

SRIKAR CHAMALA

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EDUCATION

DOCTOR OF PHILOSOPHY (PH.D)

AUG 2011 - AUG 2014

Department of Biology, University of Florida (UF), Gainesville, FL.

MASTER OF SCIENCE IN BIOINFORMATICS

AUG 2007 - OCT 2008

Department of Computer Science, University of Illinois at Urbana-Champaign (UIUC), IL.

BACHELOR OF SCIENCE WITH HONORS IN BIOINFORMATICS

JAN 2005 - DEC 2006

Department of Integrative Biology, Brigham Young University (BYU), Provo, UT.

RESEARCH SKILLS & EXPERTISE

Alternative Splicing | Chip-seq | Comparative Genomics | Copy Number Variations | Data Mining | e-QTL | Haplotyping | Genome Sequencing | Genome Annotation | Genome and Gene Evolution | Genome Methylation | Gene Expression Analyses | Genotyping | Microarray Analysis | Polyploidy Evolution | RNA-seq Analyses | Software Programming | Statistical Data Analysis | Transcriptomics | Variant Calling | Whole Genome Duplication

PEER-REVIEWED PUBLICATIONS

† Indicates equal contributions

Citations: 1600+

- [19] Patel, V., Wilkinson, E. J., Chamala, S., Lu, X., Costagno, J., and Rush D. (2016). Endometrial thickness as measured by transvaginal ultrasound and the corresponding histopathologic diagnosis in women with postmenopausal bleeding. *International Journal of Gynecological Pathology*.
- [18] Alam, S. G., Zhang, Q., Prasad, G., Li, Yuan., Chamala, S., Kuchibhotla, R., Birendra, K.C., Aggarwal, V., Shrestha, S., Jones, A., Levy S., Roux, K., Nickerson, J., & Lele, T. P. (2016). The mammalian LINC complex regulates genome transcriptional responses to substrate rigidity. *Scientific Reports*, 6:38063.
- [17] Westbrook, J. W., Chhatre, V. E., Wu, L. S., Chamala, S., Neves, L. G., Muñoz, P., Martínez-García. P. J., Neale, D.B., Kirst, M., Mockaitis, K., Nelson, C.D., Peter, G.F., Davis, J. M., & Echt, C. S. (2015). A consensus genetic map for *Pinus taeda* and *Pinus elliottii* and extent of linkage disequilibrium in two genotype-phenotype discovery populations of *P. taeda*. **G3: Genes| Genomes| Genetics**, g3-115.3.
- [16] 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).
- [15] 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*, 3, 33.

- [14] Pillon, Y., Johansen, J., Sakishima, T., Chamala, S., Barbazuk, W. B., & Stacy, E. A. (2014). Primers for low-copy nuclear genes in *Metrosideros* and cross-amplification in Myrtaceae. ***Applications in Plant Sciences***, 2(10).
- [13] †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., Wing, R. A., Xiao, N., Moore, R., Soltis, P. S., Soltis, D. E., & Barbazuk, W. B. (2013). Assembly and validation of the genome of the nonmodel basal angiosperm *Amborella*. ***Science***, 342(6165), 1516–1517.
- [12] Amborella Genome Consortium (Chamala, S. is listed as one of the four major contributors) (2013). The *Amborella* genome and the evolution of flowering plants. ***Science***, 342(6165), 1241089.
- [11] Clancy, M. A., Rosli, H. G., Chamala, S., Barbazuk, W. B., Civello, P. M., & Folta, K. M. (2013). Validation of reference transcripts in strawberry (*Fragaria* spp.). ***Molecular Genetics and Genomics***, 288(12), 671-681.
- [10] Pillon, Y., Johansen, J., Sakishima, T., Chamala, S., Barbazuk, W. B., & Stacy, E. A. (2013). Primers for Low-Copy Nuclear Genes in the Hawaiian Endemic *Clermontia* (Campanulaceae) and Cross-Amplification in Lobelioideae. ***Applications in Plant Sciences***, 1(6).
- [9] Pillon, Y., Johansen, J., Sakishima, T., Chamala, S., Barbazuk, W. B., Roalson, E. H., Price, D.K., & 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 Evolutionary Biology***, 13(1), 35.
- [8] Chambers, A., Carle, S., Njuguna, W., Chamala, S., Bassil, N., Whitaker, V., Barbazuk, W. B., & Folta, K. (2013). A genome-enabled, high-throughput, and multiplexed fingerprinting platform for strawberry (*Fragaria* L.). ***Molecular Breeding***, 1-15.
- [7] Ruzicka, D., Chamala, S., Barrios-Masias, F. H., Martin, F., Smith, S., Jackson, L. E., Barbazuk, W. B., & Schachtman, D. P. (2012). Inside arbuscular mycorrhizal roots – molecular probes to understand the symbiosis. ***The Plant Genome***, 6(0), 1-13.
- [6] Tomato Genome Consortium. (2012). The tomato genome sequence provides insights into fleshy fruit evolution. ***Nature***, 485(7400), 635-641.
- [5] Buggs, R. J., Chamala, S., Wu, W., Tate, J. A., Schnable, P. S., Soltis, D. E., Soltis, P. S., & Barbazuk, W. B. (2012). Rapid, repeated, and clustered loss of duplicate genes in allopolyploid plant populations of independent origin. ***Current Biology***, 22(3), 248-252.
- [4] Zuccolo, A., Bowers, J. E., Estill, J. C., Xiong, Z., Luo, M., Sebastian, A., Goicoechea, J. L., Collura, K., Yu, Y., Jiao, Y., Duarte, J., Tang, H., Ayyampalayam, S., Rounsley, S., Kudrna, D., Paterson, A. H., Pires, J. C., Chanderbali, A., Soltis, D. E., Chamala, S., Barbazuk, B., Soltis, P. S., Albert, V. A., Ma, H., Mandoli, D., Banks, J., Carlson, J. E., Tomkins, J., dePamphilis, C. W., Wing, R. A., & Leebens-Mack, J. (2011). A physical map for the *Amborella trichopoda* genome sheds light on the evolution of angiosperm genome structure. ***Genome Biology***, 12(5), R48.
- [3] Folta, K. M., Clancy, M. A., Chamala, S., Brunings, A. M., Dhingra, A., Gomide, L., Kulathinal, R. J., Peres, N., Davis, T. M., & Barbazuk, W. B. (2010). A transcript accounting from diverse tissues of a cultivated strawberry. ***The Plant Genome***, 3(2), 90-105.
- [2] †Buggs, R. J., †Chamala, S., Wu, W., Gao, L., May, G. D., Schnable, P. S., Soltis, D. E., Soltis, P. S., & Barbazuk, W. B. (2010). Characterization of duplicate gene evolution in the recent natural allopolyploid

Tragopogon miscellus by next-generation sequencing and Sequenom iPLEX MassARRAY genotyping. **Molecular ecology**, 19 Suppl 1, 132-146.

