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# Matias Kirst

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## Education

Cornell University	Maize Genomics	Postdoc	2004
North Carolina State University	Genetics & Genomics	Ph.D.	2003
Federal University of Viçosa (Brazil)	Genetics and Improvement	M.Sc.	1999
Federal University of Santa Maria (Brazil)	Forestry Engineering	B.S.	1996

## Professional Positions

2016-present	Director, Plant Molecular and Cellular Biology Program, University of Florida
2015-present	Professor, School of Forest Resources and Conservation, University of Florida
2014-2016	Graduate Coordinator, Plant Molecular and Cellular Biology Program, University of Florida
2011-present	Founder, Chief Executive Officer (2011-12) and scientific consultant (2013-present) of RAPiD Genomics LLC
2010-present	Associate Professor, School of Forest Resources and Conservation, University of Florida
2010-present	Co-Director Cooperative Forest Genetics Research Program, University of Florida
2005-present	Member UF Genetics Institute
2005-2009	Assistant Professor, School of Forest Resources and Conservation, University of Florida

## Professional Experience

**Research** – Research funded by over \$20M in federal grants secured since joining UF in 2005, of which \$13.9M as the principal investigator. Kirst is the currently the lead investigator in four federal grants from the NSF, USDA and DOE, on: (1) development of methods to predict phenotypes based on genomic data and (2) their application to hyper-accelerate genetic improvement, (3) training of plant breeders in modern genomic technologies, (4) identification of genes that regulate adaptation of plants to climate change and plant productivity and (5) characterization of newly discovered genes of economic value. The research derived from these activities is published in over 50 peer-reviewed articles. Kirst also participates in Scientific Advisory Boards from projects funded by the European Union and Genome Canada, and frequently acts as an external reviewer for national and international funding agencies. Kirst has also chaired some of the largest conferences in the field of forest biotechnology, including the IUFRO Tree Biotechnology Conference 2013 and the Forest Tree Workshop at the Plant and Animal Genome Conference.

**Teaching and advising** – Advises four PhD students from the inter-college programs Genetics and Genomics, and Plant Molecular and Cellular Biology, and is a member of 18 PhD/MSc student committees. Kirst is the lead instructor of GMS6231 Genomics and Bioinformatics, taught through

the College of Medicine, which commonly included students from different majors and colleges. Kirst also teach and co-teach two other graduate level courses (PCB5065 Advanced Genetics, and PCB7922 Journal Colloquium). Kirst commonly hosts 2-4 visiting scholars annually, including scientists from Brazil, Canada, Finland, France, Italy, Japan and Spain.

**Extension and Development** – Kirst acts as the co-Director of the Cooperative Forest Genetics Research Program, the oldest pine breeding cooperative in the US. Kirst also founded RAPID Genomics in 2011, a spin-off of his laboratory at the UF Genetics Institute, created to commercialize inventions and support the development of the local economy. RAPID started operations in the Florida Innovation Hub at UF in December 2012, and currently supplies genotyping and genomic data analysis services to over 100 clients in 20 countries.

