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HTIRC
HARDWOOD TREE
IMPROVEMENT
& REGENERATION
CENTER

August 4th, 20167

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ARBOR AMERICA INC.

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MANAGEMENT

Dear TACF,

We are submitting a new proposal for your consideration to fund regarding recent research completed by Nick LaBonte, an outstanding PhD student here, and as of yesterday, our newest HTIRC PhD! Nick's goal was to utilize existing genomic knowledge and from that, to probe suspected blight resistant areas to find practical and reliable DNA markers to identify blight resistant areas of the chestnut genome and ultimately, to aid blight resistance breeding. As the operational tree breeder here for the HTIRC, and after working for the last 13 years on behalf of the Indiana TACF chapter, I am excited and eager to put such technology into practice.

Nick approached me early this year for a sample of BC3 trees to test his markers on and I was pleased to organize our chapter and colleagues here to provide the resources to do just that. That preliminary validation test showed a very good fit to long term canker ratings and identified our most resistant, longest standing BC3F1 trees. I have assembled a very good team, including Dr. Jared Westbrook, to continue this work. While Nick will begin teaching this fall at Eureka College in Illinois, he is committed and very interested to continue this line of work and contribute all that he can.

My hope is that between additional material we have in the IN-TACF, and the material that Jared has at Meadowview, we may be able to develop and refine these markers to help advance all of our chestnut blight resistance breeding efforts – National and State Chapters.

Thanks for your consideration and please do not hesitate to contact Nick or me for additional details or any other information.

Sincerely,

James R. McKenna
Operational Tree Breeder
USDA-Forest Service, Northern Research Station
Hardwood Tree Improvement & Regeneration Center
Department of Forestry & Natural Resources
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Optimization of Novel SNP DNA Markers for Early Selection of Blight Resistant Hybrid Chestnut in Indiana and Virginia Backcrosses

SUMMARY

We screened a panel of highly resistant, moderately resistant, and susceptible BC3F1 chestnut samples from IN-TACF using a set of 10 preliminary SNP markers from predicted Chinese chestnut (*Cm*, *Castanea mollissima*) blight resistance genes that exhibited distinct alleles in American chestnut (*Cd*, *C. dentata*). The most resistant trees in this pilot study had more *Cm* alleles than susceptible trees. The goal of this research proposal is to validate the utility and predictive power of these SNP markers using BC3F2 and BC3F3 chestnuts, and to identify additional SNPs for targeting other blight resistance candidate genes in 'Graves'-derived and early-generation BC1F1 material.

Nick LaBonte¹, Jared Westbrook², Aziz Ebrahimi³, James McKenna⁴, Keith Woeste⁴, Shaneka Lawson⁴, Dana Nelson⁵, and Mark Coggeshall⁴

¹Eureka College, Department of Biology, 300 E College Ave, Eureka, IL, 61530; ²TACF, 50 N Merrimon Ave, Suite 115, Asheville, NC, 20804; ³Purdue University, Department of Forestry & Natural Resources, 715 W State, West Lafayette, IN, 47907; ⁴USDA Forest Service, Hardwood Tree Improvement & Regeneration Center, 715 W State, West Lafayette, IN, 47907; ⁵USDA Forest Service, Forest Health Center, 730 Rose, Lexington, KY, 40546

Total amount requested: \$10,000

Project duration: October 2017 – October 2018

Short-Term Goals

- Screen 30 SNP blight resistance-associated markers from Indiana's BC3F2 populations.
- Genotype TACF BC3F2 and BC3F3 material at selected SNP loci.
- Screen earlier-generation trees (F1, BC1, BC2F2) and supplemental species (*Cd*, *Castanea dentata*; *Cm*, *Castanea mollissima*) to provide corroborating evidence.
- Graft up to 200 new American and BC3 resistant selections for future breeding.

Long-Term Goals

- Develop an elite SNP marker panel within blight resistance candidate genes, for use in marker-assisted selection (MAS) for chestnut blight-resistance breeding.
- Use evidence from BC3F2 and marker genotyping from prior-generations to screen and validate blight resistance candidate genes.

PRELIMINARY RESULTS – JUNE/JULY 2017

Genotypes were obtained in most individuals from seven SNP loci. Of the remaining three loci, one assembled poorly to the reference sequence, one was overly polymorphic, and one was monomorphic. The SNP loci lgf:g2785 and lgc:g3384 exhibited allele frequencies for hybrid genotypes ranging from approximately 0.56-0.75 (**Table 1**). Most loci showed allele frequencies closer to the expected 0.5 for hybrid genotypes, 0.00 for *Cm* and 1.00 for *Cd* samples (**Table 1**). Allele frequencies easily conform to *Cd/Cd*, *Cd/Cm*, and *Cm/Cm* genotypes (**Table 2**). *Cd/Cd* is expected in susceptible BC3F1s while *Cd/Cm* is expected in resistant BC3F1s. Two *Cm/Cm* genotypes were observed in one of the resistant JWSF BC3F1

samples (**Sample 9; Table 2**), indicating that this tree may result from a BC2 x BC2 cross rather than the BC2 x *Cd* cross used to generate a BC3F1, or an error in sequencing/scoring. **Table 2** designates the Indiana *Cd* mothers, TACF BC2 pollen parents, canker ratings, and estimated inoculated stem lifespan.

For a BC3F1 tree, the maximum number of *Cm* alleles is equal to number of loci: one *Cm* allele and one *Cd* allele at each locus. *Cm* allele numbers were tallied across SNP loci for BC3F1 individuals using: (*Cm* allele number / number of genotyped loci). Linear regression of *Cm* allele percentage by field Canker Rating showed a highly significant correlation ($R^2 \leq 0.84$) between the two traits (**Figure 1**).

