BIOGRAPHICAL SKETCH

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NAME: Chamala, Srikar

eRA COMMONS USER NAME (credential, e.g., agency login): schamala

POSITION TITLE: Assistant Professor & Director of Biomedical Informatics

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Brigham Young University, Provo, UT	BS	12/2006	Bioinformatics
University of Illinois, Urbana-Champaign, Illinois	MS	10/2008	Bioinformatics
University of Florida, Gainesville, Florida	PhD	08/2014	Biology/Bioinformatics

A. Personal Statement

My expertise is specifically in the area of Bioinformatics and Genomics, where I have made several original contributions in the areas of alternative splicing, comparative genomics, genome sequencing and annotation, genome evolution, genetic marker development, and genetic variant calling. The current focus of my research is in understanding the genetic basis for human cancers and type 1 diabetes using genomics technologies. At the same time, I am pursuing medical informatics projects such as lab test utilization habits by health care providers, and clinical data visualization methods. Currently at University of Florida (UF), I lead bioinformatics efforts in type 1 diabetes (PO1 Award # AI042288), and NCI-supported grants, Florida-California CaRE^2 Health Equity Center (U54 Award # CA233444) and NCI-EGRP supported Prostate Cancer Transatlantic Consortium (CaPTC) (http://epi.grants.cancer.gov/captc/). As Director of Biomedical Informatics, I lead clinical bioinformatics and biomedical informatics efforts at UF Health Pathology Laboratories in developing clinical genomic or precision medicine tests (in cancer, germline, and pharmacogenomics), clinical bioinformatics data analysis & management workflows, clinical genomic variant data interpretation, solutions for integrating genomic data into health information systems, pathology analytics and quality assurance (e.g., CAP Cancer Reporting Protocols). The current proposal builds on my existing research interests and experience in cancer bioinformatics. I have successfully worked on and organized multiple international and inter-institutional projects focused on cancer disparities. These projects involved institutions in USA and West Africa.

B. Positions and Honors

Positions and Employment

2004 - 2004 Research Trainee, Dr. Satyabrata Nandi lab, University of California, Berkeley, CA
2005 - 2006 Software Programmer, Brigham Young University, Provo, UT
2005 - 2006 Research Assistant, Dr. David McClellan lab, Brigham Young University, Provo, UT
2006 - 2006 Research Assistant, Dr. David Belnap lab, Brigham Young University, Provo, UT
2007 - 2008 Bioinformatics Research Assistant, Dr. Matthew Hudson lab, University of Illinois, Urbana, IL
2007 - 2007 Programmer Analyst, Michigan Information Technology (Consultant), Lansing, MI
2008 - 2008 Functional Architect (co-op), Monsanto, St. Louis, MO
2009 - 2011 Biological Scientist, Dr. Brad Barbazuk Lab, University of Florida, Gainesville, FL
2011 - 2014 Graduate Research Assistant, Dr. Brad Barbazuk Lab, University of Florida, Gainesville, FL
2013 - 2013 Bioinformatics Research Scientist (intern), RAPiD Genomics, Gainesville, FL
2014 - 2016 Lead Bioinformatician, RAPiD Genomics, Gainesville, FL

2014 - 2016 Bioinformatics Scientist, Dr. Patrick Concannon Lab, University of Florida, Gainesville, FL
2016 - 2017 Assistant Scientist (Clinical Bioinformatics), Department of Pathology, Immunology, and Laboratory Medicine, UF, Gainesville, FL
2017 - Clinical Assistant Professor and Director of Biomedical Informatics, Department of Pathology, Immunology, and Laboratory Medicine, UF, Gainesville, FL

Other Experience and Professional Memberships

2018-present Member, American Medical Informatics Association
2016-present Member, Association for Molecular Pathology
2016-2018 Member, Health Level Seven International

Honors

2003 – 2004 Honors Academic Merit Award, Berkeley City College, Berkeley, CA
2005 Brigham Young Academic Scholarship, BYU, Provo, UT
2005 – 2006 Clarence Cottam Memorial Scholarship, BYU, Provo, UT
2006 Honors Thesis Research Grant, BYU, Provo, UT
2007 – 2008 Graduate Student Research Assistant Grant, UIUC, Urbana, IL
2011 – 2013 Grinter Fellowship, UF, Gainesville, FL
2013 Best graduate student paper award (Honorable Mention), UF, Gainesville, FL

C. Contributions to Science

1. Novel Whole-Genome Sequencing Strategies and Annotation

Recent improvements in sequencing technology have increased throughput and lowered cost. However, it is still difficult to generate high-quality reference genomes for large and complex genomes as this requires extensive genetic and physical maps which are expensive and laborious to generate. My colleagues and I in a major breakthrough published in *Science* (Chamala & Chanderbali et. al., 2013) demonstrated a new paradigm that by-passes the need for traditional genetic or physical maps. Instead, we use NGS, fluorescence in situ hybridization, and whole-genome mapping to assemble a high-quality genome sequence. Additionally, I developed a computational pipeline for improving gene annotations by constructing a highly comprehensive species-specific training set for TWINSCAN *ab initio* gene finder.

