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CURRICULUM VITAE

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EDUCATION BACKGROUND:

Ph.D. Simon Fraser University, Burnaby, British Columbia Canada 1997
Dissertation: Genetic characterization of the *Caenorhabditis elegans* rol-3(V) and srl-2(III) genes, and their molecular localizations through correlation of the genetic and physical maps.

Bachelors degree: Simon Fraser University, Burnaby, British Columbia, Canada 1990
Major: Biochemistry.
Minors: Organic Chemistry
Molecular and Cell Biology

PROFESSIONAL EXPERIENCE:

UF Department of Biology Graduate Coordinator: August 2013 - present

Associate Professor: August 16, 2011 –

Dept. of Botany and Zoology, University of Florida,
Gainesville FL.

Principal Investigator and lab head – Plant functional, comparative and computational genomics.

Assistant Professor: August 16, 2008 –

Dept. of Botany and Zoology, University of Florida,

Gainesville FL.

Principal Investigator and lab head – Plant functional, comparative and computational genomics.

Assistant Member and Principal Investigator: July 1, 2006 – August 15, 2008

Donald Danforth Plant Science Center

975 N. Warson Rd, St. Louis, MO 63141

Principal Investigator and lab head – Plant functional, comparative and computational genomics.

Senior Bioinformatics Specialist and Assistant Domain Member: Jan 21, 2003 – June 30, 2006

Donald Danforth Plant Science Center

975 N. Warson Rd, St. Louis, MO 63141

Maize genome project management, data analysis, acting lab head.

Senior Bioinformatics Scientist: Jan 1, 2001 – Jan 21, 2003

Monsanto Company, Agricultural Sector/Crop Science, Genomics Technology Division, St. Louis, MO 63167.

High-throughput Arabidopsis Functional Genomics program: Paradigm Validation Lead, Submission Lead, Nomination Co-lead, 06/2002 – 01/2003.

Enterprise Cloning support: 01/2002 – 01/2003.

Crop Genomics: Rice Physical Mapping Lead, Maize Physical Mapping Lead, Comparative analysis of the Rice and Maize genomes, 01/2001 – 01/2002.

Bioinformatics Scientist: Dec 21, 1999 – Dec 31, 2000

Monsanto company, Agricultural sector/Crop Science, Genomics Technology Division, St. Louis, MO 63167.

Crop Genomics: Rice Physical Mapping Lead, Maize Physical Mapping Lead, Comparative analysis of the Rice and Maize genomes.

Post-Doctoral Researcher: May 5, 1997 – Dec 18, 1999

Washington University School of Medicine, Genome Sequencing Center, St. Louis, MO 63108.

Participated in the development and implementation of technology used to construct the human genome map.

Zebrafish Radiation Hybrid Mapping – 12/1998 – 12/1999

Zebrafish Mapping Group Leader and analysis lead.

Physical mapping group leader 09/1999 – 12/1999.
Human Genome Physical mapping team management and data analysis.

Post-Doctoral Researcher: Jan 1, 1997 – May 1, 1997
Simon Fraser University, Burnaby, British Columbia, Canada.

PROFESSIONAL SUMMARY:

Recognized expert in Plant Genomics, Genome Analysis, Bioinformatics, and Computational Biology.

Industry experience in project management.

Eight plus years experience as head of a productive research laboratory – responsible for research direction, securing funding, fiscal management, staffing and training.

I develop and employ computational, comparative and functional genomics approaches to study genome architecture, function and evolution. While I was a post-doc working on the human genome project it became clear to me that the genome era would not only influence the scope and type of questions that would be investigated in biology, it would require a paradigm shift in the way experimentation and data analysis were performed. I work with large and complex plant and animal genomes where we apply computational sequence analysis methods to assemble and annotate large genome and transcriptomes, investigate within species and between species sequence variation, genome structure, gene structure, gene content, gene/genome organization and gene regulation. My research projects involve collecting primary genome annotation data in the form of genome sequences and catalogues of genes, developing methods and tools to leverage next generation sequence capacities, leverage genomic data and approaches to address fundamental evolutionary questions concerning genome evolution, and examining the function and regulation of RNA processing. My laboratory was the first to demonstrate the utility of NGS re-sequencing to identify and validate single nucleotide polymorphism in *Zea mays* (Maize), which enabled construction of high-resolution genetic maps, and pioneered the methodologies adopted by the Maize HapMap consortium. Additionally, my laboratory was instrumental in developing methods to identify and analyze structural variation in maize, pine and poplar; identifying sequence variation in *Brachypodium*, sequencing, assembling and annotating the genome of the basal angiosperm *Amborella tricopodia*, and performing a large scale sequence variation study among populations *Amborella* to investigate its sequence diversity to better understand its population structure and distribution to aid in conservation activities.

Lead the construction of a zebrafish radiation hybrid map (Hukriede et al. 1999 Proc Natl Acad Sci U S A 96: 9745-9750; Hukriede et al. 2001 *Genome Res* 11: 2127-2132) and generated the first whole genome synteny map between human and zebrafish (Barbazuk et al. 2000 *Genome Res* 10: 1351-1358.).

Collaborated on the whole genome physical map of human (McPherson et al. 2001. *Nature* 409: 934-941). Developed a rapid method to generate BACend sequences for map closure and a rapid method to develop hybridization probes to identify gap spanning clones.

Responsible for assembly and analysis of MONSANTO's rice physical map and sequence resource. Collaborated with public sector researcher to integrate the MONSANTO map with the public map to support the public rice genome sequence effort (Chen et al. 2002 *Plant Cell* 14: 537-545.)

Collaborated on the first large scale maize genome sequencing effort – sequenced and characterized the maize gene space (Whitelaw et al. 2003 *Science* 302: 2118-2120; Springer et al. 2004 *Plant Physiol* 136: 3023-3033).