WORK PROPOSED – ADDITIONAL SNP MARKERS

We propose to screen additional trees in the IN-TACF program and TACF selections from Meadowview, VA, to further validate and optimize these SNPs. A larger population of BC3F1, additional BC3F2, and BC3F3 progeny will be screened. Also, we will detail trends in marker inheritance for F1 (both [C x A] and [A x C] and BC1F1 trees in Indiana. Meadowview, VA selections will include BC1F2, BC2F2, and a range of BC3s with varied blight resistance. Novel *Cm* and *Cd* will be used as controls. Using our resources, we hope to genotype up to 320 samples. Additional SNP markers will be tested and optimized. Finally, we will initiate development of new SNPs that target genes potentially underlying the *cbr1* blight resistance QTL on linkage group B. We will use pools of resistant and susceptible BC3F2s with confirmed *Cm/Cm* haplotypes at blight resistance loci for Illumina whole-genome sequencing. The goal is to include 10-15 individuals in each pool, but this number will depend on the number of resistant BC3F2s four years post-inoculation. Separate pools will be sequenced for ‘Clapper’ and ‘Graves’-derived material. This will determine sizes of linkage blocks flanking blight resistance genes to optimize and improve markers. Finally, we propose to graft up to 200 trees to augment MAS research and to conserve additional breeding material at Meadowview for future studies

OUTCOMES & DELIVERABLES

If the predictive power of these SNP markers is demonstrated across a wide genetic spectrum of backcrossed hybrid chestnut, we will share these SNPs with all TACF chapters and other chestnut breeders to speed up chestnut blight resistance breeding. Furthermore, with our current long-term resistance data, we hope identification of more durable resistance will be achieved with these markers. Individual trees with the best SNP marker profile will be selected and grafted onto BC3 rootstock to develop new breeding seed orchards. We will include additional *Cd* individuals to create a new grafted American seed orchard.

REFERENCES

- Kearse, M., Moir, R., Wilson, A., Stones-Havas, S., Cheung, M., Sturrock, S., Buxton, S., Cooper, A., Markowitz, S., Duran, C., Thierer, T., Ashton, B., Mentjies, P., and Drummond, A. (2012). Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*, 28(12), 1647-1649.
- LaBonte, N., Miller, G., Nelson, C.D., Woeste, K. (*in preparation*) Genetic variants associated with blight resistance and signatures of selection near blight resistance loci.

- McKenna, J. and Beheler B. (2016) Five-year graft compatibility in an American chestnut breeding orchard. *Journal of the American Chestnut Foundation*. Winter Edition. p. 24-28.
- Stanke, M., Schöffman, O., Morgenstern, B., Waack, S. (2006) Gene prediction in eukaryotes with a generalized hidden Markov model that uses hints from external sources. *BMC Bioinformatics* 7, 62.

TIMELINE AND BUDGET

- **Fall '17** Identify individuals and genotypes, collect samples (leaves/twigs), and extract DNA
- **Winter '17 '18** Perform and optimize PCRs, sequence products, develop new markers, collect scion wood
- **Spring '18** Further optimize and identify new individuals to validate, graft trees
- **Summer '18** Test new and optimized markers on a wider array of individuals, prepare final report

Line Item	TACF
Travel	\$1,000
Grafting (200+ trees)	\$1,000
WideSeq (320+ samples)	\$6,400
Reagents	\$1,600
Grand Total	\$10,000

*HTIRC will contribute \$10,000 for technicians and post-doc salary and Illumina sequencing

FIGURES AND TABLES

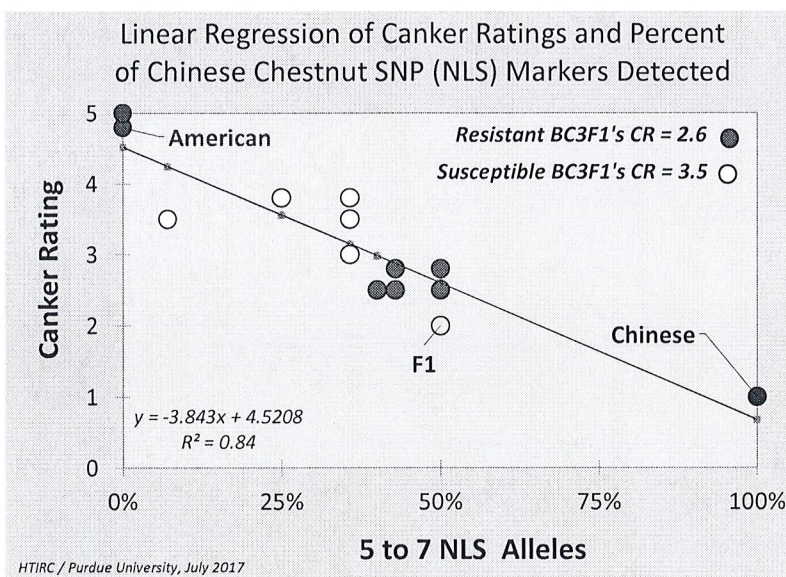


Figure 1. Correlation of NLS Markers with 6 to 16 year IN-TACF BC3F1 progeny grown in Starke, Tippecanoe, and Washington Counties of Indiana. The F1 hybrid is a novel natural cross of DOE x a Chinese chestnut in Grant Co., Indiana. The Chinese is 'Hort 14' that was purchased about 30 years ago from Empire Chestnut. American chestnuts were both grafted clones from the Duke Energy Orchard at Martell Forest, West Lafayette, IN.

Table 1. Genotypes coded for species of origin (American chestnut allele = *Cd*, Chinese chestnut allele = *Cm*) at seven SNP loci designed from exons of blight-resistance candidate genes in a panel of BC3F1 chestnuts, American chestnuts (*Cd*), Chinese chestnut (*Cm*) and one F1 hybrid.

Lab no.	Species	Blight	lgc:g3384	lgf:g1803	lgf:g1804	lgf:g2785	lgg:g3657b	lgl_g8953a	lgl_g8953b
1	BC3F1	R	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cd	Cd/Cm	Cd/Cm
2	BC3F1	M	Cd/Cm	Cd/Cd	Cd/Cm	x	x	Cd/Cm	Cd/Cm
3	BC3F1	S	Cd/Cm	Cd/Cd	Cd/Cd	Cd/Cd	x	Cd/Cm	Cd/Cm
4	BC3F1	S	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cd	Cd/Cd
5	<i>Cm</i>	R+	Cm/Cm	Cm/Cm	Cm/Cm	Cm/Cm	Cm/Cm	Cm/Cm	Cm/Cm
6	<i>Cd</i>	S+	Cd/Cd	Cd/Cd	Cd/Cd	Cd/Cd	Cd/Cd	Cd/Cd	Cd/Cd
7	<i>Cd</i>	S+	Cd/Cd	Cd/Cd	Cd/Cd	Cd/Cd	Cd/Cd	Cd/Cd	Cd/Cd
8	BC3F1	R+	x	x	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cm
9	BC3F1	R	Cm/Cm	Cd/Cm	Cd/Cm	Cd/Cd	Cm/Cm	Cd/Cd	Cd/Cd
10	BC3F1	M	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cd	Cd/Cd	Cd/Cm	Cd/Cm
11	BC3F1	S	Cd/Cd	Cd/Cd	Cd/Cd	Cd/Cd	Cd/Cm	Cd/Cd	Cd/Cd
12	BC3F1	R	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cd	Cd/Cd	Cd/Cm	Cd/Cm
13	BC3F1	M	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cm
14	F1	R	Cd/Cm	Cd/Cm	x	Cd/Cm	Cd/Cm	Cd/Cm	Cd/Cm

