DR. VIJAY SHANKAR, PH. D.

CURRENT POSITION
Bioinformatics Staff Scientist
Center for Human Genetics
College of Science
Clemson University

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EDUCATION

Ph.D.	**Wright State University,** Dayton, OH, USA *Biomedical Sciences*	**2010-2016**
Bachelor of Arts (BA)	**Miami University,** Oxford, OH, USA *Microbiology*	**2004-2008**

POSITIONS

Bioinformatics Staff Scientist	**Clemson University,** Greenwood, SC	**2019-Present**
Bioinformatics Research Associate	**Clemson University,** Clemson, SC	**2016-2018**
Research Assistant	**Wright State University,** Dayton, OH	**2016**

GRANTS, HONORS AND AWARDS

Center for Produce Safety Grant Award: 2019CPS07 – Co-PI with Dr. Jiang and Dr. Saski	**2018**
Best student poster presentation at Ohio Branch American Society of Microbiology	**2014**
Recipient of the Original Works Grant from Wright State Graduate Student Assembly	**2012**
Graduate Teaching Assistantship at Wright State University	**2009 – 2010**
Ohio Leaders Scholarship at Miami University	**2004 – 2008**
National Scholarship Survey Recognition	**2004 – 2008**
Dean’s List at Miami University	**2007**
Robotics and Mechanics Award for High School Seniors from Cuyohoga Community College	**2003**

MEMBERSHIPS

American Society for Microbiology	**2012 – present**

AREAS OF RESEARCH INTERESTS

Development and application of multivariate statistics in a wide array of subjects and fields
Development of new pipelines and improvement of current ones for analysis of NGS data
Role of intestinal microbiota in human health and disease
Metabolic interactions in complex microbial communities

PUBLICATIONS

- S. S. Mokashi, **V. Shankar**, J. A. Johnstun, W. Huang, T. F. C. Mackay and R. R. H. Anholt. (2021). Systems Genetics of Single Nucleotide Polymorphisms at the Drosophila *obp56h* Locus. ***bioRxiv***
- M. D. Lucius, H. Ji, D. Altomare, R. Doran, B. Torkian, A. Havighorst, V. Kaza, Y. Zhang, A. V. Gasparian, J. Magagnoli, **V. Shankar**, M. Shtutman and H. Kiaris. (2021). Genomic variation in captive deer mouse (*Peromyscus maniculatus*) populations. ***BMC Genomics*** 22(1), 1-15.
- N. O. Nazario-Yepiz, J. F. Sobaberas, R. Lyman, M. R. Campbell III, **V. Shankar**, R. R. H. Anholt and T. F. C. Mackay. (2021). Physiological and metabolomics consequences of reduced expression of the *Drosophila bummer* triglyceride Lipase. ***PLOS ONE*** 16(9), e0255198.
- M. Usovsky, R. Robbins, J. F. Wilkes, D. Crippen, **V. Shankar**, T. Vuong, P. Agudelo and H. T. Nguyen. (2021) Classification methods and identification of reniform nematode resistance in known soybean cyst nematode resistant soybean genotypes. ***Plant Disease*** doi: 10.1094/PDIS-01-21-0051-RE.
- J. A. Deaver, M, N, Soni, K. I. Diviesti, K. T. Finneran, **V. Shankar**, S. C. Popat. (2021) Taxonomic and Functional Variants Induced by an Overloading Event in Anaerobic Codigestion of Municipal Wastewater Sludge with Fats, Oils, and Grease. ***ACS ES&T Engineering*** 1: 1205-1216.
- S. S. Mokashi, **V. Shankar***, R. A. MacPherson, R. C. Hannah, T. F. C. Mackay and R. R. H. Anholt. (2021) Developmental Alchol Exposure in Drosophila: Effects on Adult Phenotypes and Gene Expression in the Brain. ***Frontiers in Psychiatry*** 12:699033. doi: 10.3389/fpsyt.2021.699033. *PMC8341641*. ***co-first author – equal contribution with S. S. Mokashi.**
- B. M. Baker, S. S. Mokashi, **V. Shankar***, J. S. Hatfield, R. C. Hannah, T. F. C. Mackay and R. R. H. Anholt. (2021) The Drosophila brain on cocaine at single cell resolution. ***Genome Research*** doi: 10.1101/gr.268037.120. ***co-first author – equal contribution with B. M. Baker and S. S. Mokashi.**
- J. A. Johnstun, **V. Shankar**, S. Mokashi, L. T. Sunkara, U. E. Ihearahu, R. L. Lyman, T. F. C. Mackay and R. H. A. Anholt. (2021) Functional Diversification, Redundancy, and Epistasis among Paralogs of the *Drosophila melanogaster Obp50a-d* Gene Cluster. ***Molecular Biology and Evolution*** 38(5): 2030-2044.
- I. Q. Phan, C. A. Rice, R. E. Noorai, J. McDonald, S. Subramanian, L. Tillery, L. K. Barrett, **V. Shankar**, J. C. Morris and W. C. Van Voorhis. (2020) The Transcriptome of *Balamuthia mandrillaris* trophozoites for structure-based drug design. ***bioRxiv***
- R. E. Noorai, **V. Shankar***, N. H. Freese, C. M. Gregorski and S. C. Chapman. (2019) Discovery of genomic variants by whole-genome requencing of the North American Araucana chicken. ***PLOS ONE*** 14(12): e0225834. *PMC6903725* ***co-first author – equal contribution with R. E. Noorai.**
- D. Nayduch, **V. Shankar**, M. K. Mills, T. Robl, B. Drolet, M. Ruder, E. Scully and C. Saski. (2019) Transcriptome response of female *Culicoides sonorensis* biting midges (Diptera: Ceratopogonidae) to early infection with Epizootic Hemorrhagic Disease Virus (EHDV-2). ***Viruses*** 11(5): 473. *PMC6563219*

