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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: Nematology Dept., University of California, Riverside (Feb-2008 to Sept-2010)

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

Current research activities:

BioEnergy Science Center (<http://bioenergycenter.org/besc/index.cfm>): 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.

Plant Microbe Interfaces (pmi.ornl.gov): 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 genomic intervals suggestive 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.

***Physcomitrella* Genome Improvement (http://www.phytozome.net/physcomitrella_er.php):**

Physcomitrella is an evolutionarily important model plant species that provides insight into the emergence of terrestrial flowering plant. It is the first moss to have its genome sequenced. In this project, we are working with an international consortium of scientist from the University of Freiburg - Germany, University of Leeds - UK, DOE-Joint Genome Institute - USA, HudsonAlpha Institute of Biotechnology - USA, and the University of Florida - USA to apply rapid SNP genotyping in the creation of high-density genetic maps to be used in aligning genome scaffolds in addition to QTL mapping.

Allele Mining for Biomass Quality: We are a part of USDA/DOE funded Biomass Feedstocks project in collaboration with scientists at the Michigan Technological University in which we characterize natural variants of genes discovered via activation tagging for their effect on biomass quality and quantity characteristics. We conduct targeted allele mining using whole-genome resequencing on diverse *Populus* genotypes.

Intellectual property:

1. Invention Disclosure S-124,759 A lectin-like receptor kinase leads to enhanced mycorrhization in plants.
2. Invention Disclosure S-124,857 A heavy metal transporter enhancing woody quality for biofuels production.
3. Invention Disclosure S-124,856 An Amino Acid Transporter enhancing lignin quality and sugar release.
4. Invention Disclosure: S-124,480: A gene regulating cellulose, hemicellulose biosynthesis, and biomass sugar yield.
5. Invention Disclosure: S-124,481: Allelic variants regulating cellulose, lignin biosynthesis and biomass sugar yield.
6. Invention Disclosure: S-124,482: A gene regulating cellulose, hemicellulose biosynthesis and biomass sugar yield.
7. Invention Disclosure: S-124,200: A key gene A regulating plant cell-wall recalcitrance and sugar release.
8. Invention Disclosure: S-124,201: A key gene B regulating plant cell-wall recalcitrance and sugar release.
9. Invention Disclosure: S-124,202: A key gene C regulating plant cell-wall recalcitrance and sugar release.
10. Invention Disclosure: S-124,203: A key gene D regulating plant cell-wall recalcitrance and sugar release.
11. Invention Disclosure: S-124,204: A key gene E regulating plant cell-wall recalcitrance and sugar release.
12. Invention Disclosure: S-124,205: A key gene F regulating plant cell-wall recalcitrance and sugar release.
13. Invention Disclosure: S-124,206: A key gene G regulating plant cell-wall recalcitrance and sugar release.
14. Invention Disclosure: S-124,207: A key gene H regulating plant cell-wall recalcitrance and sugar release.
15. Invention Disclosure: S-124,208: A key gene I regulating plant cell-wall recalcitrance and sugar release.
16. Invention Disclosure: S-124,209: A key gene J regulating plant cell-wall recalcitrance and sugar release.
17. Invention Disclosure: S-124,210: A key gene K regulating plant cell-wall recalcitrance and sugar release.
18. Invention Disclosure: S-124,211: A key gene L regulating plant cell-wall recalcitrance and sugar release.
19. Invention Disclosure: S-124,212: A key gene M regulating plant cell-wall recalcitrance and sugar release.
20. Invention Disclosure: S-124,213: A key gene N regulating plant cell-wall recalcitrance and sugar release.
21. Invention Disclosure: S-124,214: A key gene O regulating plant cell-wall recalcitrance and sugar release.
22. Invention Disclosure: S-124,215: A key gene G-paralog regulating plant cell-wall recalcitrance and sugar release.