- [1] Chamala, S., Beckstead, W. A., Rowe, M. J., & McClellan, D. A. (2007). Evolutionary selective pressure on three mitochondrial SNPs is consistent with their influence on metabolic efficiency in Pima Indians. **International Journal of Bioinformatics Research and Applications**, 3(4), 504-522.

BOOK CHAPTERS AND REVIEWS

- [4] Soltis, D. E., Gitzendanner, M. A., Stull, G., Chester, M., Chanderbali, A., Chamala, S., Jordon-Thaden, I., Soltis, P. S., Schnable, P. S., & Barbazuk, W. B. (2013). The potential of genomics in plant systematics. **Taxon**, 62(5), 886-898.
- [3] Godden, G. T., Jordon-Thaden, I. E., Chamala, S., Crowl, A. A., García, N., Germain-Aubrey, C. C., Heaney, J. M., Latvis, M., Qi, X., & Gitzendanner, M. A. (2012). Making next-generation sequencing work for you: approaches and practical considerations for marker development and phylogenetics. **Plant Ecology & Diversity**, 5(4), 427-450.
- [2] Soltis, D. E., Buggs, R. J. A., Barbazuk, W. B., Chamala, S., Chester, M., Gallagher, J. P., Schnable, P. S., & Soltis, P. S. (2012). The Early Stages of Polyploidy: Rapid and Repeated Evolution in *Tragopogon*. **Polyploidy and Genome Evolution** (pp. 271-292): Springer Berlin Heidelberg.
- [1] 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., & Soltis, D. E. (2012). Next-generation sequencing and genome evolution in allopolyploids. **American Journal of Botany**, 99(2), 372-382.

SCHOLARLY PRESENTATIONS

* Primary presenter

- [50] * Kim, J. T., Jahn, S. C., Newsom, K. J., Wang, H. Y., Chamala, S., & Starostik, P. (2016, November 10-12). NGS-Based Evaluation of Enteropathy-Associated T-Cell Lymphoma Mutation Profile. Poster presented at the Association for Molecular Pathology (AMP) 2016 Annual Meeting. Charlotte, North Carolina, USA.
- [49] * Jordon-Thaden, I., Gilman, I., Uribe-Convers, S., Chamala, S., Tank, D., & Martine, C. (2015, July 25-29). Selection and validation of transcriptome-mined intronic primers for Fluidigm PCR and Illumina sequencing. Poster presented at the Botany 2015 Conference. Edmonton, Alberta, Canada.
- [48] * 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, April 23). Phylogenetic Marker Development Using MarkerMiner 1.0. Invited Talk presented at the Smithsonian National Museum of Natural History. Washington DC, USA.
- [47] Chamala, S., * Godden, G. T., Garcia, N., Jordon-Thaden, I., Soltis, D. E., & Soltis, P. S. (2014, July 26-30). MarkerMiner 1.0: A New Pipeline and Tool for Phylogenetic Marker Development Using Angiosperm Transcriptomes. Talk presented at the Botany 2014 Conference. Boise, ID, USA.
- [46] * Jordon-Thaden, I., Uribe-Convers, S., Godden, G. T., Chamala, S., Tank, D. C., & Martine, C. T. (2014, July 26-30). A Research Workflow for Development of Single-Copy Nuclear Loci and High-throughput Targeted Enrichment for Two or More Phylogenetic Studies. Talk presented at the Botany 2014 Conference. Boise, ID, USA.

- [45] * Godden, G. T., Chamala, S., Soltis, D. E., & Soltis, P. S. (2014, July 26-30). 85 Nuclear Genes Largely Resolve the Phylogeny of Lamiales. Talk presented at the Botany 2014 Conference. Boise, ID, USA.
- [44] * Garcia, N., Meerow, A. W., Gitzendanner, M. A., Chamala, S., Soltis, D. E., & Soltis, P. S. (2014, July 26-30). Exploration of reticulate evolution in Amaryllidaceae tribe Hippeastreae (Asparagales) using sequence capture and NGS of low-copy nuclear markers. Talk presented at the Botany 2014 Conference. Boise, ID, USA.
- [43] * Chamala, S., Jackson, S., Schmutz, J., Town, C., & Barbazuk, B. (2014, January 12). Evolution of Alternative Splicing Across Legumes Using *Amborella* as a Reference. Poster presented at the Plant and Animal Genome XXII, San Diego, CA, USA.
- [42] * Chamala, S., Jackson, S. A., Schmutz, J., & Barbazuk, B. (2014, January 11-15). Evolution of Alternative Splicing Patterns After Whole-genome Duplication. Invited talk presented at the Plant and Animal Genome XXII, San Diego, CA, USA.
- [41] * Kirst, M., Resende Jr, M. F., Chamala, S., & Neves, L. G. (2014, January 11-15). Maize Genotyping Using Rapid-Seq (Randomly-Amplified Polymorphic DNA Sequencing). Poster presented at the Plant and Animal Genome XXII, San Diego, CA, USA.
- [40] Chamala, S., Walts, B., Chanderbali, A., Albert, V., Ayyampalayam, S., Burnette, J., dePamphilis, C., Der, J., Estill, J., Lan, T., Leebens-Mack, J., Lee, S., Ma, H., Moore, R., Palmer, J., Ralph, P., Rice, D., Rounsley, S., Schuster, S., Tomsho, L., Wessler, S., Wing, R., Yu, Y., Jiao, Y., Xiao, N., Soltis, D., Soltis, P., & Barbazuk, B. (2013, October 9-10). Assembly and validation of an evolutionary reference genome for flowering plants (*Amborella trichopoda*). Poster presented at the Florida Genetics 2013, Gainesville, FL, USA.
- [39] * Chamala, S., Jackson, S., Schmutz, J., Town, C., & Barbazuk, B. (2013, October 9-10). Evolution of Alternative Splicing Across Legumes Using *Amborella* as a Reference. Poster presented at the Florida Genetics 2013, Gainesville, FL, USA.
- [38] * Jordon-Thaden, I., Viccini, L., Buggs, R., Chester, M., Silva, A. V. C. D., Chamala, S., Davenport, R., Wu, W., Schnable, P. S., Barbazuk, W. B., Soltis, D., & Soltis, P. (2013, July 27-31). Differential gene expression and loss in two natural and synthetic allotetraploid *Tragopogon* species (*Asteraceae*) and their diploid progenitors. Talk presented at the Botany 2013 Conference, New Orleans, LA, USA.
- [37] * Ibarra-Laclette, E., Chamala, S., Barbazuk, B., Perez-Torres, C.-A., Méndez-Bravo, A., Hernandez, G., Albert, V. A., & Herrera-Estrella, L. (2013, January 12-16). Avocado Genome Sequencing Project. Talk presented at the Plant and Animal Genome XXI, San Diego, CA, USA.
- [36] * Chamala, S., Walts, B., Chanderbali, A., Albert, V. A., Ayyampalayam, S., Burnette, J., dePamphilis, C., Der, J. P., Estill, J., Lan, T., Leebens-Mack, J., Lee, S., Ma, H., Moore, R., Palmer, J., Ralph, P., Rice, D., Rounsley, S., Schuster, S. C., Tomsho, L. P., Wessler, S., Yu, Y., Jiao, Y., Xiao, N., Soltis, D. E., Soltis, P. S., & Barbazuk, B. (2013, January 12-16). Assembly and Validation of an Evolutionary Reference Genome for Flowering Plants (*Amborella trichopoda*). Poster presented at the Plant and Animal Genome XXI, San Diego, CA, USA.
- [35] * Chamala, S., Walts, B., Chanderbali, A., Albert, V., Ayyampalayam, S., Burnette, J., dePamphilis, C., Der, J., Estill, J., Lan, T., Leebens-Mack, J., Lee, S., Ma, H., Moore, R., Palmer, J., Ralph, P., Rice, D., Rounsley, S., Schuster, S., Tomsho, L., Wessler, S., Wing, R., Yu, Y., Jiao, Y., Xiao, N., Soltis, D., Soltis, P., & Barbazuk, B. (2012, November 28-29). Assembly and validation of an evolutionary

