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Education:

B.Sc Crop Science, Cum Laude, California Polytechnic State University, Pomona (2000-2003)
Ph.D Plant Pathology, University of California, Riverside (2003-2007)

Professional appointments:

Postdoctoral Scholar: University of California, Riverside (Feb-2008 to Sept-2010)

Plant Molecular Biologist: Oak Ridge National Laboratory (Oct-2010 to Present)

Joint Faculty: Plant Sciences Dept., University of Tennessee, Knoxville (May-2015 to Present)

Research activities:

PI: DOE Early Career Award 2017 – 2021 (\$2.5M). Innate host immunity poses a fundamental challenge in the utilization of beneficial microbes for the sequestration of carbon dioxide, a potent greenhouse gas, and its fixation into economically valuable biofuels plant feedstocks. The immense obstacle presented by host defense mechanisms is illustrated by the fact that up to 90% of the microbes in the rhizosphere cannot overcome this defensive barrier to establish a functional presence in the plant endosphere. In compatible interactions, biomass increases of up to 200% have been achieved in perennial feedstocks inoculated with growth-promoting endophytic microbes. However, due to the strong innate host immunity these gains are largely host-specific thereby limiting application across diverse plant species. Using *Salix*, a biofuels feedstock and pioneer species in the warming arctic region, this project seeks to characterize unique host-derived genetic factors that allow select microbes to successfully evade defense mechanisms and establish a functional presence in the host endosphere with no adverse effects. Membrane-bound pattern recognition receptors (PRRs) are a class of receptor kinases with an extracellular domain that can identify microbe-associated molecular patterns (MAMPs) with high fidelity. Upon recognition of these MAMPs, the intracellular kinase domain initiates signaling cascades which results in suppression of host defense mechanism to facilitate colonization. Understanding these molecular dynamics presents the unique opportunity to coupling growth-promoting microbes with *Salix* for the enhancement of carbon sequestration in the vulnerable arctic region while also providing major economic gains for the nascent cellulosic biofuels industry by increasing biomass yields. *Outputs from this project will inform efforts to rationally design and engineer plant-microbe interactions for application in these Department of Energy (DOE) missions.*

PI: Dissecting shared function in ancient proteins across plants and animals 2016 – 2017 (\$190,000):

Despite millions of years of evolutionary separation, fundamental genetic mechanisms governing penetrance of some plant and animal traits of major economic, social and ecological importance

exhibit surprising levels of conservation across highly divergent organisms. Recent advances in genome sequencing revealed that this conservation is not only mechanistic but is also manifested at the DNA and amino acid sequence level via conserved domains/motifs. These observations suggest that such gene structures and their associated functions have remained highly conserved and that they continue to mediate the expression of similar phenotypes between plants and animals. In this project, we harness the shared evolutionary origin of genes and proteins that mediate expression of similar phenotypes between plants and animals to advance the understanding of genetic features that underlie ecologically important traits in plants but cause detrimental and heritable diseases in humans and animals. We have successfully demonstrated that the same conserved genes underlie callus formation in plants (rapid growth of undifferentiated cells) and human cancer proliferation. Currently, my group is performing validation experiments in plants and zebrafish to demonstrate functional conservation of a conserved DiGeorge Syndrome Critical Region Gene 14 (DGCR14) gene whose molecular function has not been established in any organism. Loss-of-function of this gene is associated with developmental abnormalities in humans. In plants, we demonstrated that loss-of-function mutants exhibit significantly increased biomass and accumulation of secondary metabolites. Outputs from this project will provide targets for the genetic improvement of plants for biomass production while informing fundamental studies in heritable human diseases.

Plant Microbe Interfaces 2014 – 2017 (\$21.2M). Our primary objective is to identify and characterize genetic determinants that drive *Populus spp.* interaction with microbial symbionts. We use a combination of statistical and molecular genetics to identify rapidly evolving genomic intervals suggestive of function in microbial recognition. Currently we are validating and screening insertion/deletion (INDEL) polymorphisms occurring in tandemly duplicated receptor kinases which have been implicated in pattern recognition of carbohydrate moieties in microbial cell walls leading to host immunity or highly specific host-microbe interactions. This work is being conducted within naturally varying *P. trichocarpa* and *P. deltoides* populations in the Pacific Northwest and Eastern USA. Under this initiative, we have successfully identified membrane-bound receptors that suppress host immune responses to facilitate colonization. These genes can be used to engineer novel plant-microbe combinations to enhance carbon dioxide capture.