Co-led the first 454 transcriptome sequece project from tissue isolated by laser capture microdissection (Emrich et al. 2007 *Genome Res* 17: 69-73). This project identified novel transcripts from maize shoot apical meristem tissue and demonstrated the utility of high volume, next generation sequence technology to the acquisition of targeted transcriptome reads.

Demonstrated the first use of next-generation sequencing for rapid genetic marker detection in plant genomes (Barbazuk et al. 2007 *Plant J* 51: 910-918.). In addition, this manuscript demonstrated the use of these SNP markers for high-throughput genotyping, illustrating the utility of next generation sequencing for marker assisted breeding, association studies, variation detection and genome diversity studies. The methods in this particular manuscript were the foundation for several high throughput transcriptome analysis and marker identification studies conducted subsequently throughout the plant community.

Co-developed an array based sequence capture method for highly repetitive plant genomes (Fu et al. 2010 *The Plant Journal* 62:898-909).

Co-developed array based comparative genome hybridization (CGH) for examining genome rearrangements and gene gain/loss between inbred lines of maize (Springer et al. 2009 *PLoS Genet* 5: e1000734; Schnable et al. 2009 *Science* 326: 1112-1115.) This study revealed a level of structural diversity between the inbred lines B73 and Mo17 that is unprecedented among higher eukaryotes.

Demonstrated a novel alternative splice isoform of the *TFIIIA* gene that is highly conserved in land plants (Fu et al. 2009. *Genome Research* 2009 19:913-21). This study provides the first evidence of ancient exaptation of 5S rRNA in plants, suggesting a novel gene regulation model mediated by the alternative splicing of an anciently exonized non-coding element.

Developed a genomic assay using next-generation sequence technology to examine gene loss in polyploids (Buggs et al 2010 *Journal of Molecular Ecology*. 19: (Suppl. 1), 132-146). Such activity sheds light on genome stabilization and rearrangements that occur early after the polyploidization event. This study successfully demonstrated a general strategy to enable RNA-Seq and other next-generation sequence based analysis to be conducted in organisms that do not have reference genome sequences available.

Sequenced, assembled, annotated and analyzed the genome of Amborella, a non-model plant that is sister to all flowering plants

TEACHING

A. Courses Offered:

Course Number	Title	Level	Semester Offered
BSC2010	Integrated Principles of Biology I	Lower-division	Spring 09, Spring 10, Spring 11. Taught 1/3 of this course (the genetics section) to 3 concurrent sections.
PCB3063	Mendelian and Molecular Genetics	Upper-division	Fall 2009, Fall 2010, Fall 2011, Fall 2014
PCB7922	PMCB Journal Club	Graduate	Fall 2010, Spring 2015
BOT6935	Special Topics	Graduate	Spring 2012
BSC2930	Phage Genomics	Lower-division	Fall 2012, Spring 2013, Fall 2013, Spring 2014, Spring 2015

B. Invited Teaching:

Participation as a lecturer on bioinformatics and genomics for the St. Louis Community College *Bioinformatics* course (Bio547) 2003-2004.

Participation as a lecture in the Interdepartmental Genetics Workshop (Genet 591) "Genomic Tools and Analysis" graduate course offered by Dr. Patrick Schnable, Iowa State University. 2004

Participation as a lecturer on bioinformatics and genomics for Truman State University (Kirksville, Mo) 2005, 2007.

Designed and presented a workshop titled " Mapping of Short read NGS sequences and Analysis at the University of Hawaii, Hilo, October 26-17, 2012. This workshop was invited through the UH Hilo Fall Bioinformatics Workshop series.

Invited lecturer to the "Frontiers in Genomics" Undergraduate program offered at UNAM, Cuernavaca Mexico. Forum was a 3 hour lecture, followed by oral interviews with students in the program (2 hours). Lecture title: "Investigating plant genome structure and function with computational and comparative genomics.

HONORS, AWARDS, SCHOLARSHIPS AND FELLOWSHIPS:

Medical Research Council of Canada Studentship	1994-1996
Presidents Ph.D. Award	1995
MacMillan-Bloedel IMBB Graduate Fellowship	1994
S F U Graduate Fellowship	1993
MacMillan-Bloedel IMBB Graduate Fellowship	1993
MacMillan-Bloedel IMBB Graduate Fellowship	1992
Hemingway Nelson Architects Graduate Scholarship	1992

S F U Graduate Fellowship
N.I.H. Travel Grant

1991
06/1991, 06/1993, 06/1995

GRANT SUPPORT: (Participation as PI/Co-PI in over \$15M in federal agency awards (2003 – present))

AWARDED

Current:

PI:Kirst, **Co-PI: Barbazuk**. Genome and Transcriptome based prediction, and regular inference, of molecular and whole plant phenotypes. NSF-PGRP \$1,956,424
03/15/2015 – 02/28/19

PI: Lal, **Co-PI: Barbazuk**. Genetic, molecular, and biochemical dissection of RNA splicing factors critical for maize endosperm development. NSF. \$800,000;
08/01/2014 – 07/31/2017

PI: Settles, **Co-PI Barbazuk**, McDaniels. Efficient structure-function analysis of proteins required to control cell proliferation University of Florida –Research Opportunity Fund, \$85,000, 07/01/2014 – 06/30/2016

Maden and **Barbazuk - Co-investigators**. The transformative potential of the regenerating spiny mouse. The W. M. Keck Foundation. \$1,000,000; 01/01/2014 – 12/31/2016

PI: Soltis, **Co-PI: Barbazuk**, Schnable, Soltis. Genomic consequences of recent and ancient allopolyploid: a continuum of ages in *Tragopogon* (Asteraceae). NSF \$393,609 01/01/12-05/31/15,

Cohn & **Barbazuk – Co-Investigators**, U01DK094523-01 PI: " A GenitoUrinary Development Molecular Anatomy Project (GUDMAP). National Institutes of health. \$1,803,990; 12/01/11 – 11/30/2016.