## Publications

- Conde D, Moreno-Cortés A, Dervinis C, Ramos-Sánchez JM, Kirst M, Perales M, González-Melendi P, Allona I. Overexpression of DEMETER, a DNA demethylase, promotes early apical bud maturation in poplar. *Plant Cell Environ.* 2017 Aug 15. doi: 10.1111/pce.13056.
- Conde D, Le Gac AL, Perales M, Dervinis C, Kirst M, Maury S, González-Melendi P, Allona I. Chilling responsive DEMETER-LIKE DNA demethylase mediates in poplar bud break. *Plant Cell Environ.* 2017 Jul 13. doi: 10.1111/pce.13019.
- Müller BSF, Neves LG, de Almeida Filho JE, Resende MFR Jr, Muñoz PR, Dos Santos PET, Filho EP, Kirst M, Grattapaglia D. Genomic prediction in contrast to a genome-wide association study in explaining heritable variation of complex growth traits in breeding populations of Eucalyptus. *BMC Genomics.* 2017 Jul 11;18(1):524. doi: 10.1186/s12864-017-3920-2.
- Tieman D, Zhu G, Resende Jr. MFR, Nguyen C, Bies D, Rambla JL, Beltran KSO, Taylor M, Zhang B, Ikeda H, Liu Z, Fisher J, Monforte A, Zamir D, Granell A, Kirst M, Huang S, Klee H. (2017) A chemical genetic roadmap to improved tomato flavor. *Science* 355:391-394.
- Fahrenkrog AM, Neves LG, Resende MF Jr, Vazquez AI, de Los Campos G, Dervinis, C, Sykes R, Davis M, Davenport R, Barbazuk WB, Kirst M. (2017) Genome-wide association study reveals putative regulators of bioenergy traits in *Populus deltoides*. *New Phytol.* doi: 10.1111/nph.14154.
- Vazquez AI, Veturi Y, Behring M, Shrestha S, Kirst M, Resende MF Jr, de Los Campos G. (2016) Increased proportion of variance explained and prediction accuracy of survival of breast cancer patients with use of whole-genome multiomic profiles. *Genetics.* 103:1425-1438.
- de Almeida Filho JE, Guimarães JF, E Silva FF, de Resende MD, Muñoz P, Kirst M, Resende MF Jr. (2016) The contribution of dominance to phenotype prediction in a pine breeding and simulated population. *Heredity (Edinb).* 117:33-41.
- Ramos SL, Dequigiovanni G, Sebbenn AM, Lopes MT, Kageyama PY, de Macêdo JL, Kirst M, Veasey EA. (2016) Spatial genetic structure, genetic diversity and pollen dispersal in a harvested population of *Astrocaryum aculeatum* in the Brazilian Amazon. *BMC Genet.* 17:63.
- Ribeiro CL, Silva CM, Drost DR, Novaes E, Novaes CR, Dervinis C, Kirst M. (2016) Integration of genetic, genomic and transcriptomic information identifies putative regulators of adventitious root formation in *Populus*. *BMC Plant Biol.* 16:66.
- Goncalves EC, Wilkie AC, Kirst M, Rathinasabapathi B. (2016) Metabolic regulation of triacylglycerol accumulation in the green algae: identification of potential targets for engineering to improve oil yield. *Plant Biotechnol J.* 14:1649-1660.
- Drost DR, Puranik S, Novaes E, Novaes CR, Dervinis C, Gailing O, Kirst M. (2015) Genetical genomics of *Populus* leaf shape variation. *BMC Plant Biol.* 15:166.

