

CURRICULUM VITAE

PRIYANKA JAIN, PhD

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CAREER OBJECTIVE: To decipher new areas in genomics research.

CURRENT POSITION: Working as Research officer, National genomics and genotyping Facility (DBT-NGGF), National Institute of Plant genome Research (DBT-NIPGR), Delhi.

EDUCATIONAL QUALIFICATION:

August 2019 - Till Now: Research officer, DBT-NGGF, NIPGR, New Delhi.

February 2019 - August 2019: Post-PhD, Research Fellow at ICAR-NIPB, New Delhi.

June 2011 - Nov 2018: PhD in Bioinformatics at ICAR-NIPB, New Delhi.

Sep 2008 - May 2011: Pre-PhD, Project Fellow at CSIR-IGIB, New Delhi.

April 2006 - March 2008: Masters in Bioinformatics from BHU.

April 2003 – March 2006: Bachelors in Chemistry (Hons.) with botany & zoology from BHU.

FIELD OF SPECIALIZATION

- 1) Analysis of data generated from genotyping by sequencing, whole genome resequencing, targeted sequencing, exome sequencing, RNA sequencing, small RNA sequencing, metagenome sequencing using shell scripts, R, Perl and Python in linux environment using fast high-performance computing (HPC) server and storage.
- 2) Development of known and novel (SNP/SSR/KASP) markers for varietal differentiation, purity testing, paternity testing and marker assisted selection.
- 3) Marker discovery from from genomic/ transcriptomic/genotyping.
- 4) Quality check, filtering, identification of high-quality SNP for the designing and development of customized high throughput Affymetrix SNP array for unexplored species.
- 5) Identification of single nucleotide polymorphisms, insertions, deletions, copy number variations and large rearrangements from genotyping data.
- 6) Construction of linkage map and QTL mapping in order to identify QTL linked to trait.
- 7) Diversity analysis using high quality markers for population structure and phylogenetic cluster analysis.
- 8) Genome wide association analysis for identification of causal gene associated with trait of interest.

- 9) Draft/reference genome/organelle assembly using different assembly approaches. Annotation of genomes, comparative genomics, gene family analysis, repeat analysis, phylogenetic and homology analysis.
- 10) Analyzed in house generated RNAseq data of plants and animals to find the regulatory role of novel coding and non-coding RNAs.
- 11) Allele specific expression, isoform level analysis, long and small non-coding RNA analysis of both prokaryotic and eukaryotic data.
- 12) RNAseq data analysis of plants and animals to find the regulatory role of novel coding and non-coding RNAs.
- 13) Identification of regulatory lncRNA-miRNA-mRNA module to find interaction in coding and non-coding RNA.
- 14) Co-expression networks, various gene set enrichment strategies. Metacorrelations and discovery of hub genes.
- 15) Development of new in silico pipelines and tools using python, shell and R for analysis of high throughput and customized genotyping and genomic data analysis.
- 16) Identification of transcriptomic signature of rice in abiotic stress using machine learning models.
- 17) Identification of gene regulatory network hubs involved in metabolic adjustments of rice upon abiotic stress.
- 18) Development and revision of Standard Operating Procedures to performs genotyping and genomic bioinformatics analysis and interpretation of data with development of final reports.
- 19) Assist in development of functional LIMS for integrating the high throughput platforms for end-to-end tracking of the samples.
- 20) Database Designing and development (PHP, MySQL, HTML), Genome browser development, Open-source customization and installation of HPC server, HPC management and maintenance and FTP site maintenance.
- 21) Consultancy services to breeders and biotechnologist by guiding them in design of experiment, selection of bioinformatics tools, appropriate technology and data analysis that will help to improve research quality and product development.
- 22) Trained model on dataset using different machine learning methods with R.
- 23) Pathway, gene ontology, cluster and network analysis of functionally relevant coding and non-coding RNA.
- 24) Protein modeling, RNA structure and sequence analysis, protein visualization using PyMol, VMD and JMol etc.

PRESENT RESEARCH INTEREST

- 1) Systems biology approach to reveal genome to phenome correlation in cereals and legumes.
- 2) Meta-analysis of transcriptome data to find the regulatory role of novel coding and non-coding RNAs.
- 3) Identification of regulatory lncRNA-miRNA-mRNA module to find interaction of coding and non-coding RNA.

- 4) Meta-QTL analysis of agronomic trait linked QTL identified from published data in different mapping population of chickpea.