Publications:

1. **Muchero W** (*corresponding author*) **et al. (2014)** Multi-environment detection and molecular validation of candidate genes associated with cell wall chemistry in *Populus trichocarpa*. (Under review).
2. **Muchero W** et al. **(2014)** Genetic and genomic characterization of rare recessive traits conferring enhanced root epidermal mucilage and root hairlessness in cowpea. (Under review).
3. 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** DOI: 10.1111/nph.12815.
4. Yin H, Chen CJ, Yang J, Weston DJ, Chen JG, **Muchero W**, Ye N, Tschaplinski TJ, Wullschleger SD, Cheng ZM, Tuskan GA, Yang X. **(2014)** Functional genomics of drought tolerance in bioenergy crops. **Critical Review in Plant Science** 33:205-224.
5. **Muchero W** (*corresponding author*) **et al. (2014)** Genome resequencing in *Populus*: Revealing large-scale genome variation and implications on specialized-trait genomics. In Challenges and Opportunities for the world's Forests in the 21st Century. Springer academic publishers. **Forestry Sciences** 81: 587-595.
6. Porth I, Klápště J, Skyba O, Hannemann J, McKown AD, Guy RD, DiFazio SP, **Muchero W** et al. **(2013)**. Genome-wide association mapping for wood characteristics in *Populus* identifies an array of candidate single nucleotide polymorphisms. **New Phytologist** 200: 710-726.
7. **Muchero W** et al. **(2013)** Genetic architecture of delayed senescence, biomass, and grain yield under drought stress in cowpea. **PLoS ONE** 8(7): e70041.
8. **Muchero W** (*corresponding author*) **et al. (2013)** Genome anchored QTLs for biomass productivity in Hybrid *Populus* grown under contrasting environments. **PLoS ONE** 8: e54468.
9. Geraldles A, DiFazio S, Slavov GT, Priya R, **Muchero W** et al. **(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.
10. Porth I, Klápště J, Skyba O, Lai BSK, Geraldles A, **Muchero W** et al. **(2013)** *Populus trichocarpa* cell wall chemistry and ultrastructure trait variation, genetic control and genetic correlations. **New Phytologist** 197: 777-790.
11. Zhaoqing J, **Muchero W**, Chen J-G **(2013)** Analysis of Cell Division and Cell Elongation in the Hypocotyls of Arabidopsis Heterotrimeric G Protein Mutants. Mark P. Running (ed.), G Protein-

Coupled Receptor Signaling in Plants: Methods and Protocols, Methods in Molecular Biology 1043: 37-43.

12. Slavov GT, DiFazio SP, Martin J, Schackwitz SP, **Muchero W** et al. (2012) Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree *Populus trichocarpa*. New Phytologist 196: 713-725.
13. 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.
14. 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.
15. **Muchero** 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.
16. **Muchero** 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.
17. **Muchero** 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.
18. Agbicodo EM, Fatokun CA, Bandyopadhyay R, Wydra K, Diop NN, **Muchero W** et Al. (2010) Identification of markers associated with bacterial blight resistance loci in cowpea [*Vigna unguiculata* (L) Walp.]. Euphytica 175:215-226.
19. **Muchero** 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.
20. **Muchero** 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.
21. **Muchero** et al. (2008) Seedling stage drought-induced phenotypes and drought-responsive genes in diverse cowpea genotypes. Crop Science 48: 541-552.

Meeting presentations:

1. **Muchero et al. (2014)** Genome re-sequencing reveals a species-specific whole-gene deletion associated with *Populus-Laccaria* mycorrhizal symbiosis. **The Annual DOE JGI User Meeting**, Walnut Creek, CA.
2. **Muchero et al. (2014)** Whole genome re-sequencing-enabled discovery and functional validation of allelic variants associated with cell wall chemistry and mycorrhizal symbiosis in *Populus*. **Plant and Animal Genome XXII Conference**, San Diego, CA.
3. **Muchero et al. (2013)** Natural allelic variation shaping cell-wall recalcitrance phenotypes in *Populus trichocarpa*. **Plenary Talk: DOE Genomics Science Awardee Meeting**, Washington DC.
4. **Muchero et al. (2013)** The *Physcomitrella* illumina infinium SNP array: Informing genetics and genomics in mosses. **Plant and Animal Genome XXI Conference**, San Diego, CA.
5. **Muchero et al. (2012)** Genome-scale discovery of cell wall biosynthesis genes in *Populus*. **Seventh Annual Genomics of Energy and Environment Meeting, DOE-JGI**, Walnut Creek, CA.
6. **Muchero et al. (2012)** Partitioning cell wall recalcitrance phenotypes among individual gene effects in *Populus*. **BioEnergy Science Center (BESC) Characterization Workshop**, Riverside, CA.
7. **Muchero et al. (2011)** Genetic dissection of cell-wall recalcitrance using high-resolution SNP mapping arrays in *Populus*. **BioEnergy Science Center (BESC) Annual Retreat**, Chattanooga, TN.
8. **Muchero et al. (2010)** Genomic distribution of loci exhibiting positive pleiotropic effects on delayed senescence, grain yield and biomass accumulation under drought stress in cowpea. **5th World Cowpea Conference**, Saly, Senegal.

