

Kanhu Charan Moharana

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Campos dos Goytacazes, RJ, Brazil

EDUCATION

Ph.D. in Biosciences and Biotechnology

Universidade Estadual do Norte Fluminense Darcy Ribeiro

2016-now
 Rio de Janeiro, Brazil

Project: Genome duplication has a remarkable impact on angiosperm evolution and crop domestication. Retention transcription factors (TF) in duplicate copies plays an important role in speciation. Soybean has a paleopolyploidy genome and ~75% of its genes are still in duplicate copies. However, a systematic analysis of soybean TFs in the light of genome duplication events during soybean evolution is yet to be conducted. In my PhD, I am using 20 plant genomes to study the duplicate TF retention pattern and their functional divergence, especially in soybean and legumes.

Besides I am also involved in collaborative projects such as de novo transcriptome assembly and annotation of non-model plant species namely *Cedrela fissilis* and *Copaifera langsdorffii*.

M.Sc in Bioinformatics

Orissa University of Agriculture and Technology

2008-2010
 Odisha, India
 80.6%, first class

Dissertation title: Development of tool for operon prediction using genetic algorithm.

Project: Many approaches are available to predict bacterial operons, but an easy to use GUI based tool was not available in the public domain. We developed a graphical tool to predict cluster of genes likely to be within an operon. We combined two different approaches (along with an novel, but less sensitive heuristic algorithm) to predict bacterial operons.

B.Sc in Botany(H)

Aska science college (Berhampur University)

2005-2008
 Odisha, India
 70%, first class

Botany, chemistry, Biotechnology, Mathematics

RESEARCH EXPERIENCE

Project Scientist-I

Sanjay Gandhi Postgraduate Institute of Medical Sciences, Lucknow, India

June 2013-
 January 2016

Research advisor: Prof. Rakesh Aggarwal, MD, DM.

Projects involved:

- Predicting RNA editing sites using genome independent method.
- Analyzing meta-genomic data.
- Developing a on-line survey portal to score Systemic Lupus

Erythematosus patients.

Junior Research Fellow

National Institute of Plant Genome Research, New Delhi, India

Research advisor: Dr. Mukesh Jain, PhD.

2012 Oct -
2013 May

- I was involved in a work to identify genomic single nucleotide polymorphisms and insertions-deletions in three contrasting varieties of rice and correlate their role in contrasting water stress.
- The study involved next-generation sequencing analysis on a 48 core computation grid.
- Besides, I was also involved in other bioinformatics support.

Research Assistant

Rajendra Memorial Research Institute of Medical Sciences, Patna, India

Supervisor: Dr. Ganesh Ch. Sahoo, PhD.

2012 Mar -
2012 Oct

- 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.

TEACHING EXPERIENCE

Lecturer

Jaipur National University, Jaipur, India.

2011 Jan -
2012 Feb

- I was teaching Bioinformatics to B.Sc. and M.Sc. (Biotech.) students. The topics I was concerned with were Phylogenetic Analysis, PERL, Proteomics and Fundamentals of Bioinformatics.
- Also, I used to take topics like Biostatistics, Cytology to under graduate-students.
- The classes had strength of 15 students. Preparing questions for semester examinations and evaluation.
- Designing and revising syllabus for bioinformatics.
- Developing new teaching resources for other biological subjects using bioinformatics.

OTHER CERTIFICATIONS

1. R programming (on Coursera), April 2015.
2. Computational Molecular Evolution (on Coursera), September 2013.
3. Machine Learning by Stanford University (on Coursera), August 2016.

PUBLICATIONS

1. Rana, S., Dikhit, M. R., Rani, M., **Moharana, K. C.**, Sahoo, G. C., & Das, P. (2012). CPDB: cysteine protease annotation database in *Leishmania* species. *Integrative Biology : Quantitative Biosciences from Nano to Macro*, 4(11), 1351–7.