reference genome for flowering plants (*Amborella trichopoda*). Poster presented at the Florida Genetics 2012, Gainesville, FL, USA.

- [34] * Mei, W., * Chamala, S., & Barbazuk, B. (2012, November 28-29). Evolution of alternative splicing across land plants. Poster presented at the Florida Genetics 2012, Gainesville, FL, USA.
- [33] * Jordon-Thaden, I. E., Viccini, L. F., Buggs, R., Silva, A. V. C., Chamala, S., Davenport, R., Wu, W., Schnable, P., Barbazuk, B., Soltis, D., & Soltis, P. (2012, July 7-11). Further exploration of genome evolution and gene expression in natural and synthetic polyploids (*Tragopogon*, Asteraceae). Talk presented at the Botany 2012 Conference, Columbus, Ohio, USA.
- [32] * Der, J., Ayyampalayam, S., Burnett, J., Chamala, S., Chanderbali, A., Estill, J., Jiao, Y., Liu, K., Ralph, P., Lan, T., Lyons, E., Tang, H., Tomsho, L. P., Wafula, E., Walts, B., Albert, V., Barbazuk, B., Ma, H., Leebens-Mack, J., Palmer, J., Rounsley, S., Sankoff, D., Schuster, S. C., Soltis, D., Soltis, P., Wessler, S., Wing, R., & dePamphilis, C. (2012, July 7-11). The draft genome sequence of *Amborella trichopoda* sheds light on the ancestral angiosperm genome. Talk presented at the Botany 2012 Conference, Columbus, Ohio, USA.
- [31] * Chanderbali, A., Lan, T., Powell, A., Chang, T.-H., Albert, V., Chamala, S., dePamphilis, C., Leebens-Mack, J., Barbazuk, B., Walts, B., Der, J., Ma, H., santiago, N., Traub, G., Cellinese, N., Estill, J., Lee, S., Palmer, J., Ralph, P., P.Tomsho, L., Yu, Y., Rounsley, S., Schuster, S. C., Wessler, S., Wing, R., Soltis, P., & Soltis, D. (2012, July 7-11). Fluorescence In Situ Hybridization (FISH) in the Evolutionary Reference Plant *Amborella* to Verify Genome Sequence Assembly and Generate a Karyotype. Talk presented at the Botany 2012 Conference, Columbus, Ohio, USA.
- [30] * Estill, J., Leebens-Mack, J., Ayyampalayam, S., Soltis, D. E., Soltis, P. S., Barbazuk, B., Albert, V. A., Ma, H., Wessler, S., Burnett, J., Chamala, S., Jiao, Y., Wafula, E., Walts, B., Schuster, S. C., Der, J. P., & dePamphilis, C. (2012, January 14-18). A genome browser for the basal angiosperm, *Amborella trichopoda*. Poster presented at the Plant & Animal Genome XX, San Diego, CA, USA.
- [29] * Lan, T., Chanderbali, A., Chang, T.-H., Powell, A., Santiago, N., Traub, G., Cellinese, N., Chamala, S., Estill, J., Lee, S., Ralph, P., Tomsho, L. P., Walts, B., Yu, Y., Der, J. P., dePamphilis, C., Leebens-Mack, J., Ma, H., Palmer, J., Rounsley, S., Schuster, S. C., Wessler, S., Wing, R. A., Soltis, D. E., Soltis, P. S., & Albert, V. A. (2012, January 14-18). Using Fluorescence In Situ Hybridization (FISH) in the Evolutionary Reference Plant *Amborella* to Verify Genome Sequence Assembly and Generate a Karyotype. Poster presented at the Plant & Animal Genome XX, San Diego, CA, USA.
- [28] * Der, J. P., Ayyampalayam, S., Burnett, J., Chamala, S., Chanderbali, A., Chang, T.-H., Estill, J., Jiao, Y., Liu, K., Lee, S., Ralph, P., Lan, T., Tomsho, L. P., Wafula, E., Walts, B., Yu, Y., Albert, V. A., Barbazuk, B., Leebens-Mack, J., Ma, H., Palmer, J., Rounsley, S., Schuster, S. C., Soltis, D. E., Soltis, P. S., Wessler, S., Wing, R. A., & dePamphilis, C. (2012, January 14-18). The *Amborella* Genome Sequencing Project: Generating An Evolutionary Reference Sequence for Flowering Plants. Poster presented at the Plant & Animal Genome XX, San Diego, CA, USA.
- [27] * Estill, J., Leebens-Mack, J., Ayyampalayam, S., Soltis, D. E., Soltis, P. S., Barbazuk, B., Albert, V. A., Ma, H., Wessler, S., Burnett, J., Chamala, S., Jiao, Y., Wafula, E., Walts, B., Schuster, S. C., Der, J. P., & dePamphilis, C. (2012, January 14-18). A genome browser for the basal angiosperm, *Amborella trichopoda*. Talk presented at the Plant & Animal Genome XX, San Diego, CA, USA.
- [26] * Chamala, S., Walts, B., Estill, J., Lee, S., Ralph, P., Tomsho, L. P., Yu, Y., Der, J. P., Albert, V. A., dePamphilis, C., Leebens-Mack, J., Ma, H., Palmer, J., Rounsley, S., Schuster, S. C., Soltis, D. E., Soltis, P. S., Wessler, S., Wing, R. A., & * Barbazuk, B. (2012, January 14-18). A Whole Genome