Co-PI: BioEnergy Science Center 2008 – 2017 (\$250M). The BioEnergy Science Center is one of three Bioenergy Research Centers established by the United States Department of Energy in part to come up with genetic solutions to overcome the key constraint of cell wall recalcitrance in enabling the economic conversion of plant biomass to biofuels. I lead efforts to target cell-wall recalcitrance phenotypes in naturally varying populations of *P. trichocarpa* and interspecific mapping pedigrees to identify genes that affect lignin content, sugar release, and fermentation efficiency. We established 4 common gardens with replicated clones of *P. trichocarpa* natural variants in the Pacific Northwest for phenotypic characterization and evaluation of genotype x environment interactions. To complement this phenotypic data, we apply high-density SNP genotyping and whole-genome resequencing to characterize DNA polymorphisms segregating in these populations. We have successfully identified key genes affecting cell wall recalcitrance using a combination of QTL and Linkage Disequilibrium (LD)-

based Association Mapping. With this approach we demonstrated unprecedented speed of gene discovery, validation and commercial deployment in less than 4 years.

Intellectual property:

Licenses:

1. Greenwood Resources Inc. and ORNL successfully negotiated a license for patent US 20,150,353,948 (April 2016).

Patents:

1. **Muchero W**, Chen J, Gunter LE, Jawdy S, Tuskan GA, Bryan AC, Difazio S, Guo HB, inventors. Transcription Factor Which Regulates Flavonoid, Phenylpropanoid, Tyrosine, and Tryptophan Pathways. United States patent US 20,150,353,948. 2015 Dec 10.
2. Chen J, Gunter LE, Jawdy S, **Muchero W**, Tuskan G, Guo J, Ranjan P, DiFazio SP, Bryan AC, inventors; UT-BATTELLE, LLC, assignee. KEY GENE REGULATING PLANT CELL WALL RECALCITRANCE. United States patent US 20,160,053,275. 2016 Feb 25.

Invention disclosures:

1. **S-138,286**: Transcriptional regulator of phosphoenolpyruvate shunt between shikimate and glycolysis pathways.
2. **S-124,759**: A lectin-like receptor kinase leads to enhanced mycorrhization in plants.
3. **S-124,857**: A heavy metal transporter enhancing woody quality for biofuels production.
4. **S-124,856**: An amino acid transporter enhancing lignin quality and sugar release.
5. **S-124,480**: A gene regulating cellulose, hemicellulose biosynthesis, and biomass sugar yield.
6. **S-124,481**: Allelic variants regulating cellulose, lignin biosynthesis and biomass sugar yield.
7. **S-124,482**: A gene regulating cellulose, hemicellulose biosynthesis and biomass sugar yield.
8. **S-124,200**: A key gene A regulating plant cell-wall recalcitrance and sugar release.
9. **S-124,201**: A key gene B regulating plant cell-wall recalcitrance and sugar release.
10. **S-124,202**: A key gene C regulating plant cell-wall recalcitrance and sugar release.
11. **S-124,203**: A key gene D regulating plant cell-wall recalcitrance and sugar release.
12. **S-124,204**: A key gene E regulating plant cell-wall recalcitrance and sugar release.
13. **S-124,205**: A key gene F regulating plant cell-wall recalcitrance and sugar release.
14. **S-124,206**: A key gene G regulating plant cell-wall recalcitrance and sugar release.

15. **S-124,207**: A key gene H regulating plant cell-wall recalcitrance and sugar release.