TOTAL YEARS OF RESEARCH EXPERIENCE (Since M Sc): 12 years

RESEARCH EXPERIENCE

1) **August 2019 - Till Now:** Research Officer, National Genomics and Genotyping Facility (DBT-NGGF), National Institute of Plant genome Research (DBT-NIPGR), Delhi.

Work Summary: Experiment designing and development of known and novel markers for fluorescent dye-labelled SNP genotyping platform (LGC Array tape/KASP) and data analysis. Sample preparation for array-based SNP genotyping platform (Affymetrix gene titan multichannel instrument) and data analysis. Collected markers of cereals and legumes from publicly available markers in order to make repository for genotyping/fingerprinting. Pipeline for reference/de-novo based variant (SNP/Indel/structural variants) identification from core collection, wild germplasm and biparental mapping population data. Identification of gene variants associated with aspirin resistance from exome sequencing data. Involved in computation infrastructure of HPC and storage.

2) **February 2019 - July 2019:** Post PhD worked as research fellow at National Institute for plant Biotechnology (ICAR-NIPB), Pusa, New Delhi under Dr T K Mondal in project entitled “Decoding of tea genome for identification of agronomically important genes”.

Work Summary: Draft genome assembly, evaluation and annotation of a popular Indian tea genotype TV-1. Identification of repeat region in tea genome and *de-novo* assembly of tea transcriptome.

3) **June 2011 - November 2017:** PhD in Bioinformatics at National Institute for Plant Biotechnology (NIPB) under supervision of Dr T R Sharma (DDG-Crop Sciences, ICAR) and Dr Vinay Sharma (Dean-Academics, Amity University). During PhD initially worked as senior research fellow in the NAIP project entitled, “Allele mining and expression profiling of resistance and avirulence genes in rice blast pathosystem for development of race non-specific disease resistance”. Later worked as CSIR-SRF in NIPB and my PhD work entitled “Computational Analysis of Molecular Interactions Involved in Rice-*Magnaporthe oryzae* Pathosystem”

Work Summary: Screening of best NIL in PBI background containing different blast resistance genes against *M. oryzae*. Transcriptome profiling of three NILs and their control at two time point against *M. oryzae*. Understanding the rice fungal interaction and signaling network in the broad spectrum NIL. I have used transcriptomics and network biology approach to propose a novel approach to analyze the molecular interactions involved in Rice-*Magnaporthe oryzae* pathosystem. I also focused in identifying signature set of small and long noncoding RNAs involved in rice blast disease.

During PhD, i was involved in several other project with the following scientists, Dr Tapan Mondal, Dr Amol Solanki, Dr Amitha, Dr Deepak Bisht, Dr Ramawatar Nagar, Dr Devana, Dr Archana and Dr Shruti. I have performed the diverse work with the above-mentioned scientists. Comparative transcriptome profiling to identify the signaling network in the broad spectrum Tetep against sheath blight and panicle blast using RNA sequencing at different time point to identify the key regulatory genes. Comparative genomic to identify the high copy number variation of

retrotransposon in different *Magnaporthe* isolates. Discovery and profiling of small RNAs from *Puccinia triticina* by deep sequencing and identification of their potential targets in wheat. Discovery of small RNA from sheath blight infected rice and their potential target in host plant. Draft level assembly of of alloplasmic *Brassica juncea* line.

4) **September 2008 - May 2011:** Pre PhD worked as project fellow at Institute of Genomics and Integrative Biology (CSIR-IGIB), New Delhi in the project entitled “Diabetes mellitus - New drug discovery R & D, molecular mechanisms and genetic and epidemiological factors” under guidance of Dr Abhay Sharma and Dr Dwaipayan Bharadwaj. During this period, I have used system biology approach to study genome to phenome correlation in type 2 diabetes.

5) **June 2007 - June 2008:** M.Sc. Dissertation at BHU under Dr Rajeev Mishra, Coordinator of Bioinformatic department. I have worked on genome wide repeat identification. Meta-QTL analyses. Comparative secondary structure and repeats analysis of large non-coding RNA: Computational study across the twelve species of *Drosophila*”.

Two-month training at Indian Institute of Chemical Biology (CSIR-IICB) worked on “Improved filtration based method for fast and sensitive protein quantification”. Supervised by Dr T K Dhar, Head drug development, Diagnostic and Biotechnology Division, Indian Institute of Chemical Biology, Jadavpur, Kolkata.

PUBLICATION

First Author: 5

- 1) **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**).
- 2) **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 *Magnaporthe oryzae*. *Scientific Reports*. 9: 16939 (2019) (**IF=5**).
- 3) **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**).
- 4) **Jain P**, Sharma V, Dubey H, Singh PK, Kapoor R, Kumari M, Singh J, Pawar D, Bisht D, Solanke AU, Mondal TK, Sharma TR. Identification of long non-coding RNA in rice lines resistant to Rice blast pathogen *Magnaporthe oryzae*. *Bioinformatics*.13:249-55 (2017) (**IF=0**).
- 5) **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**).