- Westbrook JW, Chhatre VE, Wu LS, Chamala S, Neves LG, Muñoz P, Martínez-García PJ, Neale DB, Kirst M, Mockaitis K, Nelson CD, Peter GF, Davis JM, Echt CS. (2015) A consensus genetic map for *Pinus taeda* and *Pinus elliottii* and extent of linkage disequilibrium in two genotype-phenotype discovery populations of *Pinus taeda*. *G3* (Bethesda). 5:1685-1694.
- Munoz PR, Resende MF Jr, Gezan SA, Resende MD, de Los Campos G, Kirst M, Huber D, Peter GF. (2014) Unraveling additive from nonadditive effects using genomic relationship matrices. *Genetics* 198:1759-1768.
- Neves LG, Davis JM, Barbazuk WB, Kirst M. (2014) A high-density gene map of loblolly pine (*Pinus taeda* L.) based on exome sequence capture genotyping. *Genes, Genetics and Genomes* 10:29-37.
- Munoz PR, Resende MF Jr, Huber DA, Quesada T, Resende MDV, Neale DB, Wegrzyn JL, Kirst M, Peter GF. (2014) Genomic relationship matrix for correcting pedigree errors in breeding populations: impact on genetic parameters and genomic selection accuracy. *Crop Sci.* 54:1115-1123.
- Quesada T, Resende Jr MF, Muñoz P, Wegrzyn JL, Neale DB, Kirst M, Peter GF, Gezan SA, Nelson CD, Davis JM. (2014) Mapping fusiform rust resistance genes within a complex mating design of loblolly pine. *Forests* 5:347-362.
- White T, Davis J, Gezan S, Hulcr J, Jokela E, Kirst M, Martin TA, Peter G, Powell G, Smith J. (2014) Breeding for value in a changing world: past achievements and future prospects. *New Forests* 45:301-309.
- Zhang, J., E. Novaes, M. Kirst and G.F. Peter. (2014) Comparison of pyrolysis mass spectrometry and near infrared spectroscopy for genetic analysis of lignocellulose chemical composition in *Populus*. *Forests* 5:466-481.
- Albert VA et al. The Amborella genome and the evolution of flowering plants. *Science* 342: 1516-1517.
- Maron LG, Guimarães CT, Kirst M, Albert PS, Birchler JA, Bradbury PJ, Buckler ES, Coluccio AE, Danilova TV, Kudrna D, Magalhaes JV, Piñeros MA, Schatz MC, Wing RA, Kochian LV. (2013) Aluminum tolerance in maize is associated with higher MATE1 gene copy-number. *Proc. Natl. Acad. Sci. USA.* 110:5241-5246.
- Neves LG, Davis JM, Barbazuk WB, Kirst M. (2013) Whole-exome targeted sequencing of the uncharacterized pine genome. *Plant J.* 75:146-156.
- Westbrook JW, Resende MF Jr, Munoz P, Walker AR, Wegrzyn JL, Nelson CD, Neale DB, Kirst M, Huber DA, Gezan SA, Peter GF, Davis JM. (2013) Association genetics of oleoresin flow in loblolly pine: discovering genes and predicting phenotype for improved resistance to bark beetles and bioenergy potential. *New Phytol.* 199:89-100.
- Resende MF Jr, Muñoz P, Resende MD, Garrick DJ, Fernando RL, Davis JM, Jokela EJ, Martin TA, Peter GF, Kirst M. (2012) Accuracy of genomic selection methods in a standard dataset of loblolly pine (*Pinus taeda* L.). *Genetics.* 190:1503-1510.
- Harfouche A, Meilan R, Kirst M, Morgante M, Boerjan W, Sabatti M, Mugnozza GS. (2012) Accelerating the domestication of forest trees in a changing world. *Trends in Plant Sciences.* 17:64-72.
- Resende MFR, Muñoz P, Acosta JJ; Peter GF, Davis JM, Grattapaglia D, Resende MDV, Kirst M. (2012) Accelerating the domestication of trees using genomic selection: accuracy of prediction models across ages and environments. *New Phytologist.* 193:617-624.
- Villar E, Klopp C, Noirot C, Novaes E, Kirst M, Plomion C, Gion JM. (2011) RNA-Seq reveals genotype-specific molecular responses to water deficit in eucalyptus. *BMC Genomics.* 12:538.
- Neves LG, Mc Mamani E, Alfenas AC, Kirst M, Grattapaglia D. (2011) A high-density transcript linkage map with 1,845 expressed genes positioned by microarray-based Single Feature Polymorphisms (SFP) in *Eucalyptus*. *BMC Genomics.* 12:189.

