Mansi Srivastava

Doctoral Candidate, Molecular and Cell Biology, Department of Cell Biology and Molecular Genetics, University of Maryland, College Park
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I study how bacteria regulate the expression of long biosynthetic gene clusters. My work focuses on LoaP, a specialized paralog of the transcription factor NusG that promotes RNA-dependent transcriptional antitermination across polyketide synthase operons, combining bacterial genetics in non-model species with reporter assays, transcriptomics and proteomics.

Research Experience

Doctoral Candidate, University of Maryland, College Park **2023–present**

Department of Cell Biology and Molecular Genetics, laboratory of Dr. Wade C. Winkler
Processive antitermination in bacteria: LoaP, a NusG paralog that enhances post-initiation expression of long antibiotic biosynthesis operons. Established conjugation-based genetic methods in the laboratory and extended them to non-model bacteria that previously had no genetic tools. Heterologous reporter assays, RNA-seq and proteomics.

Graduate Researcher, University of Maryland, College Park **2021–2023**

Laboratory of Dr. Stephen M. Mount
Computational methods for sequence data: latent Dirichlet allocation for 5′ splice site prediction and discovery of latent sequence subtypes, and low-rank tensor methods for high-dimensional data.

Junior Research Fellow, National Centre for Biological Sciences **2018–2019**

Laboratory of Dr. Shashi Thutupalli
Single-nucleotide polymorphism and copy-number analysis of yeast populations surviving repeated freeze–thaw cycles, identifying genomic regions associated with increased survival and trehalose production.

M.Sc. Thesis Research, Institute of Bioinformatics and Applied Biotechnology **2018**

Laboratory of Dr. Sanjay Ghosh
Master's thesis project on metal toxicity: development of a whole-cell biosensor in engineered yeast for detecting heavy metals in the environment, harnessing the yeast's native defence mechanisms against toxic metals. Designed and constructed a promoter–reporter assay using arsenic-responsive promoter sequences not previously tested in biosensor applications. Assembled multi-fragment DNA constructs by sequence overlap extension PCR and Gibson assembly and integrated them into the yeast genome to give a stable, self-sustaining biosensor, with reporter efficiency evaluated by FACS. Established a streamlined protocol for assembling complex transgenic constructs to support future biosensor development.

Education

Ph.D. candidate, Molecular and Cell Biology, University of Maryland, College Park **in progress**

Department of Cell Biology and Molecular Genetics.

M.Sc., Bioinformatics and Applied Biotechnology **2018**

Institute of Bioinformatics and Applied Biotechnology, Bengaluru. CGPA 8.49.

B.Sc. (Honours), Biomedical Sciences **2016**

Shaheed Rajguru College of Applied Sciences for Women, University of Delhi. 77.5%.

Selected Research Contributions

LoaP-Mediated Antitermination in Non-Model Bacterial Species

With Madison D. Jermain, Conor C. Jenkins and Wade C. Winkler
Tested LoaP homologs from *Bacillus inaquosorum*, *B. cereus*, *B. thuringiensis* ser. *pondicherriensis* and *Paenibacillus polymyxa* in a heterologous *B. subtilis* reporter built from the *B. velezensis dfn* leader fused to *yfp*. Diverse homologs promoted readthrough of the *dfn* terminator in an RNA hairpin-dependent manner, supporting a conserved antitermination mechanism.

Regulation of the Macrolactin Pathway

With Conor C. Jenkins and Wade C. Winkler
Deletion of *loaP* in *B. inaquosorum* reduced macrolactin protein levels in stationary phase, while overexpression during exponential growth did not activate the pathway, indicating that LoaP-mediated regulation of the macrolactin cluster is context-dependent.

Conjugation-Based Genetic Tools for Non-Model Bacteria

With Wade C. Winkler

Established conjugation-based gene transfer in the laboratory and extended it to non-model species including *Bacillus thuringiensis*, *B. cereus*, *Rossellomorea vietnamensis*, *Priestia megaterium* and *Paenibacillus alvei*, enabling targeted knockout and reporter studies in organisms with no previously established genetic tools.

Mixtures of Position Weight Matrices for Sequence Subtype Discovery

With Shashwat Kumar and Stephen M. Mount

Used canonical polyadic decomposition to factorize the joint probability distribution over splice site sequences, recovering each subtype's consensus as an interpretable latent factor. A rank-3 decomposition recovered the major (U2) consensus, two subclasses of major sites, and the minor (U12) consensus when minor sites were only 12% of the data. Mutual information estimated from the fitted distribution identified the most discriminating positions, and classification was comparable to MaxEntScan.

Conference Presentations

1. *LoaP, a NusG Paralog, Promotes Off-target Effects in Bacillus Species* (poster)
   M. Srivastava, C. C. Jenkins, M. D. Jermain, W. C. Winkler. 22nd Biennial Meeting on Post-Initiation Activities of RNA Polymerases (Mountain Lake Termination Meeting), Mountain Lake Lodge, Virginia, 1–4 October 2026
2. *LoaP Mediated RNA-Based Anti-termination in Non-Model Bacterial Species* (poster, abstract MECH-SAT-460)
   M. Srivastava, M. D. Jermain, W. C. Winkler. ASM Microbe 2026, Washington, DC, June 2026
3. *Investigation of LoaP, a NusG Paralog, Across Non-Model Bacterial Species* (talk)
   Molecular and Cell Biology RIPS seminar, University of Maryland, March 2026
4. *Investigation of LoaP, a NusG Paralog, Across Non-Model Bacterial Species* (talk)
   Molecular and Cell Biology Retreat, University of Maryland, August 2025
5. *LoaP Regulated Operons in Diverse Bacterial Groups* (lightning talk)
   CAFPA–ASM DC, October 2024
6. *Mixture of Position Weight Matrices for Sequence Subtype Discovery* (poster)
   M. Srivastava, S. Kumar, S. M. Mount. NCI RNA Biology Symposium, 27–28 April 2023

Teaching

- Teaching Assistant, BSCI223: General Microbiology Laboratory, University of Maryland (2023)
- Teaching Assistant, BSCI410: Molecular Genetics, University of Maryland (2022)
- Teaching Assistant, BSCI103: The World of Biology, University of Maryland (2022)
- Teaching Assistant, BSCI161: Principles of Ecology and Evolution Laboratory, University of Maryland (2021)
- Teaching Assistant, BSCI171: Principles of Molecular and Cellular Biology Laboratory, University of Maryland (2021)

Professional Service

Reviewer for ACM Transactions on Computing for Healthcare (2022–2023).

Technical Skills

- **Molecular biology:** cloning and primer design, conjugation-based gene knockouts, PCR, RT-PCR and qPCR, restriction digestion, ligation, transformation, cell lysis and nucleic acid isolation
- **Genomics:** RNA-seq and differential expression analysis, proteomics, ChIP-seq and methylation analysis, metagenomics, genome annotation
- **Computational:** Python, R, shell scripting, Linux
- **Modelling:** homology modelling and docking (Chimera, PyMOL, Maestro); topic models and low-rank methods
- **Databases:** NCBI, UCSC, RCSB PDB, UniProt

Workshops

- Transcriptomics Workshop, University of Maryland, Baltimore County (2025)
- Mathematical and Statistical Explorations in Disease Modelling and Public Health, ICTS Bengaluru (2019)
- Exome Sequencing Workshop, IBAB (2017)
- StartUp Bio, IBAB (2017)
- Spectroscopic and Chromatographic Techniques, SRCASW (2016)