Dr. Priyanka Jain, PhD
Assistant Professor

Specialization: Bioinformatics, Systems biology, Deep Learning, Machine learning (ML) and Artificial Intelligence (AI) in genomics, Transcriptional regulation via LncRNA-miRNA-mRNA regulatory axis, Multi-omics/NGS pipelines for data integration, host pathogen interaction.
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Priyanka Jain did her graduation and post-graduation from Banaras Hindu University, Varanasi. She obtained her PhD in Bioinformatics under joint mentorship from the National Institute for Plant Biotechnology (NIPB), New Delhi and Banasthali Vidyapith, Rajasthan. During PhD she worked on transcriptional changes during blast disease. She worked for three years at the Institute of Genomics and integrative biology (IGIB). Further, she worked at National Institute of plant genome research (NIPGR) and Indian Agricultural Statistical Research Institute (IASRI), New Delhi for her post-doctoral work. She has a total of **30 publications** in Scopus indexed journals with **h-index of 16 and citations of 947**. She has presented number of posters and oral presentations at national and international conferences. She served as a reviewer for several international journals like Frontiers and BMC. She has been involved in regular teaching and training programs for master students and scientific faculty. She has generated and analyzed several genomic resources which are submitted at NCBI. She is interested in the development of new omics pipelines for coding and non-coding RNA identification and interaction. She is also interested in the development of a marker kit for deciphering gene regulatory network in host pathogen interaction using integrative multi-omic approaches. Her areas of expertise include analysis of different types of genomics (whole/organelle genome assembly, bulk and single-cell transcriptome sequencing, exome sequencing, Bisulphite seq, Chip-Seq, ATAC-Seq) data, Network Analysis, R, Python, shell scripting, and development of Deep Learning, Machine learning (ML) and Artificial Intelligence (AI) based model for genomics studies.

Fellowship /Awards/Achievements:
1) ICMR DHR Women Scientist Fellowship 2023.
2) Artificial intelligence program by DBT-STUTI in 2023.
3) INSc Young Researcher Award 2022.
4) INSc Young Researcher Award 2023.
5) CSIR-SRF conducted by CSIR-UGC, India for the year 2013.
6) Graduate aptitude test examination (GATE) for the year 2009 and 2010.
7) CSIR-NET conducted by CSIR-UGC, India for the year 2008 and 2009.
8) Summer research Fellowship from Indian Academy of Sciences (IAS), Bangalore, Indian National Science Academy New Delhi, National Academy of sciences, Allahabad for the year 2008.

Grant Received as PI:
1) ICMR-DHR scientist grant entitled "Genome wide identification of Liquid-Liquid Phase Separation (LLPS)-related gene signature as potential therapeutic biomarker for breast cancer progression".

Running Projects:
1) Deep learning-based model for identification of Liquid-Liquid Phase Separation (LLPS)-related gene signature as potential therapeutic biomarker for breast cancer progression.
2) Machine learning based tool for lncRNA/microRNA/mRNA network reconstruction in different disease models.

Selected Recent Publications

1) Pandey V., **Jain P**., Chatterjee S., Rani A., Tripathi A., Dubey P.K. Variants in exon 2 of MED12 gene causes uterine leiomyoma's through over-expression of MMP-9 of ECM pathway. **Mutation Research** 828,111839 (2024) [**IF=2**]

2) Singh, P., Kumari, A., Khaladhar, V.C., Singh, N.; Pathak, P.K., Kumar, V.; Kumar, R.J., **Jain, P**., Thakur, J.K., Fernie, A.R. et al. Serine Hydroxymethyltransferase6 is involved in growth and resistance against pathogens via ethylene and lignin production in *Arabidopsis*. **Plant Journal** , *119*, 1920–1936 (2024) [**IF=6.2**]

3) Singh, G., Ambreen, H., **Jain, P**., Chakraborty, A., Singh, B., Manivannan, A. et al. Comparative transcriptomic and metabolite profiling reveals genotype-specific responses to Fe starvation in chickpea. **Physiologia Plantarum**, 175(2), e13897 (2023) [**IF=4.5**]

4) Panda AK, Rawal HC, **Jain P**, Mishra V, Nishad J, Chowrasia S, Sarkar AK, Sen P, Naik SK, Mondal TK.

Identification and analysis of miRNAs-lncRNAs-mRNAs modules involved in stem-elongation of deepwater rice (Oryza sativa L.). **Physiol Plant**. 174(4):e13736 (2022) [**IF=4.5**]

5) **Jain P.**, Singh A., Iquebal M.A., Jaiswal S., Kumar S., Kumar D., Rai A. Genome-Wide Analysis and Evolutionary Perspective of the Cytokinin Dehydrogenase Gene Family in Wheat (*Triticum aestivum* L.). *Frontiers in Genetics* 19;13:931659 (2022) [**IF=4.8**].