PI: Settles, **Co-PI Barbazuk**, Analysis of imprinted genes with developmental functions in the maize seed. Agency: National Institute for Food and Agriculture; \$497,725 (UF-total); 09/01/2010 – 08/31/2014 – on NCE

PI: de Pamphilus, **Co-PI Barbazuk**, Soltis, Soltis, Leebens-Mack, Rounsley, Albert TRPGR: The Amborella Genome: An evolutionary reference for plant biology, NSF Plant genome research Program, \$8,179,788, 04/1/10 – 31/12/15

Previous:

PI: Chen, **Co-PI Barbazuk**, Soltis, Soltis and McIntyre. "Proteomic Analysis of Plant Polyploidy" University of Florida –Research Opportunity Fund, \$99,392,
05/01/2011 – 04/30/2014

PI: Barbazuk (equally shared with McIntyre, Riva, Settles and Swanson). Understanding alternative RNA processing with computational methods. UF Seed Grant Proposal for Interdisciplinary Working Groups in Computational Biology, \$155,829, 09/01/2010 – 02/28/2014,

PI: Barbazuk, Co-PI: Brent, Giovanonni, Mueller. “Developing an Accurate Program to Identify Potential Genes in Tomato Genome Sequence”. USDA-NRI, \$398,000 09/01/08 – 08/31/12

PI: Davis, **Co-PI Barbazuk**, Burleigh, Soltis. The enormous genome challenge: how and why did gymnosperms acquire so much DNA?, University of Florida –Research Opportunity Fund, \$98,800, 05/01/2009 – 04/30/2012

PI: Soltis, **Co-PI Barbazuk**, Schnable Soltis. Genome evolution in natural populations and synthetic lines of allopolyploids in *Tragopogon* (Asteraceae), NSF Plant Genome Project \$389,794 07/01/09-11/01/11

PI: Schachtman, Co-PI: Barbazuk, Jackson. “A genomic and physiology approach to understanding the impact of mycorrhizal fungal colonization on root metabolism and nutrient acquisition from nutrient patches.” NSF, \$985,238 09/01/07 – 08/31/10

PI: Barbazuk, Co-PI: Brent. “Ab initio gene prediction in maize.” NSF-PGRP-0501758 \$720,968 08/01/05 – 01/01/09.

PI: Schubert, **Co-PI: Barbazuk**, Bennetzen, Quackenbush. “Consortium for maize genomics.” NSF-PGRP-0221536; \$5,928,755 09/01/02 –12/31/05

PI: Goldman, **Co-PI: Barbazuk**, Forst, Goodner, Goodrich-Blair. “Microbial Genome sequencing: Complete Sequence of two entomopathogenic *Xenorhabdus sp.*” USDA 2004-03560-14181; \$499,827 12/01/03 –11/30/06

SERVICE ACTIVITIES (PROFESSIONAL):

A. Grant Reviews

Member: USDA-NRI Plant genome competition panel – 2006 (12 proposals handled)

Ad Hoc reviewer:

2003 NSF-Plant Genome (1)

2004 USDA-NRI (1)

(2005) USDA-NRI (1)

(2008) USDA-NRI (1)

2009 NSF GGS (1)

2010 NSF 2010 program (1)

Site visit teams:

Chairman of the NSF site visit team for National Science Foundation Plant Genome Research Program – Proposal Number 0321467 “Molecular and Functional Diversity in the Maize genome”, June 4-6, 2003.

Chairman of the NSF site visit team for National Science Foundation Plant Genome Research Program – Proposal Number 0321467 “Leveraging untapped genetic diversity in Soybean”, October, 2008.

Member of the on-site progress review team for the DOE Bioenergy Research Center at Madison WI. – 2008

Member of the on-site progress review team for the DOE Bioenergy Research Center at Oakridge TN. - 2011

B. Editorial Service

Member of the Editorial Board for the journal "Genome Research" 2005-2008.

Review Editor for the Journal: Frontiers in Plant Genetics and Genomics

C. Journal Reviews:

Ad hoc reviewer for (2001–2011): "American Journal of Botany", "Annals of Botany", "Bioinformatics", "Biotechniques", "BMC Bioinformatics", "BMC Biology", "BMC Genomics", "BMC Plant Biology", "Briefings in Functional Genomics and Proteomics", "Chemical Reviews", "Frontiers of Science", "Genome Research", "Genomics", "Nature Methods", "New Phytologist", "Nucleic Acids Research", "Planta", "Plant Molecular Biology", "Plant Physiology", "Plant Science", "Proceedings of the National Academy of Science", "Rice", "The Journal of Experimental Botany", "The Plant Cell", "Tropical Plant Biology".

D. Committee Seats:

Member of External Advisory Committee for the Missouri Maize Mapping Project (PI: Ed Coe), 2001 – 2003.

Member of a scientific team consisting of representatives of the Syngenta Foundation, ILRI, ICRASAT and US research institutions to advise on the activities of the 'Biosciences East and Central Africa' (BECA) research institution. 2004 – 2006.

Member of the Advisory Board for the University Of Missouri, St. Louis Super Computer center (2007-2008).

Member of the Scientific Advisory Board for NSF-PGRP Project 0321467 "Leveraging untapped genetic diversity in Soybean" PI-Scott Jackson, University of Georgia (2010-2014).

Member of the Scientific Advisory Board for Genome Canada Project "Genomics of Sunflower" PI-Loren Rieseberg, University of British Columbia (2009-2013).

Consultant to the SAB of the Forestry Health Initiative funded project: "Conservation Genomics: Genome sequence of the American Black Chestnut" (Feb. 2010).

E. Consulting

The Monsanto Company, September 2007 – 2008.

SERVICE ACTIVITIES (COLLEGE, DEPARTMENT, AND UNIVERSITY):

Donald Danforth Plant Science Center Seminar Committee (2007-2008).

Chair of Florida Genetics Institute high performance computing committee – representative of the College of Liberal Arts and Science (2008 – present).

Member of the Plant Molecular and Cellular Biology (PMCB) curriculum committee (2009).