- Grattapaglia D, Silva-Junior OB, Kirst M, de Lima BM, Faria DA, Pappas GJ Jr. (2011) High-throughput SNP genotyping in the highly heterozygous genome of *Eucalyptus*: assay success, polymorphism and transferability across species. *BMC Plant Biology* 11:65.
- Lourenço VM, Pires AM, Kirst M. Robust linear regression methods in association studies. (2011) *Bioinformatics*. 27:815-21.
- Prosdociimi F, Bittencourt D, da Silva FR, Kirst M, Motta PC, Rech EL. (2011) Spinning gland transcriptomics from two main clades of spiders (order: Araneae) - insights on their molecular, anatomical and behavioral evolution. *PLoS One*. 6:e21634.
- Novaes, E., M. Kirst, V. Chiang, H. Winter-Sederoff and R. Sederoff. (2010) Lignin and biomass: a negative correlation for wood formation and lignin content in trees. *Plant Physiology* 154:555-561.
- Mattiello, L., M. Kirst, F.R. da Silva, R.A. Jorge and M. Menossi. (2010) Transcriptional profile of maize roots under acid soil growth. *BMC Plant Biology* 10:196.
- Visscher, A.M., A.L. Paul, M. Kirst, C.L. Guy, A.C. Schuerger and R.J. Ferl. (2010) Growth performance and root transcriptome remodeling of *Arabidopsis* in response to Mars-like levels of magnesium sulfate. *PLoS One*. 5:e12348.
- Drost, D.R., C.I. Benedict, A. Berg, E. Novaes, C.R. Novaes, Q. Yu, C. Dervinis, J.M. Maia, J. Yap, B. Miles and M. Kirst. (2010) Diversification in the genetic architecture of gene expression and transcriptional networks in organ differentiation of *Populus*. *Proc. Natl. Acad. Sci. USA*. 107:8492-8497.
- Krill, A.M., M. Kirst, L.V. Kochian, E.S. Buckler and O.A. Hoekenga. (2010) Association and linkage analysis of aluminum tolerance genes in maize. *PLoS One*. 5:e9958.
- Brunings, A.M., L.E. Datnoff, J.F. Ma, N. Mitani, Y. Nagamura, B. Rathinasabapathi and M. Kirst. (2009) Differential gene expression of rice in response to silicon and rice blast fungus *Magnaporthe oryzae*. *Annals of Applied Biology* 155: 161-170.
- Visscher, A.M., A-L. Paul, M. Kirst, A.K. Alling, S. Silverstone, G. Nechitailo, M. Nelson, W.F. Dempster, M. Van Thillo, J.P. Allen and R.J. Ferl. (2009) Effects of a spaceflight environment on heritable changes in wheat gene expression. *Astrobiology* 9: 359-367.
- Drost, D.R., E. Novaes, C. Boaventura-Novaes, C.I. Benedict, R.S. Brown, T. Yin, G.A. Tuskan and M. Kirst. (2009) A microarray-based genotyping and genetic mapping approach for highly heterozygous outcrossing species localizes a large fraction of the unassembled *Populus trichocarpa* genome sequence. *Plant Journal* 58: 1054-1067.
- Grattapaglia, D., C. Plomion, M. Kirst and R.R. Sederoff. (2009) Genomics of growth traits in forest trees. *Current Opinion in Plant Biology* 12: 148-156.
- Novaes, E., L.F. Osorio, D.R. Drost, B.L. Miles, C. Boaventura-Novaes, C.I. Benedict, C. Dervinis, Q. Yu, R. Sykes, M. Davis, T.A. Martin, G.F. Peter and M. Kirst. (2009) Quantitative genetic analysis of biomass and wood chemistry of *Populus* under different nitrogen levels. *New Phytologist* 182: 878-890.
- Quesada, T., Z. Li, C. Dervinis, Y. Li, P.N. Bockock, G.A. Tuskan, G. Casella, J.M. Davis and M. Kirst. (2008) Comparative analysis of the transcriptomes of *Populus trichocarpa* and *Arabidopsis thaliana* suggests extensive evolution of gene expression regulation in angiosperms. *New Phytologist* 180: 408-420.
- Novaes, E., D.R. Drost, W.G. Farmerie, G.J. Pappas Jr., D. Grattapaglia, R.R. Sederoff and M. Kirst. (2008) High-throughput gene and SNP discovery in *Eucalyptus grandis*, an uncharacterized genome. *BMC Genomics* 9: 312-325.
- Grattapaglia, D. and M. Kirst. (2008) *Eucalyptus* applied genomics: from gene sequences to breeding tools. *New Phytologist* 179: 911-929.
- Maron, L.G., M. Kirst, C. Mao, M. Menossi and L.V. Kochian. (2008) Transcriptional profiling of Al toxicity and tolerance responses in maize roots. *New Phytologist* 179: 116-128.

