

# Migun Shakya, PhD

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## EDUCATION

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- Ph.D** Genome Sciences ◇ University of Tennessee ◇ Knoxville, TN 2013  
*Dissertation:* Validating approaches for studying microbial diversity to characterize communities from roots of *Populus deltoides*
- B.S** Biology ◇ Southwestern Oklahoma State University ◇ Weatherford, OK 2008

## RESEARCH EXPERIENCE

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- Post-doc** 2016 - present
- Bioscience Division, Los Alamos National Laboratory, Los Alamos, NM
  - Developing RNA-seq analysis pipeline to detect differentially expressed genes in eukaryotes and prokaryotes.
  - Developing pipelines to conduct evolutionary analyses directly from raw sequences.
- Post-doc** 2013 - 2016
- Department of Biology, Dartmouth College, Hanover, NH
  - Describe evolution of Gene Transfer Agents (GTAs) across *Alphaproteobacteria*.
  - Developed SVM-based algorithm to distinguish phage genes from their GTA homologs.
- Graduate Research Assistant** 2009 - 2013
- University of Tennessee and Oak Ridge National Lab, Oak Ridge, TN
  - Analysis of microbiomes from roots of *P. deltoides*.
  - Tested the accuracy of describing microbiome using amplicons.

## PUBLICATIONS

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- Shakya M.**, Soucy S.M., Zhaxybayeva O. (2017). Insights into Origin and Evolution of  $\alpha$ -proteobacterial Gene Transfer Agents. *Submitted to Viral Evolution*
- Hynes A.P\*, **Shakya M.**\*, Mercer R.G, Grull M.P, Brown L., Davidson F, Steffen E., Matchem H., Peach M.E, Berger T, Grebe K., Zhaxybayeva O., Lang A.S (2016). Functional and evolutionary characterization of a gene transfer agent's multi-locus "genome"?, *Molecular Biology and Evolution* \*These authors contributed equally
- DAmore R., Ijaz, U. Z., Schirmer M., Kenny J. G., Gregory R., Darby A. C., **Shakya M.**, Podar M., Quince C. and Hall N. (2016). A comprehensive benchmarking study of protocols and sequencing platforms for 16S rRNA community profiling. *BMC genomics* doi:10.1186/s12864-015-2194-9
- Hurt, R.A., Robeson II M.S., **Shakya M.**, Moberly, J.G., Vishnivetskaya, T.A., Gu B., and Elias, D.A. (2014). Improved Yield of High Molecular Weight DNA Coincides with Increased Microbial Diversity Access from Iron Oxide Cemented Sub-Surface Clay Environments. *Plos ONE*. doi:10.1371/journal.pone.0102826
- Shakya, M.**, Gottel N., Castro H., Yang Z.K., Gunter L., Labbe J., Muchero W., Bonito G., Vilgalys R., Tuskan G., Podar M., Schadt C.W. (2013). A Multifactor Analysis of Fungal and Bacterial Community Structure in the Root Microbiome of Mature *Populus deltoides* Trees. *Plos ONE*. doi:10.1371/journal.pone.0076382

**Shakya, M.**, Quince, C., Campbell, J., Yang, Z., Schadt, C.W., Podar, M (2013). Comparative metagenomic and rRNA microbial diversity characterization using Archaea and Bacteria synthetic communities *Environmental Microbiology*.doi:10.1111/1462-2920.12086

Flores E.G.,**Shakya, M.**, Meneghin J.,Podar, M., Seewald., J.S., Reysenbach A-L (2012). Inter-field Variability in the Microbial Communities of Hydrothermal Vent Deposits from a Back-Arc Basin.*Geobiology*. doi:10.1111/j.1472-4669.2012.00325.x

## BOOK CHAPTERS

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Culley A.I., **Shakya M.**, Lang A.S. (2015) Viral evolution at the limits. In *Microbial Evolution under Extreme Conditions* (pp.209-222).Germany.degruyter.

## SELECTED SCIENTIFIC CONFERENCES

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**Shakya M.** Lets make a tree! PhaME: A tool for Phylogenetic and Molecular Evolution Analysis. In:*LANL B Division Day*, September 14, 2017. Talk.

**Shakya M.**, Senin P., Feng S., Lo C., Hu. B, Chain P.S.G. PiReT: Pipeline for Reference Based Transcriptomics. In:*LANL Postdoc Research Symposium and Career Fair*, August 29-31, 2017. Poster.

Li P.E., Lo C-C., Anderson J., Davenport K., Bishop-Lilly K., Xu Y., Voegtly L., Feng S., Senin P., **Shakya M.**, Philipson C., Gans J., Miller N., Challacombe J., Hamilton T., Chain P.S.G. Addressing the Analysis Bottleneck Created by Next Generation Sequencing (NGS) Using EDGE Bioinformatics. In:*asm microbe*, June 1-5, 2017. Poster and Selected talk.