University of Florida Department of Biology Graduate Admission Committee (2009, 2010,2011,2012,2013,2014,2015)

Member of the UF Computational Biology Committee. 2011- present.

Chair of the Genetics Institute high performance computing committee.

May 2012 – present.

Member of the Genetics Institute Executive committee. June 2012 – present.

Member of the UF “Initiative on Dense, Intense, and Complex Data” working group

Chaired by David Norton, VP of research. Feb 2012 – present.

Member of the UF CLAS pre-eminence hiring committee 2013 – 2105

Graduate Coordinator (UF-Biology). August 2013 –

Member of the UF Biology advisory council. August 2013 –

Member of the University of Florida Informatics Institute Steering Committee. November 2013 –

Member of the UG Genetics Institute Statagic Planning Committee. December 2014 –

PUBLICATION RECORD:

Refereed Manuscripts (Published, 69 Total):

Chamala, S., Feng, G., Chavarro, C., **Barbazuk, W.B.** 2015. Genome-wide Identification of evolutionarily conserved alternative splicing events in flowering plants. *Frontiers in Bioengineering and Biotechnology*. 2015 3:33. doi: 10.3389/fbioe.2015.00033.

Chamala, S., García, N., Godden, G. T., Krishnakumar, V., Jordon-Thaden, I. E., De Smet, R., Barbazuk, W. B., Soltis, D. E., Soltis, P. S. 2015. MarkerMiner 1.0: A new application for phylogenetic marker development using angiosperm transcriptomes. *Applications in Plant Sciences*. 3(4). pii: apps.1400115. doi: 10.3732/apps.1400115.

Pope, W. H., Bowman, C. A., Russell, D.A., Jacobs-Sera, D., Asai, D. J., Cresawn, S. G., Jacobs, W. R., Hendrix, R. W., Lawrence, J. G., Hatfull, G. F., Science Education Alliance Phage Hunters Advancing Genomics and Evolutionary Science; Phage Hunters Integrating Research and Education; Mycobacterial Genetics Course. 2015. Whole genome comparison of a large collection of mycobacteriophages reveals a continuum of phage genetic diversity. *Elife*. 2015 Apr 28;4. doi: 10.7554/eLife.06416.

Pillon, Y., Johansen, J., Sakishima, T., Chamala, S., **Barbazuk, W.B.** and Stacy E. A. 2014. Primers for low-copy number nuclear genes in *Metrosideros* and cross-amplification in Myrtaceae. *Applications in Plant Sciences*. 2(10). pii: apps.1400049. doi: 10.3732/apps.1400049.

Xiong, Y., Mei W., Kim E. D., Mukherjee K., Hassanein H., Barbazuk W. B., Sung S., Kolaczowski B. and Kang B. H. 2014 Adaptive expansion of the maize maternally expressed gene (Meg) family involves changes in expression patterns and protein secondary structures of its members. *BMC Plant Biol*. 14:204.

Corrales J., Fang X., Thornton C., Mei W., Barbazuk W. B., Duke M., Scheffler B. E.,

Willett K. L. 2014 Effects on specific promoter DNA methylation in zebrafish embryos and larvae following benzo[a]pyrene exposure. **Comp Biochem Physiol C Toxicol Pharmacol**. pii:S15320456(14)000155.doi:10.1016/

Neves, L. G., Davis, J. M., **Barbazuk, W. B***, and Kirst M*. 2014 A High-Density Gene map of loblolly pine (*Pinus taeda* L.) based on Exome Sequence Capture Genotyping. **G3: GENES, GENOMES, GENETICS** 4:29-37

*Corresponding authors

Chamala S., Chanderbali A. S., Der J. P., Lan T., Walts B., Albert V. A., dePamphilis C. W., Leebens-Mack J., Rounsley S., Schuster S. C., Wing R. A., Xiao N., Moore R., Soltis P. S., Soltis D. E. and **Barbazuk W. B.** 2013 Assembly and validation of the genome of the nonmodel basal angiosperm Amborella. **Science**. 342:1516-7

Amborella Genome Project. 2013 The Amborella genome and the evolution of flowering plants. **Science**. 342:1241089. doi: 10.1126/science.1241089.

Clancy M. A., Rosli H. G., Chamala S., **Barbazuk W. B.**, Civello P. M. and Folta K. M. 2013 Validation of reference transcripts in strawberry (*Fragaria* spp.). **Mol Genet Genomics** 288:671-81

Soltis, D. E., Gitzendanner, M. A., Stull, G., Chester, M., Chanderbali, A., Chamala, S., Jordon-Thaden, I., Soltis, P. S., Schnable, P. S. and **Barbazuk W. B.** 2013. The potential of genomics and plant systematics. **Taxon** 62:886-898

Pillon, Y., Johansen, J., Sakishima, T., Chamala, S., **Barbazuk, W.B.** and Stacy E. A. 2013. Primers for low-copy number nuclear genes in the Hawaiian endemic *Clermontia* (Campanulaceae) and cross-amplification in Lobelioideae. **Applications in Plant Sciences**. 1(6):1200450

Neves, L. G., Davis, J. M., **Barbazuk, W. B.*** and Kirst M*. 2013 Whole-exome targeted sequencing of the uncharacterized pine genome. **The Plant Journal** 75:146-156

*Corresponding authors

Pillon, Y., Johansen, J., Sakishima, T., Chamala, S., **Barbazuk, W.B.**, Roalson, E. H. and Stacy E. A. 2013. Potential use of low-copy nuclear genes in DNA barcoding: a comparison with plastid genes in two Hawaiian plant radiations. **BMC Evol Biol**. 13:35.

