

# Yogendra Kumar Bhaskar

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<https://github.com/bhaskar-hub/>

Department of Biology, SRMIST

Delhi-NCR Campus, Ghaziabad

## Employment

22 Sep. 2025 **Assistant Professor**

to Department of Biology, SRM Institute of Science and Technology

Present Delhi-NCR Campus, Ghaziabad, Uttar Pradesh

**Role:** Responsible for teaching undergraduate courses in Computational Biology (*21BTB102T*) and Environmental Science (*21CYM101T*), mentoring students, developing independent research directions, and pursuing external grant opportunities.

12 Jul. 2023 **Project Scientist-II** (Bioinformatics)

to Division of Genomic Resources, ICAR-National Bureau of Plant Genetic Resources

19 Sep. 2025 Pusa Campus, New Delhi

**Role:** Responsible for managing and analyzing genotype and whole-genome sequencing data from diverse plant species, including Wheat, Chickpea, Lentil and Mung Bean.

20 Feb. 2023 **Research Associate-III** (Bioinformatics)

to Centre for Agricultural Bioinformatics, ICAR-Indian Agricultural Statistics Research

11 Jul. 2023 Institute, Pusa, New Delhi

**Role:** Engaged in the analysis of next-generation sequencing data, including RNA-Seq, whole-genome sequencing, and 16S-rRNA sequencing.

29 Jun. 2021 **Project Scientist-I** (Bioinformatics)

to ICMR-AIIMS Computational Genomics Centre, Indian Council of Medical Research

31 Dec. 2022 (ICMR), New Delhi

**Role:** Managing and analyzing the high throughput sequencing data of Covid-19 and Human from different institutes and developing the pipeline for data analysis.

## Education

2014-2021 **PhD**, Biochemistry and Molecular Biology

University of Chinese Academy of Sciences, Qingdao Institute of Bioenergy and Bioprocess Technology, Beijing, China

**Thesis title:** Genome-wide protein stoichiometry prediction in Selective RNA Processing

and Stabilization operons and its implications on bacterial environmental adaptation

**Supervisor:** Prof. Jian Xu

**Honors:** UCAS Scholarship for International Students recipient (100% tuition+fellowship)

2012-2014 **Master of Technology**, Computational and Systems Biology

School of Computational and Integrative Sciences, Jawaharlal Nehru University, India

**Thesis title:** Assembly, annotation and differential expression analysis from RNA-Seq data using Trinity: Application to *De-novo* sequences of the Indian Pitcher plant

**Supervisor:** Prof. Andrew Lynn

2007-2011 **Bachelor of Technology**, Information Technology

Babu Banarasi Das National Institute of Technology & Management,  
Uttar Pradesh Technical University, India

**Final year project:** On-Line recruitment system

## Research Interest

- Next/Third generation sequencing data analysis
- Genome-Wide Association Study (GWAS) and genomic selection
- Gene regulation and evolution in prokaryotes
- Bioinformatics tools development
- Data classification and prediction using Machine Learning

## Research Experience

12 Jul. 2023 **Project Scientist-II,**

to

19 Sep. 2025

- Performing a comprehensive analysis of the **whole genome sequencing** data for Mung bean, which includes sequencing reads alignment to reference genome, **variant calling**, filtration and annotation.
- Development of a **variant Map** of Mung bean samples from across the globe.
- Conducted a **Genome-wide Association Study** (GWAS) by utilizing both genotype and phenotype data of Chickpea to identify significant genetic variants associated with observable traits.
- Development of diverse **core collection** of Wheat and Mung bean using genotyping data.
- Perform a GWAS on wheat genotyping data, followed by the **Quantitative Trait Loci** (QTL) identification and **genomic selection**.
- **Classifying** Lentil roots based on root images using **machine learning** algorithms.