^aR+ = highly resistant; R = resistant, M = moderately resistant, S = susceptible, S+ = highly susceptible

Table 2. Summary of BC3F1 selections, F1, and chestnut species used to validate seven novel SNP loci.

Lab No.	Geno.	IN-TACF			IN-		TACF		Yrs. Live Stem	Loci	
		BC3F1 Selection	Blight Resist	Orchard	TACF Line	IN <i>Cd</i> Mother	BC2 Father	CR (2017)		Geno-typed	<i>Cm</i> alleles
1	BC3F1	Wake. A	R	Culver	1A	IW2	GR226	2.5	16	7	6
2	BC3F1	Wake. B	R	Culver	1B	IW2	GR226	2.5	14	5	4
3	BC3F1	Wake. C	S	Culver	1C	IW2	GR226	3.8	5	6	3
4	BC3F1	Wake. D	S	Culver	1D	IW2	BE325	3.5	7	7	5
5	<i>Cm</i>	Hort #14	R+	Lugar- <i>Cm</i>	-	-	-	1.0	30	7	14
6	<i>Cd</i>	'Sieg #2'	S+	Duke- <i>Cd</i>	-	-	-	5.0	2	7	0
7	<i>Cd</i>	'Johnson'	S+	Duke- <i>Cd</i>	-	-	-	4.8	2	7	0
8	BC3F1	JWSF 'A'	R+	JWSF	3A	BURKE	AB185	2.5	14	5	5
9	BC3F1	JWSF 'B'	R	JWSF	3B	BURKE	AB185	2.8	14	7	6*
10	BC3F1	JWSF 'C'	M	JWSF	3C	BURKE	AB185	3.8	9	7	5
11	BC3F1	JWSF 'D'	S	JWSF	2E	RL3	GR97	3.5	6	7	1
12	BC3F1	JWSF 'E'	R	JWSF	2D	RL3	GR97	3.0	14	7	5
13	BC3F1	JWSF 'F'	R	JWSF	3D	BURKE	AB185	2.8	14	7	7
14	F1	Line 4A	R+	Lugar-BC3	4A	DOE	CHIN op	2.0	12	6	6

^aR+ = highly resistant, R = resistant, M = moderately resistant, S = susceptible, S+ = highly susceptible, CR = canker rating, Years stem lived after inoculation, * two loci homozygous for *Cm* we need to investigate further.

Nicholas R. LaBonte

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Education

University of Wisconsin-Madison

B.S., Forest Ecology August 2007 - May 2011
Cumulative GPA: 3.865

Purdue University

M.S., Forest Genetics August 2011 - August 2013
Ph.D., Forest Genetics August 2013 – December 2017
Cumulative GPA: 3.80

- Graduate coursework includes: Plant Breeding Methods and Techniques, Plant Genetics, Intro Bioinformatics, Advanced Plant Pathology, Practical Bio-Computing, Quantitative Genetics, Intro QTL Mapping, Quantitative Methods for Ecologists, Intro Computer Science, and Design of Experiments.

Academic Appointments

August 2011- Present

Graduate student at Purdue University, West Lafayette, IN

Recent Publications

LaBonte, N.R., Ostry, M.E., Ross-Davis, A., Woeste, K.E. (2015) Estimating heritability of disease resistance and factors that contribute to long-term survival in butternut (*Juglans cinerea* L.). *Tree Genetics and Genomes* 11(3): 63.

LaBonte, N.R., McKenna, J.R., Woeste, K.E. (2016) Effectiveness of a detached leaf assay as a proxy for stem inoculations in backcrossed chestnut (*Castanea*) blight resistance breeding populations. *Forest Pathology* doi:10.1111/efp.12313

LaBonte, N.R., Hartel, C., Tonos, J., Woeste, K.E. (2017) Genetic diversity and differentiation of yellowwood [*Cladrastis kentukea* (Dum.Cours.) Rudd] growing in the wild and in planted populations outside the natural range. *New Forests* doi:10.1007/s11056-017-9566-8

Additional Anticipated Publications from Dissertation

Characteristics of genomic loci associated with variation in blight resistance among chestnut species ((*Castanea*) and interspecific hybrids

Conservation and divergence at putative disease-resistance gene loci in chestnut (*Castanea*) and walnuts (*Juglans*)

Signatures of selection in the genomes of Chinese chestnuts (*Castanea mollissima*) from orchards versus trees from wild stands: the genomic roots of small stature and large seeds

Genomic loci associated with differential seed dispersal by a scatter-hoarding rodent in hybrid chestnut (*Castanea*).

Profiling epi- and endophytic fungal communities using short-read DNA sequences from plant samples: a case study in chestnut (*Castanea*) and (*Juglans*).

Research Grants Awarded

Assessing the functional diversity of blight resistance in Chinese chestnut (*Castanea mollissima* Blume) by whole-genome resequencing of a diverse germplasm collection: Proposal awarded \$8000 by the American Chestnut Foundation, October 2015.

Sequencing the genome of Indiana's largest surviving American chestnut (*Castanea dentata* (Marsh.) Borkh.): Proposal awarded \$2000 by the Indiana Academy of Sciences, March 2015

Assessing diversity of blight resistance genes in Chinese chestnut (*Castanea mollissima* Blume) by whole-genome resequencing of a diverse germplasm collection: Proposal awarded \$5000 by Northern Nut Growers Association, August 2014

Recent Presentations and Posters

"Genetic variation in genomic regions associated with blight resistance in chestnut (*Castanea*)" (Presentation) Southern Forest Tree Improvement Conference, Melbourne, FL, 6/19/2017-6/22/2017

"Presentation on Northern Nut Growers funded research: Whole-genome resequencing of Chinese chestnut" (Presentation) Northern Nut Growers 107th Annual Meeting, Nebraska City, NE 7/31/2016-8/3/2016.

