

NOELLE A BARKLEY

USDA-ARS Plant Genetic Resources Conservation Unit
1109 Experiment St.
Griffin, GA. 30223
(770) 412-4035
nbarkley@uga.edu

360 Darren Drive
Fayetteville, GA. 30215
(404) 805-3828 cell
plantdnadoc@yahoo.com

PROFESSIONAL/RESEARCH EXPERIENCE

Geneticist, USDA-ARS Plant Genetic Resources Conservation Unit, Griffin, GA, 10/2010-present. Acquire, regenerate, and propagate the cultivated and wild *Arachis* species collection maintained in Griffin, GA in order to preserve genetic diversity and provide genetic resources for distribution to scientists worldwide. Maintain six greenhouse bays of cultivated and wild peanut plants. Process germplasm imported from other countries through quarantine and ensure material is disease free (via ELISA) for USDA germplasm collection and peanut CRSP scientists. Plans and seeks funding for research to address issues pertaining to genetic diversity, phylogeny, population structure, and nutritional quality in wild and cultivated peanuts utilizing classical, biochemical, and molecular techniques. Develop and employ marker assisted selection to expedite breeding in peanut. Evaluate genetic diversity with molecular markers (SSRs, SNPs, or GBS) and collect phenotyping data to associate markers with agronomic traits. Perform interspecific crossing of wild species in order to introgress wild species genes into cultivated peanut. Part of peanut CRSP project to promote sustainable agriculture and increase peanut production in Bolivia, South America, and Africa, as well as, assisting in developing disease resistant cultivars, capacity training on germplasm conservation, and molecular technology transfer to host countries. Prepare manuscripts and presentations for publication and scientific meetings. Direct research and training on laboratory equipment and safety practices for postdoctorals, graduate, undergraduate students, and technicians.

Molecular Geneticist, USDA-ARS Plant Genetic Resources Conservation Unit, Griffin, GA, 2003-2010. Collaborate with curators and develop independent research projects to address issues regarding germplasm diversity, characterization, and novel traits for the purpose of breeding and/or crop improvement. Marker development for various agronomic traits in crop plants such as high oleic acid and disease resistance. Overview of projects and responsibilities follow. Develop qPCR protocol to detect sweet potato leaf curl virus (SPLCV), screen sweet potato collection for presence of the virus, sequence SPLCV isolates, and determine phylogenetic relationships among related viruses. Develop real-time PCR SNP genotyping assay to determine high oleic acid in peanut seeds or leaves, evaluate mutant alleles and effect on phenotype in segregating population. Test clover accessions for infection with TSWV using RT-PCR. Perform RT-PCR to examine the change in expression of resveratrol synthase and chalcone synthase in various peanut tissues under stress. Develop and carry out EcoTILLING on a mung bean (*Vigna radiata*) population to evaluate genetic variation, sequence positive samples and design SNP markers for horticultural traits. Apply TILLING in sorghum to detect mutations in targeted genes and determine putative gene function. Evaluation of genetic diversity and phylogenetic relationships of various crops (peanut, bamboo, sorghum, legumes, etc.) utilizing various molecular markers. Sequencing SSR alleles to determine the mode of their evolution (stepwise or infinite allele) and assess variation among same sized alleles. Identify and sequence segments of peanut DNA for variation in resistant gene analogs. Perform data analysis (including phylogenetics and statistical) for all marker and sequence data collected. Separate and identify flavonoids in various legumes using HPLC. Prepare manuscripts and presentations for publication and scientific meetings. Direct research and training on laboratory equipment and safety practices for postdoctorals, graduate, undergraduate students, and technicians.

Graduate Student Researcher, University of California, Riverside, 1998-2003. Determine the level of genetic diversity among 370 *Citrus* accessions and establish a core collection. Development and evaluation of forty SSR markers for the *Citrus* population to develop a detailed linkage map and determine phylogenetic relationships between *Citrus* accessions. Identify hybrid accessions and determine putative parentage. Cloning and sequencing genes from the population to determine an evolutionary history of the *Citrus* accessions. Evaluate homoplasy in SSR alleles from *Citrus* and its near relatives.

Lab Assistant I, USDA-ARS National Germplasm Repository for Citrus and Dates, Riverside, CA, 1995-1998. Screened *Citrus* seedlings for genetic variability using Isozymes (Starch Gel Electrophoresis), and other DNA based methodologies (ISSRs) to determine how many accessions in the population should be maintained in the collection. Additionally, I was involved in other various lab projects including: annual viral testing of plants via ELISA, identifying inclusion bodies using light microscopy, determining a protocol for analyzing ploidy level of *Citrus* via root tip squashes, culturing *Spiroplasma citri* for stubborn detection, and fruit quality measurements. Other responsibilities included performing a bioassay to detect various *Citrus* viruses and plant propagations. Collected material as needed for distributions of *Citrus* seed, budwood, date palm offshoots and pollen to requestors worldwide and was involved in cleaning material, packaging and providing necessary paperwork to the county inspector.