- Chambers, A., Carle, S., Njuguna, W., Chamala, S., Bassil, N., Whitaker, V. M., Barbazuk, W. B., and Folta, K. M. 2013. A Genome-Enabled, High-Throughput, and Multiplexed Fingerprinting Platform for Strawberry (*Fragaria L.*) ***Molecular Breeding*** 31:615-629
- Ruzicka, D., Chamala, S., Barrios-Masias F. H., Martin, F., Smith, S., Jackson, L. E., **Barbazuk, W. B***, and Schachtman D. P. 2012. Inside arbuscular mycorrhizal roots – Molecular probes to understand the symbiosis. ***The Plant Genome*** 6:1-13
*Corresponding author
- Tomato Genome Consortium. 2012 The tomato genome sequence provides insights into fleshy fruit evolution. ***Nature*** 485:635-41
- Buggs, R. J., Renny-Byfield, S., Chester, M., Jordon-Thaden, I. E., Viccini, L. F., Chamala, S., Leitch, A. R., Schnable, P. S., **Barbazuk, W. B.**, Soltis, P. S. and Soltis D. E. 2012. Next-generation sequencing and genome evolution in allopolyploids. ***Am J Bot.*** 99:372-82.
- Buggs, R. J., Chamala, S., Wu, W., Tate, J. A., Schnable, P. S., Soltis, D. E., Soltis, P. S. and **Barbazuk, W. B.** 2012. Rapid, repeated, and clustered loss of duplicate genes in allopolyploid plant populations of independent origin. ***Curr Biol.*** 22:248-52.
- Burleigh, J. G., **Barbazuk, W. B.**, Davis, J. M., Morse, A. M. and Pamela S. Soltis, 2012. Exploring Diversification and Genome Size Evolution in Extant Gymnosperms through Phylogenetic Synthesis. ***Journal of Botany***, vol. 2012, Article ID 292857, doi:10.1155/2012/292857
- Chaston, J. M., Suen, G., Tucker, S. L., Andersen, A. W., Bhasin, A., Bode, E., Bode, H. B., Brachmann, A. O., Cowles, C. E., Cowles, K. N., Darby, C., de Léon, L., Drace, K., Du, Z., Givaudan, A., Herbert Tran, E. E., Jewell, K. A., Knack, J.J., Krasomil-Osterfeld, K. C., Kukor, R., Lanois, A., Latreille, P., Leimgruber, N. K., Lipke, C. M., Liu, R., Lu, X., Martens, E. C., Marri, P. R., Médigue, C., Menard, M. L., Miller, N. M., Morales-Soto, N., Norton, S., Ogier, J. C., Orchard, S.S, Park, D., Park, Y., Qurollo, B. A., Sugar, D. R., Richards, G. R., Rouy, Z., Slominski, B., Slominski, K., Snyder, H., Tjaden, B. C., van der Hoeven, R., Welch, R. D., Wheeler, C., Xiang, B., **Barbazuk, B.**, Gaudriault, S., Goodner, B., Slater, S. C., Forst, S., Goldman, B. S. and Goodrich-Blair, H. 2011. The entomopathogenic bacterial endosymbionts *Xenorhabdus* and *Photorhabdus*: convergent lifestyles from divergent genomes. ***PLoS One.*** 6:e27909.
- Zuccolo, A., Bowers, J. E., Estill, J. E., Xiong, Z., Luo, M., Sebastian, A., Goicoechea, J. L., Collura, K., Yu, Y., Jiao, Y., Duarte, J., Tang, H., Rounsley, S., Kudrna, D., ¹, Paterson, A. H., Pires, J. C., Soltis, D. E., Chamala, S., **Barbazuk,**

- W. B., Soltis, P. S., Albert, V. A., Ma, H., Mandoli, D., Banks, J., Carlson, J., Tomkins, J., dePamphilis, C., Wing, R. A. and Leebens-Mack, J. 2011 A Physical Map for the *Amborella* Genome Sheds Light on the Evolution of Angiosperm Genome Structure BMC Genomics. **Genome Biology** 12:R48
- Buggs, R. J. A., Zhang, L., Miles, N., Tate, J. A., Gao, Lu., Wu, W., Schnable P. S., **Barbazuk, W. B.**, Soltis, P. S. and Soltis D. E., 2011 Transcriptomic Shock Generates Evolutionary Novelty in a Newly Formed, Natural Allopolyploid Plant. **Current Biology** 21:551-6
- Schmidt, M., **Barbazuk, W. B.**, Sandford, M., May, G. D., Song, Z., Zhou, W., Nikolau, B. J. and Herman, E. M. 2011 Silencing of soybean seed storage proteins results in a rebalanced protein composition preserving seed protein content without major collateral changes in the metabolome and transcriptome. **Plant Physiol.** 156:330-45
- Fu, Y., Springer, N. M., Ying, K., Yeh, C. T., Iniguez, A. L., Richmond, T., Wu, W., **Barbazuk, B.**, Nettleton, D., Jeddelloh, J., and Schnable, P. S. 2011 High-resolution genotyping via whole genome hybridizations to microarrays containing long oligonucleotide probes. **PLoS One.** 5:e14178.
- Folta, K. M., Chamala, S., **Barbazuk, W. B.**, Brunings, A. M., Rosli, H., Pombo, M. and Civello, M. 2010. Tissue and Developmental Transcriptome Differences in Strawberry Revealed with Next-Generation Sequencing. **Hortscience** 45:S6-S7
- Barbazuk W. B.**, 2010 A conserved alternative splicing event in plants reveals an ancient exonization of 5S rRNA that regulates TFIIIA. **RNA Biol.** 7:397-402.
- Folta, K. M., Clancy, M. A., Chamala, S., Dhingra, A., Brunings, A. M., Gomide, L., Kulathinal, R. J., Peres, N., Davis, T. M. and **Barbazuk, W. B.** 2010. A Transcript Accounting from Diverse Tissues of a Cultivated Strawberry (*Fragaria xananassa*). **The Plant Genome** 3: 90-105
- Ordiz, M. I., Yang, J., **Barbazuk, W. B.** and Beachy, R. N. 2010. Functional analysis of The activation domain of RF2a, a rice transcription factor. **Plant Biotechnology Journal** 8: 835-844
- Buggs, R. J. A., Chamala, S., Wu, W., Gao, L., May, G. D., Schnable, P. S., Soltis, D. E., Soltis, P. S., and **W. Brad Barbazuk.** 2010. Characterization of duplicate gene evolution in the recent natural allopolyploid *Tragopogon miscellus* by next-generation sequencing and Sequenom iPLEX MassARRAY genotyping. **Journal of Molecular Ecology.** 19: (Suppl. 1), 132-146
- Marsh E, Alvarez S, Hicks L.M., **Barbazuk W.B.**, Qiu W, Kovacs L, Schachtman D. 2010 Changes in protein abundance during powdery mildew infection of leaf

tissues of Cabernet Sauvignon grapevine (*Vitis vinifera* L.). *Proteomics* 10:2057-2064.