"Genetic differences between yellowwood (*Cladrastis kentukea*) in wild populations versus urban forests." (Presentation) Gene Conservation of Tree Species Workshop, Chicago, IL 5/16/2016-5/19/2016.

"Exploring patterns of sequence variation in regions associated with chestnut blight resistance using whole-genome sequencing of Chinese chestnut (*Castanea mollissima*)" (Presentation and Poster) Plant and Animal Genome Conference XXIV, San Diego, CA 1/08/2016-1/13/2016

Aziz Ebrahimi

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EDUCATION AND TRAINING

2005 B.S. Tehran University Horticulture
2007 M.S. Tehran University Horticulture
2013 Ph.D. National Institute of Genetic Engineering and Biotechnology (NIGB)

RESEARCH EXPERIENCE

2013-present Research Scholar, Purdue University, West Lafayette, IN.
2009-2013 Graduate Research Assistant, National Institute of Genetic Engineering and Biotechnology (NIGB), Tehran, Iran.
2007-2009 Breeding Assistant/Lab Manager, Plant Production Institute, Tehran, Iran.
2005-2007 Graduate Research Assistant, Tehran University, Tehran, Iran.

GRANTS RECEIVED

2014 Indiana Nut and Fruit Growers Foundation (INGF)
\$2500.00

HONORS AND AWARDS

2013 Research Scholar Position, Purdue University, West Lafayette, IN.

PUBLICATIONS (Selected)

Ebrahimi, A., Zarei, A., McKenna, J. R., Bujdoso, G., & Woeste, K. E. (2017). Genetic diversity of Persian walnut (*Juglans regia*) in the cold-temperate zone of the United States and Europe. *Scientia Horticulturae*, 220, 36-41.

Erica A Di Pierro, Luca Gianfranceschi, Mario Di Guardo, Herma JJ Koehorst-van Putten, Johannes W Kruisselbrink, Sara Longhi, Michela Troggio, Luca Bianco, Hélène Muranty, Giulia Pagliarani, Stefano Tartarini, Thomas Letschka, Lidia Lozano Luis, Larisa Garkava-Gustavsson, Diego Micheletti, Marco CAM Bink, Roeland E Voorrips, **Ebrahimi Aziz**, Riccardo Velasco, François Laurens and W Eric van de Weg. (2016). A high-density, multi-parental SNP genetic map on apple validates a new mapping approach for outcrossing species. *Horticulture Research*. 16057; doi:10.1038/hortres.2016.57.

Ebrahimi, A., Zarei, A., Lawson, S., Smulders, M. J. M. (2016). Genetic diversity and genetic structure of Persian walnut (*Juglans regia*) accessions from 14 European, African, and Asian countries using SSR markers. *Tree genetics & genomes*. DOI: 10.1007/s11295-016-1075-y

Ebrahimi, A. Nosrati, Z and Khadivi-Khub, A. (2015). Identification of superior walnut (*Juglans regia*) genotypes with late leafing and high kernel quality in Iran. *Scientia Horticulturae* 193: 195-201.

- Khadivi-Khub, A., **Ebrahimi, A.**, Sheibani, F., Esmaceli, A. (2015). Phenological and pomological characterization of Persian walnut to select promising trees. *Ephytica* 205:557-567.
- Khadivi-Khub, A., **Ebrahimi, A.**, Mohammadi, A., Kari, A. (2015). Characterization and selection of walnut (*Juglans regia* L.) genotypes from seedling origin trees. *Tree Genetics & Genomes*. DOI 10.1007/s11295-015-0882-x.
- Khadivi-Khub, A., **Ebrahimi, A.** (2014). The variability in walnut (*Juglans regia* L.) germplasm from different regions in Iran. *Acta Physiologiae Plantarum*. 37:1-11.
- Khadivi-Khub, A., Kameli, M., Moshfeghi, N., **Ebrahimi, A.** (2014). Phenotypic characterization and relatedness among some Iranian pomegranate Accessions. *Trees*. 29: 893-901.
- Ebrahimi, A.**, Fatahi, R., and Zamani, Z. (2011). Analysis of genetic diversity among some Persian walnut genotypes (*Juglans regia* L.) using morphological traits and SSRs marker. *Scientia Horticulturae*. 130: 146-151.
- Fatahi, R., **Ebrahimi, A.**, and Zamani, Z. (2010). Characterization of some Iranians and foreign walnut genotypes using morphological traits and RAPD markers. *Hort. Environ. Biotechnol*. 51:51-60.
- Ebrahimi, A.**, Zarei, A., Fatahi, R., and Ghasemi, V. (2009). Study on some morphological and physical attributes of walnut used in mass models. *Scientia Horticulturae*. 121: 490–494.
- Ebrahimi, A.**, Vahdati, K and Fallahi, E. (2007). Improved success of persian walnut grafting under environmentally controlled conditions. *International Journal of Fruit Science*. 6: 3-12.

CONFERENCE PRESENTATIONS

- Aziz Ebrahimi.** Pollen flow in an isolated and non-isolated black walnut seed orchard. National Walnut Council Annual Meeting, West Lafayette, IN. June 2017.
- Aziz Ebrahimi** and Abdolkarim Zarei. Assessment of Genetic Diversity and Comparative Analysis of *Juglans regia* Accessions from Different Countries Using SSR Markers. *ASHS Conference*, Atlanta, Georgia, USA, 2016.
- Aziz Ebrahimi** and James Mckenna. Genetic Diversity of Persian Walnut from the Midwestern USA Determined by Microsatellite Markers. *ASHS Conference*. New Orleans, Louisiana, USA, 2015.
- Aziz Ebrahimi** and Eric Van De Weg. Genetic evaluation of partial resistance to race 6 of venturia inaequalis in apple with SSR marker. *Next Generation Plant Breeding Conference*, Wageningen, Netherlands, 2012.