- Ma, C.-X., Q. Yu, A. Berg, D. Drost, E. Novaes, G. Fu, J.S. Yap, A. Tang, M. Kirst, Y. Cui and R. Wu. (2008) A pleiotropic model for mapping phenotypic plasticity of a count trait. *Genetics* 179: 627-636.
- Gore, M., P. Bradbury, R. Hogers, M. Kirst, E. Verstege, J. van Oeveren, J. Peleman, E. Buckler and M. van Eijk. (2007) Evaluation of target preparation methods for single feature polymorphism detection in large complex plant genomes. *Crop Science* 47: S135-S148.
- Kirst, M., R. Caldo, P. Casati, G. Tanimoto, V. Walbot, R.P. Wise and E.S. Buckler. (2006) Genetic diversity contribution to errors in short-oligonucleotide microarray analysis. *Plant Biotechnology Journal* 4: 489-498.
- Tuskan, G.A., et al. (2006) The genome of western black cottonwood, *Populus trichocarpa* (Torr. & Gray ex Brayshaw). *Science* 313:1596-1604.
- Tieman, D.M., M. Zeigler, E.A. Schmelz, M.G. Taylor, P. Bliss, M. Kirst and H.J. Klee. (2006) Identification of loci affecting flavour volatile emissions in tomato fruits. *Journal of Experimental Botany* 57:887-896.
- Kirst, M., C.J. Basten, A. Myburg, Z.-B. Zeng and R. Sederoff. (2005) Genetic architecture of transcript level variation in differentiating xylem of *Eucalyptus* hybrids. *Genetics* 169: 2295-2303.
- Kirst, M., C.M. Cordeiro, G.D.S.P. Rezende and D. Grattapaglia. (2005) Power of microsatellite markers for fingerprinting and parentage analysis in *Eucalyptus grandis* breeding populations. *Journal of Heredity* 96:161-166.
- Egertsdotter, U., L.M. van Zyl, J. MacKay, G. Peter, M. Kirst, C. Clark, R. Whetten and R. Sederoff. (2004) Gene expression during formation of earlywood and latewood in loblolly pine: expression profiles of 350 genes. *Plant Biology* 6:654-663.
- Kirst, M., A. Myburg, M.E. Kirst, J. Scott and R. Sederoff. (2004) Quantitative analysis of transcript variation on microarrays reveals coordinated downregulation of lignin gene transcripts associated with two quantitative trait loci for growth in a *Eucalyptus* hybrid backcross. *Plant Physiology* 135:2368-2378.
- Kirst, M., A.F. Johnson, C. Baucom, E. Ulrich, K. Hubbard, R. Staggs, C. Paule, E. Retzel, R. Whetten and R. Sederoff. (2003) Apparent homology of expressed genes from wood-forming tissues of loblolly pine (*Pinus taeda* L.) with *Arabidopsis thaliana*. *Proceedings of the National Academy of Sciences of the U.S.A* 100:7383-7388.
- Brondani, R.P.V., Gaiotto, F.A., Missiaggia, A.A., Kirst, M., Gribel, R. and Grattapaglia, D. (2003) Microsatellite markers for *Ceiba pentandra* (Bombacaceae), an endangered tree species of the Amazon forest. *Molecular Ecology Notes* 3:177-179.