Reference Sequence of *Amborella*. Poster presented at the Plant & Animal Genome XX, San Diego, CA, USA.

- [25] *Jordon-Thaden, I., Viccini, L. F., Buggs, R., Chester, M., Chamala, S., Wu, W., Barbazuk, B., Schnable, P. S., Soltis, D. E., & Soltis, P. S. (2012, January 14-18). Using Sequenom to study gene expression and gene loss in natural and synthetic polyploid generations (*Tragopogon*, *Asteraceae*). Poster presented at the Plant & Animal Genomes XX Conference, San Diego, CA, USA.
- [24] *Chambers, A., Carle, S., Chamala, S., Barbazuk, W. B., Whitaker, V. M., & Folta, K. M. (2011, November 09-10). Multiplexing eight SSR molecular markers to fingerprint diverse *Fragaria* germplasm. Poster presented at the Florida Genetics 2012, Gainesville, FL, USA.
- [23] *Neves, L. G., Chamala, S., Davis, J. M., Barbazuk, W. B., & Kirst, M. (2011, November 09-10). Exploring the megagenome of pine by targeted resequencing. Poster presented at the Florida Genetics 2011, Gainesville, FL, USA.
- [22] *Chamala, S., Walts, B., Chanderbali, A., Albert, V., Ayyampalayam, S., Burnette, J., dePamphilis, C., Der, J., Estill, J., Lan, T., Leebens-Mack, J., Lee, S., Ma, H., Rounsley, S., Schuster, S., Soltis, D., Soltis, P., Tomsho, L., Wessler, S., Wing, R., Yu, Y., & Barbazuk, B. (2011, November 09-10). The Amborella Genome Project: generating a reference sequence for angiosperm evolutionary analysis. Poster presented at the Florida Genetics 2011, Gainesville, FL, USA.
- [21] Chamala, S., *Walts, B., Albert, V., dePamphilis, C., Der, J., Estill, J., Leebens-Mack, J., Lee, S., Ma, H., Rounsley, S., Schuster, S., Soltis, D., Soltis, P., Tomsho, L., Wessler, S., Wing, R., Yu, Y., & Barbazuk, W. B. (2011, November 2-5). The Amborella genome project: generating a reference sequence for angiosperm evolutionary analysis. Poster presented at the Genome Informatics 2011, Cold Spring Harbor, New York, USA.
- [20] Brunings, A., Clancy, M. A., Rosli, H. G., Chamala, S., Carle, S., Varn, F., Civello, M., Babazuk, W. B., Davis, T. M., & *Folta, K. M. (2011, September 23-30). Genome-enabled development of new tools to accelerate strawberry (*Fragaria spp*) research. Poster presented at the American Society for Horticultural Science (ASHS) Annual Conference 2011, Waikoloa, Hawaii, USA.
- [19] *Soltis, D., Buggs, R., Chamala, S., Chester, M., Symonds, V., Tate, J., Mavrodiev, E., Schnable, P., Barbazuk, W. B., & Soltis, P. (2011 July 9-13). *Tragopogon* - A model for recent and recurring allopolyploidy. Talk presented at the Botany 2011 Conference, St. Louis, MO, USA.
- [18] *Jordon-Thaden, I., Facio, L. V., Buggs, R., Chester, M., Silva, A. V., Chamala, S., Davenport, R., Wu, W., Schnable, P., Barbazuk, B., Soltis, D., & Soltis, P. (2011 July 9-13). Exploring genome evolution and gene expression in natural and synthetic polyploids (*Tragopogon*, *Asteraceae*) based on growth chamber experiments. Talk presented at the Botany 2011 Conference, St. Louis, MO, USA.
- [17] *Buggs, R. J., Renny-Byfield, S., Chamala, S., Jordon-Thaden, I. E., Viccini, L. F., Leitch, A. R., Schnable, P. S., Barbazuk, W. B., Soltis, P. S., & Soltis, D. E. (2011 July 4-8). Ongoing evolution in allopolyploid genomes examined using next-generation sequencing. Invited Talk presented at the 8th Biennial Meeting of the Systematics Association, Queen's University, Belfast, UK.
- [16] *Soltis, D. E., Soltis, P. S., Buggs, R. J., Viccini, L. F., Chester, M., Jordon-Thaden, I.E., Silva, A. V. C. D., Tate, J. A., Symonds, V. V., Wu, W., Schnable, P. S., Chamala, S., Davenport, R., & Barbazuk, W. B. (2011 July 23-30). Genetic, karyotypic and genomic evolution in *Tragopogon* allotetraploids. Invited Talk presented at the *International Botanical Congress XVIII*, Melbourne, Australia.

