

CURRICULUM VITAE

Vikash Kumar Yadav, PhD

Email: vikash@unigoa.ac.in; yadav.vikash0301@gmail.com

Research Area

Chromatin Biology, Epigenetics and Single Cell Genomics, Transcription Regulation, Biology of non-coding RNA, Cellular Heterogeneity, Molecular Biology, Marine Genomics and NGS Data Analysis, Bioinformatics and Computational Biology.

Projects

1. Deciphering Chromatin Rewiring during Chickpea Seed Development (Ongoing, Funded by Department of Biotechnology, Govt. of India).

Research Experience

- ❖ **Assistant Professor (October 2024- Present)** at School of Biological Sciences and Biotechnology, Goa University, Goa, India.
- ❖ **Staff Scientist II (August 2023- October 2024)** at the National Institute of Plant Genome Research, New Delhi, India.
- ❖ **Post-doctorate (DBT-RA, March 2022- July 2023)** at the School of Biological Sciences and Biotechnology, Goa University, Goa, India.
- ❖ **Post-doctorate (October 2019- March 2021)** at Louvain Institute of Biomolecular Science and Technology (LIBST), UCLouvain, Belgium.
- ❖ **Post-doctorate (April 2017-July 2019)** at the Department of Plant Biology, Uppsala BioCenter, Swedish University of Agricultural Sciences, Sweden.
- ❖ **Ph.D. (2010-2017)** at Plant Molecular Biology Lab, Council of Scientific & Industrial Research-National Botanical Research Institute, Lucknow, India.

Awards, fellowships and other achievements:

- ❖ CSIR- Senior Research Associateship (SRA)/Scientists Pool Scheme fellowship (2023).
- ❖ DBT-Research Associateship from the Department of Biotechnology, India (2022).
- ❖ Cleared the Joint CSIR-UGC NET for JRF, ARS-NET -2015, GATE and CEEB.
- ❖ Editorial Board Member for BMC Research Notes.
- ❖ Members of the reviewer board of Plants (MDPI).

Research Directions

(A). Role of higher-order chromatin organization in seed biology.

Seeds constitute a significant part of our diet; however, our understanding of the molecular mechanisms underlying seed biology remains limited, thereby affecting the foundation of seed yield in agriculture. Thus, investigating the molecular mechanisms that regulate seed development presents an exciting research avenue with immense relevance for enhancing agricultural productivity.

To comprehensively comprehend seed biology, I am keen on exploring epigenetic approaches to identify enhancer elements using techniques such as Chromosome Conformation Capture (3C) based methods, ChIP-Seq, BS-Seq, RNA-Seq and Computational data analysis. These methods can help identify enhancer-like elements that govern the expression of genes associated with seed vigour. These enhancers represent potential targets for engineering agronomic traits and will open exciting avenues to develop climate-ready crops toward global food security.

(B). Dissecting cell heterogeneity in the context of the epigenomics landscape

Multicellular organisms harbor nearly identical genomes, yet distinct cells within these organisms perform specialized functions primarily due to their diverse epigenomes. Consequently, characterizing individual cell genomes holds immense significance, considering each cell encounters diverse physiological, environmental, and developmental cues. Single-cell sequencing technology, renowned for its unmatched resolution, has emerged as a potent tool for unraveling cellular heterogeneity.

Generating plant cell atlases based on epigenomic and transcriptomic data from diverse single-cell and developmental stages could serve as a valuable resource for comprehending gene function at the single-cell level. This approach could potentially address pivotal biological questions that traditional technologies relying on complex multicellular tissues cannot adequately answer.

