor-like kinases in Populus. BMC Genomics 17:699 (2016)
47. Kalluri UC, Payyavula RS, Labbé JL, Engle N, Bali G, Jawdy SS, Sykes RW, Davis M, Ragauskas A, Tuskan GA, Tschaplinski TJ. Down-Regulation of KORRIGAN-Like Endo-β-1,4-Glucanase Genes Impacts Carbon Partitioning, Mycorrhizal Colonization and Biomass Production in Populus. Frontiers in Plant Science 7:1455 (2016)
48. Timm CM, Pelletier DA, Jawdy SS, Gunter LE, Henning JA, Engle N, Aufrecht J, Gee E, Nookaew I, Yang Z, Lu TY, Tschaplinski TJ, Doktycz MJ, Tuskan GA, Weston DJ. Two Poplar-Associated Bacterial Isolates Induce Additive Favorable Responses in a Constructed Plant-Microbiome System. Frontiers in Plant Science 7:497 (2016)
49. Bible AN, Fletcher SJ, Pelletier DA, Schadt CW, Jawdy S, Weston DJ, Engle N, Tschaplinski TJ, Masyuko R, Polisetti S, Bohn PW, Coutinho TA, Doktycz MJ, Morrell-Falvey JL. A Carotenoid-Deficient Mutant in Pantoea sp. YR343, a Bacteria Isolated from the Rhizosphere of Populus deltoides, Is Defective in Root Colonization. Frontiers in Microbiology. 7:491 (2016)
50. Bryan AC, Jawdy S, Gunter LE, Gjersing E, Sykes R, Hinchee M, Winkler K, Collins C, Engle NL, Tschaplinski TJ, Yang X, Tuskan GA, Muchero W, Chen JG. Knockdown of a laccase in Populus deltoides confers altered cell wall chemistry and increased sugar release. Plant Biotechnology Journal 14:2010-2020 (2016)
51. Czarnecki O, Bryan AC, Jawdy S, Yang X, Cheng ZM, Chen JG, Tuskan GA. Simultaneous knock-down of six non-family genes using a single synthetic RNAi fragment in Arabidopsis thaliana. Plant Methods 12:16 (2016)
52. Muchero W, Guo J, Difazio SP, Chen JG, Ranjan P, Slavov GT, Gunter LE, Jawdy S, Bryan, AC, Sykes R, Ziebell A, Klapste J, Porth I, Skyba O, Unda F. High-resolution genetic mapping of allelic variants associated with cell wall chemistry in Populus. BMC Genomics 16:24 (2015)
53. Timm CM, Campbell AG, Utturkar SM, Jun SR, Parales RE, Tan WA, Robeson MS, Lu TY, Jawdy S, Brown SD, Ussery DW, Schadt CW, Tuskan GA, Doktycz MJ, Weston DJ, Pelletier DA. Metabolic functions of Pseudomonas fluorescens strains from Populus deltoides depend on rhizosphere or endosphere isolation compartment. Frontiers in Microbiology 6:1118 (2015)
54. Weston DJ, Rogers A, Tschaplinski TJ, Gunter LE, Jawdy SS, Engle NL, Heady LE, Tuskan GA, Wullschleger SD. Scaling nitrogen and carbon interactions: what are the consequences of biological buffering? Ecology and Evolution 14:2839-2850 (2015)
55. Muchero W, Guo J, DiFazio SP, Chen JG, Ranjan P, Slavov GT, Gunter LE, Jawdy S, Bryan AC, Sykes R, Ziebell A, Klápště J, Porth I, Skyba O, Unda F, El-Kassaby YA, Douglas CJ, Mansfield SD, Martin J, Schackwitz W, Evans LM, Czarnecki O, Tuskan GA. High-resolution genetic mapping of allelic variants associated with cell wall chemistry in Populus. BMC Genomics 16:24 (2015)
56. Payyavula RS, Tschaplinski TJ, Jawdy SS, Sykes RW, Tuskan GA, Kalluri UC. Metabolic profiling reveals altered sugar and secondary metabolism in response to UGPase overexpression in Populus. BMC plant biology 14:265 (2014)
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58. Martin MZ, Gunter LE, Jawdy SS, Wullschleger SD, Wheeler CS, Jha AK. Genetic Improvement, Sustainable Production and Scalable Small Microenterprise of Jatropha as a Biodiesel Feedstock. OMICS: Journal of Bioremediation and Biodegradation 4:4172 (2013)
59. Karve AA, Jawdy SS, Gunter KE, Allen SM, Yang X, Tuskan GA, Wullschleger SD, Weston DJ. Initial characterization of shade avoidance response suggests functional diversity between Populus phytochrome B genes. New Phytologist 196: 726-737 (2012)