- [15] *Chamala, S., Walts, B., Albert, V., dePamphilis, C., Der, J., Estill, J., Leebens-Mack, J., Lee, S., Ma, H., Rounsley, S., Schuster, S., Soltis, D., Soltis, P., Tomsho, L., Wessler, S., Wing, R., Yu, Y., & Barbazuk, W. B. (2011, May 18-21). The *Amborella* genome project: generating a reference sequence for angiosperm evolutionary analysis. Poster presented at the 18th Plant Biology Symposium, University Park, Pennsylvania, USA.
- [14] *Chamala, S., Walts, B., Albert, V., dePamphilis, C., Der, J., Estill, J., Leebens-Mack, J., Lee, S., Ma, H., Rounsley, S., Schuster, S., Soltis, D., Soltis, P., Tomsho, L., Wessler, S., Wing, R., Yu, Y., & Barbazuk, W. B. (2011, January 15-19). The *Amborella* genome project: generating a reference sequence for angiosperm evolutionary analysis. Poster presented at the Plant & Animal Genomes XIX Conference, San Diego, CA, USA.
- [13] *Barbazuk, W. B., Chamala, S., Brent, M. R., Mueller, L., & Giovannoni, J. (2011, January 15-19). Tomato trained TWINSKAN and *ab initio* gene finding in tomato. Poster presented at the Plant & Animal Genomes XIX Conference, San Diego, CA, USA.
- [13] *Neves, L. G., Chamala, S., Davis, J. M., Barbazuk, W. B., & Kirst, M. (2011, January 15-19). Whole-Exome Sequencing And Genotyping In The Loblolly Pine (*Pinus taeda*) Megagenome. Talk presented at the Plant & Animal Genomes XIX Conference, San Diego, CA, USA.
- [12] *Jordon-Thaden, I. E., Viccini, L. F., Buggs, R., Chester, M., Silva, A. V., Chamala, S., Davenport, R., Wu, W., Schnable, P. S., Barbazuk, W. B., Soltis, D. E., & Soltis, P. S. (2011, January 15-19). Exploring Genome Evolution And Gene Expression In Natural And Synthetic Polyploids (*Tragopogon*). Poster presented at the Plant & Animal Genomes XIX Conference, San Diego, CA, USA.
- [11] *Zuccolo, A., Bowers, J. E., Estill, J. C., Xiong, Z., Luo, M., Sebastian, A., Goicoechea, J. L., Collura, K., Yu, Y., Jiao, Y., Tang, H., Duarte, J., Rounsley, S., Kudrna, D., Paterson, A. H., Pires, J. C., Soltis, D., Chamala, S., Barbazuk, B., Soltis, P., Albert, V. A., Ma, H., Der, J. P., Mandoli, D., Banks, J., Carlson, J., Tomkins, J., dePamphilis, C., Wing, R. A., & Leebens-Mack, J. (2011, January 15-19). A Physical Map For The *Amborella* Genome Sheds Light On The Evolution Of Angiosperm Genome Structure. Poster presented at the Plant & Animal Genomes XIX Conference, San Diego, CA, USA.
- [10] *Chambers, A., Chamala, S., Barbazuk, W. B., Whitaker, V. M., & Folta, K. M. (2010, October 27-28). Universal fingerprinting platform for strawberry (*Fragaria* species). Poster presented at the Florida Genetics 2010, Gainesville, FL, USA.
- [9] *Clancy, M. A., Brunings, A. M., Chamala, S., Barbazuk, W. B., Davis, T. M., & Folta, K. M. (2010, October 27-28). Empirically-designed tools for molecular biology: exploiting a deeply-sequenced transcriptome of octoploid strawberry. Poster presented at the Florida Genetics 2010, Gainesville, FL, USA.
- [8] *Neves, L. G., Chamala, S., Davis, J. M., Barbazuk, W. B., & Kirst, M. (2010, October 27-28). Towards genome-wide association studies in forest trees. Poster presented at the Florida Genetics 2010, Gainesville, FL, USA.
- [7] *Clancy, M. A., Brunings, A. M., Chamala, S., Barbazuk, W. B., & Folta, K. M. (2010, July 31-August 4). Empirically-designed tools for molecular biology: exploiting a deeply-sequenced strawberry transcriptome. Poster presented at the Plant Biology 2010 Annual Conference, Montreal, Quebec, Canada.
- [6] *Folta, K. M., Chamala, S., Barbazuk, W. B., Dhingra, A., Brunings, A., Clancy, M. A., Rosli, H. G., Pombo, M., Civello, M., & Davis, T. M. (2010, August 2-5). Tissue and Developmental Transcriptome Differences in strawberry revealed with Next-Gen Technology. Talk presented at the American Society for Horticultural Science (ASHS) Annual Conference 2010, Palm Desert, California, USA.

- [5] *Chamala, S. (2008, April 4). Developing assembly Strategies for emerging sequencing technologies. Talk presented at the Advanced Seminar in Biomedical Informatics, UIUC, Urbana, IL, USA.
- [4] *Chamala, S., Beckstead, W. A., Rowe, M. J., & McClellan, D. A. (2006, October 20-21). Evolutionary selective pressure on three mitochondrial SNPs is consistent with their influence on metabolic efficiency in Pima Indians. Talk presented at the Biotechnology and Bioinformatics Symposium, Brigham Young University, Provo, Utah, USA.
- [3] *Chamala, S., Beckstead, W. A., Rowe, M. J., & McClellan, D. A. (2006, June 23-27). Evolutionary selective pressure on three mitochondrial SNPs is consistent with their influence on metabolic efficiency in Pima Indians. Poster presented at the Evolution 2006, Society of Systematic Biology, State University of New York-Stony Brook, Stony Brook, New York, USA.
- [2] *Chamala, S., Beckstead, W. A., Rowe, M. J., & McClellan, D. A. (2006, May 24-28). Evolutionary selective pressure on three mitochondrial SNPs is consistent with their influence on metabolic efficiency in Pima Indians. Poster presented at the Genomes, Evolution, and Bioinformatics 2006, Society for Molecular Biology and Evolution, Arizona State University, Tempe, Arizona, USA.
- [1] *Chamala, S. (2006, March 18). Contribution of conserved nucleotides for the RNA folding in picornaviruses. Talk presented at the 20th Annual Spring Research Conference 2006, Brigham Young University, Provo, Utah, USA.

TEACHING EXPERIENCE

GRADUATE TEACHING ASSISTANT (GENETICS COURSE)

FALL 2011 & SPRING 2013

Department of Biology, University of Florida, Gainesville, FL.

Responsibilities include:

- Lead discussion and tutoring sections.
- Schedule and maintain regular office hours to meet with students.
- Evaluate and grade examinations, assignments, and papers, and record grades.
- Fill-in lectures in case of instructor's absence.