SOFTWARE PROFICIENCIES

Statistical: SAS, SPSS, Ntysis, Joint Map, Map QTL, GeneMapper, GenAlex and Bioinformatics software.

JAMES R. McKENNA

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EDUCATION AND TRAINING

1993	B.S.	University of California, Davis	International Ag. Development
1997	M.S.	University of California, Davis	Plant Biology

RESEARCH AND PROFESSIONAL EXPERIENCE

2001-present	Operational Tree Breeder (USDA Forest Service), Purdue University, West Lafayette, IN.
1997-2001	Research Associate. UC Davis, UC Riverside, UCCE, Davis, CA. Pomology, Horticulture, Nematology Department

RECENT GRANTS RECEIVED

2015-	Butternut Restoration: breeding to mitigate butternut canker disease:	\$30,000
2016	USDA Forest Service Northern Area	
2013-	Screening a Range-wide collection of black walnut against TCD and	\$55,000
2015	establishing common garden plots. USDA Forest Service State & Private Forestry, Special Technology Development Program	
2011	Support for IN-TACF chestnut blight resistance breeding. Duke Energy Foundation	\$20,000
2010	Creating a grafted American chestnut breeding orchard. Duke Energy Foundation	\$10,000

SELECTED PUBLICATIONS

McKenna J.R. and M.V. Coggeshall. 2018. Breeding Black Walnut for Timber Production. Plant Breeding Reviews, Volume 41, 2nd Edition. 2018 John Wiley & Sons, Inc. Published 2018 by John Wiley & Sons, Inc. p. 263-289. (in press)

Ebrahimi, A., Zarei, A., **McKenna, J. R.**, Bujdoso, G., & Woeste, K. E. 2017. Genetic diversity of Persian walnut (*Juglans regia*) in the cold-temperate zone of the United States and Europe. Scientia Horticulturae, 220, 36-41.

Griffin, Jason J.; Jacobi, William R.; McPherson, E. Gregory; Sadof, Clifford S.; **McKenna, James R.**; Gleason, Mark L.; Gauthier, Nicole Ward; Potter, Daniel A.; Smitley, David R.; Adams, Gerard C.; Gould, Ann Brooks; Cash, Christian R.; Walla, James A.; Starrett, Mark C.; Chastagner, Gary; Sibley, Jeff L.; Krischik, Vera A.; Newby, Adam F. 2017. Ten-year performance of the United States national elm trial. Arboriculture & Urban Forestry. 43(3): 108-121.

LaBonte, N., **J. McKenna**, and K. Woeste. 2016. Effectiveness of a detached leaf assay as a proxy for stem inoculations in backcrossed chestnut. Forest Pathology Online. DOI 10.1111/efp.12313

McKenna, J. and Beheler B. (2016) Five-year graft compatibility in an American chestnut breeding orchard. *Journal of the American Chestnut Foundation*. Winter Edition. p. 24-28.

McKenna, James R.; Geyer, Wayne A.; Woeste, Keith E.; Cassens, Daniel L. 2015. Propagating figured wood in black walnut. *Open Journal of Forestry*. 05 (05): 518-525.

McKenna J.R., O'Connor P.A. 2014. Performance of Select Walnut in Indiana after 10 Years. In: Wilkinson KM, Haase DL, Pinto JR, technical coordinators. National Proceedings: Forest and Conservation Nursery Associations—2013. Fort Collins (CO): USDA Forest Service, Rocky Mountain Research Station. Proceedings RMRS-P-72. 6-11. Available at: http://www.fs.fed.us/rm/pubs/rmrs_p072.html

Utle, C., Nguyen, T., Roubtsova, T., Coggeshall, M., Ford, T.M., Grauke, L.J., Graves, A.D., Leslie, C.A., **McKenna, J.**, Woeste, K., Yaghmour, M.A., Cranshaw, W., Seybold, S.J., Bostock, R.M., and Tisserat, N. 2013. Susceptibility of walnut and hickory species to *Geosmithia morbida*. *Plant Dis.* 97(5): 601–607.

Buzo T., **J. McKenna**, S. Kaku, S. A. Anwar, M. V. McHenry. 2009. VX211, A Vigorous New Walnut Hybrid Clone with Nematode Tolerance and a Useful Resistance Mechanism. *Journal of Nematology* 41(3):211–216. 2009.

Mahoney N., R. Molyneux, **J.R. McKenna**, and G. McGranahan. 2003. Resistance of ‘Tulare’ Walnut (*Juglans regia* cv. Tulare) to Aflatoxigenesis. *Journal of Food Science*. 68(2):0619-0622.

McKenna J.R. and L. Epstein. 2003. Relative Susceptibility of Different Genotypes of *Juglans* Species and Interspecific Hybrids to *Agrobacterium tumefaciens*. *HortScience*. 38(3) 435-439.

D. Potter, F. Gao, S. Baggett, **J. McKenna**, and G. McGranahan. 2002. Defining the Sources of Paradox: DNA Sequence Markers for North American Walnut (*Juglans* L.) Species and Hybrids. *Scientia Horticulturae*. 94:157-170.

PROFESSIONAL AFFILIATIONS

USDA Juglans Crop Germplasm Committee, 1999 – present

Indiana Nut Growers Association, 2002 – present

Indiana Walnut Council, 2003 – present

Indiana Chapter of the American Chestnut Foundation, 2005 – present

Northern Nut Growers Association, 2016 – present

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A. Education and Training

University of Florida	Botany	BS	1980
Jesuit School of Theology, Berkeley, CA	Theology	M.Div.	1986
University of California, Davis, CA	Horticulture	MS	1990
University of California, Davis, CA	Genetics	PhD	1995
University of Illinois, Chicago, IL	Post-doctoral, Hormone signal transduction		1995 – 1998

B. Research Experience

Research Molecular Geneticist (1999–present). GS-12, 13, 14. RWU 4157 USDA Forest Service North Central Research Station Hardwood Tree Improvement and Regeneration Center, West Lafayette, IN and Adjunct Asst. Professor, Purdue University, Department of Forestry and Natural Resources (1999–present).

