Kanhu Charan Moharana

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Campos dos Goytacazes, RJ, Brazil

EDUCATION

Universidade Estadual do Norte Fluminense Darcy Ribeiro   Campos dos Goytacazes, Rio de Janeiro
Ph.D. in Biosciences and Biotechnology   *2016 - Expected March 2020*

Thesis: Effects of whole genome duplication in the evolution of Glycine max (soybean): tissue-specific expression and diversity of transcription factors

Relevant skills: Phylogenomics, functional genomics, genome and transcriptome assembly, RNA-seq, technical writing, hypothesis testing, Data Visualization, R, Python

Orissa University of Agriculture and Technology   Bhubaneswar, Odisha
Master of Sciences in Bioinformatics; OGPA: 8.06/10.0   *2008 - 2010*

Thesis: Development of tool for operon prediction using genetic algorithm.

Relevant skills: Bioinformatics, Molecular biology, statistics, PERL, UNIX, Shell, Genetic algorithm, Fuzzy logic, RDBMS

SKILLS

- **NGS read mapping tools**: Bowtie, BWA, Tophat, STAR.
- **Computing languages**: Advanced R; Advanced Perl; Intermediate Python
- **Database**: MySQL, SQLite
- **Libraries**: BioConductor,Dplyr, Numpy, Pandas, jQuery.js, Google App script
- **Data visualization**: ggplot2, iGraph, plotly, matplotlib

Gene expression analysis: Cufflinks, StringTie, HTSeq, DESeq, edgeR.
Scripting languages: Shell scripting, awk
Web technology: Apache/LAMP, HTML/CSS/Javascript, R Shinny
Version control technologies: GitHub
Report generation: Rmarkdown, R-studio, Jupyter, R shinny web app

RESEARCH EXPERIENCE

Sanjay Gandhi Postgraduate Institute of Medical Sciences   Lucknow, India
Project Scientist-I   *June 2013 - January 2016*

- **RNA editing site**: Predicting RNA editing sites using genome independent method.
  - Employed various Bioinformatics tools to map billions of short DNA sequences on human genome and used, next, various in-house scripts to identify locations with nucleotide variations.
- **Co-expression gene network**: Used gene expression data generated using RNA-seq method to create gene network.
  - Used R to create gene network for normal and Non-alcoholic Fatty Liver Disease (NAFLD) liver samples
  - Employed network based statistics to compare the gene connectivity and identify candidate disease causing genes.
- **Patience data collection platform**: Developed an web based survey portal to collect Systemic Lupus Erythematosus patients.

National Institute of Plant Genome Research   New Delhi, India
Junior Research Fellow   *2012 Oct - 2013 May*

- **Rice genomic variation**: I was involved in a work to identify genomic single nucleotide polymorphisms and insertions-deletions in three contrasting verities of rice and correlate their role in contrasting water stress.

Rajendra Memorial Research Institute of Medical Sciences   Patna, India
Research Assistant   *2012 Mar - 2012 Oct*

- **Leishmanial polymorphic repeat database**: I was involved in a project aimed at analyzing publicly available genomic sequences of six different Leishmanial species and extracted sequence repeats. Later, using in silico approaches the polymorphic repeats among these species were predicted and created a database using SQL and CGI-Perl.

PUBLICATIONS

- Sindhuprava Rana, Manas Ranjan Dikhit, Mukta Rani, Kanhu Charan Moharana, Ganesh Chandra Sahoo, and Pradeep Das. CPDB: cysteine protease annotation database in Leishmania species. *Integrative biology : quantitative biosciences from nano to macro*, 4(11):1351–7, 2012

- Mukesh Jain, Kanhu Charan Moharana, Rama Shankar, Romika Kumari, and Rohini Garg. Genomewide discovery of DNA polymorphisms in rice cultivars with contrasting drought and salinity stress response and their functional relevance. *Plant Biotechnology Journal*, 12(2):253–264, 2014

- Manas R Dikhit, Kanhu C Moharana, Bikash R Sahoo, Ganesh C Sahoo, and Pradeep Das. LeishMicrosatDB: open source database of repeat sequences detected in six fully sequenced Leishmania genomes. *Database : the journal of biological databases and curation*, 2014, 2014

- Ganesh Chandra Sahoo, Mukta Rani, Md Yousuf Ansari, Chanda Jha, Sindhuprava Rana, Manas Ranjan Dikhit, Kanhu Charan Moharana, Rakesh Kumar, and Pradeep Das. Structure, evolution and virtual screening of NDM-1 strain from Kolkata. *International journal of bioinformatics research and applications*, 10(3):235–63, 2014