a. †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. Assembly and validation of the genome of the nonmodel basal angiosperm *Amborella*. Science. 2013 Dec 20;342(6165):1516-7. doi: 10.1126/science.1241130. PMID: 24357320.
† *Indicates equal contributions*
b. Amborella Genome Consortium (Chamala, S. is listed as one of the four major contributors). The *Amborella* genome and the evolution of flowering plants. Science. 2013 Dec 20;342(6165):1241089. doi: 10.1126/science.1241089. PMID: 24357323.
c. Tomato Genome Consortium. The tomato genome sequence provides insights into fleshy fruit evolution. Nature. 2012 May 30;485(7400):635-41. doi: 10.1038/nature11119. PMID: 22660326; PMCID: PMC3378239.
d. 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. A physical map for the Amborella trichopoda genome sheds light on the evolution of angiosperm genome structure. Genome Biol. 2011;12(5):R48. doi: 10.1186/gb-2011-12-5-r48. Epub 2011 May 27. PMID: 21619600; PMCID: PMC3219971.

2. Study of Early Polyploidy with a *Tragopogon miscellus* Evolutionary Model

The scientific community's understanding of whole genome duplication (WGD) processes has relied on model species which have undergone WGD hundreds of thousands of years ago or synthetic polyploids

without accurate ecological and historical contexts. Thus, we lack insight into early, naturally-occurring polyploidy evolutionary stages. To overcome these limitations, we used natural allotetraploid *Tragapogon miscellus* (Asteraceae) as a model system, which possesses a history of approximately 40 generations with extant diploid parents. I developed genomic resources and computational pipelines for accelerating the identification of differential gene expression, gene loss, and gene gain events in a high-throughput manner in the polyploids compared to their diploid parents. The findings from this work were published in high impact journals and were highlighted on the journal covers.

a. †Buggs, R. J., †Chamala, S., Wu, W., Gao, L., May, G. D., Schnable, P. S., Soltis, D. E., Soltis, P. S., & Barbazuk, W. B. Characterization of duplicate gene evolution in the recent natural allopolyploid *Tragopogon miscellus* by next-generation sequencing and Sequenom iPLEX MassARRAY genotyping. Mol Ecol. 2010 Mar;19 Suppl 1:132-46. doi: 10.1111/j.1365-294X.2009.04469.x. PMID: 20331776.
   † *Indicates equal contributions*
b. Buggs, R. J., Chamala, S., Wu, W., Tate, J. A., Schnable, P. S., Soltis, D. E., Soltis, P. S., & Barbazuk, W. B. Rapid, repeated, and clustered loss of duplicate genes in allopolyploid plant populations of independent origin. Curr Biol. 2012 Feb 7;22(3):248-52. doi: 10.1016/j.cub.2011.12.027. Epub 2012 Jan 19. PMID: 22264605.
c. 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. Am J Bot. 2012 Feb;99(2):372-82. doi: 10.3732/ajb.1100395. Epub 2012 Jan 20. PMID: 22268220.

3. Development & Application of MarkerMiner 1.0 to SCN Loci Discovery

Discovering alternative single-copy nuclear (SCN) loci is a difficult process for species without sequenced genomes. I developed MarkerMiner 1.0, a fully-automated, open-access, bioinformatics workflow and application for discovering SCN loci. With tabular and alignment outputs for efficient evaluations of primer/probe development, locus selection, phylogenetic utility, and intron-exon boundary predictions, MarkerMiner application has already revealed hundreds to thousands of different SCN loci. Availability of these loci is key to the identification of evolutionary relationships between genes, enriching the fields of biological systematics, ecology, evolution, population biology, and phylogeography. MarkerMiner's command line and graphical user interface is written in Python and can be found at the website below: https://bitbucket.org/srikarchamala/markerminer