- Development of a **next-generation SNP genotyping array** for wheat to enhance precision and efficiency in genomic studies and breeding programs.
- Compose final manuscripts of original research for peer-reviewed academic journals.
- Advise graduate students and technicians on professional development (scientific design, management, and presentation skills).
- Evaluate new data and research innovation as **peer reviewer for leading academic journals**.

20 Feb. 2023 **Research Associate-III,**

to ● Analysis of miRNA based on next generation sequencing data of Cattle and Buffalo.

11 Jul. 2023

- Characterization of enzymatic activity of *Trichoderma asperellum* using next and third generation sequencing data.
- Assembling the mitochondrial genome of Tree Bean using the whole genome sequencing data and performing the comparative analysis with related species.

29 Jun. 2021 **Project Scientist-I,**

to ● Working with Covid-19 data from third generation sequencing technologies such as

31 Dec. 2022

- Oxford Nanopore MinION technology.
- Performing various kinds of analysis, such as genome guided/*de-novo* assembly, variant-calling, lineage prediction, etc, on **exome** and **RNA-Seq** sequencing data.
- Clinical reporting based on exome and whole genome sequencing data.
- Development of pipeline for the Covid-19 data analysis from three sequencing platforms, *i.e.*, **Illumina, IonTorrent** and **Oxford Nanopore technologies**.
- Study to evaluate the changes in gastric microbiota in the presence and absence of *H. pylori* infection using **16s-rRNA** sequencing data.
- Investigating Effective Diagnostic Biomarkers and Immune Cell Infiltration in Breast and Lung Cancer through bioinformatics analysis and **machine learning** Strategies.
- Providing training to bachelor's and master's students from different institutes and universities.

Oct. 2014 **Doctorate,**

to ● Developed a genome-wide strategy to predict stable stem-loops in Clostridium species

Sep. 2020

by analyzing stem-loop parameters. This work involved unraveling the intricate folding patterns of RNA molecules, contributing to our understanding of gene regulation.

- Identified SRPS operons within the whole genome, shedding light on how bacteria fine tune their gene expression.
- Predicted protein stoichiometry in SRPS operons using stem-loop  $\Delta G$ -ratios, bridging the gap between RNA structure and protein abundance.
- Implemented these functions as a tool using Perl and awk for the Linux platform (SLOFE-RatioCalculation). <https://github.com/bhaskar-hub/SLOFE-RatioCalculation>
- Phylogenetically explored the evolutionary features of the genes and operons in mesophilic *Clostridium* species.
- Applied the Bacterial Systematics to explore the environmental adaptation of bacteria.
- Proposed a novel theory for the evolution of SRPS operons in Gram-positive bacteria, emphasizing the role of  $\Delta G$ -ratios in shaping bacterial genomes.
- Acquired proficiency in various experimental techniques, including bacterial cell culture ,plasmid extraction, RNA/DNA extraction, PCR, gel electrophoresis, bacterial transformation, and qRT-PCR. Successfully validated results using these techniques.
- Investigated bacterial transcription and post-transcriptional sites using dRNA-Seq data.
- Analyzed 16S-rRNA and ITS regions of oral microbiome data to profile the microbial diversity.
- Utilized an ensemble machine learning approach to classify a diverse range of microalgal species based on Raman spectroscopy data.

Jul. 2013

**M. Tech,**

to

- Contributed to the development of an RNA-seq data analysis pipeline using R.

Aug. 2014

- Designed and deployed a workflow for assembly, annotation, and differential expression analysis using the Trinity suite of software.
- Performed the *De-novo* transcriptome analysis of the Indian Pitcher plant.