- S. K. Krombeen, **V. Shankar**, R. E. Noorai, C. Saski, J. Sharp, M. Wilson and T. Wilmoth. (2019) The identification of differentially expressed genes between extremes of placental efficiency in maternal line gilts on day 95 of gestation. ***BMC Genomics*** 20(1): 254.
- T. Zhebentyayeva, **V. Shankar**, R. Scorza, A. Callahan, M. Ravelonandro, S. Castro, T. Dejong, C. Saski and C. Dardick. (2019) Genetic characterization of world-wide Prunus domestica (plum) germplasm using sequence-based genotyping. ***Horticulture Research*** 6(1): 12. *PMC6312543*
- Y. Qiu, J. E. Milanes, J. A. Jones, R. E. Noorai, **V. Shankar**, and J. Morris. (2018) Glucose signalling is important for nutrient adaptation during differentiation of pleomorphic African trypanosomes. ***mSphere*** 3(5), e00366-18. *PMC6211221*.
- A. Ramos-Garcia, **V. Shankar**, C. Saski, T. Hsiang and D. Freedman. (2018) Draft Genome Sequence of the 1,4-Dioxane-Degrading Bacterium *Pseudonocardia dioxanivorans* BERK-1. ***Genome Announc*** 6(14), e00207-18. *PMC5887028*
- **V. Shankar**, R. Agans, and O. Paliy. (2017) Advantages of phylogenetic distance based constrained ordination analyses for the examination of microbial communities. ***Sci Rep*** 7(1): 6481. *PMC5526943*
- **V. Shankar**, M. Gouda, J. Moncivaiz, A. Gordon, N. V. Reo, L. Hussein, and O. Paliy. (2017) Differences in gut metabolites and microbial composition and functions between Egyptian and US teenagers are consistent with consumed diets. ***mSystems*** 2(1): e00169-16. *PMC5296411*
- O. Paliy and **V. Shankar**. (2016) Application of multivariate statistical techniques in microbial ecology. ***Mol. Ecol.*** 25(5), 1032-57. *PMC4769650*
- **V. Shankar**, N. Reo, and O. Paliy. (2015) Simultaneous fecal microbial and metabolite profiling enables accurate classification of pediatric irritable bowel syndrome. ***Microbiome*** 3:73. *PMC4675077.*
- **V. Shankar**, D. Homer, L. Rigsbee, H. J. Khamis, S. Michail, M. Raymer, N. V. Reo, and O. Paliy. (2015) The networks of human gut microbe-metabolite associations are different between health and irritable bowel syndrome. ***ISME J*** 9(8), 1899-903. *PMID25635640.*
- **V. Shankar**, M. J. Hamilton, A. Khoruts, A. Kilburn, T. Unno, O. Paliy, and M. J. Sadowsky. (2014) Species and genus level resolution analysis of gut microbiota in *Clostridium difficile* patients following fecal microbiota transplantation. ***Microbiome*** 2:13. *PMC4030581*.
- **V. Shankar**, R. Agans, B. Holmes, M. Raymer, and O. Paliy. (2013) Do gut microbial communities differ in pediatric IBS and health? ***Gut Microbes*** 4(4): 347-352. *PMID23674073.*
- L. Rigsbee, R. Agans, **V. Shankar**, H. Kenche, H. Khamis, S. Michail, and O. Paliy. (2012) Quantitative profiling of gut microbiota of children with diarrhea-predominant Irritable Bowel Syndrome. ***Am. J. Gastroenterol.*** 107(11), 1740-51. *PMID22986438.*

BOOK CHAPTERS

- O. Paliy, **V. Shankar**, and M. Sagova-Mareckova. (2014). Chapter 9: Phylogenetic Microarrays. *Bioinformatics and Data Analysis in Microbiology*. Ed. Ozlem Tastan Bishop. ***Horizon/Caister press***. 207-229. Print.
- O. Paliy, **V. Shankar**. (2014). Chapter 11: Applications of Phylogenetic Microarrays in Profiling of Human Microbiomes. *Microarrays: Current Technology, Innovation and Applications*. Ed Melanie Woodward. ***Horizon press***. 195-215. Print.