Student Assistant (Senior Research), Department of Botany and Plant Sciences, UC Riverside. 1994-1995. Determined nuclease activity in hypoxic maize root seedlings using 12.5% polyacrylamide gels and gel photography. Assisted in RNA fractioning, spectrophotometer readings of RNA and protein fractions, and cesium chloride centrifugation.

SKILLS

Molecular Biology: Proficient with molecular biology techniques including DNA & RNA extraction, primer and marker development, gene cloning, bacterial transformation, bacterial culturing, restriction enzyme digestion, minipreps, sequencing (direct PCR product and vectors), PCR, RT-PCR, Real-Time PCR, TILLING, EcoTILLING, molecular markers (SSRs, ISSRs, AFLPs, Isozymes), mapping markers, root tip squashes to determine ploidy level, flow cytometry to determine DNA content and ploidy, tobacco transformation, polyacrylamide and agarose gel electrophoresis. Skilled in operating automated sequencers including the ABI 377, Beckman CEQ 8000, and LI-COR 4200 & 4300.

Bioinformatics/Computer Software: Experienced with most data analysis software programs including Microsat, Popgene, Phylip, PAUP, NTSYSpC, Clustal, Cervus, Sequencher, AlignR, Structure, Fstat, Joinmap, Primer3, BLAST, Sequin, SAGA, e-Seq, Genescan, Genotyper, Genographer, GraphPad Prism, jModelTest, MAFFT, TCS, Mega, TASSEL, and DNAsp. Familiar with AWTY, MrBayes, Arlequin, BEAST, GARLI, LAMARC, PAML, MacClade, PowerMarker, JMP, QTL Cartographer, and Mapmaker software programs for data analysis. Proficient with MS Office, EndNote, and Photoshop for preparing reports, presentations, and manuscripts.

Viral Detection: Experienced with viral detection methods (for DNA and RNA viruses) including RT-PCR and Real-Time PCR, ELISA, biological indexing for citrus and sweet potato viral detection, identifying inclusion bodies using light microscopy, and culturing *Spiroplasma citri* for stubborn detection. Developed methods to evaluate germplasm for infection of SPLCV, TSWV, PMMoV, PMV, AMV, PSTV, and PeMoV using molecular and/or serological techniques. Experienced with viral elimination by thermotherapy and shoot tip micrografting.

Biochemistry: Adept with detection and separation of flavonoids, phytoalexins (resveratrol) and designing methods to separate compounds using HPLC Agilent 1100. Familiar with methods and procedures for gas chromatography for fatty acid composition analysis. Employed NMR to collect oil and moisture content in seeds.

INVITED SPEAKER

Preservation and evaluation of plant germplasm. Presentation, Master Gardeners of Fayette County, Peachtree City, GA July 2013.

Why preserve and evaluate genetic resources in peanut? Presentation, Advances in Arachis through Genomics and Biotechnology (AAGB), Zhengzhou, China June 2013.

USDA plant germplasm collections. Presentation. Exchange Club, Tifton, GA April 2013.

Activities and Status of the *Arachis* germplasm collection. Presentation, Peanut Foundation Project Review College Park, GA March 2013.

USDA *Arachis* germplasm collection: A valuable resource for mining traits to improve peanuts. International Congress on legume Genetics and Genomics (ICLGG), Hyderabad, India, October 2012.

Genotyping and phenotyping the *Arachis* germplasm collection to track functional mutations and evaluate genetic diversity. University of Florida, September 2012.

Employing SNP and microsatellite markers to track functional mutations and evaluate genetic diversity in the USDA *Arachis* germplasm collection. Advances in Arachis through Genomics and Biotechnology (AAGB), Brasilia, Brazil. June 2011

TILLING: A reverse genetics approach for functional genomics. Clayton State University. November 2008.

Fundamentals of recombinant DNA cloning. University of Georgia. October 2006.

Do not be bamboozled by bamboo: the real story from the cradle to the coffin. American Bamboo Society National Meeting. Houston, TX. October 2005.

Genetic diversity and phylogeny in the Citrus Variety Collection. USDA Salinity Laboratory. Riverside, CA. September 2002.

TEACHING EXPERIENCE

University of Georgia. 2006. Recombinant DNA Cloning guest lecture and lab demonstration. Genetics 3200.

University of California, Riverside. 2000-2002. SSR genotyping demonstration. Plant Biotechnology BPSC153. Molecular marker lecture and demonstration of SSR markers on Li-Cor 4200.