May 2013

**Summer Trainee**, Bioinformatics Center, Bose Institute, Kolkata

to

Supervisor: Dr. Zhumar Ghosh

June 2013

- Conducted Express Path Analysis (EPA) on microarray data from cancer cells, unraveling intricate molecular pathways and shedding light on potential therapeutic targets.
- Contributed to the design and development of the piRNAQuest database using Perl and PHP. <http://bicesources.jcbose.ac.in/zhumur/pirnaquest/>

## Editorial work

Critique and evaluate novel manuscripts and recommend acceptance/rejection for publication

- Microbiology Spectrum, American Society for Microbiology
- Journal of Advanced Research, Elsevier
- Advanced Science, Wiley
- Plos One, PLOS
- Applied and Environmental Microbiology, American Society for Microbiology
- mSystems, American Society for Microbiology

## Conferences

- 2014 Attended 8th International Conference on Systems Biology/ 4th Translational Bioinformatics Conference, Qingdao, China
- 2017 Presentation at Sino-Israel Bioenergy seminar, Qingdao, China
- 2022 Member of Organizing Committee for the 2nd International colloquium RMBPD 2022 organized by Department of Zoology, University of Delhi, Delhi
- 2022 Organized research seminar on Biomedical Engineering at ICMR-NIMS, New Delhi
- 2022 Participated as delegate in Training Program on “Traditional Medicine: Modern Approaches for Affordable and Accessible Healthcare” sponsored by Department of Science & Technology (DST)

## Publications

- Dkhar J, **Bhaskar YK**, Lynn A, Pareek A. Pitchers of *Nepenthes khasiana* express several digestive-enzyme encoding genes, harbor mostly fungi and probably evolved through changes in the expression of leaf polarity genes. *BMC Plant Biology* 20, 524 (2020).
- **Bhaskar Y**, Su X, Xu C, Xu J. Predicting Selective RNA Processing and Stabilization operons in *Clostridium* spp. *Frontiers in Microbiology* 9;12:673349 (2021).
- Nair S S D, Zhu P, **Bhaskar Y**, Xu J, Teng F. Influence of DNA extraction methods and 16S-rRNA targeted hypervariable regions on microbial diversity profiling of dental plaque and saliva. *Science Asia* 47(5) (2021).
- **Bhaskar Y**, Heidari B M, Xu C, Xu J. Evolution of Selective RNA Processing and Stabilization operons in cellulosome-harboring *Clostridium* spp. (**Under review**; DOI: <https://doi.org/10.1101/2021.06.12.447814>)

- Heidari B M, Hekmat A M, He Y, **Bhaskar Y**, Ji Y, Xu J. Culture-Free Identification and Metabolic Profiling of Microalgal Single Cells via Ensemble Learning of Ramanomes. *Analytical Chemistry* 93, 25, 8872–8880 (2021).
- Zheng S, Meng Z, Min L, **Bhaskar Y**, Jinshan Z, Youran J, Hongbing C, Heping Z. Interactions between Human Gut Microbiome Dynamics and Sub-Optimal Health Symptoms during Seafaring Expeditions. *Microbiology Spectrum* Vol. 10, No. 1 (2022).
- Singh P, **Bhaskar Y**, Verma P, Rana S, Goel P, Kumar S, Gouda K C, Singh H. Impact of comorbidity on patients with COVID-19 in India: A nationwide analysis. *Frontiers in Public Health*, 10. (2023)
- Arfi S, Sharma P, Das K, **Bhaskar Y**, Goel I, Singh H, Das R. Low abundance of healthy bacteria in the gastric microbiota can be a potential biomarker for gastrointestinal diseases: A pilot study. *Indian Journal of Medical Research*, 159(2) (2024)
- Singh A, Sharma P, Das K, **Bhaskar Y**, Goel I, Singh H, Das R. Alteration in the gastric microbiota of Erosive Reflux Disease and Non-erosive Reflux Disease patients: An indicator for disease progression. *Biomedicine* 44(1) (2024).
- Sharma P, Singh A, Singh S, Das K, **Bhaskar Y**, Goel I, Singh H, Das R. Alteration of gastric microbiota in Helicobacter pylori-infected individuals suffering from GERD, DU, and gastritis. *Indian Journal of Pathology and Microbiology* 1015, 23 (2024).
- Mathur A, Sharma P, Singh S, Das K, **Bhaskar Y**, Goel I, Singh H, Das R. Aging-related Alterations in Gastric Microbiota: A Potential Contributor to Gastrointestinal Diseases. *Journal of Preventive, Diagnostic and Treatment Strategies in Medicine* 3(2), (2024)
- Goel I, **Bhaskar Y**, Singh S, Dhar R, Karmakar S. Role of AI in empowering and redefining the oncology care landscape: Perspective from a developing nation. *Frontiers in Digital Health*, 7, p.1550407 (2025).