Fu, Y., Springer, N. M., Gerhardt, D. J., Ying, K., Yeh, C., Wu, W.,¹ Swanson-Wagner, R. A., D'Ascenzo, M., Millard, T., Freeberg, L., Ayoyama, N., Kitzman, J., Burgess, D., Richmond, T., Albert, T. J., **Barbazuk, W. B.**, Jeddelloh, J. A., and Patrick S. Schnable. 2010. Repeat subtraction-mediated sequence capture from a complex genome. *The Plant Journal* 62:898-909

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Book Chapters:

W. Brad Barbazuk and Wenbin Mei Chapter 8 “Genome Sequencing: Past and Present” in **Compendium of Bioenergy Plants: Corn**. Stephen L. Goldman ed. CRC Press

W. Brad. Barbazuk and Patrick S. Schnable. 2011. SNP discovery by transcriptome pyrosequencing. In “**cDNA libraries: methods and applications**”. (Chaofu Lu Ed.) Humana Press

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Patrick S. Schnable, An-Ping Hsia, Ling Guo, **W. Brad Barbazuk**. 2008 Molecular Markers. In “**Molecular Genetic Approaches to Maize Improvement**” (Alan Kriz and Brian Larkins eds.) Springer-Verlag

W. Brad Barbazuk, An-Ping Hsia, Hsin D. Chen, Yan Fu, Kazuhiro Ohtsu and Patrick S. Schnable. 2007 High Throughput Molecular Genetic Maps and SNP discovery in maize. In “**Genetic Variation: A Laboratory Manual**”, CSHL press.

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Published Abstracts:

Neves, L., Davis, J., **Barbazuk, B.** and Kirst, M. (2011) Targeted sequencing in the loblolly pine (*Pinus taeda*) megagenome by exome capture. **BMC Proceedings** 5(Suppl 7):048

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Manuscripts in press or submitted for publication

Gault, C. M., Martin, F., Mei, W., Black, J. B., **Barbazuk, W. B.**, Settles, A. M. Mark Settles. 2015 Aberrant U12-type intron splicing due to the hypomorphic *rough endosperm3* splicing factor locus. *Submitted to **Nature Plant***.

Professional Presentations:

A. Invited Presentations:

2014 Illinois Wesleyan University, Department of Biology, Bloomington Illinois
"Characterization and conservation of alternative mRNA splicing events in plants." Host Dr. David Bollivar, Chair of Department of Biology.

2014 Florida Genetics Symposia, University of Florida "The *Amborella* Genome Sequence: A reference for the evolution of flowering plants".

2014 Nantong University, Department of Biology, Nantong, China "Comparative genomics to identify conserved Alternative Splicing across plant lineages; examining the relationship between Alternative Splicing and Whole Genome Duplication. Host Dr. Ping Li

2014 China Academy of Agricultural Sciences, Beijing, China "Investigating the extent, function and evolution of Alternative Splicing in Plants" Host Dr. Yunbi Xu

2013 Frontiers in Genomics, UNAM, Cuernavaca Mexico "Investigating plant genome structure and function with computational and comparative genomics

2013 Frontiers in Genomics, UNAM, Cuernavaca Mexico. "Using Next Generation Sequence and Comparative Genomics to investigate Alternative Splicing in Plants"

- 2013 Plant Genomics Congress, St. Louis MO. “A survey of alternative splicing in maize.”
- 2012 DOW AgroChemical, Indianapolis, Indiana “NGS: making models out of non-model species.”
- 2010 Alternative Splicing Workshop at the 18th annual Plant and Animal genome meeting, January 8-13, 2010 San Diego, CA. U.S.A. “Comparative sequence analysis in plants reveals an alternatively spliced exon that regulates Plant Transcription Factor TFIIIA”.
- 2009 Florida Genetics Symposia, University of Florida “A conserved alternative splicing event in plants reveals an ancient exonization of 5sRNA”.
- 2009 Cancer and Genetics Research Center, University of Florida. “Comparative sequence analysis in plants reveals an alternatively spliced exon that regulates Plant Transcription Factor TFIIIA”.
- 2009 Dept. of Agronomy, Purdue University, West Lafayette IN. “Comparative sequence analysis in plants reveals an alternatively spliced exon that regulates Plant Transcription Factor TFIIIA”. Host Dr. Scott Jackson.
- 2008 Dept. of Plant Genetics & Breeding, China Agricultural University, Beijing, China “Finding genes in maize: Identifying transcription units, training gene finders and investigating alternative splicing.” Host: Dr. Zhiyong Liu
- 2008 Chinese Academy of Agricultural Sciences, Beijing, China “Sequencing transcripts with 454: applications in large scale gene discovery, annotation and polymorphism identification.” Host: Dr. Guoying Wang
- 2007 University of Georgia “Maize transcriptome sequencing with 454: applications in large scale gene discovery, annotation and polymorphism identification.” Host: Dr. Jeff Bennetzen.
- 2007 University of Illinois at Urbana-Champaign “Maize transcriptome sequencing with 454– applications for large scale gene discovery, annotation and polymorphism identification.” Host: Dr. Torbert Rocheford
- 2007 University Florida “Maize transcriptome sequencing with 454– applications for large scale gene discovery, annotation and polymorphism identification.” Host: Dr. Doug Soltis
- 2007 Roche Applied Science and 454 Workshop at the 15th annual Plant and Animal genome meeting, January 14-18, 2004 San Diego, CA. U.S.A. Topic: Maize transcriptome sequencing with 454: applications in large scale gene discovery, annotation and polymorphism identification.
- 2006 University of Missouri, Columbia “Maize transcriptome sequencing with 454– applications for large scale gene discovery, annotation and polymorphism identification.” Host: Dr. Dong Xu
- 2006 GDEST India Workshop - Agricultural Biotechnology for the Global Public Good (Oct 3-6), Chennai India. “Comparative analysis and genome tool development in maize “Host: National Academy of Agricultural Sciences of India and the U.S. National Academies.
- 2006 Agriculture Biotechnology: The Next Generation, Sept 29, Science Museum of Minnesota, St. Paul MN. – “What cracking the corn genome means for farmers and consumers.” Host: Minnesota Agri-Growth Council, BioteCanada, the University of Minnesota, and the Office of the Canadian Consulate General