60. Weston DJ, Pelletier DA, Morrell-Falvey JL, Tschaplinski TJ, Jawdy SS, Lu T-Y, Allen SM, Melton SJ, Martin MZ, Schadt CW, Karve AA, Chen J-G, Yang X, Doktycz MJ, Tuskan GA. Pseudomonas fluorescens induces strain-dependent and strain-independent host plant responses in defense networks, primary metabolism, photosynthesis, and fitness. Molecular Plant-Microbe Interactions 25: 765-778 (2012)
61. Foston M, Hubbell CA, Samuel R, Jung S, Fan H, Ding SY, Zeng Y, Jawdy S, Davis M, Sykes R, Gjersing E, Tuskan GA, Kalluri U, Ragauskas AJ. Chemical, ultrastructural and supramolecular analysis of tension wood in Populus tremula x alba as a model substrate for reduced recalcitrance. Energy and Environmental Science 4:4962-4971 (2011)
62. Weston DJ, Karve AA, Gunter LE, Jawdy SS, Yang X, Allen SM, Wullschleger SD. Comparative physiology and transcriptional networks underlying the heat shock response in Populus trichocarpa, Arabidopsis thaliana and Glycine max. Plant Cell and Environment. 34:1488-1506 (2011)
63. Yang X, Tschaplinski TJ, Hurst GB, Jawdy SS, Abraham PE, Lankford PK, Adams RM, Manesh BS, Hettick RL, Lindquist E, Kalluri UC, Gunter LE, Pennacchio C, Tuskan GA. Discovery and annotation of small proteins using genomics, proteomics, and computational approaches. Genome research 21: 634-664 (2011)
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65. Ranjan P, Yin T, Zhang X, Kalluri UC, Yang X, Jawdy SS, Tuskan GA. Bioinformatics-based identification of candidate genes from QTLs associated with cell wall traits in Populus. BioEnergy Research 3: 172-182 (2010)
66. Yang X, Jawdy S, Tschaplinski TJ, Tuskan GA. Genome-wide identification of lineage specific genes in Arabidopsis, Oryza and Populus. Genomics 93:473-480 (2009)
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68. Yin TM, DiFazio SP, Gunter LE, Jawdy S, Boerjan W, Tuskan GA. Genetic and physical mapping of Melampsora rust resistance genes in Populus and characterization of linkage disequilibrium and flanking genomic sequence. New Phytologist 164:95-105 (2004)
69. Norby RJ, Sholtis J, Gunderson CA, Jawdy S. Leaf dynamics of a deciduous forest canopy: no response to elevated CO2. Oceologia 136:574-584 (2003)

PRESENTATIONS AND SEMINARS:

* (Poster) **Jawdy S,** Sreedasyam A, Schmutz J, Tuskan G, “JGI Plant Gene Atlas: Use of Transcriptome Expression Analysis to Study Nitrogen Uptake in Root and Leaf Tissue of *Populus trichocarpa*”, CROPS conference, Huntsville, AL, May 2015.
* (Oral Presentation) **Jawdy S**, Tschaplinski T, Kalluri U, Yin Y, Gunter L, Martin M, Engle N, Yang X, Busov V, Strauss S, Davis M, Sykes R, Tuskan GA, “Extreme Wood Chemistry Phenotypes in a *Populus* Activation Tagged Population”, BESC Retreat, Asheville, NC, June 2010.
* (Poster) **Jawdy S**, Tschaplinski T, Kalluri U, Yin T, Gunter L, Martin M, Engle N, Yang X, Busov V, Strauss S, Ma C, Davis M, Sykes R, Tuskan GA, “The Use of TAIL PCR to Identify Genes Controlling Extreme Phenotypes in a *Populus* Activation Tagged Population”, GTL meeting, 2009.
* (Oral Presentation) **Jawdy S**. Expression analysis of genes in *Populus* induced by exogenous auxin treatment. Department of Plant Sciences, University of Tennessee, May 2006.
* (Poster) **Jawdy S**, DiFazio SP, Kalluri UC, Davis JM, Morse AM, Dervinis C, Smith KE, Tuskan GA. Using SSH and RCA to identify auxin-responsive transcripts in *Populus.* 12th New Phytologist Symposium: Functional genomics of environmental adaptation in *Populus*. Gatlinburg, TN, October 2004.