Teaching Assistant, University of California, Riverside. 1999. Genetics 102. Supervisor: Dr. Mikeal Roose. Developed lectures for discussion sections to reinforce the vital points made in class. Developed and graded weekly quizzes to evaluate student progress in solving basic genetic word problems. Helped students work through homework problems in an informal genetics clinic. Created study worksheets for each midterm. Assisted the genetics instructor in the final grade determination.

EDUCATION

PhD, Molecular Genetics, University of California, Riverside 2003. Advisor: Dr. Mike Roose, Dept. of Botany and Plant Sciences. Dissertation: Genetic diversity in a *Citrus* germplasm collection characterized with simple sequence repeat (SSR) markers.

BS, Biology, University of California, Riverside, 1996.

PUBLICATIONS

Chen CY, **Barkley NA**, Wang ML, Holbrook CC, Dang P. Registration of purified accessions for the U.S. peanut mini core germplasm collection. *Journal of Plant Registrations* (in press).

Barkley NA, Isleib TG, Wang ML, Pittman RN. 2013. Genotypic effect of *ahFAD2* on fatty acid profiles in six segregating peanut (*Arachis hypogaea* L.) populations. *BMC Genetics* 14:62.

Wang ML, Chen CY, Tonnis B, **Barkley NA**, Pinnow DL, Pittman RN, Davis J, Wu Y, Holbrook CC, Stalker HT, Pederson GA. 2013. Seed fatty acid composition and oil, flavonoid, and resveratrol content variability in the US peanut mini core collection. *Journal of Agricultural and Food Chemistry* 61:2875-2882.

Barthe S, Gugerli F, **Barkley NA**, Maggia L, Cardi C, Lemes MR, Gribel R, Scotti I. 2012. Always look on both sides: phylogenetic information conveyed by SSR allele sequences. *PLoS One* 7:e40699.

Wang ML, Chen CY, Pinnow DL, **Barkley NA**, Pittman RN, Lamb M, Pederson GA. 2012. Seed dormancy variability in the US peanut mini core collection. *Research Journal of Seed Science*. 5(3):85-95.

Jenkins TM, Wang ML, **Barkley NA**. 2012. Microsatellite markers in plants and insects: Part II: Databases and *in silico* tools for microsatellite mining and analyzing population genetic stratification. Invited review, *Genes, Genomes, and Genetics* 1: 60-75.

Wang ML, **Barkley NA**, Chen Z, Pittman RN. 2011. *FAD2* gene mutation significantly alters fatty acid profiles in cultivated peanuts. *Biochemical Genetics* 49:748-759.

Wang ML, Sukumaran S, **Barkley NA**, Chen Z, Chen Y, Guo B, Pittman RN, Stalker HT, Holbrook CC, Pederson GA, Yu J. 2011 Population structure and marker trait association analysis of the U.S. peanut mini-core collection. *Theoretical and Applied Genetics* 123:1307-1317.

Barkley NA, Ling KS, Pinnow DL, Wang ML, Jarret RL. 2011. Detecting and classification of sweet potato leaf curl virus (SPLCV) isolates in the U.S. sweet potato germplasm collection via a Real-Time PCR assay and phylogenetic analysis. *Plant Disease* 95(11):1385-1391.

Barkley NA, Chenault Chamberlin KD, Wang ML, Pittman RN. 2011. Genotyping and fatty acid composition analysis in segregating peanut (*Arachis hypogaea* L.) populations. *Peanut Science* 38(1): 11-19.

Barkley NA, Wang ML, Pittman RN. 2011. A real-time PCR assay to detect SNPs in *FAD2A* in peanuts (*Arachis hypogaea* L.). *Electronic Journal of Biotechnology* 14(1):1-9, DOI: 10.2225/vol14-issue1-fulltext-12.

Wang ML, **Barkley NA**, Chinnan M, Stalker HT, Pittman RN. 2010. Oil content and fatty acid composition variability in wild peanut species. *Plant Genetic Resources. Plant Genetic Resource* 8:232-234.