## Grants and Contracts

- 2017 – 2022 Phylogenomic discovery and engineering of nitrogen fixation into the bioenergy woody crop poplar (PI, Amount: \$7,300,000; Source: DOE)
- 2015 – 2019 Genome and transcriptome based prediction, and regulator inference, of molecular and whole-plant phenotypes (PI; Amount: \$1,956,424; Source: NSF)
- 2013 – 2017 Accelerated development of optimal pine feedstocks for bioenergy and renewable chemicals using genome-wide selection (PI; Amount: \$1,000,000; Source: USDA)
- 2013 – 2017 Accelerated breeding by improved accuracy and mate allocation using genome-wide selection (PI; Amount: \$500,000; Source: USDA)
- 2010 – 2015 A systems biology, whole-genome association analysis of the molecular regulation of biomass growth and composition in *Populus deltoides* (PI; Amount: \$873,327; Source: DOE)

- 2009 – 2014 Advanced pine breeding through association genetics and biotechnology (PI; Amount: \$500,000; Source: USDA)
- 2009 – 2013 Mechanism of carbon partitioning regulation by cp<sub>g13</sub> in the bioenergy woody crop poplar (PI; Amount: \$642,148; Source: USDA)
- 2009 – 2012 Identification and functional characterization of insect resistance genes in poplar using forward genetics (Co-PI; Amount: \$617,637; Source: NSF)
- 2009 – 2012 Energy intensive crop development (Co-PI; Amount: \$432,000; Source: Florida Energy Systems Consortium)
- 2008 – 2009 Gene expression networks and their regulators in a model perennial plant (PI; Amount: \$250,000; Source: NSF)
- 2008 – 2011 The Agricultural Genomics, Education and Metabolomics (GEM) Graduate Fellows Program (Co-PI; Amount: \$229,500; Source: USDA)
- 2006 – 2008 Genome-enabled discovery of carbon allocation genes in Populus: Molecular control of root proliferation and production of recalcitrant compounds (Co-PI; Amount: \$4,084,481; Source: DOE)
- 2006 – 2008 Genes for more efficient land use and conversion of forest trees into wood products (Co-PI; Amount: \$236,978; Source: CPBR)
- 2005 – 2008 Genomic mechanisms of carbon allocation and partitioning in poplar (PI; Amount: \$1,029,658; Source: DOE)
- 2005 – 2007 Genomic regulation of growth and lignin in Eucalyptus (Co-PI; Amount: \$236,000; Source: CPBR)
- 2005 – 2009 Association genetics of natural genetic diversity and complex traits in pine (Co-PI; Amount: \$5,902,886; Source: NSF)

### **Patents** (*granted and provisional*)

- M. Kirst, M. Resende, C. Dervinis. Four provisional patents currently submitted on the application of CRISPR to genome complexity reduction and genotyping.
- M. Kirst, M. Resende, L. Neves, C. Dervinis. A method for genome complexity reduction and polymorphism detection (patent granted in 2012, currently licensed to RAPiD Genomics)
- M. Kirst. Material and methods to increase plant growth and yield (patent granted in 2013, currently licensed to Benson Hill Biosystems)

### **Invited Presentations** (*international, invited*)

- Vessel Development and the Evolution of Land Plants. University of British Columbia – Michael Smith Laboratory. November 2017. Vancouver, Canada.
- From academia to industry – Can genomic selection be implemented in commercial tree breeding? IUFRO Tree Biotechnology 2017. June 2017. Concepcion, Chile.
- The application of genome-wide information to tree breeding – what is coming next? Forest Genetics Conference. June 2017. Edmonton, Canada.
- EVE regulation of vessel size and number. Plant Vascular Biology Conference. July 2016. Shenzhen, China.
- Populus deltoides genetic and structural variation and comparison to related species. ProCoGen Conference. December 2015. Orléans, France.

From QTL to GWAS to genomic selection and back to genes. 8th Brazilian Congress of Plant Breeding. August 2015. Goiânia, Brazil.

EVE regulation of vessel development. IUFRO Tree Biotechnology Conference 2015. June 2015. Florence. Italy.

A whole-genome association analysis of *Populus deltoides* implicates rare alleles in phenotypic variation for biomass growth and composition. IUFRO Tree Biotechnology Conference 2015. June 2015. Florence, Italy.