RESEARCH EXPERIENCE

CLINICAL BIOINFORMATICS FACULTY (ASSISTANT SCIENTIST)

MAY 2016 TO PRESENT

Department of Pathology, Immunology, and Laboratory Medicine, University of Florida, Gainesville, FL

My current work at the UF involve leading clinical bioinformatics efforts at Molecular Laboratory at UF Health Pathology Laboratories in developing **next-generation sequencing clinical assays** and data management for **personalized cancer medicine**. Additionally, I am conducting research in understating genetic basis for **cancer** and **Type 1 diabetes** using sequencing and array based genomics technologies.

Responsibilities include:

- Development and execution of a bioinformatics platform in support of personalized medicine initiatives
- Develop algorithms for integrating sequence-based/functional knowledge about genes to help scientists/physicians analyze and interpret genomic data
- Assist in clinical and academic projects related to high-throughput omics data, for the analysis and interpretation of next generation sequencing (NGS), microarray, and genotyping data

- Maintenance of genomic and biologic database information used for record keeping, validation, quality control, quality monitoring, data storage, as well as assessment and implementation of new technology and software releases associated with NGS testing
- Development of software and custom scripts to automate data input, data retrieval, manipulation, and analysis; application of statistics, and visualization tools
- Develop and maintain operational and validation standard operating procedure (SOP) documents for NGS diagnosis assay meeting CLIA/CAP requirements.
- Develop independent scholarly effort in bioinformatics research, taking advantage of the outstanding environment for clinical, translational, and basic research in the department in particular and in the institution in general
- Establish collaborations with medical center investigators to assist with their extramurally-funded research

BIOINFORMATICS SCIENTIST

JANUARY 2014 TO MAY 2016

Dr. Patrick Concannon's Lab, University of Florida, Gainesville, FL

As a Bioinformatics Scientist at University of Florida Genetics Institute in Dr. Patrick Concannon's lab, my research involves bioinformatic analyses of array and sequence-based data sets from several different projects in the laboratory. Below are brief details of the some of the main projects that I impacted.

Project: Identification of genomic sequence variants associated with contralateral breast cancer in WECARE Study

The Women's Environment, Cancer, and Radiation Epidemiology (WECARE) Study was designed to identify genetic and environmental determinants of contralateral breast cancer (CBC). The study I am working on currently involves 1,536 WECARE Study participants, who underwent full mutation screening for cancer related genes *ATM* and *PPM1D* using targeted re-sequencing of these genes. Studying these genetic variations in *ATM* and *PPM1D* will help understand their interactions with cancer treatments and the association with second primary cancers.

Project: Expression quantitative trait loci (e-QTL) to identify associations between genotype and gene expression in human Type 1 diabetes (T1D)

Most of the top SNPs that are associated with human Type 1 diabetes (T1D) in previously published GWAS studies are not located in coding regions. In this project we attempt to identify possible regulatory roles for these mutations. One of these regulatory roles that I am investigating is associations between genotype and gene expression in T1D using genotype and expression arrays derived from various cell types isolated from T1D human patients and controls.

Project: Human exome sequencing in T1D families

In this study we are searching for rare, highly penetrant risk variants by sequencing exomes of 114 probands of high-risk T1D families defined as having three or more siblings diagnosed with T1D at early ages.

Responsibilities include:

- Developed quality control methods and pipelines for NGS, array based genotyping and microarray-based gene expression datasets.
- Performed NGS data alignments using BWA-MEM and implemented post-alignment QC methods.
- Explored and evaluated various variant callers like GATK, FreeBayes, VarScan and bcftools for their effectiveness.
- Developed high-throughput variant calling computational pipelines (in **Python**) for targeted and exome sequencing.
- Implemented variant filtering and annotation pipelines using ANNOVAR, SnpEff, and VEP software.
- Genetic variations and their annotations were explored using integrated database framework called GEMINI.

- Explored and evaluated various e-QTL computational frameworks like eQtlBma, eQTLA, and Matrix eQTL.
- Developed R software programming based visualization scripts.

LEAD BIOINFORMATICIAN (PART-TIME)

AUGUST 2014 TO MAY 2016

RAPiD Genomics, Gainesville, FL

RAPiD Genomics is a DNA genotyping and genetic data analysis company. They provide the full suite of tools and analytical methods to researchers and breeders that wish to characterize genetic variation and/or advance breeding.

Responsibilities include:

- Lead bioinformatics related projects.
- Develop and improve high-throughput and efficient bioinformatics methodologies and pipelines for cost-effective DNA genotyping and probe design.

GRADUATE RESEARCH ASSISTANT

JULY 2011 TO AUGUST 2014

Dr. Brad Barbazuk Lab, University of Florida, Gainesville, FL

Project: Examine the evolutionary conservation and divergence of alternative splicing (AS)

This study investigated the evolutionary conservation and divergence of AS patterns in genes duplicated by independent whole genome duplication events during the evolutionary histories of flowering plants.

Responsibilities include:

- Transcriptome sequence collection and quality filtering.
- Transcriptome assembly using Trinity, Cufflinks, and Newbler.
- Global AS events identification using PASA.
- Gene orthogrouping using OrthoMCL.
- Investigated correlation between gene methylation patterns and AS events in plants.
- Developed software pipeline for identifying conserved cross species AS events.
- Developed software pipeline for analyzing fate of AS events in duplicated genes from recent WGD.

Project: The *Amborella* Genome Project: Generating a reference sequence for angiosperm evolutionary analysis

This project generated a high-quality genome sequence for the non-model plant *Amborella*, using a **novel and relatively inexpensive genome assembly and validation strategy** facilitated by next-generation sequencing (NGS) technologies, *fluorescence in situ hybridization* (FISH), and Whole Genome Mapping. Until now, extensive genomic resources like genetic and physical maps were essential for generating high-quality genome sequences of species with large and complex genomes, which is a expensive and labor intensive process. Results from these studies were published as two publications at *Science* journal and are listed above under peer-reviewed publications as *Chamala et al., 2013* and *Amborella Genome Consortium 2013*.

Responsibilities include:

- **Quality filtering and screening** of sequenced data, for organellar contaminants, short read lengths, poor quality, artificial duplicates, and chimeras.
- *De novo* sequence assembly using **Newbler**.
- Monitoring assembly progress.
- Super-scaffolding of *de novo* assembled scaffolds using **OpGen's Genome-Builder™**.
- Evaluation of fidelity of assembly mainly using combination of chromosomal **FISH** (fluorescence in situ hybridization) analysis and **OpGen's whole genome mapping** (optical mapping).
- Evaluating the potential of OpGen's Genome-Builder™ to serve as a surrogate to using long-range PE libraries (like BAC ends) to increase the contiguity of a genome assembly.
- To construct a highly comprehensive training set of well annotated *Amborella* genes, and then use this set to re-train **TWINSKAN *ab initio* gene finder** to accurately identify genes in the *Amborella* whole

genome sequence.