- Barkley NA**, Chenault Chamberlin KD, Wang ML, Pittman RN. 2010. Development of a real-time PCR genotyping assay to identify high oleic acid (18:1) peanuts (*Arachis hypogaea* L.). *Molecular Breeding* 25: 541-548.
- Chen Z, Wang ML, **Barkley NA**, Pittman RN. 2010. A simple allele-specific PCR assay for detecting FAD2 alleles in both the A and B genome of cultivated peanut for high oleate trait selection. *Plant Molecular Biology Reporter* 28: 542-548.
- Barkley NA**, Krueger RR, Federici CT, Roose ML. 2009. What phylogeny and gene genealogy analyses reveal about homoplasy in citrus microsatellite alleles. *Plant Systematics and Evolution* 282: 71-86.
- Barkley NA**, Pinnow DL, Wang ML, Pederson GA. 2009. First report of tomato spotted wilt virus (TSWV) infecting African clover [*Trifolium temense* (Fresen.)] in Georgia. *Plant Disease* 93: 202.
- Wang ML, Zhu C, **Barkley NA**, Chen Z, Erpelding JE, Murray SC, Tesso T, Pederson GA, Yu J. 2009. Genetic diversity and population structure analysis of sweet sorghum accessions in the US historic collection. *Theoretical and Applied Genetics* 120: 13-23.
- Wang ML, **Barkley NA**, Jenkins TM. 2009. Microsatellite markers in plants and insects: Part I: Applications of biotechnology. Invited review, *Genes, Genomes, and Genetics* 3: 54-67.
- Wang ML, Pinnow DL, **Barkley NA**, Pittman RN. 2009. Plant resistance to TSWV and seed accumulation of resveratrol within peanut germplasm and its wild relatives in the US collection. *Plant Pathology Journal* 8: 53-61.
- Wang ML, Mosjidis J, Morris JB, Chen Z, **Barkley NA**, Pederson GA. 2009. Evaluation of *Lespedeza* germplasm genetic diversity and its phylogenetic relationship with the genus *Kummerowia*. *Conservation Genetics* 10: 79-85.
- Wang ML, **Barkley NA**, Gillaspie AG, Pederson GA. 2008. Phylogenetic relationships and genetic diversity of the USDA *Vigna* germplasm collection revealed by gene derived markers and sequencing. *Genetics Research* 90: 467-480.
- Xin, Z, Wang ML, **Barkley NA**, Burow GB, Franks CD, Pederson GA, Burke JJ. 2008. Applying genotyping (TILLING) and phenotyping analyses to elucidate gene function in a chemically induced sorghum mutant population. *BMC Plant Biology* 8: 103.
- Jarret RL, Gillaspie AG, **Barkley NA**, Pinnow DL. 2008. The occurrence and control of pepper mild mottle virus (PMMoV) in the USDA/ARS *Capsicum* germplasm collection. *Seed Technology* 30: 26-37.
- Barkley NA**, Gillaspie AG, Dean RE, Wang ML, Jenkins TM. 2008. Discovering and verifying DNA polymorphisms in a mung bean [*V. radiata* (L.) R. Wilczek] collection by EcoTILLING and sequencing. *BMC Research Notes* 1: 28.
- Barkley NA**, Wang ML. 2008. Application of TILLING and EcoTILLING as reverse genetic approaches to elucidate the function of genes in plants and animals. Invited review, *Current Genomics* 9: 212-226.
- Barkley NA**, Dean RE, Pittman RN, Wang ML, Holbrook CC, Pederson GA. 2007. Genetic diversity of cultivated and wild type peanuts evaluated with M13-tailed SSR markers and sequencing. *Genetics Research* 89: 93-106.
- Wang ML, Morris JB, **Barkley NA**, Dean RE, Jenkins TM, Pederson GA. 2007. Evaluation of genetic diversity of the USDA *Lablab purpureus* germplasm collection using SSR markers. *Journal of Horticultural Science and Biotechnology* 82: 571-578.
- Barkley NA**, Roose ML, Krueger RR, Federici CT. 2006. Assessing genetic diversity and population structure in a *Citrus* germplasm collection utilizing simple sequence repeat markers (SSRs). *Theoretical and Applied Genetics* 112: 1519-1531.
- Gillaspie AG, **Barkley NA**, Morris JB. 2006. An unusual strain of *Alfalfa* mosaic virus detected in *Crotalaria spp.* L. germplasm in Georgia. *Plant Pathology Journal* 5: 397-400.
- Wang ML, Chen ZB, **Barkley NA**, Newman ML, Kim W, Raymer P, Pederson GA. 2006. Characterization of seashore paspalum (*Paspalum vaginatum* Swartz) germplasm by transferred SSRs from wheat, maize, and sorghum. *Genetic Resources and Crop Evolution* 53: 779-791.
- Barkley NA**, Newman ML, Wang ML, Hotchkiss MW, Pederson GA. 2005. Assessment of the genetic diversity and phylogenetic relationships of a temperate bamboo collection using transferred EST-SSR markers. *Genome* 48: 731-737.
- Wang ML, **Barkley NA**, Yu JK, Dean RE, Newman ML, Sorrells ME, Pederson GA. 2005. Transfer of simple sequence repeat (SSR) markers from major cereal crops to minor grass species for germplasm characterization and evaluation. *Plant Genetic Resources* 3: 45-57.