6) Priya S., Tripathi G., Singh DB., **Jain P**., Kumar A. Machine learning approaches and their applications in drug discovery and design. *Chemical Biology & Drug Design*. https://doi.org/10.1111/cbdd.14057. (2022) [**IF=2.817**].

7) **Jain P**, Hussain S, Nishad J, Dubey H, Bisht DS, Sharma TR, Mondal TK. Identification and functional prediction of long non-coding RNAs of rice (*Oryza sativa L.*) at reproductive stage under salinity stress. *Molecular Biology Reports*. 10.1007/s11033-021-06246-8 (2021) [**IF=2.4**].

8) **Jain P**, Dubey H, Singh PK, Solanke AU, Singh AK, Sharma TR. Deciphering signalling network in broad spectrum Near Isogenic Lines of rice resistant to *Magnaportheoryzae*. *Scientific Reports*. 9: 16939 (2019) [**IF=5**].

9) **Jain P**, Singh PK, Kapoor R, Khanna A, Solanke AU, Singh AK, Gopala Krishnan S, Sharma V, Sharma TR. Understanding Host-Pathogen Interactions with Expression Profiling of NILs Carrying Rice-Blast Resistance Pi9 Gene. *Frontiers in Plant Science* 8:1-20 (2017) [**IF=5.7**].

10) **Jain P**, Vig S, Datta M, Jindel D, Mathur AK, Mathur SK, Sharma A. Systems Biology Approach Reveals Genome to Phenome Correlation in Type 2 Diabetes. *PLoS One* 8: e53522 (2013) [**IF=3.24**].

11) Panda, A.K., Rawal, H.C., **Jain, P.**, Mishra, V., Nishad, J., Chowrasia, S. et al. Identification and analysis of miRNAs-lncRNAs-mRNAs modules involved in stem-elongation of deepwater rice (*Oryza sativa* L.). *Physiologia Plantarum*, 174(4), e13736. (2022) [**IF=4.5**].

12) Devanna, B. N., **Jain, P.**, Solanke, A. U., Das, A., Thakur, S., Singh, P. K.,Sharma, T. R. et al. Understanding the Dynamics of Blast Resistance in Rice-Magnaportheoryzae Interactions. *Journal of Fungi*, 8(6), 584(2022) [**IF=5.816**].

13) Kumar V, **Jain P**, Venkadesan S, Karkute SG, Bhati J, Abdin MZ, Sevanthi AM, Mishra DC, Chaturvedi KK, Rai A, Sharma TR, Solanke, AU. Understanding Rice-*MagnaportheOryzae* Interaction in Resistant

and Susceptible Cultivars of Rice under Panicle Blast Infection Using a Time-Course Transcriptome Analysis. *Genes*-Basel.12 (2021) **[IF=4]**.

14) Devanna BN, Jaiswal R, Singh PK, Kapoor R, **Jain P**, Kumar G, Sharma Y, Sharma TR. Role of transporters in plant disease resistance. ***Physiologia Plantarum*** ppl.13377 (2021) [**IF=4.5**]

GITHUB RESOURCES GENERATED

https://github.com/Dr-Priyanka-Jain/RNAseq-analysis-using-R-and-Python-

GENOMIC RESOURCES GENERATED

1**) SRP153207** (24 samples): Comparative transcriptome study of resistant NILs PB1+Pi1 and PB1+Pi54 and susceptible rice line (PB1) after M. oryzae inoculation (2019).

2) **GSE136672** (16 samples): RNA-seq profiling of Tetep (resistant) and HP2216 (susceptible) in rice lines at 0, 48, 72, and 96 hours post infection after M. oryzae inoculation in panicle (2019).

3) **SRP075722** (12 samples): Expression profiling of resistant NIL (PB1+Pi9) and susceptible rice line (PB1) 24 hours after M. oryzae inoculation (2017).

4) **GSE29221** (24 samples) Global gene expression profiles of skeletal muscle in males with Type 2 Diabetes (2012).

5) **GSE29226** (24 samples) Global gene expression profiles of subcutaneous adipose in females with type 2 Diabetes (2012).

6) **GSE29231** (24 samples) Global gene expression profiles of Visceral Adipose in Females with type 2 Diabetes (2012).

7) **GCST001759** Genome-wide genotyping array (2012)

Discovery samples:1,101 Indo-European ancestry cases and 1,027 Indo-European ancestry controls.

Replication samples: 3,607 Indo-European ancestry cases, 2,924 Indo-European ancestry controls, 1,184 Dravidian ancestry cases, 1,061 Dravidian ancestry controls, 11,28 European ancestry cases, 11,285 European ancestry controls.