Selected publications:

1. Bryan AC, Jawdy S, Gunter L, Gjersing E., Sykes R, Hinchee MA, Winkeler KA, Collins CM, Engle N, Tschaplinski J., Yang X, Tuskan GA, **Muchero W** (co-senior author)., Chen JG. (2016). Knockdown of a laccase in *Populus deltoides* confers altered cell wall chemistry and increased sugar release. *Plant biotechnology Journal* 14: 2010-2020.
2. Stevenson SR, Kamisugi Y, Trinh CH, Schmutz J, Jenkins JW, Grimwood J, **Muchero W**, Tuskan GA, Rensing SA, Lang D, Reski R. (2016). Genetic analysis of *Physcomitrella patens* identifies ABCISIC ACID NON-RESPONSIVE (ANR), a regulator of ABA responses unique to basal land plants and required for desiccation tolerance. *The Plant Cell*, pp.tpc-00091.
3. Bhagia S, **Muchero W**, Kumar R, Tuskan GA, Wyman CE. (2016). Natural genetic variability reduces recalcitrance in poplar. *Biotechnology for biofuels* 9: 1.
4. Yang Y, Labbé J, **Muchero W**, Yang X, Jawdy SS, Kennedy M, Johnson J, Sreedasyam A, Schmutz J, Tuskan GA, Chen JG. (2016). Genome-wide analysis of lectin receptor-like kinases in *Populus*. *BMC genomics* 17: 699.
5. Zheng K, Wang X, Weighill DA, Guo HB, Xie M, Yang Y, Yang J, Wang S, Jacobson DA, Guo H **Muchero W**, Chen JG. (2016). Characterization of DWARF14 Genes in *Populus*. *Scientific reports* 6: 21593.
6. Dumitrache A, Akinosho H, Rodriguez M, Meng X, Yoo CG, Natzke J, Engle NL, Sykes RW, Tschaplinski TJ, **Muchero W**, Ragauskas AJ. (2016). Consolidated bioprocessing of *Populus* using *Clostridium (Ruminiclostridium) thermocellum*: a case study on the impact of lignin composition and structure. *Biotechnology for biofuels*, 9: 1.
7. **Muchero W** (corresponding author), Guo J, DiFazio SP, Chen J-G, Ranjan P, Slavov GT, Gunter L, Jawdy S, Bryan AC, Sykes R, Ziebell A, Klápště J, Porth I, Skyba O, Unda F, El-Kassaby Y, Douglas CJ, Mansfield SD, Martin J, Schackwitz W, Evans LM, Czarnecki O, Tuskan GA. (2015) High-resolution Genetic Mapping of Allelic Variants Associated With Cell Wall Chemistry in *Populus*. *BMC Genomics* 16:24.
8. Evans LM, Slavov GT, Rodgers-Melnick, Martin J, Ranjan P, **Muchero W**, Schackwitz, Chen J-G, Brunner A, Tuskan GA, DiFazio SP. (2014). *Populus trichocarpa* population genomics, signatures of selection and adaptive trait associations. *Nature Genetics* 46:1089-1096.
9. **Muchero W** (corresponding author), Labbé J, Ranjan P, DiFazio S, Tuskan GA (2014) Genome re-sequencing in *Populus*: Revealing large-scale genome variation and implications on specialized-trait genomics. T. Fenning (ed.) Challenges and Opportunities for the world's Forests in the 21st Century. Springer Academic Publishers. *Forestry Sciences* 81: 587-595.