- 2006 Ceres Inc., Thousand Oaks, CA “Maize transcriptome sequencing with 454 – applications for large scale gene discovery, annotation and polymorphism identification.” Host: Dr. *Richard Schneeberger*
- 2006 Washington University, St. Louis MO. “Computational methods for gene discovery and comparative genomic analysis in maize.” Host: Dr. Erik Richards.
- 2005 Tuman State University, Kirksville, MO. “Progress Towards an Effective Large Scale Whole Sequencing Strategy for the Maize Genome.” Host: Dr. Jason Miller and Dr. Jon Beck.
- 2005 University of Arizona, BIO5, Tucson, AZ. “Identifying an effective large scale sequencing strategy for the maize genome.” Host: Dr. Vicki Chandler.
- 2005 Cornell University, Institute of Genomic Diversity, Ithaca NY. “Consortium for Maize Genomics – Identifying an effective large scale whole GENOME sequencing strategy for maize.” Host: Dr. Stephen Kresovich.
- 2005 Second sorghum/millet annotation and improvement workshop, Nairobi, Kenya. “Gene annotation and identification for transgenic and marker selected breeding programs.”
- 2004 The Syngenta Foundation’s Cereal Annotation and Improvement Workshop, University of Arizona, Tucson, AZ. “Leveraging a sorghum sequence resource.”
- 2004 TechConnect2004, St. Louis Science Center, St. Louis MO. “InSilico Biology: merging IT with biology to drive discovery.”
- 2004 Simon Fraser University, Burnaby, BC, Canada. “Exploring the gene space of *Zea mays* by sequencing reduced representation clones.” Host: Dr. Bruce Brandhorst.
- 2004 University of British Columbia, Vancouver, BC. Canada. Topic: “Getting to the good stuff... an investigation of gene recovery and biases observed in two reduced representation sequencing techniques when applied to the genome of *Zea mays*.” Host: Dr. Francis Oullette.
- 2004 Iowa State University, Ames, Iowa. Topic: “Getting to the good stuff”... an investigation of gene recovery and biases observed in two reduced representation sequencing techniques when applied to the genome of *Zea mays*.” Host: Dr. Pat Schnable
- 2004 Keystone Symposia on Comparative Plant Genomics, Taos, New Mexico “Maize Gene Recovery and Coverage from a Reduced Representation Sequencing approach.”
- 2004 University of British Columbia, Vancouver, BC. Canada. Topic: “Getting to the good stuff... an investigation of gene recovery and biases observed in two reduced representation sequencing techniques when applied to the genome of *Zea mays*.” Host: Dr. Francis Oullette.
- 2003 The Plant Molecular Genetics Institute and the Center for Microbial and Plant Genomics, University of Minnesota. Topic: “Progress on the evaluation of gene-enrichment strategies for sequencing the maize genome.” Host : Dr. Ronald Phillips.
- 2003 6th Annual Awardee Meeting of the National Science Foundation’s Plant genome Research Program. Topic: “How well are gene enrichment strategies working?”
- 2001 International Rice Genome Sequencing Project Interim meeting, TIGR. Topic: Draft rice genome sequence and physical map update. Topic: “Integration of the

- Monsanto and CUGI physical maps. The Monsanto rice genome resource." Host: Dr. Takuji Sasaki/ Dr. Ben Burr.
- 2000 International Rice Genome Sequencing Project Interim meeting, Clemson University. Topic: The Monsanto rice genome resource." Host: Dr. Takuji Sasaki/ Dr. Ben Burr.
- 1998 University of British Columbia, Vancouver, BC. Canada. Topic: "A physical map of human chromosome 7." Host: Dr. David Baillie.