Publications

1. Brahmam, G. S., Mishra, D., & Yadav, V. K*. (2024). ReDtool: a Python-based command line tool for restriction digestion analysis of large DNA sequences. **Journal of Plant Biochemistry and Biotechnology**, 1-4. **(Corresponding Author)**
2. Yadav V.K.*, Jalmi S.K., Tiwari S, Kerkar S.K. (2023). Deciphering shared attributes of plant long non-coding RNAs through a comparative computational approach. **Scientific Reports**, 13, 15101. **(Corresponding Author)**
3. Yadav V.K.*, Sawant S.V., Yadav A, Jalmi S.K., Kerkar S.K. (2022). Genome-wide analysis of long non-coding RNAs under diel light exhibits role in floral development

and the circadian clock in *Arabidopsis thaliana*. **International Journal of Biological Macromolecules**, 223, 1693-1704. (Corresponding Author)

4. Yadav, V.K., Singh, S., Yadav A., Agarwal, N., Singh B., Jalmi, S.K., Yadav, V.K., Tiwari, V.K., Kumar, V., Singh, R and Sawant, S.V. (2022). Stress conditions modulate the chromatin interactions network in *Arabidopsis*. **Frontiers in Genetics**, 12:799805.
5. Yadav, V.K., Santos-González, J. and Köhler, C. (2021). INT-Hi-C reveals distinct chromatin architecture in endosperm and leaf tissues of *Arabidopsis*. **Nucleic Acids Research**, 49(8), 4371-4385.
6. Yadav V.K. and Claeys Bouuaert C. (2021). Mechanism and Control of Meiotic DNA Double-Strand Break Formation in *S. cerevisiae*. **Frontiers in Cell and Developmental Biology**, 9:642737.
7. Moreno-Romero, J., De León, G. D. T., Yadav, V. K., Santos-González, J., & Köhler, C. (2019). Epigenetic signatures associated with imprinted paternally-expressed genes in the *Arabidopsis* endosperm. **Genome Biology**, 20(1), p.41.
8. Yadav, V. K., Yadav, V. K., Pant, P., Singh, S. P., Maurya, R., Sable, A., & Sawant, S. V. (2017). GhMYB1 regulates SCW stage-specific expression of the GhGDSL promoter in the fibres of *Gossypium hirsutum* L. **Plant Biotechnology Journal**, 15(9), 1163-1174.
9. Sable, A., Rai, K. M., Choudhary, A., Yadav, V. K., Agarwal, S. K., & Sawant, S. V. (2018). Inhibition of Heat Shock proteins HSP90 and HSP70 induce oxidative stress, suppressing cotton fiber development. **Scientific Reports**, 8(1), 3620.
10. Dixit, G., Praveen, A., Tripathi, T., Yadav, V. K., & Verma, P. C. (2017). Herbivore-responsive cotton phenolics and their impact on insect performance and biochemistry. **Journal of Asia-Pacific Entomology**, 20(2), 341-351.
11. Singh, N., Kumar, R., Kumar, S., Singh, P. K., Yadav, V. K., Ranade, S. A., & Yadav, H. K. (2017). Genetic diversity, population structure and association analysis in linseed (*Linum usitatissimum* L.). **Physiology and Molecular Biology of Plants**, 23(1), 207-219.
12. Yadav, V.K., Rai, K.M., Yadav, V.K. and Sable, A. (2016). An overview of transcription regulatory elements in plant. **Journal of Biological Sciences and Medicine**, 2(4), pp.13-23.
13. Yadav, V.K. and Yadav, V.K. (2017). Impact of different carbon supplement on extraction of c-phycocyanin (C-PC) followed by poly-β-hydroxybutyrate (PHB) from *Nostoc muscorum*. **International Journal of Pharmaceutical Sciences and Research**, 620, p.A280.
14. Mishra, D. K., Agrawa, N., Choudhary, A., Yadav, V. K., & Yadav, V. K. (2018). An overview on advances in cotton genome and regulation of fiber development. *ISJR*, 7, 294-300.
15. Yadav, V. K., Rai, K. M., Kumar, N., & Yadav. V.K. (2019). Regulation of Gene Expression by Global Methylation Pattern in Plants Development. **In OMICS-Based Approaches in Plant Biotechnology**. <https://doi.org/10.1002/9781119509967.ch13>.

Interested in joining the lab?

Motivated researchers (Postdoc/Ph.D./Trainee) interested in Genomics and epigenomic regulation are welcome to contact the PI.