10. Mckown AD, Klápště J, Guy RD, Geraldles A, Porth I, Hannemann J, Friedmann M, **Muchero W**, et al. (2014) Genome-wide association implicates numerous genes underlying trait variation in natural populations of *Populus trichocarpa*. **New Phytologist** 203:535-553.
11. Czarnecki O; Yang J; Wang X; Wang S; **Muchero W**, Tuskan GA, Chen J-G (2014) Characterization of MORE AXILLARY GROWTH Genes in *Populus*. **PLoS ONE** 9: e102757.
12. Weston DJ, Timm CM, Walker AP, Gu L, **Muchero W** et al., (2014) Sphagnum physiology in the context of changing climate: Emergent influences of genomics and host-microbiome interactions to ecosystem function. *Plant Cell & Environment* (in press).
13. **Muchero W** (corresponding author), Sewell MM, Ranjan P, Gunter LE, Tschaplinski TJ, Yin T, Tuskan GA (2013) Genome anchored QTLs for biomass productivity in Hybrid *Populus* grown under contrasting environments. **PLoS ONE** 8: e54468.
14. Porth I, Klápště J, Skyba O, Hannemann J, Mckown AD, Guy RD, DiFazio SP, **Muchero W**, Ranjan P, Tuskan GA, Friedman C, Ehlting J, Cronk QCB, El-Kassaby Y, Douglas CJ, Mansfield SD (2013) Genome-wide association mapping for wood characteristics in *Populus* identifies an array of candidate single nucleotide polymorphisms. **New Phytologist**: 200:710-726.
15. Porth I, Klápště J, Skyba O, Lai BSK, Geraldles A, **Muchero W**, Tuskan GA, Douglas CJ, El-Kassaby Y, Mansfield SD (2013) *Populus trichocarpa* cell wall chemistry and ultrastructure trait variation, genetic control and genetic correlations. **New Phytologist** 197:777-790.
16. Geraldles A, DiFazio S, Slavov GT, Priya R, **Muchero W**, Hannemann J, Gunter L, Wymore AM, Grassa CJ, Farzaneh N, Porth I, Mckown AD, Skyba O, Li E, Fujita M, Klápště J, Martin J, Schackwitz W, Pennacchio C, Rokhsar D, Friedmann MC, Wasteneys GO, Guy RD, El-Kassaby Y, Mansfield SD, Cronk QCB, Ehlting J, Douglas CJ, Tuskan GA (2013) A 34K SNP genotyping array for *Populus trichocarpa*: Design, application to the study of natural populations and transferability to other *Populus* species. **Molecular Ecology Resources** 13:306-323.
17. Slavov GT, DiFazio SP, Martin J, Schackwitz SP, **Muchero W**, Rodgers-Melnick E, Lipphardt MF, Pennacchio CP, Hellsten U, Pennachio LA, Gunter LE, Ranjan P, Vining K, Pomraning KR, Wilhelm LJ, Pellegrini M, Mockler T, Freitag M, Geraldles A, El-Kassaby YA, Mansfield SD, Cronk QCB, Douglas CJ, Strauss SH, Rokhsar D, Tuskan GA (2012) Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree *Populus trichocarpa*. **New Phytologist** 196:713-725.
18. Guo J, Morrell-Falvey JL, Labbé JL, **Muchero W**, Kalluri UC, Tuskan GA, Chen JG (2012) Highly efficient isolation of *Populus* mesophyll protoplasts and its application in transient expression assays. **PLoS ONE** 7(9): e44908.
19. Induri BR, Ellis DR, Slavov GT, Yin T, Zhang X, **Muchero W** et al. (2012) Identification of quantitative trait loci and candidate genes for cadmium tolerance in *Populus*. **Tree Physiology** 32: 626-638.
20. **Muchero W** et al. (2011) Genic SNP markers and legume synteny reveal candidate genes underlying QTL for *Macrophomina phaseolina* resistance and maturity in cowpea [*Vigna unguiculata* (L) Walp.] **BMC Genomics** 12:8.

21. **Muchero W et al. (2010)** Restriction site polymorphism-based candidate gene mapping for seedling drought tolerance in cowpea [*Vigna unguiculata* (L.) Walp.]. ***Theoretical and Applied Genetics*** 120: 509-51.
22. **Muchero W et al. (2010)** QTL analysis for resistance to foliar damage caused by *Thrips tabaci* and *Frankliniella schultzei* (Thysanoptera: Thripidae) feeding in cowpea (*Vigna unguiculata* L. Walp.). ***Molecular Breeding*** 25: 47-56.
23. **Muchero W et al. (2009)** A consensus genetic map of cowpea [*Vigna unguiculata* (L) Walp.] and synteny based on EST-derived SNPs. ***Proceedings of the National Academy of Sciences USA*** 106: 18159-18164.
24. **Muchero W et al. (2009)** Mapping QTL for drought stress-induced premature senescence and maturity in cowpea [*Vigna unguiculata* (L.) Walp.] ***Theoretical and Applied Genetics*** 118: 849-863.

Synergistic Activities:

1. Professional membership: American Phytopathological Society (2006 – Present), American Society for Plant Biologists (2010 – Present).
2. Adjunct reviewer: *Plant Cell & Environment, New Phytologist, PLoS ONE, BMC Genomics, BMC Plant Biology, Biotechnology for Biofuels, GCB Bioenergy, African Journal of Microbiology, Theoretical and Applied Genetics, Molecular breeding, Crop science Journal, Euphytica, African Journal of Biotechnology, The Plant Genome.*