B. Contributed Presentations:

- 2007 Advances in Genome Biology and Technology Meeting, February 6-9, Marco island FL. U.S.A. Brad Barbazuk, □ "Maize Transcriptome Sequencing with 454: Applications in Gene Discovery, Annotation and Polymorphism Identification"
- 2006 48th annual maize genetic conference, Pacific Grove Ca. Mar. 9 -12, "Maize gene discovery and annotation using 454 transcriptome sequencing."
- 2005 Cold Spring Harbor Laboratory Conference on Genome Informatics, CSHL, Long Island NY, Oct 28 – Nov 1, Reduced representation sequencing in maize.
- 2004 46th Annual Maize genetics Conference, March 11-14, Mexico City, Mexico "Consortium for Maize Genomics – An examination of maize gene coverage obtained from shotgun sequences derived from methyl-filtered and High Cot selection libraries.
- 2004 Advances in Genome Biology and Technology Meeting, February 4-7, Marco island FL. "Consortium for Maize Genomics - evaluation of methods for targeted sequencing of maize genes."
- 2004 12th annual Plant and Animal genome meeting, January 10-14, 2004 San Diego, CA. "Consortium for Maize Genomics – An examination of maize gene coverage obtained from shotgun sequences derived from methyl-filtered and High Cot selection libraries.
- 2003 2nd European plant genome / 4th Genomic Arabidopsis resource network meeting, Sept. 3 – 6, York University, York, UK. "Consortium for Maize Genomics - evaluation of methods for targeted sequencing of maize genes."
- 2003 45th Annual Maize genetics Conference, March 6-9, "The Maize Genome Sequencing Project at the Donald Danforth Plant Science Center."
- 1999 9th International Beyond the identification of transcribed sequences workshop: Functional and Expression Analysis. Oct 28-31, Reston, VA. "Construction of a whole genome transcribed sequence map for the zebrafish *Danio rerio*."
- 1998 Genome Mapping, Sequencing and Biology Meeting May 13-17, CSHL, Long Island, NY. "Closing gaps in the Chromosome 7 sequence-ready map."
- 1996 West Coast *C. elegans* meeting. July 25-28, 1996, U.B.C. Vancouver, B. C. Canada. "Molecular localization of rol-3(V) and srl-2(III) through correlation of the genetic and physical maps."
- 1993 Northwest Regional Developmental Biology Conference, May 6-8, 1993, U.B.C. Vancouver, B. C. Canada. "The Isolation and Genetic Characterization of srl-Suppressor of Roller Lethal."
- 1992 West Coast *C. elegans* meeting. June 5–7, 1992, Berkeley, CA. A Genetic

Characterization of rol-3, and Suppressors of rol-3 lethal alleles.”

POSTDOCTORAL ASSOCIATES SUPERVISED:

Xiequn (Tony) Xu, 08/03 – 11/04; Currently with Invitrogen Corporation, San Diego CA.

Yucheng Feng 09/03 – 06/05; Currently with Washington University at St. Louis
Genome Center.

Yan Fu, 09/05 – 05/08; Currently with the Monsanto Company, St. Louis MO

Hao Peng, 05/07 – 12/07; Currently a Postdoc in the Department of Crop and Soil
Sciences, Washington State University.

Xiaoguo Zhang 01/09-01/10 UF

Rob Kulathinal, 01/09 – 12/09; Currently tenure track faculty in the Department of
Biology, Temple University, Philadelphia PA.

Stela Palli 05/2014 –

Jason Brant-Orr 04/2014 -

GRADUATE STUDENTS ADVISED:

As Supervisor:

Leandro Gomide, 2009 – 2013 (PhD granted Summer 2013). University of Florida Plant
Molecular and Cellular Biology Program. (Research: Sequence capture and
association genetics in poplar to identify genes that are the basis for variation in
biomass and bio-fuel related productivity traits.) (PhD granted December 2013)

Shaojun Tang, 2009 – 2012 (PhD granted Fall 2012). University of Florida Genetics
Institute. (Research: development of novel algorithms for identifying and
quantifying expression of alternative splice variants and from next generation
sequence).

Christy Gault, 2010 – 2014 (PhD granted Summer 2014). University of Florida Plant
Molecular and Cellular Biology Program. (Research: Expression analysis and
molecular function of the maize U2AF³⁵ homologue, which is associated with the
minor U12 spliceosome)

Srikar Chamala, 2010 – 2014 (PhD granted Summer 2014). University of Florida
Department of Biology. (Assembly, annotation and structural analysis of the
Amborella genome).

Wenbin Mei, 2010 – Present. PhD candidate University of Florida Department of
Biology. (Analysis of alternative splicing in *Zea mays*).

Xiaoxian Liu, 2011 – Present. PhD candidate University of Florida Department of
Biology. (Analysis of alternative splicing in polyploid *Tragopogon*).

Jon Lucas Boatwright, 2013 – Present. PhD candidate University of Florida Department
of Biology. (Analysis of gene loss and gene expression in polyploid *Tragopogon*).

Nathan Catlin 2014 – Present. University of Florida Department of Biology.
(Characterization and Evolution of Alternative splicing in the genus *Oryza*)
Guanqiao Feng 2014 – Present University of Florida Plant Molecular and Cellular
Biology Program. (The Evolutionary history of the *MYB* transcription factor family
of proteins in Plants).

As Graduate Committee Member:

Yijie Yang, 2008 – 2013. PhD Candidate: University of Florida Genetics Institute.
Oscar Tarazona, 2010 – Present. PhD candidate: University of Florida Department of
Biology.
Jennifer Fernandez, 2011 – 2012. MSc candidate: University of Florida Department
of Biology.
Marianne Goodwin, 2011 – 2014. PhD Candidate: University of Florida Genetics
Institute.
Justin Fear 2012 – 2014. PhD Candidate: University of Florida Genetics Institute.
Jessica Sabo 2012 – 2013. PhD candidate: University of Florida Department
of Biology.
Marcio Resende 2012 – 2014. PhD Candidate: University of Florida Genetics
Institute.
Annette Fahrenkrop 2012 – Present. PhD Candidate: University of Florida Plant and
Molecular Cell Biology Program.
Heather Rose Kates 2012– Present. PhD candidate: University of Florida Department
of Biology.
Clayton Visger 2013 – Present. PhD candidate: University of Florida Department
of Biology.
Blaine Marchant 2013 – Present. PhD candidate: University of Florida Department
of Biology.
George Tiley 2013 – Present. PhD candidate: University of Florida Department
of Biology.
Justyna Resztak 2014 – Present. PhD Candidate: University of Florida Genetics and
Genomics program.
Peng Liu 2014 – Present. PhD candidate: University of Florida Plant and
Molecular Cell Biology Program.

UNDERGRADUATE STUDENTS SUPERVISED:

Donald Danforth Plant Science Center: Josif Neitzke, Kim Morrell, Maxim
Schillebeeckx, Matt Turnure, James Schnable

University of Florida: Shane Mooney, Nicole Stanford, Michael Sanchez. Tales
Sideronio (HHMI Science for Life Award)