

# Biodata

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**Present Designation:** Chief Scientist

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**Qualification:**

Degree	University	Stream	Year
Ph. D.	University of Delhi	Plant Molecular Biology	2004
M.Sc.	G. B. Pant University of Agriculture and Technology, Pantnager, Uttarakhand, INDIA	Molecular Biology & Biotechnology	1998

**Area of Specialization**

***Plant Molecular Biology and Plant Genomics***

***Present Research Activities and Contributions***

Dr. Vikrant's lab has been working in the area of Plant Molecular Biology & Plant Genomics. Current focus of the laboratory is on structural & functional genomics of economically important Medicinal & Aromatic Plants (MAPs). Secondary metabolites that are produced by MAPs have pharmaceutical importance for health and wellbeing of human kind. These are synthesized in very limited amounts *in planta*, and their biosynthesis is tightly regulated at the molecular and developmental levels. In many medicinal/aromatic plants these metabolites are synthesized or stored in specialized tissue/organs such as glandular trichomes, root tissue, etc. Generation of genomics/transcriptomis resources for gene mining and utilization is the key for improving the quality of medicinal/aromatic plants in terms of bioactive secondary molecules. His laboratory has been focusing on the modulation of secondary metabolism in selected MAPs through genomics and molecular interventions. To understand the regulation of secondary metabolism, few transcription factor encoding genes from selected medicinal/aromatic plants have been identified and are being functionally characterized. Apart from transcription factors, miRNAs from medicinal plants are also identified to investigate their role(s) in secondary metabolism.

Moreover, the laboratory has been focusing in understanding the molecular aspects of development of glandular trichomes and root biomass in selected MAPs. Few trichome development-related gene homologs from *Artemisia annua* as a model medicinal plant have been identified and studied in details at the molecular level. Root development gene homolog(s) are being studied in *Withania somnifera* for improvement in root architecture and biomass. The aspect of abiotic stresses and signal transduction through kinases that affect the secondary metabolism in medicinal plants are also being investigated. Such genes have immense potential as biotechnological tool for metabolic engineering in plants and have great industrial impact and societal benefits. Moreover, the trichome- and root-specific genes would provide tissue-specific promoters for targeted expression of genes plants.

➤ ***Ocimum* genome sequence and transcriptomic resources of *Ocimum* species**

The laboratory contributed towards sequencing the draft genome of *Ocimum tenuiflorum*. Transcriptome of leaf tissue of different *Ocimum* species and distinct chemotypes were sequenced to generate transcriptomic resources.

➤ **Tissue-abundant/specific EST resources generated from medicinal plants**

Several ESTs (including subtractive ESTs) were generated from *Artemisia annua* and *Azadirachta indica* (neem) tissues. Few Cytochrome p450s from *A. indica* which are related to secondary metabolism, such as *Trans*-cinnamate 4-monoxygenase, Taxane 5 $\alpha$  hydroxylase, and Terpene synthases such as  $\beta$ -amyrin synthase, cycloartenol synthase and squalene epoxidase genes were identified and few of them were studied.

➤ **Studies on regulation of secondary metabolism in medicinal plants for modulating the content of important compounds in planta**

Few transcription factors were characterized from medicinal plants like *Artemisia annua* and *Catharanthus roseus* that were found to regulate secondary metabolism. The overexpression and silencing studies of these deciphered their probable role(s) in the regulation of secondary metabolism leading to pharmaceutically important secondary metabolites has emerged.

➤ **A Sterol biosynthesis pathway gene characterized**

A C4-sterol methyl oxidase (*SMO*) gene of *Artemisia annua* was structurally and functionally characterized. Total sterol content was found to be enhanced in transgenic tobacco plants upon ectopic over-expression of *AaSMO1* gene. *AaSMO1* transcript was found to be highly induced upon dehydration stress and its ectopic expression in tobacco plants conferred dehydration stress tolerance.

➤ **Understanding the trichome and root development: site for secondary metabolites biosynthesis/accumulation**

The development of trichome and root is a very important aspect in terms of storage of bioactive compounds in case of many medicinal/aromatic plants. Trichome development-related gene homologs from *Artemisia annua* (as model medicinal plant) were identified and functionally characterized. Few identified *A. annua* gene homologs like *AaGL2* and *AaMIXTA-Like2* reverted the mutant phenotype in *Arabidopsis* trichome mutants. Gene homolog(s) that influence root development and leaf biomass including *DWARF4* (*DWF4*), *SHORT-ROOT* (*SHR*), *BIG BROTHER* (*BB*) and few other putative candidates have been identified in *Withania somnifera* and are being studied.

➤ **Trichome-specific promoters: tool for tissue-specific metabolic engineering**

Trichome-specific promoters were characterized from *Artemisia annua*. Both these promoters confer the reporter gene activities in the trichomes of *Arabidopsis thaliana* and *A. annua*. These promoters have immense biotechnological importance and could be used to target a gene of interest specifically in trichomes.

➤ **MicroRNAs from medicinal plants**

Conserved and novel microRNAs (*trans*-acting regulators) were identified from *Catharanthus rosues*, *Rauvolfia serpentina* and *Azadirachta indica* through high-throughput sequencing or *in-silico* analysis of available nucleotides in public databases. These miRNAs may have immense importance in regulating secondary metabolism and stresses.

➤ **Signal transduction affecting secondary metabolism**

For investigating the molecular components involved in stress-induced signal transduction pathways that affect secondary metabolism in *Catharanthus rosues*, calcium-dependent protein kinases (CDPKs) were identified and studied.