Conifer genotyping approaches, and applications to population and quantitative genetics. Conifer Genome Summit. September 2015. Gysinge Herrgård, Sweden.

Tree breeding using genome information-resistant traits. University of Helsinki. October 2014. Helsinki, Finland.

Genotyping using nextgen sequencing – from GBS to sequence capture. University of São Paulo. October 2014. Piracicaba, Brazil.

How EVE led the flowering plants to dominate the world. Universidad de Alcala. February 2014. Alcala de Henares, Spain.

Maize genotyping using RAPiD-Seq (Randomly-Amplified Polymorphic DNA Sequencing). Maize Workshop, Plant and Animal Genome Conference XXI. January 2014. San Diego, USA.

Accelerated breeding of pines using advanced methods and applications of genomic prediction. Scion New Zealand Crown Research Institute and Radiata Pine Breeding Company Meeting. October 2013. Rotorua, New Zealand.

Population genomics of forestry species: in search for the genes that regulate adaptation and domestication. II International Symposium of Applied Botany. September 2013. Manaus, Brazil.

From QTL to genomic prediction – and the joys and challenges of academia in between. North Carolina State University Genetics Colloquium. August 2013. Blowing Rock, USA.

What do we need to apply genome-wide prediction? Phenotype Prediction Using Genomic Data Workshop. August 2013. Gainesville, USA.

From genetical genomics to genomic selection – adapting our forests to a changing world. Federal University of Goiás. June 2013. Goiânia, Brazil.

Advanced Pine Breeding through Association Genetics and Biotechnology. USDA and DOE Principal Investigators Meeting. January 2013. San Diego, USA.

Technology transfer from University to Industry: The experience of RAPiD Genomics. SMarT Forests Technology Advisory Transfer Committee Meeting. December 2012. Quebec City, Canada.

Accelerated, precision breeding using genome wide selection and next-generation sequencing. Horticultural Sciences Department, University of Florida. November 2012. Gainesville, USA.

Accelerating the domestication of forest species using genome-wide selection and next-generation sequencing. Noveltree Conference: Tree Breeding, Genomics and Evolutionary Biology. October 2012. Helsinki, Finland.

Exome sequencing for GWAS and genomic selection in pines. Noveltree Workshop: Genome analysis tools applied to forest tree breeding. October 2012. Vantaa, Finland.

Biociência e Genômica no setor Florestal (in portuguese). VII Simpósio de Pós-Graduação em Ciências Florestais. September 2012. Viçosa, Brazil.

Surveying the genic diversity in megagenomes: exome-capture and sequencing of pines. Genome Sequencing and Annotation Symposium. April 2012. Gainesville, USA.

A systems biology, whole-genome association analysis of the molecular regulation of biomass growth and composition in *Populus deltoids*. DOE Investigator Meeting. April 2012. Washington, USA.

High-throughput targeted resequencing of plant complex genomes using sequence capture. Agilent Workshop. Plant and Animal Genome XX Conference. January 2012. San Diego, USA.

Evolutionary conservation of gene networks implicated in lignin biosynthesis. NESCent Meeting – Evolutionary Origins and Development of Woody Plants. October 2011. Durham, USA.

Genome-wide selection to hyper-accelerate genetic gain and adaptation of conifers to climate change. Virginia Tech. September 2011. Blacksburg, USA.

Capturing and genotyping the genome-wide diversity of trees for association mapping and genomic selection. IUFRO Tree Biotechnology Conference. June 2011. Arraial d’Ajuda, Brazil.

20 years in 5: Hyper-accelerating genetic gain and adaptation of conifers using genomic selection. The Conifer Translational Genomics Network Workshop. June 2011. Davis, USA.

Hyper-accelerating breeding and adaptation of loblolly pine using genomic selection. Southern Forest Tree Improvement Conference. June 2011. Biloxi, MS.