Co-author: 15

- 6) 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-*Magnaporthe Oryzae* Interaction in Resistant and Susceptible Cultivars of Rice under Panicle Blast Infection Using a Time-Course Transcriptome Analysis. *Genes*-Basel.12 (2021) (**IF=4**).

- 7) 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).
- 8) Singh PK, Mahato AK, **Jain P**, Rathour R, Sharma V, Sharma TR. Comparative Genomics Reveals the High Copy Number Variation of a Retro Transposon in Different *Magnaporthe* Isolates. *Frontiers in Microbiology* 10:966 (2019) (IF=5.64).
- 9) Kapoor R, Kumar G, Arya P, Jaswal R, **Jain P**, Singh K, Sharma TR. Genome-Wide Analysis and Expression Profiling of Rice Hybrid Proline-Rich Proteins in Response to Biotic and Abiotic Stresses, and Hormone Treatment. *Plants* (Basel). 8 (2019) (IF=4).
- 10) Dubey H, Kiran K, Jaswal R, **Jain P**, Kayastha AM, Bhardwaj SC, Mondal TK, Sharma TR. Discovery and profiling of small RNAs from *Puccinia triticina* by deep sequencing and identification of their potential targets in wheat. *Functional Integrative Genomics*. 19:391-407 (2019) (IF=3.6).
- 11) Sharma TR, Devanna BN, Kiran K, Singh PK, Arora K, Jain P, Tiwari IM, Dubey H, Saklani B, Kumari M, Singh J, Jaswal R, Kapoor R, Pawar DV, Sinha S, Bisht DS, Solanke AU, Mondal TK. Status and Prospects of Next Generation Sequencing Technologies in Crop Plants. *Current Issues in Molecular Biology* 27:1-36 (2018) (IF=2.1).
- 12) Singh J, Devanna BN, Mishra P, **Jain P**, Upadhyay A, Sharma TR. Comparative evaluation of independent blast resistance transgenic lines containing Pi54 and its orthologue genes *Pi54rh* and *Pi54of*. *Oryza* 55: 493-499 (2018) (IF=0).
- 13) Pawar DV, Singh PK, Singh J, Dubey H, **Jain P**, Sharma TR, Singh NK. An Efficient Protocol for Embryogenic Callus Induction and Whole Plant Regeneration in *Oryza Rufipogon* WRA21. *Indian Research Journal of Genetics and Biotechnology* 10:1-11 (2018) (IF=0).
- 14) Kumari A, **Jain P**, Kamboj R, Sharma TR. RNA Seq reveals Differential Regulation of Genes in Resistant and Susceptible rice varieties during early phases of infection with *Rhizoctonia solani*. *Indian Journal of Genetics and Plant Breeding*. 77:475 (2017) (IF=0.5).
- 15) Sharma TR, Das A, Thakur S, Devanna BN, Singh PK, **Jain P**, Vijayan J, Kumar S. Oscillating Transcriptome during Rice *Magnaporthe* Interaction. *Current Issues in Molecular Biology*. 19:99-120 (2015) (IF=2.1).
- 16) Krishnan V, **Jain P**, Vinutha T, Hada A, Manickavasagam M, Ganapathi A, Rai RD, Sachdev A. Molecular modeling and in silico characterization of *Glycine max* Inositol (1,3,4) tris 5/6 kinase-1 (*Gmitpk1*)- a potential candidate gene for developing low phytate soybean transgenics. *Plant Omics Journal* 8:381-391 (2015) (IF=0.6).
- 17) Mathur SK, **Jain P**, Mathur P, Punjabi P, Agarwal A, Sharma A. Transcriptomic analysis of visceral adipose from healthy and diabetic obese subjects. *Indian Journal of Endocrine Metabolism* 17:446-50 (2013) (IF=1.21).
- 18) Tabassum R, Chauhan G, Dwivedi OP, Mahajan A, Jaiswal A, Kaur I, INDICO et al. Genome-Wide Association Study for Type 2 Diabetes in Indians Identifies a New Susceptibility Locus at 2q21. *Diabetes* 62: 977-8 (2013) (IF=9.5).
- 19) Consortium IND. **INDICO**: the development of a resource for epigenomic study of Indians undergoing socioeconomic transition. *Hugo Journal* 5:65-9 (2011) (IF=0.24).