SUBMITTED MANUSCRIPTS

He G, **Barkley NA**, Zhao Y, Yuan M, Prakash CS. Phylogeny of the *Arachis* genus based on genic sequences. *Plant Systematics and Evolution*.

Jenkins TM, Eaton TD, Eger JE, **Barkley NA**, Chen Z, Suiter DR, Gardner WA, Buntin D, Roberts PM, Ruberson JR, Toews MD, Sparks AN, Greene JK, Choi DS. The GA1 haplotype of *Megacopta cribraria*: The three year phylogeographic odyssey of a new Asian invasive symbiosis in the Western hemisphere. *Molecular Phylogenetics and Evolution*.

Chamberlin KD, **Barkley NA**, Tillman BL, Dillwith JW, Madden R, Payton ME, Bennett RS. A comparison of methods used to determine the oleic/linoleic acid ratio in cultivated peanut (*Arachis hypogaea* L.) *Journal of Agriculture and Food Chemistry*.

MANUSCRIPTS IN PREPARATION

Barkley NA, Jenkins TM, Wang ML. Microsatellite markers in plants and insects: Part III: The good, bad and ugly of microsatellites. Invited review, *Genes, Genomes, and Genetics*.

Barkley NA, Roose ML, Krueger RR, Federici CT. Construction of a core collection from a *Citrus* germplasm collection.

BOOK CHAPTERS

Barkley NA, Wang ML. Oleic Acid: Natural variation and potential enhancement in oil seed crops. In: *Oleic Acid: Dietary sources functions and health benefits*. 2012, Editor: Luciano Paulino Silva, Nova Science Publishers Inc. p 60-73.

Barkley NA, Wang ML. Revealing gene function and genetic diversity in plants and animals via TILLING and EcoTILLING. Invited book chapter, 2012, Editor: Christian Neri, *Current Genome Science Vol 1* 306-341.

PROCEEDINGS

Barkley NA, Roose ML, Krueger RR. 2007. Diversity and phylogenetic relationships of the Citrus Variety Collection. *Proceedings, International Society of Citriculture X Cong 2004*, 178-182.

Barkley NA, Roose ML, Krueger RR. 2003. Assessing genetic diversity in *Citrus* by utilizing molecular markers. *Proceedings, International Society of Citriculture IX Cong 2000*, 126-127.

PRESENTATIONS AT PROFESSIONAL MEETINGS

Wang ML, Chen CY, Tonnis B, **Barkley NA**, Pederson GA. 2013. Seed chemical composition variability and FAD2A functional SNP genotypes in the US peanut mini core collection. Poster, ASA-CSSA-SSSA, Tampa, FL November 2013.

Isleib TG, **Barkley NA**. Contributions of plant introductions to the ancestry of current U.S. peanut cultivars. Presentation, American Peanut Research and Education Society (APRES). Braselton, GA. July 2013.

He GH, **Barkley NA**, Zhao YL, Yuan M. Use of EST-SSR loci flanking regions for phylogenetic analysis of the genus *Arachis*. Poster, American Peanut Research and Education Society (APRES). Braselton, GA. July 2013.

Chen CY, Wang ML, **Barkley NA**, Tonnis B. Effect of GXE interaction on oil and oleic fatty acid contents of cultivated peanuts. Presentation, American Peanut Research and Education Society (APRES). Braselton, GA. July 2013.

Varsheny RK, Froencike L, Pandey MK, Upadhyaya HD, Liao B., **Barkley NA**, Guo B, Gowda MVC, Holbrook CC, Brenneman TB, Bhat RS, Chen CY, Damicone J, Burrow MD, Isleib TG, Dean L, Wang ML, Vadez V, Jackson S, Michelmore RW. An international initiative for genome wide association studies (GWAS) in peanut (*Arachis hypogaea* L.) Poster, *Advances in Arachis through Genomics and Biotechnology (AAGB)*, Zhengzhou, China June 2013.

Qiao L, Pandey M, **Barkley NA**, Feng S, Wang H, Culbreath A, Varshney R, Guo B. A modified PCR protocol for consistent amplification of fatty acid desaturase (FAD) alleles in marker assisted backcross breeding for high oleic trait in peanut. Presentation, *Advances in Arachis through Genomics and Biotechnology (AAGB)*, Zhengzhou, China June 2013.

Chen C, Wang ML, **Barkley NA**, Dang P, Holbrook CC, Liu L. Genetic variation of purified U.S. peanut (*Arachis hypogaea* L.)

mini core collection. Presentation, Advances in Arachis through Genomics and Biotechnology (AAGB), Zhengzhou, China June 2013.