B. Publications/Products

- Woeste, K., G. McGranahan, and R. Bernatzky. 1995. The identification and characterization of a genetic marker linked to hypersensitivity to the cherry leafroll virus in walnut. *Molecular Breeding* 2 (3):261-266.
- Woeste, K.E., and Beineke, W. 2001. An efficient method for evaluating the susceptibility of black walnut to walnut anthracnose in field plots and the identification of resistant genotypes. *Plant Breeding* 120:454-456.
- Michler, C. H., K. E. Woeste, P. M. Pijut, D. F. Jacobs, R. Meilan, and M. Ostry. 2006. Improving disease resistance of butternut (*Juglans cinerea*) a threatened fine hardwood: a case for single tree selection through genetic improvement. *Tree Physiology* 26:113-120.
- Worthen, L., C. Michler, and K. Woeste. 2010. Breeding American Chestnuts for Blight Resistance. *Plant Breeding Reviews* 33: 305 – 339.
- LaBonte, N., J. McKenna, and K. Woeste. 2016. Effectiveness of a detached leaf assay as a proxy for stem inoculations in backcrossed chestnut. *Forest Pathology Online*. DOI 10.1111/efp.12313
- Alexander, L., K. Woeste (2017) Pollen gene flow, male reproductive success, and genetic correlations among offspring in a northern red oak (*Quercus rubra*) seed orchard. *PLoS One* (refereed). 12 (2) e0171598.
- Crystal, P., N. Lichti, K. Woeste, D. Jacobs. 2016. Vegetative and adaptive traits predict different outcomes for restoration using hybrids. *Frontiers in Plant Science*. Doi: 10.3389/fpls.2016.01741
- Dang, M., T. Zhang, Y. Hu, H. Zhou, K. Woeste, P. Zhao. 2016. De Novo assembly and characterization of bud, leaf, and flowers transcriptome from *Juglans regia* for the identification and characterization of new EST-SSRs. *Forests* doi:10.3390/f7100247
- Worthen, L., K. Woeste. 2015. Phenology, dichogamy, and floral synchronization in a northern red oak (*Quercus rubra*) seed orchard. *Canadian Journal of Forest Research* DOI 10.1139/cjfr-2015-0312

- LaBonte, N., M. Ostry, A. Ross-Davis, K. **Woeste** 2015. Estimating heritability of disease resistance and factors that contribute to long-term survival in butternut (*Juglans cinerea* L.). *Tree Genetics and Genomes* 11: 63-74.

C. Synergistic Activities

Significant accomplishments include service on science board of TACF, development and application of nuclear microsatellites for genetic analysis in *Juglans*, in collaboration with Dr. Michael Ostry, the establishment and maintenance of largest and most comprehensive germplasm repository for the threatened species *Juglans cinerea*, collaboration with Paul Berrang to establish USDA Forest Service R9 butternut seed source tree testing orchard, development of SSRs for study of genetic diversity of *Geosmithia morbida*, the fungal component of Thousand Cankers Disease of walnut.

D. Collaborators and Other Affiliations

Collaborators and Co-Editors:

Preston Aldrich (Benedictine Univ.) Malli Aradhya (USDA NCGR) Malli Aradhya (USDA ARS) John Bickham (Purdue Univ.) Greg Boland (Univ. Toronto) Richard Bostock (UC Davis) Kirk Broders (Univ. New Hampshire) Francesca Cannata (CNR-IBAF Italy) Mark Coggeshall (Univ. Missouri) Whitney Cranshaw (CO State Univ.) G.S. Dangl (UC Davis) Andrew DeWoody (Purdue Univ.) Fulvio Ducci (Italian Institute of Forestry) Youran Fan (Purdue Univ.) Junfeng Fan (Northwest A&F Univ. China) Lenny Farlee (Purdue University) Tim Ford (IPFB UT) Marco Gallitelli (Univ. Naples Federico II) T. Gireesh (RRI India) Jeffery Glaubitz (Cornell Univ.) Susumu Goto (Univ. Tokyo) Maria Gras (CRA Rome) LJ Grauke (USDA ARS) Andrew Graves (USDA FS) Zhonglian Huang (Purdue Univ.) Douglass Jacobs (Purdue Univ.) Daisuke Kihara (Purdue Univ.) M.K. Koehmstedt (UCDavis) Charles Leslie (UC Davis) Christian Lexer (Univ. Fribourg) Zhenhua Ma (Northwest A&F Univ. China) A. Major (CNR, Italy) Maria Malvolti (Italian National Res. Council) JG Marattukalam (RRI India) Gale McGranahan (UC Davis) James McKenna (USDA FS) Mike Jenkins (Purdue Univ.) Megumi Kimura (FFPRI Ibaraki Japan) Danilo Marandola (NIEA-FO Italy) Masaki Matsui (Univ. Tokyo) Richard Meilan (Purdue Univ.) VC Mercykutty (RRI India) Charles Michler (USDA FS) Karen Moldenhauer (Univ. Arkansas) Luigi Monti (Italian National Res. Council) G.S. Mugnozza (DISAFRI, Università della Tuscia) Dana Nelson (USDA FS) Krista Nichols (NOAA) Tivonne Nguyen (UC Davis) Irene Olimpieri (IBAF-Italy) Michael Ostry (USDA FS), Amanda Parks (PA DNR) Paula Pijut (USDA FS) Paola Pollegioni (Italian National Research Council) Dan Potter (University of California, Davis), Allen Pursell (The Nature Conservancy) Rodney Robichaud (Hartmann's Plants) Tatiana Roubtsova (UC Davis) K Rupert (Purdue Univ.) Philip San Miguel (Purdue Univ.) Kenji Seiwa (Tohoku Univ. Japan) Marcus Selig, Steve Seybold (USDA FS) Jack Siefert (Indiana DNR) Giovanni De Simioni (CNR-IBAF) Chuck Simon (USDA NCGR) Blanche Sterling (Louisiana State Univ.) Pinku Surana (Purdue Univ.) Yoshihisa Suyama (Tohoku Univ. Japan) Ned Tisserat (CO State Univ.) C.J. Tsai (Univ. Georgia) Curtis Utley (CO State Univ.) Khoroush Vadahti (Univ. Tehran) Y. Annamma Varghese (RRI India) Diane Velasco (USDA ARS) Erin Victory (Connecticut DNR) G. Vengadesan (Purdue Univ.) Sally Weeks (Purdue Univ.) Rick Westerman (Purdue Univ.) Alex Weidenhoeft (USDA FS-FPL) Lisa Worthen-Alexander (Univ. Tenn.-Knox.) Mohammad Yaghmour (UC Davis) Peihua Yang (Northwest A&F Univ. China) Shuoxin Zhang (Northwest A&F Univ. China) Peng Zhao (Northwest A&F Univ. China)

Thesis Advisor and Postgraduate-Scholar Sponsor:

Phillip Crystal (Jackson Labs) Zhonglian Huang (Purdue University) James Jacobs (Purdue University) Oriana Rueda Krauss (Purdue University) Nicholas LaBonte (Purdue University) Kejia Pang (Purdue University) Amanda Parks (PA DNR) Scott Rogers (USDA FS) Micah Stevens (Purdue University) Lisa Worthen Alexander (Univ. TN-Knoxville) Peng Zhao (Northwest A&F University).

