

SHUBHAM S. TUPE

M.Tech Bioinformatics, School of Life Sciences, University of Hyderabad

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EDUCATION

University of Hyderabad, Institute of Eminence

Telangana, India

2 year M. Tech Bioinformatics (CGPA: 8.76/10*)

2023 -2025

- **Relevant coursework:** Bio-informatics, Drug Design, Computational Systems Biology, Machine Learning Methods and Data Analytics, Molecular Modeling and Simulations, R programming, Python, Genomics, Proteomics, Mathematics and Statistics

Mahatma Phule Krishi Vidyapeeth, Rahuri

Maharashtra, India

4 Year B. Tech Biotechnology. CGPA: 8.76/10

2019-2023

- **Relevant coursework:** Cell Biology, Basic Genetics, Molecular Biology, Microbiology, Basic Statistics, Nanobiotechnology, Molecular Marker Technology, Introductory Bioinformatics, Fundamentals of Crop Protection, Bio-mathematics, General Biochemistry

Maharashtra State Board of Higher Secondary Education, Pune

India

Class XII. Marks: 74%

2017-18

Maharashtra State Board of Higher Secondary Education, Pune

India

Class X. Marks: 92%

2015-16

ACHIEVEMENTS

- Student of the Year 2023 (B. Tech)
- Qualified JAM-BT 2023
- Qualified GATE -XL 2023
- 1st Academic Topper (III Year, B. Tech)
- 3rd Academic Topper (II Year, B. Tech)
- 3rd Position in state level science exhibition held (Air Scrubber Model, 9th std)

RESEARCH EXPERIENCE

Master's Dissertation, School of Life Sciences, UoH

Jul 2024 – June 2025

Supervised by: Prof. JSS Prakash

Hyderabad, Telangana

Title: Computational prediction of cAMP Receptor Protein, SyCRP1's, Regulon in genome of Synechocystis sp. PCC 6803

Aim: To reveal the regulatory role of SyCRP1 by using gene expression data. Following the Pathway enrichment analysis of genes having SyCRP1 binding sites to identify key pathways

- Identification of all the possible SyCRP1 binding sites in Synechocystis genome - using experimentally (ChIP-seq) discovered binding site information
- Classification of all the possible target genes into their functional category- to understand the possible regulation of SyCRP1 under different stresses
- Integration of motif position information with gene expression data- to evaluate the significant region of the DNA responsible for transcriptional regulation

Mentored by: Dr. S. K. Holkar , Prof. B. B. Ghorpade**Title:** Molecular Identification and Evaluation of Fungal Endophytes for the Management of Grapevine Diseases**Aim:** To identify fungal endophytes from grapevine leaves and evaluate their bio-control potential against grapevine pathogens.

- Maintained the pure culture and microscopic identification of fungal endophytic isolates from leaves of grapevine cultivars
- Isolated total genomic DNA from isolated fungal endophytes and PCR amplification of genomic DNA using ITS universal primers and amplicon sequencing.
- Studied the compatibility assay of fungal endophytes against different fungicides of Downy mildew
- Studied antagonistic activity of all fungal endophytes against NRCG Colletto isolate of (*Colletotrichum* species)

Undergraduate Dissertation, CABT College, Loni

Quencher Biotech Private Limited

1 Nov 2022 - 10 Apr 2023

Sangamner, Maharashtra

Mentored by: Dr. Sandeep Kale , Prof. B. B. Ghorpade**Title:** DNA barcoding Primers for Molecular Characterization Species Discrimination of Wheat Genotypes**Aim:** To construct the standard DNA barcode for the discrimination of *Triticum aestivum* species.

- * Extraction of genomic DNA of wheat genotypes
- * PCR amplification using rbcL and matK gene primers
- * Identification, Genetic variation, and DNA barcode analysis of wheat genotypes using rbcL and matK gene sequences

Skills

- * **Wet Lab Skills:** Fungal cell culture, DNA/Protein extraction and purification, qPCR, Agarose gel electrophoresis, Protein estimation (Bradford assay), SDS-PAGE, Column chromatography
- * **Programming Languages:** Python, R, C
- * **Operating Systems & Scripting:** Linux (command-line and scripting), Windows
- * **Bioinformatics Tools & Software:**
 - Sequence Analysis: BLAST, HISAT2, STAR, FeatureCounts, DESeq2
 - Quality Control: FastQC, MultiQC
 - Structural Biology: AutoDock, GROMACS, AlphaFold, Modeller
 - Other Tools: SnapGene, Nextflow
- * **Database Management:** PostgreSQL

CERTIFICATIONS

Hands-on Introduction to Linux Commands and Shell Scripting**Oct 2024**

Linux architecture — file, content, navigational, compression, and networking command — shell scripts — Schedule cron jobs in Linux with crontab

Bioinformatics: Learn Bulk RNA-Seq Data Analysis From Scratch**Sep 2024**

1. Basic molecular biology and the Central Dogma 2. Explored RNA-Seq experimentation and its applications. 3. Analyzed FASTQ files in a Linux environment. 4. Worked with various file formats, including SAM, BAM, FASTQ, and GTF. 5. Utilized R and RStudio for data analysis. 6. Conducted differential gene expression analysis using the DESeq2 package. 7. Created visualizations such as PCA, MA, heatmaps, and volcano plots to present data effectively. 8. Performed GO and pathway analysis

Drug Discovery Using CRISPR**15 Days**

Biotechnika Info Labs Pvt. Ltd.

CONFERENCES ATTENDED

International Conference on Frontiers in Basic Biology, Biotechnology & Bioinformatics

Attended various talks and seminars focusing on advancements in biotechnology and bioinformatics. 15-18 Feb 2024