Wang ML, Chen Z, **Barkley NA**, Morris JB, Pederson GA. Genetic and chemical evaluation of the U.S. castor germplasm collection for biodiesel production. Poster, Plant and Animal Genome Conference, San Diego, CA. January 2013.

Chamberlin KD, Tillman BL, **Barkley NA**. 2012 Determining the oleic/linoleic acid content of a single seed: A comparison of available methods. Poster, ASA CSSA SSSA, Cincinnati OH October 2012.

Pandey MK, Feng S, Culbreath A, Wang ML, **Barkley NA**, Holbrook CC, Zhang XY, Wu YT, Varshney RK, Guo B. Construction and use of saturated genetic map for identification of QTLs associated with disease resistance, oil quality, morphological descriptors, and yield components in cultivated peanut (*Arachis hypogaea* L.) Presentation, VI International Conference on Legume Genetics and Genomics, Hyderabad, India October 2012.

Chamberlin KD, **Barkley NA**, Tillman B. Comparing three methods used to determine the oleic/linoleic acid ratio in a single peanut seed. Poster, American Peanut Research and Education Society (APRES). Raleigh, NC. July 2012.

Pandey, MK, Feng S, Culbreath A, Varshney RK, Wang ML, **Barkley NA**, Holbrook CC, Guo B. Saturation of genetic maps for the identification of QTLs controlling biotic resistance, morphological descriptors, and oil quality in tetraploid peanut (*Arachis hypogaea* L.). Poster, American Peanut Research and Education Society (APRES). Raleigh, NC. July 2012.

Wang ML, **Barkley NA**, Chen Z, Pittman RN, Pederson GA. FAD2 gene mutations significantly alter fatty acid composition in peanuts. Poster, Plant and Animal Genome Conference, San Diego, CA. January 2012.

Barkley NA, Wang ML, Pittman RN. Utilization of SNP, SSR, and biochemical data to evaluate genetic and phenotypic diversity in the U.S. peanut germplasm collection. Poster, Peanut CRSP Strategic Research Conference. St Julian, Malta December 2011.

Barkley NA, Wang ML, Pittman RN. Can high quality DNA be extracted and utilized from *Arachis* seeds in long term storage with zero percent germination? Poster, American Peanut Research and Education Society (APRES). San Antonio, TX. July 2011.

Chen CY, Dang P, Lamb M, Wang ML, Pinnow DL, **Barkley NA**, Pittman RN. Variability in seed dormancy within the U.S. peanut mini core collection. Presentation, American Peanut Research and Education Society (APRES). San Antonio, TX. July 2011.

Wang ML, Sukumaran S, **Barkley NA**, Chen Z, Chen Y, Guo B, Pittman RN, Stalker HT, Holbrook CC, Pederson GA, Yu J. Genetic diversity and population structure analysis of the accessions in the U.S. peanut mini-core collection. Poster, Plant and Animal Genome Conference, San Diego, CA. January 2011.

Barkley NA, Wang ML, Pittman RN. Utilizing real-time PCR to reveal *ahFAD2* genotypes in segregating peanut populations. Presentation, American Peanut Research and Education Society (APRES). Clearwater, FL. July 2010.

Barkley NA, Wang ML, Pittman RN. Improving fatty acid composition in peanuts (*Arachis hypogaea* L.) by SNP genotyping and traditional breeding. Poster, Gordon Research Conference. Holden, NH. July 2010.

Wang ML, **Barkley NA**, Chinnan M, Stalker T, Pittman RN. Oil content and fatty acid composition variability in wild peanut species. Poster, American Peanut Research and Education Society (APRES). Clearwater, FL July 2010.

Barkley NA, Ling KS, Pinnow DL, Wang ML, Jarret RL. Detection of sweet potato leaf curl virus (SPLCV) in the U.S. germplasm collection via Real-Time PCR. Presentation, PGOC, CGC chair, and S-9 joint meeting. Geneva, NY. July 2010.

Barkley NA, Wang ML, Pittman RN. Rapid and accurate detection of high oleic peanuts using Real-Time PCR. Presentation, Peanut Commission, Tifton, GA. February 2010.

Wang ML, Zhu C, **Barkley NA**, Chen Z, Erpelding JE, Pederson GA, Yu J. Assessment of genetic diversity and population structure of sweet sorghum accessions in the US historic germplasm collection. Presentation, Plant and Animal Genome Conference, San Diego, CA. January 2010.

Barkley NA, Wang ML, Pittman RN. Real-Time PCR genotyping using Taqman probes to detect high oleic acid peanuts. Presentation, American Peanut Research and Education Society (APRES). Raleigh, NC. July 2009.