○ K.C. Moharana, M.R. Dikhit, B.R. Sahoo, G.C. Sahoo, and P. Das. GAOPP: Operon prediction in prokaryotes using genetic algorithm. *Current Bioinformatics*, 10(3), 2015

○ Hemanoel Passarelli-Araujo, Jussara Palmeiro, Kanhu Moharana, Francisnei Pedrosa-Silva, L\'\ibera Maria Dalla-Costa, and Thiago Venancio. Molecular epidemiology of 16S rRNA methyltransferase in Brazil: RmtG in Klebsiella aerogenes ST93 (CC4). *Annals of the Brazilian Academy of Sciences*, 90(3 (Supl.1)), 2018

○ Rajesh K Gazara, Kanhu C Moharana, Daniel Bellieny-Rabelo, and Thiago M Venancio. Expansion and diversification of the gibberellin receptor GIBBERELLIN INSENSITIVE DWARF1 (GID1) family in land plants. *Plant molecular biology*, 97(4-5):435–449, jul 2018

○ Monica Danilevicz, Kanhu Moharana, Thiago Venancio, Luciana Franco, Sérgio Cardoso, Mônica Cardoso, Flávia Thiebaut, Adriana Hemerly, Francisco Prosdocimi, and Paulo Ferreira. Copaifera langsdorffii Novel Putative Long Non-Coding RNAs: Interspecies Conservation Analysis in Adaptive Response to Different Biomes. *Non-Coding RNA*, 4(4):27, oct 2018

○ Bikash R. Sahoo, Takuya Genjo, Kanhu C. Moharana, and Ayyalusamy Ramamoorthy. Self-Assembly of Polymer-Encased Lipid Nanodiscs and Membrane Protein Reconstitution. *The Journal of Physical Chemistry B*, 123(21):4562–4570, may 2019

○ Kanhu C Moharana and Thiago M Venancio. Polyploidization events shaped the transcription factor repertoires in legumes (Fabaceae). *bioRxiv*, page 849778, jan 2019

○ Fabricio Brum Machado, Kanhu C. Moharana, Fabricio Almeida-Silva, Rajesh K. Gazara, Francisnei Pedrosa-Silva, Fernanda S. Coelho, Clícia Grativol, and Thiago M. Venancio. Systematic analysis of 1,298 rna-seq samples and construction of a comprehensive soybean (glycine max) expression atlas. *bioRxiv*, 2019

ADDITIONAL EXPERIENCE & ACHIEVEMENTS

Teaching:
- Worked as lecturer in *Jaipur National University, Jaipur, India* for one year Jan, 2011 - Feb, 2012. I taught subjects like Phylogenetic Analysis, PERL, Proteomics and Fundamentals of Bioinformatics to undergraduate students.
- Conducted a three day hands on workshop *PERL for Bioinformatics* at UENF. June 12-13, 2017.
- Conducted a three day mini-course titled *Introduction to programming in R*, organised by NEBBIO,UENF. 25-27 November, 2019

Certifications:
- R programming (on Coursera), April 2015.
- Computational Molecular Evolution (on Coursera), September 2013.
- Machine Learning by Stanford University (on Coursera), August 2016.

Conference and poster presentations:
- Research Methodology, data management and Biostatistics using web based statistical software, *National Institute of Animal Nutrition and Physiology, Bangalore, India*. December 10-11, 2010.
- Sarangi AN, Moharana KC, Aggarwal R, Aggarwal A. Differences in bacterial community composition in healthy Indian children and adults compared to those in healthy persons in the United States. Poster presented at: *Big Data analysis and Translation in Disease Biology;January 18-22, 2015; Jawaharlal Nehru University, New Delhi, India*. **(Best poster award)**
- Moharana KC, Venancio TM. Impact of non-synonymous mutations in adaptive diversification and domestication of soybean. Poster presented at: *X-meeting 2016, 12th International conference of AB3C on Bioinformatics; November 16-18, 2016; Universidade Federal de Minas Gerais, Belo Horizonte, Brazil.*
- Moharana KC, Venancio TM. Phylogenomic analysis of transcription factor families and the evolution of nitrogen fixation in legumes. Poster presented at: *III CONGRESSO FLUMINENSE DE PÃŞS-GRADUAÃĞÃČO, Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes, RJ, Brazil*. **(Honorary Award)**

PROFESSIONAL RECOMMENDATIONS

Available on request