a. García, N., Folk, R.A., Meerow, A.W., Chamala, S., Gitzendanner, M.A., de Oliveira, R.S., Soltis, D.E., & Soltis, P.S. Deep reticulation and incomplete lineage sorting obscure the diploid phylogeny of rain-lilies and allies (Amaryllidaceae tribe Hippeastreae). Mol Phylogenet Evol. 2017 Jun;111:231-247. doi: 10.1016/j.ympev.2017.04.003. Epub 2017 Apr 6. PMID: 28390909.
b. 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. MarkerMiner 1.0: A new application for phylogenetic marker development using angiosperm transcriptomes. Appl Plant Sci. 2015 Apr 6;3(4). pii: apps.1400115. doi: 10.3732/apps.1400115. eCollection 2015 Apr. PMID: 25909041; PMCID: PMC4406834.
c. Pillon, Y., Johansen, J., Sakishima, T., Chamala, S., Barbazuk, W. B., & Stacy, E. A. Primers for low-copy nuclear genes in Metrosideros and cross-amplification in Myrtaceae. Appl Plant Sci. 2014 Oct 2;2(10). pii: apps.1400049. doi: 10.3732/apps.1400049. eCollection 2014 Oct. PMID: 25309837; PMCID: PMC4189496.
d. Pillon, Y., Johansen, J., Sakishima, T., Chamala, S., Barbazuk, W. B., Roalson, E. H., Price, D.K., & Stacy, E. A. Potential use of low-copy nuclear genes in DNA barcoding: a comparison with plastid genes in two Hawaiian plant radiations. BMC Evol Biol. 2013 Feb 9;13:35. doi: 10.1186/1471-2148-13-35. PMID: 23394592; PMCID: PMC3605094.

4. Novel Bioinformatics Methodologies for Identification of Conserved Alternative Splicing Patterns Across Species of Large Phylogenetic Distances

I created multiple scalable computational methodologies that incorporate massive transcriptome datasets generated from next generation sequencing platforms to find and classify alternative splicing events within

different species. These methods can identify alternative splicing conservation that occurs between certain species and large phylogenetic lengths. We discovered that AS events are important and have been retained during the course of evolution. I also explored how the identification of conserved AS events allows for the examination of AS conservation and changes among different gene family members within single species or across several species. Overall, my work reveals the need for molecular-level experiments to unpack the roles of newly-identified AS events.

a. Chamala, S., Feng, G., Chavarro, C., & Barbazuk, W. B. (2015). Genome-wide identification of evolutionarily conserved alternative splicing events in flowering plants. Front Bioeng Biotechnol. 2015 Mar 26;3:33. doi: 10.3389/fbioe.2015.00033. eCollection 2015. PMID: 25859541; PMCID: PMC4374538.

Complete List of Published Work in MyBibliography:
https://www.ncbi.nlm.nih.gov/sites/myncbi/srikar.chamala.1/bibliography/40163595/public/?sort=date&direction=ascending

Ongoing Research Support

U54 CA233444 Odedina & Wilkie (MPIs) 09/17/2018-08/31/2023
NIH/NCI
2/3 Florida-California Cancer Research, Education & Engagement (CaRE2) Health Equity Center
The overarching goals of the Florida-California CaRE2 Health Equity Center will be to address cancer health disparities in Black and Latino populations in Florida and California through cutting-edge translational science, training and education of URM scientists and students, and development of culturally-sensitive tools and programs for community initiatives tailored to the needs of Black and Latino populations.
Role: UF Bioinformatics Core Leader

P01 AI042288 Atkinson (PI) 06/20/2018-05/31/2023
NIH
Immune Function and the Progression to Type 1 Diabetes.
The goals are to elucidate the mechanisms by which genes impart immunoregulatory abnormalities that result in aberrant iNKT development, inflammatory antigen presenting cells, expansion of autoreactive lymphocytes, and defective regulatory/effector mechanisms in T cells.
Role: Co-Investigator, Core A

2018PG-T1D071 Brusko (PI) 4/1/2018-3/31/2021
Helmsley Charitable Trust
Human Atlas of Neonatal Development and Early-Life Immunity
The goal is to acquire key insights into immune system development in peripheral tissues, ultimately leading to novel interventional strategies.
Role: Co-Investigator

1838316 Lele (PI) 08/01/2018-07/31/2020
NSF
RoL:FELS:EAGER Rules for cellular adaptation to the mechanical properties of their environment
The goals of this proposal are to use experimental evolution to uncover evolutionary rules underlying the adaptation of Eukaryotic somatic cells to the mechanical properties of their environment.
Role: Co-Investigator

Pending Research Support

PRO00025382 Odedina (PI) 2019 – 2024
Leidos Biomedical Research Inc.
Prostate Cancer Transatlantic Consortium (CaPTC) CPTAC Tissue Source Sites
The purpose of this project is to provide high-quality, clinically annotated primary, untreated tumor specimens and whole or processed blood specimens from prostate cancer patients in West Africa.
Role: Co-Investigator (Pending Release)

PRO00024739 Lele (PI) 2019 – 2024
NIH/NIGMS
Cellular Evolution on a Soft Biomaterial
The purpose of this project is to develop a new line of research by establishing the concept of cellular evolution in soft environments. If successful, this research will reveal the genomic basis of cellular adaptation to the rigidity of the ECM, and will promote an appreciation for experimental evolution on biomaterials as a tool to engineer somatic cells.
Role: Co-Investigator

Completed Research Support
None