BIOINFORMATICS RESEARCH SCIENTIST (PART-TIME)

AUGUST 2013 TO DECEMBER 2013

RAPiD Genomics, Gainesville, FL

RAPiD Genomics is a DNA genotyping and genetic data analysis company. They provide the full suite of tools and analytical methods to researchers and breeders that wish to characterize genetic variation and/or advance breeding.

Responsibilities include:

- Developed high-throughput and efficient bioinformatics methodologies and pipelines for cost-effective DNA genotyping and probe design.
- Improved methods for sequence variant discovery.

BIOLOGICAL SCIENTIST (COMPUTATIONAL BIOLOGY)

FEBRUARY 2009 TO JUNE 2011

Dr. Brad Barbazuk Lab, University of Florida, Gainesville, FL

As a Biological Scientist in computational biology at UF's Genetics Institute in Dr. Brad Barbazuk's lab, I was involved in wide variety of genomic and transcriptomic projects. Below are brief details of the some of the main projects that I impacted.

Project: Computational gene prediction in Tomato Whole Genome

A computational pipeline was developed to construct a highly comprehensive training set of well annotated tomato genes, and then used this set to re-train TWINSCAN *ab initio gene finder* to accurately identify genes in the tomato whole genome sequence. The tomato specific version of TWINSCAN is integrated into the tomato whole genome sequencing project annotation pipeline. This work is published and listed above under peer-reviewed publications as *Tomato Genome Consortium, 2012*.

Project: Strawberry global gene expression

A novel computational approach was developed to obtain comprehensive coverage of the cultivated strawberry (*Fragaria × ananassa* Duchesne) transcriptome. This study led to the identification of large number of **novel expressed genes**, and thus substantially increasing the available expressed sequence information in the genus. Predictions of **cellular localization and function** were made for these expressed genes by using tissue pool tags sequencing information. This information allows the design of molecular markers that can speed development of new cultivars to meet challenges, such as emerging pathogens, high labor and fuel costs, and diminishing water resources, to name a few. This work was published and listed above under peer-reviewed publications as *Folta et al., 2010*.

Project: Genome evolution in natural populations and synthetic lines of *Tragopogon*

This project involved understanding the impact of polyploidization on **genome evolution** and gene function using *Tragopogon* (sunflower family) as a model organism. Computational pipelines were developed to accelerate the identification of differential gene expression, gene loss, and gene gain events in a high-throughput manner in the polyploids compared to their diploid parent. This work was published and listed above under peer-reviewed publications as *Buggs et al., 2010* and *Buggs et al., 2012*.

Responsibilities include:

- **Genome and transcript sequence assemblies.**
- Characterization and **annotation** of genomes and transcriptomes.
- **Polymorphism discovery** and **gene expression analysis.**
- Develop computational pipelines to automate various biological data analysis.
- Review genome annotation, bioinformatics research procedures, literature, and evaluate their impact on research goals.
- Perform scientific experiments for analysis and standardization.
- Prepare written reports of research findings for publication and presentation.

- **Train graduate students** and biologists at UF in the use of new bioinformatics methods.
- Identifying, implementing and maintaining available software packages that will aid our research projects and developing software and analysis methods when required to complete the research.

FUNCTIONAL ARCHITECT (INTERNSHIP)

JUNE TO DECEMBER 2008

Monsanto, Technology Pipeline Solutions, St. Louis, MO

Monsanto is a leading multinational agricultural biotechnology corporation. I worked in Pipeline Management Team (PMT) of **LEADS** project; it's a joint Biotechnology and IT project aimed to develop Integrated Pipeline Reporting (IPR) tool, automate process tracking, and optimize work flow process for Monsanto's Biotechnology pipeline.

Responsibilities include:

- As part of PMT team, served as liaison between Biotechnology and software application development teams to enhance Biotechnology pipeline process.
- Captured and analyzed "**As Is**" business process and proposed improved "**To Be**" business processes using **BEA AquaLogic BPM** suite.
- Calculated **business value** metrics for **Gap Analysis** between "As Is" and "To Be" processes.
- Developed **user interface (UI)** screen flow prototypes using **Axure RP Pro** and presented to end users and development team for feasibility and feedback.
- Translated business requirements into **Test Driven Requirements (TDR)**, which were then passed on to software development and testing teams.
- Participated in **Bug bash** meetings and helped in analyzing bugs and prioritizing bug fixes.

BIOINFORMATICS RESEARCH ASSISTANT

AUGUST 2007 TO MAY 2008

Dr. Matthew Hudson Laboratory, University of Illinois, Urbana-Champaign, IL

Responsibilities include:

- Assembly **simulation** of genomic reads produced by Sanger, 454, and Solexa sequencing technologies for **quality** and **cost efficiencies**.
- Short read sequence analysis and functional annotation in *Polistes metricus* (Paper Wasp).
- Developing Sequence annotation pipelines using **distributed processing** and web-based interfaces using **Perl, MySQL, PHP**.

PROGRAMMER ANALYST

FEBRUARY TO AUGUST 2007

Regal Computer Systems, Consultant for Michigan Information Technology Dept, Lansing, MI

Goal of **BRIDGES** project is to automate eligibility and benefit determination for Michigan's Cash, Medical, Food, and Child Day Care Assistance programs.

Responsibilities include:

- Developed Multi-Tier Web applications using **Java, J2EE, JSP, Servlets, EJB 2.1, JDBC, XML, HTML, JavaScript**.
- Used software revision control tool **Rational ClearCase** and work-flow automation tool **Rational ClearQuest**.
- Worked on **Oracle 10g/9i, SQL, PL/SQL, Stored Procedures, TOAD, PL/SQL Developer**.
- Developed Financial Management reports using **Crystal Report 11**.
- Developed **Shell Scripts** for Batch Programs in **UNIX** environment.
- Scheduled and managed batch jobs using **OPCON 3.11.05** scheduler.

RESEARCH ASSISTANT**JANUARY TO DECEMBER 2006**

Dr. David Belnap Laboratory, Dept of Chemistry and Biochemistry, BYU, Provo, UT

Responsibilities include:

- Examined the **conserved secondary structure** in RNA of poliovirus.
- This information will help to develop a model for **RNA folding** and also to identify those nucleotides involved in RNA folding. This will be used in conjunction to another project to determine RNA fold by 3D electron microscopy.