Total number of graduate students advised (in your career): 11

Total number of postdoctoral scholars sponsored (in your career): 3

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EDUCATION AND TRAINING

2001	B.S.	Morgan State University	Biology / Chemistry
2002	Certification	Professional Career Development Institute	Animal Care Specialist
2006	M.S.	Johns Hopkins University	Biotechnology, Biodefense
2011	Ph.D.	Purdue University	Tree Physiology / Genetics

RESEARCH AND PROFESSIONAL EXPERIENCE

2011-present	Plant Physiologist (USDA Forest Service), Purdue University, West Lafayette, IN.
2007-2011	Graduate Research Assistant (Forestry) Purdue University, West Lafayette, IN.
2006-2007	Laboratory Manager (Neuroscience) Johns Hopkins University, Baltimore, MD.
2002-2006	Laboratory Manager (Human Genetics) Johns Hopkins University, Baltimore, MD.
2000-2002	Laboratory Technician (Biology) Morgan State University, Baltimore, MD.

GRANTS RECEIVED

2015-2017	Civil Rights Diversity Committee Special Project Fund (CRDC-SPF) Understanding Our Nation's Resources: Environmental Investment Challenge	14,000
2016	Civil Rights Diversity Committee Special Project Fund (CRDC-SPF), The World of Trees: Finding Nature in an Urban Environment III	3,500
2016	Civil Rights Diversity Committee Special Project Fund (CRDC-SPF), Building Bridges: Encouraging Interests in Forest Products	2,500
2014	Louis Stokes Alliance for Minority Participation (LSAMP)	\$300
2013-2016	Atherton Family Foundation	\$100,000
2013-2016	Civil Rights Diversity Committee Special Project Fund (CRDC-SPF), The World of Trees: Finding Nature in an Urban Environment I	\$8,300
2013	United States Department of Agriculture Forest Service (USDA-FS), New Scientist Research Assistance Grant	\$30,000
2013	Louis Stokes Alliance for Minority Participation (LSAMP)	\$300
2012	United States Department of Agriculture Forest Service (USDA-FS), New Scientist Research Assistance Grant	\$30,000
2011	Alliance for Graduate Education & Professoriate (AGEP) Research Grant	\$10,000

HONORS AND AWARDS

2017	Featured Researcher Life-Ology magazine
2016	USDA FS Gold Presidential Volunteer Service Award

	Purdue University Forestry & Natural Resources Community Service Highlight
	Purdue University Highlighted “Research at Purdue” Scientist
	Journal of Forestry Research Citation Award
2015	USDA FS Silver Presidential Volunteer Service Award
	USDA FS Outstanding Woman Award for Outreach
	LSAMP Mentor Award
	Society of Toxicology Eye on CDI Communiqué Spotlighted Scientist
2014	SACNAS Chapter Governance Award
	USDA FS Northern Research Station Director’s Award for Multicultural Achievement

PUBLICATIONS

Rezaei, M., Shamlu, F., **Lawson, S.S.**, Ebrahimi, A. 2017. Genetic diversity of superior Persian walnut genotypes in Azadshahr, Iran. *Genetic Resources and Crop Evolution* (Submitted)

Rezaei, M., Ghanbarpor, E., **Lawson, S.S.**, Khoshghalb, H., Ghorbani Ghogdi, H. 2017. Reduction of cracking in pomegranate fruit after foliar application of humic acid, calcium-boron, and kaolin during water stress. *Scientia Horticulturae* (Submitted)

Lawson, S.S., Pike, C. 2017. Characterization of naturally abundant stable isotopes in *Acacia koa* populations on Hawai’i. *Annals of Forest Research* (DOI: 10.15287/afr.2017.805)

Lawson, S.S. 2016. Overexpression of *AtWIN1/SHN1* in poplar mimics the *Arabidopsis* phenotype and results in changes in stomatal density and wax morphology. *Research Journal of Botany* 12: 1–13.

Ebrahimi, A., Zarei, A.K., **Lawson, S.S.**, Woeste, K.E., Smulders, M.J.M. 2016. Genetic diversity and genetic structure of Persian walnut (*Juglans regia*) accessions from 14 European, African, and Asian countries using SSR markers. *Tree Genetics & Genomes* 12:114 1–12.

Lawson, S.S., Michler, C.H. 2014. Overexpression of *AtSTO1* leads to improved salt tolerance in *Populus tremula* x *P. alba*. *Transgenic Research* 23(5): 817-826.

Lawson, S.S., Pijut, P.M., Michler, C.H. 2014. Comparison of *Arabidopsis* stomatal density mutants indicates variation in water stress responses and potential epistatic effects. *Journal of Plant Biology* 57(3): 162-173.

Lawson, S.S., Pijut, P.M., Michler, C.H. 2014. The cloning and characterization of a poplar stomatal density gene. *Genes and Genomics* 36(4): 427-441.

Lawson, S.S., Michler, C.H. 2014. Afforestation, restoration and regeneration — Not all trees are created equal. *Journal of Forestry Research* 25 (1): 3–20.

Alexander, L.W., **Lawson, S.S.** Genomics in hardwood tree improvement: applications of a growing resource. *Omics Technologies in Crop Improvement* ed. N. Benkeblia. CRC Press, Boca Raton.

Lawson, S.S., Pijut, P.M., Michler, C.H. 2012. Species selection in hardwoods research: Variations in baseline physiological responses of select temperate hardwood tree species. *Journal of Forestry Research* 24 (2): 285-292.