Wang ML, Pinnow DL, **Barkley NA**, Pittman RN. Plant response to TSWV and seed accumulation of resveratrol in peanut. Poster, American Peanut Research and Education Society (APRES). Raleigh, NC. July 2009.

Pittman RN, **Barkley NA**, Todd JW. Increasing the genetic diversity of cultivated peanuts (*Arachis hypogaea*). Presentation.

Peanut Commission Board. Tifton, GA. February 2009.

Wang ML, **Barkley NA**, Gillaspie GA, Pederson GA. Phylogenetic relationships and genetic diversity of the USDA Vigna germplasm collection revealed by gene derived markers and sequencing. Poster, Plant and Animal Genome Conference. San Diego, CA. January 2009.

Wang ML, Mosjidis J, Morris JB, Chen Z, **Barkley NA**, Pederson GA. Assessing the genetic diversity of *Lespedeza* germplasm and analysis of its phylogenetic relationship with the genus *Kummerowia*. Poster, Plant and Animal Genome Conference. San Diego, CA. January 2008.

Barkley NA, Wang ML, Gillaspie AG, Dean RE, Pederson GA, Jenkins TJ. Mining SNPs and indels in mung bean (*V. radiata*) by Ecotilling. Poster, Convergence of Genomics and the Land Grant Mission: Emerging trends in the application of genomics in agricultural research. WestLafayette, IN. September 2007.

Barkley NA, Dean RE, Pittman RN, Wang ML, Holbrook CC, Pederson GA. Diversity of peanut mini core and wild relatives using M13 tailed SSR markers. Presentation, S009: Plant Genetic Resources Conservation and Utilization Meeting. Charleston, SC. August 2007.

Zhanguo X, Wang ML, **Barkley NA**, Franks CD, Burow GB, Pederson GA, Burke JJ. Development of a TILLING population for sorghum functional genomics. Poster, Plant and Animal Genome Conference. San Diego, CA. January 2007.

Wang ML, Morris JB, **Barkley NA**, Dean RE, Jenkins TM, Pederson GA. Genetic diversity of lablab (*L. purpureus*) germplasm assessed by SSR markers. Poster, Plant and Animal Genome Conference. San Diego, CA. January 2007.

Barkley NA, Dean RE, Pittman RN, Wang ML, Holbrook CC, Pederson GA. Genetic diversity of the peanut (*Arachis hypogaea* L.) mini core. Poster, American Peanut Research and Education Society (APRES). Savannah, GA. July 2006.

Wang ML, Harrison-Dunn ML, Chen Z, **Barkley NA**, Dean RE, Pederson GA. *Cynodon Dactylon*: A very dynamic species with extensive variation. Presentation, American Society of Agronomy Annual Meeting. Salt Lake City, UT. November 2005.

Barkley NA, Gillaspie AG, Dean RE, Wang ML, Jenkins TM. TILLING: No plow, blood, sweat or tears required. Presentation, S009: Plant Genetic Resources Conservation and Utilization Meeting. Knoxville, TN. August 2005.

Wang ML, **Barkley NA**, Yu JK, Dean RE, Sorrells ME, Pederson GA. Transfer of simple sequence repeat (SSR) markers from major cereal crops to minor grass species for germplasm characterization and evaluation. Poster, Plant and Animal Genome Conference. San Diego, CA. January 2005.

Morris JB, **Barkley NA**, Wang ML. Molecular characterization of guar (*Cyamopsis tetragonoloba*) germplasm. Poster, Crop Science Society of America Annual Meeting. Seattle, WA. November 2004.

Wang ML, Chen Z, **Barkley NA**, Newman ML, Kim W, Raymer P, Pederson GA. Development of a full set of molecular genetic markers for assessment of germplasm genetic diversity and protection of cultivar patent right of turfgrass. Poster, Crop Science Society Annual Meeting. Seattle, WA. November 2004.

Newman ML, Dean RE, Wang ML, **Barkley NA**. Evaluation of the USDA finger millet collection. Poster, American Society of Agronomy Annual Meeting. Seattle, WA. November 2004.

Wang ML, **Barkley NA**, Dean RE, Holbrook CC, Pittman RN. 2004. Transfer of *Medicago* EST-SSRs to peanut for germplasm evaluation and cross-species cloning. Presentation, American Peanut Research and Education Society. San Antonio, TX. July 2004.

Barkley NA, Roose ML, Krueger RR. Diversity and phylogenetic relationships of the Citrus Variety Collection. Poster, International Society of Citriculture X Congress. Agadir, Morocco February 2004.

Barkley NA, Roose ML, Krueger RR. Utilizing simple sequence repeat markers to analyze the genetic diversity present in the Citrus Variety Collection. Poster, Gordon Agricultural Conference. Ventura, CA. February 2003.