RESEARCH ASSISTANT**JANUARY 2005 TO DECEMBER 2006**

Dr. David McClellan Laboratory, Dept of Integrative Biology, Brigham Young University, Provo, UT

Responsibilities include:

- Examined specific **single nucleotide polymorphisms (SNPs)** in the **mtDNA** of the Pima Indian population of the Sonora desert, focusing on genes coding for electron transport chain proteins which affect efficiency of energy metabolism, thereby affecting survival during historical famines and resulting in obesity during extended times of plenty.
- Determined the effect of **natural selection** acting on these residues, and made inferences regarding these mutations as selective adaptations in particular dietary environments.

SOFTWARE PROGRAMMER**NOVEMBER 2005 TO MARCH 2006**

Office of Information Technology - Engineering, Brigham Young University, Provo, UT

Responsibilities include:

- Developed web applications in **C** with embedded **SQL**.
- Debugged and maintained software code written by other software developers.
- Developed web pages using **HTML, DHTML, PHP, CSS**.

RESEARCH TRAINEE**JUNE TO AUGUST 2004**

Dr. Satyabrata Nandi Laboratory, Cancer Research Laboratory, University of California, Berkeley, CA

Responsibilities include:

- **RNA extraction** from frozen mammary tissues of various rat groups.
- RNA amplification using real-time **RT-PCR**.
- Staining and labeling of mammary tissue using **Immunocytochemistry** technique.

RELEVANT COURSE WORK

COMPUTER SCIENCE & STATISTICS

Advanced Programming Concepts | Agile Software Development | Applied Statistics Methods | Data Structures | Database Systems | Discrete Structure | Introduction to Computer Programming | Introduction to Data Mining | Linear Regression

BIOLOGY & BIOINFORMATICS

Advanced Genetics | Bioinformatics | Computational Biology | Evolutionary Biology | Genetics | Genomics | Molecular Biology | Molecular Systematics | Principles of Plant Breeding

TECHNICAL SKILLS & EXPERTISE

BIOINFORMATICS SOFTWARES

Genome Annotation: MAKER, FGENESH, TWINSKAN, TWINSKAN_EST

Microarray and Pathway Analysis: Affymetrix Expression and Transcriptome Analysis Console, Bioconductor, DAVID, GSEA, KEGG, GeneSpring, PathVisio

Phylogeny Software: ClustalW, MAFFT, MEGA, MUSCLE, PHYLIP, PAUP*, RAxML

Sequence Assemblers: Arachne, Celera, Newbler, TGICL, Trinity, Phrap, EULER-SG, Velvet, ABySS

Sequence Alignment: BLAT, BowTie, TopHat, FASTA, GMAP, GSNAP, HMMER, MOSAIK, NCBI-BLAST, SOAP WU-BLAST

Variant Discovery and Annotation: BCFtools, FreeBayes, GATK, GEMINI, GigaBayes, Hydra, Lumpy, VarScan, ANNOVAR, SnpEff, and VEP

PROGRAMMING AND SCRIPTING LANGUAGES

Java, JSP, Servlets, EJB 2.1, JDBC, C, C++, Perl, CGI programming with Perl, Python, PHP, Korn Shell Script, Bourne Shell Script, SQL, SAS, R.

APPLICATION/WEB SERVERS

IBM Websphere, Tomcat

DESIGN/VERSION/WORK-FLOW CONTROL TOOLS

BEA AuaLogic BPM, Axure RP Pro, TeamTrack, MS Visio, UML, Rational ClearCase & ClearQuest, CVS, GIT.

DATABASES

MySQL, Oracle, MongoDB, Elasticsearch.

WEB RELATED

XML, HTML, JavaScript, CSS.

SOFTWARE TECHNOLOGIES

Crystal Report 11, FindBugs, OPCON, Microsoft Office, OpenOffice.

OPERATING SYSTEMS

Linux, Mac OSX, Rocks Cluster Distribution, Windows, Sun Grid Engine, TORQUE Resource Manager, SLURM Resource Manager, UNIX

REFEREE/REVIEW EDITOR

Applications in Plant Sciences – www.bioone.org/loi/apps

BMC Genomics – www.biomedcentral.com

Frontiers in Bioinformatics and Computational Biology – www.journal.frontiersin.org

Frontiers in Plant Science – www.journal.frontiersin.org

Horticulture Research – www.nature.com

Molecular BioSystems – www.rsc.org

Molecular Ecology Resources – www.wiley.com

Molecular Plant – www.cell.com

Nucleic Acids Research – www.nar.oxfordjournals.org

PlosOne – www.plosone.org

MEMBERSHIPS

Sigma Xi The Scientific Research Society (Nominated Full Membership) - www.sigmaxi.org

Association for Molecular Pathology (AMP) - www.amp.org

Health Level Seven (HL7) International - www.hl7.org

SCHOLARSHIPS & AWARDS

| | |
|--|---------------|
| Best graduate student paper award (Honorable Mention) | 2013 |
| UT-Austin Symposium and Workshop on New Methods for Phylogenomics and Metagenomics | 2013 |
| Grinter Fellowship, University of Florida | 2011 TO 2013 |
| Travel Award from Graduate Student Council, University of Florida | 2012 |
| Travel Award from Celera Assembler User Group Meeting | 2012 |
| Travel Award from 18 th Plant Biology Symposium at Penn State | 2011 |
| Graduate Student Research Assistant Grant | 2007 AND 2008 |
| Honors Thesis Research Grant | 2006 |
| Integrative Biology Research Travel Grant | 2006 |
| Recipient, Clarence Cottam Memorial Scholarship | 2005 AND 2006 |
| Recipient, Brigham Young Academic Scholarship | 2005 |
| Honors Academic Merit Award | 2003 AND 2004 |

VOLUNTEER

| | |
|--|--------------------------------------|
| CO-PROJECT LEAD , IT Education Project, Monsanto, St. Louis, MO | JUNE TO DECEMBER 2008 |
| ACTIVE VOLUNTEER , Food & Care Coalition, Provo, UT | JUNE TO DECEMBER 2006 |
| TREASURER , Molecular Evolution Research Club, BYU, UT | JANUARY TO DECEMBER 2006 |
| TREASURER , Amnesty International USA, BYU, UT | JANUARY 2005 TO DECEMBER 2006 |