**Shakya M.**, Senin P., Feng S., Lo C., Hu. B, Chain P.S.G. PiReT: Pipeline for Reference Based Transcriptomics. In:*Sequencing, Finishing, analysis In the Future Meeting*, May 16-18, 2017. Poster.

**Shakya M.** and Zhaxybayeva O. Do bacteria domesticate viruses?. In:*Microbiology and Molecular Pathogenesis Program Retreat*, February 11-12, 2016. Poster and Talk.

**Shakya M.** and Zhaxybayeva O. Origin and Evolution of gene transfer agents in  $\alpha$ -proteobacteria. In:*Mobile Genetic Elements: In Silico, In Vitro, In Vivo*, September 3-5, 2015. Selected talk.

**Shakya M.** and Zhaxybayeva O. Origin and Evolution of gene transfer agents in  $\alpha$ -proteobacteria. In:*Gordon Research Conference: Microbial Population Biology*, July 19-24, 2015. Poster.

**Shakya M.**, Drivers of microbial community structure in rhizosphere and endosphere of *Populus deltoides*.In: *American Society for Microbiology KY-TN Branch Meeting* , October 26-27, 2012.Talk.

**Shakya M.**, Gottel,N.R., Castro,H.F.,Yang Z.K.,Kerley M., Podar M.,Doktcyz, M.J., Schadt, C.W. Archaea associated with Populus and its surrounding soil and trees.In: *International Society of Microbial Ecology 14, Copenhagen, Denmark*, August 19-24, 2012.Poster.

**Shakya M.**, Gottel,N.R., Castro,H.F.,Yang Z.,Kerley M., Podar M.,Doktcyz, M.J.,Schadt, C.W. Plant-Microbe Interface: Dynamics of Bacterial Microbiome of *Populus deltoides* In: *2012 Department of Energy Genomic Science Awardee Meeting X*, February 26-29, 2012.Poster.

**Shakya M.**, Campbell, J.C., Schadt, C.W.,Podar M. Experimental and Computational Approaches for Microbial Diversity Characterization Using Artificial Communities.In: *2011 Genomic Science Awardee Meeting IX* , April 10-13 , 2011.Poster and Talk.

**Shakya M.**, Campbell, J.C.,Yang,Z.K., Podar M. Experimental and Computational Approaches for Microbial Diversity Characterization Using Artificial Communities In: *International Society of Microbial Ecology 13*, August 22-27, 2010.Poster.

## TEACHING EXPERIENCES

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### **Los Alamos National Laboratory, Los Alamos, NM**

Taught a class on phylogenetic analysis for annual workshop (2017).

Taught a class on Transcriptomics analysis for annual workshop (2017).

### **University of Tennessee, Knoxville**

Teaching Assistant for BCMB 230 : Human Physiology Fall 2009 (2 sections)

Teaching Assistant for BIO 140 : Organization and Function of the Cell Spring 2010 (2 sections)

### **Southwestern Oklahoma State University**

Teaching Assistant for Biological Sciences Fall 2007-Spring 2008

Grader for College Algebra and Trigonometry Spring 2007-Spring 2008

## HONORS AND AWARDS

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### **University of Tennessee, Knoxville**

2011 Genomic Sciences Meeting Student Travel Grant

### **Southwestern Oklahoma State University,**

In-State Tuition Waiver 2003-2008

Ottis and Buena Ballard Memorial Scholarship 2007

Who is Who Among American Universities 2008

## PEER REVIEW ACTIVITIES

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Reviewer for: FEMS Microbiology Ecology, Canadian Journal of Microbiology, Frontiers in Microbiology, Molecular Biology and Evolution, BMC Microbiology, MDPI - *Toxins*

## MENTORSHIP EXPERIENCE

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Irene Feng, Dartmouth College (2013-2015).

Dan Birnbaum, Dartmouth College (2015).

Taylor Neely, Dartmouth College (2015-2016).

Camille Hankel, Georgetown College (2016).

Wafa Kooli, LANL (2017).

## OUTREACH

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Poster Judge in Los Alamos National Lab Annual Student Symposium (August 9, 2017).

## RELEVANT SKILLS

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**Programming/Scripting:** Python, Perl, R, Bioconductor

**Bioinformatics:** Analysis of Microbiome, Genome, Microbial ecology, Metagenome, Metagenetics, Methylo-  
lome, RNA-seq, phylogenetics, etc.

**Other:** Linux, shell scripting, high performance computing