- 20) Mathur SK, **Jain P**, Mathur P. Microarray Evidences the Role of Pathologic Adipose Tissue in Insulin Resistance and Their Clinical Implications. *Journal of Obesity* 2011:16 (2011) (IF=0).

BOOK CHAPTER

Devanna BN, Rajashekara, H, Raghu S, Singh PK, Jain P, Parameswaran C, Singh J, K Arora, Samantaray S, Katara JL, Verma RL. Blast Disease of Cereal Crops - Evolution and Adaptation in Context of Climate Change. Chapter: Advances in Genetics and Genomics for Management of Blast Disease in Cereal Crops. DOI: 10.1007/978-3-030-60585-8_12 April 2021. (<https://www.springer.com/gp/book/9783030605841>).

ABSTRACTS AND PROCEEDINGS

- 1) **Jain P**, Singh PK Singh AK, Gopala Krishnan S, Sharma V, Sharma TR. Expression profiling of NILs carrying rice blast resistance gene *Pi9* to understand molecular basis of host-pathogen interactions. International Symposium on Plant Signaling and Behavior, Delhi University, New Delhi, India (2011).
- 2) **Jain P**, Singh PK, Singh AK, Gopala Krishnan S, Sharma V, Sharma TR. RNA-Seq Study Reveals Candidate Genes for blast Resistance in Rice *Magnaportheae* pathosystem NextGen Genomics, Biology, Bioinformatics and Technologies (NGBT) Conference, HICC, Hyderabad, India (2015).

ACADEMIC ACHIEVEMENTS

- 1) Qualified CSIR NET JUNE 2008 and 2009.
- 2) Qualified GATE 2009 and 2010.
- 3) Qualified CSIR SRF 2014.
- 4) Received summer fellowship from Indian Academy of Sciences (IAS), Bangalore, Indian National Science Academy New Delhi, National Academy of sciences, Allahabad.

GENOMIC RESOURCE 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.

SIGNIFICANT RESEARCH CONTRIBUTION

These research contributions in the field of Genomics, Transcriptomic, Metabolomic and system biology helped me to earn 20 publications in internationally reputed journal with **total impact of 44, h-index 9 and citation of 372.**

SEMINARS/CONFERENCES/WORSHOP ATTENDED

- 1) Delivered insightful lecture on Variant calling in the workshop Understanding COVID-19 Genomes from 5th to 7th of February (2021).
- 2) Delivered lecture in National webinar on topic entitled Biotechnological challenges in drug discovery for covid-19, of TMBU on 16th May (2020).
- 3) National Workshop on Computation for Biomedicine and Healthcare at Indraprastha Institute of Information Technology, New Delhi, from 10th Dec to 14th Dec (2018).
- 4) Workshop on Data Science Using R at Indraprastha institute of information technology, New Delhi (2018).
- 5) Symposium on Network Biology at the Center for Computational Biology, Indraprastha institute of information technology, New Delhi on 28th October (2017).
- 6) Big data in Genomics workshop at Indraprastha institute of information technology, New Delhi on 4th Feb (2017).
- 7) NexGen Genomics Biology Bioinformatics and Technologies (NGBT) Conference HICC Hyderabad from 1st to 3rd October (2015).
- 8) International Symposium on Plant Signaling and Behavior at Delhi University, New Delhi from March 7th to 10th March (2014).
- 9) Next generation Genomics Data Analysis Workshop C-Camp, NCBS-TIFR, Bangalore, 13th to 16th January (2013).
- 10) National Conference on Drug Discovery & Development at S. P University of Delhi South Campus, New Delhi from 21st to 23rd January (2009).
- 11) HGM Satellite Meeting on Clinical Genomics held, at New Delhi on 25th September (2008).
- 12) National level Entrepreneurship Awareness Camp sponsored by National Science and Technology Entrepreneurship Development Board (NSTEDB), Department of science and Technology, Government of India, co coordinated by IIP cell, IT, BHU (2008).
- 13) National Symposium on Recent Advances in Toxicology Studies: Molecular and Physiological Aspects. NSTS at BHU (2008).
- 14) National level Workshop and Symposium in Statistical methods in computational biology at MMV, from 28th to 29th December BHU (2007).

PERSONAL DETAILS

Date of Birth: 01/07/1985

Gender: Female

Marital Status: Married

Religion: Jainism

Language Known: English and Hindi

REFERENCES:

1) Dr Tilak Raj Sharma, PhD

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Declaration: I hereby declare that above mentioned statements are true.

Date 22/05/2021

Place New Delhi

Priyanka Jain