Accelerating the domestication of bioenergy trees: from genetical genomics to genomic selection. New Phytologist Symposium: Bioenergy Trees. May 2011. Nancy, France.

A systems biology, whole-genome association analysis of the molecular regulation of biomass growth and composition in *Populus deltoids*. DOE Investigator Meeting. April 2011. Washington, USA.

Genomic selection to hyper-accelerate tree breeding. Plant Biotechnology and Genomics Center. December 2010, Madrid, Spain.

Evolution of poplar transcriptional networks and their regulation of growth and development. Spanish Forest Genetic Diversity and Functional Genomics Network Meeting. December 2010. Las Navas del Marqués, Spain.

*Populus* genome networks and the regulation of growth and development. 5th International Poplar Symposium, September 2010, Orvieto, Italy.

Integrating quantitative genetics and genomics. VI Encontro em Genética e Melhoramento da Universidade Federal de Viçosa, November 2009, Viçosa, Brazil.

Gene and microRNA expression QTL analysis unravels transcription networks implicated in *Populus* growth and development. International Plant Molecular Biology Congress (Tree Genomics and Biotechnology Symposium), October 2009, St. Louis, USA.

The Eucalypts Genome Network (EUCAGEN) and the sequencing of the *E. grandis* genome. International Symposium on New Frontiers in Forest Genomics: Sequencing and Functional Understanding of the Conifer Genome, February 2009, Madrid, Spain.

Bridging genomics and breeding in hardwood tree models. IUFRO-CTIA Joint Conference, August 2008, Quebec City, Canada.

Plant gene expression regulatory networks. 20<sup>th</sup> South African Genetics Society Congress, March 2008, Pretoria, South Africa.

## Honors and Awards

2015 University of Florida Doctoral Dissertation Advisor/Mentoring Award

2013 University of Florida Research Foundation Professorship Award



- 2012 Science Without Borders – Special Visiting Scientist Fellowship (Brazilian Ministry of Science and Technology)
- 2009 Richard Jones Outstanding New Faculty Research Award (University of Florida)
- 2007 Elected Coordinator of “Division 2.04.10 – Genomics” of the International Union of Forest Research Organizations.
- 2005 Elected Deputy of “Division 2.04.06 – Molecular Biology of Forest Trees” of the International Union of Forest Research Organizations.

### **Scientific Community Participation**

Proposal panel member and reviewer for NSF, USDA, DOE, BARD - United States & Israel Binational Agricultural Research and Development Fund, Deutsche Forschungsgemeinschaft, PLANT-KBBE, French National Research Agency, CPBR, Netherland Council for the Earth and Life Sciences, ERA-NET Plant Genomics, Austrian Science Fund

Reviewer for Annals of Botany, Australian Journal of Botany, BMC Genomics, BMC Plant Biology, Euphytica, Genetica, Genetics, Genetics and Molecular Research, Genome Research, Heredity, Journal of Experimental Botany, Journal of Heredity, Journal of Plant Physiology, New Forest, Molecular Breeding, Molecular Ecology, Nature Genetics, New Phytologist, Oecologia, Plant Biotechnology Journal, Plant Cell, Plant Cell and Environment, Plant Journal, Plant Physiology, Plant Molecular Biology, Plant Molecular Biology Reporter, Planta, Proceedings of the National Academy of Sciences USA.

Advisory Board for Genome Canada Project Arborea II and CoAdaptTree, EU funded project NovelTree and ProCoGen.

Member of editorial board of Genetics (2009-2012) and BMC Plant Biology (2009-2012).

Chair Forest Trees Workshop (Plant and Animal Genome Conference, 2007 – 2010); IUFRO Tree Biotechnology Meeting 2013.

Scientific Advisory Committee IUFRO Tree Biotechnology Meeting 2005, 2007, 2011; IUFRO – CTIA Join Meeting: Adaptation, Breeding and Conservation in the Era of Forest Tree Genomics and Environmental Change.