PRESENTATIONS

- **V. Shankar,** D. Homer, L. Rigsbee, H. Khamis, S. Michail, M. Raymer, N. Reo and O. Paliy. Fecal metabolites in pediatric IBS. *American Society of Microbiology, National Conference, Washington DC, 2014.*
- **V. Shankar,** D. Homer, L. Rigsbee, H. Khamis, S. Michail, M. Raymer, N. Reo and O. Paliy. Fecal metabolites in pediatric IBS. *Ohio Branch American Society of Microbiology, Ohio State University, OH, 2014.* **Won the award for the best graduate student poster presentation**.
- **V. Shankar,** L. Rigsbee, H. Kenche, S. Michail, and O. Paliy. Effects of VSL#3 on the composition of intestinal microbiota in IBS-D patients. *FASEB Probiotics, Intestinal Microbiota and the Host, Carefree, AZ, 2011*.

SKILLS

- Highly skilled in the use multivariate statistical and mathematical approaches to draw biological inferences from complex datasets (main focus of my doctoral dissertation). Also skilled in application of integrative approaches across multiple datasets to extract biological insights at the systems level (Systems Biology).
- Expertise in the use of Next-Generation Sequencing technologies such as Illumina MiSeq, Ion Torrent PGM and Proton, and 454 Pyrosequencing to profile complex microbial communities.
- Proficient at analyzing data acquired from Next-Generation Sequencing technologies and microarrays, and in building analysis pipelines for such datasets.
- Highly skilled at analyzing and interpreting single cell transcriptomics data.
- Proficiency in Matlab, Python and R scripting languages, and in UNIX environment.
- Experienced in laboratory molecular biological techniques such as PCR, RT-PCR, qPCR, Nucleic Acid extraction and in molecular techniques required for NGS library prep and sequencing (Illumina and Life Technologies based).
- Proficient as Systems Admin for HPC maintenance and in most operating systems and office related softwares. Also proficient in designing and building analysis workstations (hardware expertise) and cluster infrastructure.

CLEMSON® UNIVERSITY
CENTER FOR
HUMAN GENETICS

September 24, 2021

Letter of Application

Dear Members of the **RNA Society Awards Committee,**

I am writing this letter to be considered for the RNA Society Outstanding Career Researcher Award. Described below is a summary of the position that I hold currently at Clemson University and of the accomplishments related to RNA research.

My current position at the Clemson Center for Human Genetics is titled Bioinformatics Staff Scientist. In this role, I provide bioinformatics and statistical insights, training and analytical assistance to the center's faculty, staff and students. This position has a supervisory role in the bioinformatics and statistics core at the center, where I guide our bioinformatics staff member Ms. Maria Adonay in several of the challenging bioinformatics problems. I regularly meet with students and faculty directly to guide them with analyses that are tailored toward their specific scientific questions. I also organize bioinformatics workshops as part of our training and outreach program to share our knowledge and expertise to the center and university community. In addition to these responsibilities, I function as a systems administrator for our in-house high performance computing cluster and oversee data storage, protection, redundancy and maintenance.

My role as a bioinformatician and statistician at the Clemson Center for Human Genetics has enabled our labs to uncover novel insights in transcriptional responses to drug exposure, genetic variation and gene perturbation in the *Drosophila melanogaster* model system. My analyses, using cutting-edge statistical methods, of single-cell transcriptomics data was critical toward uncovering the cell-type membership, characterizing transcriptional responses associated with acute cocaine and developmental ethanol exposures and, building transcriptional regulatory networks within specific cell-types of the *Drosophila* brain. We also uncovered novel responses in genes encoding for long non-coding RNAs in *Drosophila* brain due to drug exposure. These studies led to co-first authorships in peer-reviewed publications within prestigious journals such as *Genome Research* and *Frontiers in Psychiatry*. My analytical expertise was also instrumental in characterizing the differences in transcriptional responses to changes in gene membership of a *Drosophila* gene cluster. Specifically, transcriptome profiles were used to characterize functional diversification as well as relationships of individual paralogs within a specific olfactory gene cluster (*Obp50*). Insights from this study highlight the emergence of functional diversification after gene-duplication events in multi-gene clusters. These results culminated in a peer-reviewed publication in the prestigious journal *Molecular Biology and Evolution*.

The skill set I have developed in this current position has been an important factor toward establishing highly productive collaborations with the Greenwood Genetics Center. As part of this collaboration, my team was responsible for developing bioinformatics pipelines to analyze short and long read whole genome as well as transcriptome sequencing data for the diagnosis of rare genetic diseases in multiple TRIO cases.

Thank you for your consideration.

Sincerely,

Vijay

Vijay Shankar, Ph.D
Bioinformatics Staff Scientist
Clemson Center for Human Genetics