Barkley NA. Genetic diversity in *Citrus* utilizing SSR markers. Presentation, Annual Genetics and Microbiology Symposia at Lake Arrowhead. Lake Arrowhead, CA. 1998-2002.

Barkley NA, Roose ML, Krueger RR. Assessing genetic diversity in *Citrus* by utilizing molecular markers. Poster, International Society of Citriculture IX Congress. Orlando, FL. December 2000.

Barkley NA, Roose ML, Krueger RR. Constructing a core collection utilizing simple sequence repeat markers. Poster, Conservation Biology. Riverside, CA. June 1998.

SEQUENCE SUBMISSIONS TO GENBANK: 107

CERTIFICATIONS

Molecular Evolution Workshop, August 2009
Statistical Genetics and Genomics, July 2008
Real-Time PCR and Pathogen Detection, March 2008
Chemstation Operation, February 2007
Techniques of Modern HPLC, August 2006
Biosafety and Biosecurity Certificate, July 2005
Molecular Phylogenetics and Bioinformatics Certificate, May 2005
CPR/AED Certified, March 2003-2012
Hazardous Waste Management, July 2003-2010
Lab Safety training at Environmental Health and Safety, 1995
EPA Blue Card, 1995

AWARDS AND HONORS

SAA Support Scientist of the Year 2009
Young Scholars Program Award 2004, 2006, 2007, 2008, 2010, 2012
Gordon Research Fellowship 2003
GSA mini grant 2000 and 2003
Nominated for membership in the honor society, Gamma Sigma Delta. 2000

EXTERNAL SUPPORT

Chen C, Barkley NA, Sanders T, Dean L. 2013. An association mapping study to identify loci contributing to desirable traits in the U.S. peanut mini core collection and elite germplasm for cultivar development. The Peanut Foundation. \$ 49,000.

Barkley NA, MacDonald GE, Tillman BL, Holbrook CC. 2013. Phenotyping and genotyping the US peanut core collection. The Peanut Foundation. \$35,000.

Barkley NA, MacDonald GE, Tillman BL, Holbrook CC. 2013. Characterization, evaluation, and regeneration of the US peanut core collection. GA Peanut Commission. \$15,000.

Pittman RN and Barkley NA. 2012. Genotyping-by-Sequencing (GBS) of a small segment of the cowpea (*Vigna unguiculata*) core collection. USDA Specialty Crops Grant 6607-21000-010-00D. \$8,500.

Tillman BL, Culbreath AK, Pittman RN, Barkley, NA. 2008-2013. Breeding peanut for disease resistance valuable to the U.S., Latin America and the Caribbean. USAID ECG-A-00-07-00001-00 grant to the Peanut Collaborative Research Support Program at UGA. \$220,000 (distributed among University of Florida, University of Georgia, and USDA).

Pittman RN, Wang ML, Barkley NA. 2004. Evaluating sequence content of resistant gene analogs in TSWV susceptible and resistant peanuts. Peanut Commission. \$8,500.

Graduate research partially funded by USDA Germplasm Evaluation Grant 1997-2000

SUBMITTED EXTERNAL SUPPORT

Barkley NA, Ozias-Akins P, Scheffler B. 2012. The Peanut Foundation. Assessing the genomic diversity in the U.S. peanut mini core collection via genotyping by sequencing (GBS).. \$28,500.

UNFUNDED EXTERNAL SUPPORT

Barkley NA, MacDonald GE, Tillman BL, Holbrook CC. 2012. Characterization, evaluation, and regeneration of the US peanut core collection. Southeastern Peanut Research Initiative. \$17,500.

Pittman RN, Barkley NA, Wang ML, Isleib TG. 2009. The effect of mutant and wild type alleles at *ahFAD2* loci controlling the

high oleate trait in peanuts. Southeastern Peanut Research Initiative. \$50,000.

Pittman RN, Wang ML, Barkley NA, Moore KM, Isleib TG. 2012. Genotyping and phenotyping peanut germplasm using real-time PCR and gas chromatography. Peanut Foundation. \$32,000.

PROFESSIONAL ORGANIZATION MEMBERSHIPS

Gamma Sigma Delta, Honor Society for Agriculture
American Peanut Research and Education Society

OUTREACH ACTIVITIES

Member of editorial board for Diversity and BMC Plant Biology journals
Demonstrating molecular techniques to high school teachers 2006-2007
High School Science Fair Judge, Griffin, GA. 2003-2012
Presenter, UC Riverside Citrus Variety Display, Riverside Orange Blossom Festival, 1998–2003

COMMITTEES

Bailey Award 2012, 2013
PGOC plant germplasm patents 2011, 2012
3rd Curator's Workshop 2009, 2010