### **Publications (In submission)**

- Rajendran S, Tripathi S, **Bhaskar Y**, Singh AK, Parida SK, Kumar A, Chinnusamy V. *Genome-wide association mapping identifies critical genomic regions for tissue tolerance traits and stress signalling modules associated with seedling stage salinity tolerance in chickpea.* (Under review)

- **Bhaskar Y**, Kumar D, Iquebal MA. *Assembly and annotation of mitochondrial genome of an underutilized leguminous tree bean with rich nutritional value: Parkia roxburghii*.
- **Bhaskar Y**, Velmurugan S, Iquebal MA, Kamil D, *Comparative analysis of Whole Genome, metabolome, and biocontrol efficacy of High and Low Potential Strains of Trichoderma asperellum*.
- Bharti D, **Bhaskar Y**, Singh H, Kumar A. *Global mutational analysis in spike protein of SARS-CoV-2*.
- Goel I, Kumar A, **Bhaskar Y**, Singh H, Katiyar A. *Genome-wide screening of novel diagnostic and therapeutic targets in Esophageal squamous cell carcinoma using meta-analysis of Whole-exome sequencing data*.

### Book chapter

- Singh A, Priyadarshi M and **Bhaskar Y**; Tools for Identification of Duplicates in Gene Bank Accessions Using Molecular Markers. In: G.P. Singh, R. Singh, S. Rajkumar and D.P. Wankhede (Eds) *Genomic Tools in Plant Genetic Resource Management- A Practical Manual; ICAR - National Bureau of Plant Genetic Resources, New Delhi; (2023); pp 69-72. ISBN: 978-81-937111-7-0*.
- **Bhaskar Y**, Goel I, Ranga V and Singh C.H. Challenges and Fate of Bio-nanomaterials in Industrial Applications. In: N.K. Sharma, R. Sharma and T.C. Dakal (Eds) *Bio-Nanomaterials in Environmental Remediation. Wiley (2024). ISBN: 978-3-527-35420-7*.

### Honours

2014	Awarded with University of Chinese Academy of Sciences international PhD scholarship
2012	Qualified GATE-exam
2010	Microsoft certified for the Core web application technologies
2009	IBM certified for Database Associate with DB2 9 fundamentals

**Languages** English (Proficient), Hindi (Native) and Chinese (Beginner)

### Skills

Computer Languages:	Perl, R, Awk, Shell scripting and Python (Beginner)
Operating Systems:	Linux

Experimental techniques: Bacterial cell culture, Plasmid extraction, RNA/DNA extraction, PCR, Gel electrophoresis, Bacterial transformation and qRT-PCR

## References

- Prof. Andrew Lynn  
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New Delhi, India
- Prof. Jian Xu  
E-mail: [xujian@qibebt.ac.cn](mailto:xujian@qibebt.ac.cn)  
Single Cell Center, Qingdao Institute of Bioenergy and Bioprocess Technology,  
Chinese Academy of Sciences, Qingdao, China
- Dr. Mir Asif Iquebal, Principal Scientist  
Email: [ma.Iquebal@icar.gov.in](mailto:ma.Iquebal@icar.gov.in)  
Centre for Agricultural Bioinformatics (CABin)  
ICAR-Indian Agricultural Statistics Research Institute, New Delhi, India