2. Jain, M., **Moharana, K. C.**, Shankar, R., Kumari, R., & Garg, R. (2014). 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.
3. Sahoo, G. C., Rani, M., Ansari, M. Y., Jha, C., Rana, S., Dikhit, M. R., **Moharana K.C.**, Kumar, R., Das, P. (2014). Structure, evolution and virtual screening of NDM-1 strain from Kolkata. *International Journal of Bioinformatics Research and Applications*, 10(3), 235–63.
4. Dikhit, M. R., **Moharana, K. C***, Sahoo, B. R., Sahoo, G. C., & Das, P. (2014). LeishMicrosatDB: open source database of repeat sequences detected in six fully sequenced Leishmania genomes. *Database : The Journal of Biological Databases and Curation*, 2014.
5. **Moharana, K. C.**, Dikhit, M. R*, Sahoo, B. R., Sahoo, G. C., & Das, P. (2015). GAOPP: Operon prediction in prokaryotes using genetic algorithm. *Current Bioinformatics*, 10(3).
6. Gazara, R. K., **Moharana, K. C.**, Bellieny-Rabelo, D., & Venancio, T. M. (2018). Expansion and diversification of the gibberellin receptor GIBBERELLIN INSENSITIVE DWARF1 (GID1) family in land plants. *Plant Molecular Biology*, 97(4–5), 435–449.
7. Danilevycz, M.F.; **Moharana, K.C.***; Venancio, T.M.; Franco, L.O.; Cardoso, S.R.S.; Cardoso, M.; Thiebaut, F.; Hemerly, A.S.; Prosdocimi, F.; Ferreira, P.C.G. (2018) *Copaifera langsdorffii* Novel Putative Long Non-Coding RNAs: Interspecies Conservation Analysis in Adaptive Response to Different Biomes. *Non-Coding RNA*, 4, 27.
8. Passarelli-Araujo, H., Palmeiro, J., **Moharana, K.**, Pedrosa-Silva, F., Dalla-Costa, L. M., & Venancio, T. (2018). 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)).
9. Sahoo BR, Genjo T, **Moharana KC**, Ramamoorthy A. (2019) Self-Assembly of Polymer-Encased Lipid Nanodiscs and Membrane Protein Reconstitution. *J Phys Chem B*;123(21):4562-4570.
10. Passarelli-Araujo, H., Palmeiro, J., **Moharana, K.**, Pedrosa-Silva, F., Dalla-Costa, L. M., & Venancio, T.(2019) Genomic analysis unveils important aspects of population structure, virulence, and antimicrobial resistance in *Klebsiella aerogenes*. bioRxiv 581645; doi: <https://doi.org/10.1101/581645> (accepted in The FEBS Journal)

*Co-first author

CONFERENCES AND POSTER PRESENTATION

1. Second Science Conclave: A congregation of Novel Laureates, Indian Institute of Information Technology, Allahabad, India. December 08-14, 2008.
2. Application of Bioinformatics in Medical Sciences with an Introduction to SOLiD, Biomedical Informatics Centre, Rajendra Memorial Research Institute of Medical Sciences, Patna, India. October 22-23, 2010.

3. Research Methodology, data management and Biostatistics using web based statistical software, National Institute of Animal Nutrition and Physiology, Bangalore, India. December 10-11, 2010.
4. 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**)
5. 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.
6. 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 PÓS-GRADUAÇÃO, Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes, RJ, Brazil. (**Honorary Award**)

KEY BIOINFORMATICS SKILLS

Programming skills: Python, PERL, R, Bash. **Phylogenetic tools:** RAxML, PhyML, ETE3 python package, APE R-package. **NGS read mapping tools:** Bowtie, BWA, Tophat, STAR. **De novo assembler:** SPADIS, Trinity. **Gene expression analysis:** Cufflinks, StringTie, HTSeq, DESeq, edgeR. **Database skills:** MySQL, sqlite3, PHP. **UI development:** Tk-perl, Shiny web app development.

PROFESSIONAL REFERENCES

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|---|---|
| <p>1. Ganesh ch. Sahoo, Ph.D
Scientist-C, Biomedical Informatics Division,
Rajendra Memorial Research Institute of Medical Sciences (RMRIMS)
Agam kuan, Patna, Bihar, India.
Mobile: +91-9472508523
E-mail: ganeshiitkqp@gmail.com</p> | <p>2. Gaurav Agarwal, Ph.D.
Special Project Scientist, Applied Genomics
Center of Excellence in Genomics
International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)
Patancheru, Telengana, India
Mobile: +91-9618126648
E-mail: gaurav.agarwal@cgiar.org</p> |
| <p>3. Sukant ku Pradhan.
HOD, Department of Bioinformatics, Odisha University of Agriculture and Technology (OUAT),
Bhubaneswar, Odisha, India.
Mobile: +91-9437442622
E-mail:- ksukantapradhan@gmail.com</p> | <p>4. Thiago Motta Venancio, Ph.D.
Ph.D., Associate Professor,
Universidade Estadual do Norte Fluminense Darcy Ribeiro,
Av. Alberto Lamago, 2000,
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