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715 W. State St., West Lafayette, IN 47907 and
202 ABNR Building, Columbia, MO 65211
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EDUCATION AND TRAINING

University of Massachusetts	Forest Management	B.Sc.	1976
Mississippi State University	Forest Genetics	M.Sc.	1978
University of Missouri	Horticulture	Ph.D.	2008

RESEARCH EXPERIENCE

- 2017-present Supervisory Plant Biologist and Project Leader, USDA Forest Service, Northern Research Station and Co-Director, Hardwood Tree Improvement and Regeneration Center, Purdue University, West Lafayette, IN
- 2017-present Adjunct Assistant Professor, Department of Forestry and Natural Resources, Purdue University
- 2010-2017 Research Assistant Professor Department of Forestry, University of Missouri
- 2000-2010 Research Analyst Center for Agroforestry, University of Missouri
- 2000-2010 Tree Improvement Specialist Missouri Department of Conservation
- 1998-2000 Nursery Manager/Propagator Bernheim Arboretum, Clermont, KY
- 1978-1998 Tree Improvement Specialist Indiana Department of Natural Resources

PUBLICATIONS (Selected)

1. Konar, A.; Choudhury, O.; Bullis, R.; Fiedler, L.; Kruser, J.M. Stephens, M.T.; Gailing, O.; Schlarbaum, S.; **Coggeshall, M.V.**; Staton, M.E.; Carlson, J.E.; Emrich, S.; Romero-Severson, J. 2017. High-quality genetic mapping with ddRADseq in the non-model tree *Quercus rubra*. BMC Genomics.18:417. DOI 10.1186/s12864-017-3765-8
2. Lane, T.; Best, T.; Zembower, N.; Davitt, J.; Henry, N.; Xu, Y.; Koch, J.; Liang, H.; McGraw, J.; Schuster, S.; Shim, D.; **Coggeshall, M.**; Carlson, J.E.; Staton, M. 2016. The green ash transcriptome and identification of genes responding to abiotic and biotic stresses. BMC Genomics. 17:702 DOI: 10.1186/s12864-016-3052-0 URL: <http://www.biomedcentral.com/1471-2164/17/702>.
3. Hefty, A.R.; **Coggeshall, M.V.**; Aukema, B.H.; Venette, R.C.; Seybold, S.J. 2016. Reproduction of walnut twig beetle in black walnut and butternut. HortTechnology 26(6):727-734.
4. Staton M, Best T, Khodwekar S, Owusu S, Xu T, Xu Y, Jennings, J.; Cronn, R.; Arumuganathan, A.K.; **Coggeshall, M.V.**; Gailing, O.; Liang, H.; Romero-Severson, J.; Schlarbaum, S. Carlson, J.E. 2015 Preliminary Genomic Characterization of Ten Hardwood Tree Species from Multiplexed Low Coverage Whole Genome Sequencing. PLoS ONE 10(12): e0145031. doi:10.1371/journal.pone.014503
5. McCleary, T.; McAllister, M.; **Coggeshall, M.**; Romero-Severson, J. 2013. EST-SSR markers reveal synonymies, homonymies and relationships inconsistent with putative pedigrees in chestnut cultivars. Genetic Resources and Crop Evolution. 60 (4) 1209-1222

<http://www.springerlink.com/openurl.asp?genre=article&id=doi:10.1007/s10722-012-9912-9>

6. Huang, Y.-N.; Zhang, H.; **Coggeshall, M.V.**; Rogers, S.; Woeste, K. 2015. White oak growth after 23 years in a three-site provenance / progeny trial on a latitudinal gradient in Indiana. *Forest Science* 61(_):000-000. <http://dx.doi.org/10.5849/forsci.15-013>.
7. Khodwekar S; Staton M; **Coggeshall M.V.**, Carlson J.E.; Gailing O. 2015. Nuclear microsatellite markers for population genetic studies in sugar maple (*Acer saccharum* Marsh.). *Ann. For. Res.* 58(2) DOI:10.15287/afr.2015.360. 12 pp.
8. **Coggeshall, M.V.**; Romero-Severson, J. 2013. Breeding black walnuts in the age of genomics. In: VanSambeek, J.W., ed. and four others. Managing fine hardwoods after a half century of research, *Proceedings, 7th Walnut Research Symposium*; 2011 August 1-3; Madison, WI. Gen. Tech. Rep. NRS-P-115. St. Paul, MN: U.S.D.A. Forest Service, Northern Research Station. p75.
9. Owusu, S.; Staton, M.; Jennings, T.; Schlarbaum, S.; **Coggeshall, M.**; Romero-Severson, J.; Carlson, J.; Gailing, O. 2013. Development of genomic microsatellites in *Gleditsia triacanthos* (Fabaceae) using Illumina sequencing. *Applications in Plant Sciences* 1(12):1300050. doi: <http://dx.doi.org/10.3732/apps.1300050>.
10. **Coggeshall, M.V.** 2011. Use of microsatellite markers to develop new eastern black walnut cultivars in Missouri, USA, 28th International Horticultural Congress. Lisboa, Portugal. *Acta Horticulturae* 918(1):221-226.

Five Synergistic activities:

1. Service to the forest genetics community

Co-PI on NSF project entitled, "TRPGR: Comparative genomics of environmental stress responses in North American hardwoods". Responsible for development, hosting and ongoing phenotyping of full sib mapping populations for *Quercus rubra*, *Q. alba*, *Juglans nigra* and *Fraxinus pennsylvanica* at the University of Missouri.

2. Other project-related activities

Co-PI on USDA-SCRI project entitled, "Development of disease resistant walnut rootstocks: Integration." (2012-2017).

3. Education

Mentored five undergraduates (2016-2017), Advised two M.S. students: one at Purdue who graduated in 2014, one at Missouri who graduated in 2016; currently serving on two graduate committees at University of Missouri.

4. Other recent networking experiences in the forest genetics community

Previously served as co-PI on an USDA AFRI project focused on screening of *Juglans* and *Carya* for resistance to the thousand cankers disease and evaluation of insecticidal controls for use in management.

5. Other relevant service

Member, *Juglans* Crop Germplasm Committee (2000-present); Member, USDA Forest Service Hardwood Tree Improvement and Regeneration Center Advisory Board (2005-present); Missouri Forest Resources Advisory Council Board Member (2011-present).