Conference abstracts and contributed presentations:

1. **Muchero et al. (2013)** Plant-Microbe Interfaces: Intra- and inter-specific variations in indel polymorphisms co-segregating with QTLs for *Populus-Laccaria* interaction. **DOE Genomics Science Awardee Meeting**, Washington DC.
2. Yee et al. (2013) Implications of the improved dedicated feedstock *Populus* spp. **DOE Genomics Science Awardee Meeting**, Washington DC.
3. Ehlers et al. (2013) Accessing the genome of cowpea to provide climate resilient crops. **Plant and Animal Genome Conference**, San Diego, CA.

4. Chen et al. (2013) Genome-wide association studies of shoot branching in *Populus*. **Plant and Animal Genome Conference**, San Diego, CA.
5. Evans et al. (2013) Comparative genetics of *Populus angustifolia* and *P. trichocarpa*. **Plant and Animal Genome Conference**, San Diego, CA.
6. Slavov et al. (2013) Prospects of applying genomic selection in natural populations of *Populus trichocarpa*. **Plant and Animal Genome Conference**, San Diego, CA.
7. **Muchero** et al. (2012) Mining genomic signatures of species-specific microbe interactions in *Populus* using high density SNP arrays and whole genome resequencing. **US Dept. of Energy Contractors Meeting**, Washington D.C.
8. **Muchero et al.** (2012) Post-GWAS in-silico and molecular validation of genic and Intergenic loci associated with cell-wall recalcitrance in *Populus*. **Plant and Animal Genome Conference**, San Diego, CA.
9. Schmutz et al. (2012) An improved reference genome for *Physcomitrella*. **Plant and Animal Genome Conference**, San Diego, CA.
10. Sims et al. (2012) Genome Improvement of DOE JGI Flagship Plant Genomes. **US Dept. of Energy Contractors Meeting**, Washington D.C.
11. Schadt et al. (2012) Genotype-by-environment interactions drive root-associated microbiome composition in natural populations of *Populus deltoides*. **US Dept. of Energy Contractors Meeting**, Washington D.C.
12. Geraldès et al. (2012) Levels and patterns of nucleotide variability and population differentiation in *Populus*: insights from transcriptome resequencing and SNP genotyping. **Plant and Animal Genome Conference**, San Diego, CA.
13. Ilga Porth et al. (2012) Association genetics of traits underlying secondary cell wall chemistry and ultrastructure in *Populus trichocarpa*. **Plant and Animal Genome Conference**, San Diego, CA.
14. DiFazio et al. (2012) Population genomics of vegetative phenology in *Populus*. **Plant and Animal Genome Conference**, San Diego, CA.
15. **Muchero** et al. (2011) Genome-wide association mapping for characterization of the genetic architecture of recalcitrance and biomass productivity in *Populus*. **US Dept. of Energy Contractors Meeting**, Washington D.C.

16. Diop et al. (2010) QTL mining for drought avoidance mechanisms at flowering time in cowpea [*Vigna unguiculata* (L) Walp.] **Plant and Animal Genomes XVIII Conference**, San Diego, CA.
17. **Muchero** et al. (2009) Interrogating the common genetic determinants for delayed drought-induced premature senescence and yield enhancement traits in cowpea (*Vigna unguiculata*) using association mapping. **Generation Challenge Program MAB workshop**, Zaragoza, Spain.
18. **Muchero** et al. (2009) QTL mapping of root-knot nematode resistance in cowpea (*Vigna unguiculata*) using EST-derived SNP markers. **Society of Nematology 48th Annual Meeting**, Burlington, VT.
19. **Muchero** et al. (2007) Mapping Quantitative Trait Loci (QTL) for seedling drought tolerance and ashy stem blight resistance in cowpea (*Vigna unguiculata*) Abstract: **Phytopathology** Volume: 97 Issue: 7, Suppl. S Pages: S80-S81

Press:

1. 10 Questions for a Quantitative Geneticist: Wellington Muchero
<http://energy.gov/articles/10-questions-quantitative-geneticist-wellington-muchero>
2. UC research to benefit African farmers (12-03-07):
<http://www.ucop.edu/sciencetoday/article/16901>
3. Genetic Map For Cowpea Accelerates Development Of New Varieties (10-14-09):
<http://www.sciencedaily.com/releases/2009/10/091013171231.htm>

Languages:

English (Fluent)

Shona (Fluent)

Spanish (Advanced)