## Research Publications

### Selected Research Publications:

1. Soni R, Shankar G, Mukhopadhyay P, **Gupta V** (2022) A concise review on *Artemisia annua* L.: a major source of diverse medicinal compounds. *Industrial Crops & Products* 184: 115072 (doi.org/10.1016/j.indcrop.2022.115072).
2. Rajakani R, Prakash P, Ghosliya D, Soni R, Singh A, **Gupta V** (2021) *Azadirachta indica* MicroRNAs: Genome-wide identification, target transcript prediction, and expression analyses. *Applied Biochemistry and Biotechnology* 193: 1924-1944 (doi: 10.1007/s12010-021-03500-4).
3. Biswas T, Mathur, A, **Gupta V**, Luqman S, Mathur AK (2020) Elicitation and phenylalanine precursor feeding based modulation of *in vitro* anthocyanin production, enzyme activity and gene expression in an Indian ginseng congener- *Panax sikkimensis* Ban. *Industrial Crops & Products* 145: 111986. (doi.org/10.1016/j.indcrop.2019.111986).
4. Biswas T, Mathur A, **Gupta V**, Singh M, Mathur AK (2019) Salicylic acid and ultrasonic stress modulated gene expression and ginsenoside production in differentially affected *Panax quinquefolius* (L.) and *Panax sikkimensis* (Ban.) cell suspensions. *Plant Cell Tiss Organ Cult (PCTOC)* 136: 575-588. (doi.org/10.1007/s11240-018-01538-7).
5. Biswas T, Pandey SS, Maji D, **Gupta V**, Kalra A, Singh M, Mathur A, Mathur AK (2018) Enhanced expression of ginsenoside biosynthetic genes and *in vitro* ginsenoside production in elicited *Panax sikkimensis* (Ban) cell suspensions. *Protoplasma* 255 (4): 1147-1160. (doi: 10.1007/s00709-018-1219-z).
6. Khan S, Upadhyay S, Khan F, Tandon S, Shukla RK, Ghosh S, **Gupta V**, Banerjee S, Rahman L (2017) Comparative transcriptome analysis reveals candidate genes for the biosynthesis of natural insecticide in *Tanacetum cinerariifolium*. *BMC Genomics* 18(1): 54. (doi: 10.1186/s12864-016-3409-4).
7. Prakash P, Rajakani R, **Gupta V** (2016) Transcriptome-wide identification of *Rauvolfia serpentina* microRNAs and prediction of their potential targets.

- Computational Biology and Chemistry* 61: 62-74. (doi: 10.1016/j.compbiolchem.2015.12.002.).
8. Jindal S, Longchar B, Singh A, **Gupta V** (2015) Promoters of *AaGL2* and *AaMIXTA-Like1* gene of *Artemisia annua* direct reporter gene expression in glandular and non-glandular trichomes. *Plant Signaling & Behavior* 10: 12, e1087629. (doi: 10.1080/15592324.2015.1087629.).
  9. Rastogi S, Kalra A, **Gupta V**, Khan F, Lal RK, Tripathi AK, Parameswaran S, Gopalakrishnan C, Ramaswamy G, Shasany AK (2015) Unravelling the genome of Holy basil: an "incomparable" "elixir of life" of traditional Indian medicine. *BMC Genomics* 16: 413. (doi: 10.1186/s12864-015-1640-z.).
  10. Singh A, Jindal S, Longchar B, Khan F, **Gupta V** (2015) Overexpression of *Artemisia annua* sterol C-4 methyl oxidase gene, *AaSMO1*, enhances total sterols and improves tolerance to dehydration stress in tobacco. *Plant Cell Tiss Organ Cult* 121: 167-181. (doi: 10.1007/s11240-014-0692-0.).
  11. Prakash P, Ghosliya D, **Gupta V** (2015) Identification of conserved and novel microRNAs in *Catharanthus roseus* by deep sequencing and computational prediction of their potential targets. *Gene* 554(2): 181-195. (doi: 10.1016/j.gene.2014.10.046.).
  12. Rastogi S, Meena S, Bhattacharya A, Ghosh S, Shukla RK, Sangwan NS, Lal RK, Gupta MM, Lavania UC, **Gupta V**, Nagegowda DA, Shasany AK (2014) De novo sequencing and comparative analysis of holy and sweet basil transcriptomes. *BMC Genomics* 15(1): 588. (doi: 10.1186/1471-2164-15-588.).
  13. Rajakani R, Narnoliya L, Sangwan NS, Sangwan RS, **Gupta V** (2014) Subtractive transcriptomes of fruit and leaf reveal differential representation of transcripts in *Azadirachta indica*. *Tree Genetics & Genomes* 10: 1331-1351. (doi: 10.1007/s11295-014-0764-7.).
  14. Narnoliya LK, Rajakani R, Sangwan NS, **Gupta V**, Sangwan RS (2014) Comparative transcripts profiling of fruit mesocarp and endocarp relevant to secondary metabolism by suppression subtractive hybridization in *Azadirachta indica* (neem). *Molecular Biology Reports* 41(5): 3147-3162. (doi: 10.1007/s11033-014-3174-x.).
  15. Rajakani R, Narnoliya L, Sangwan NS, Sangwan RS, **Gupta V** (2013) Activated charcoal-mediated RNA extraction method for *Azadirachta indica* and plants highly rich in polyphenolics, polysaccharides and other complex secondary compounds. *BMC Research Notes* 6(1): 125. (doi: 10.1186/1756-0500-6-125.).
  16. Nair P, Misra A, Singh A, Shukla AK, Gupta MM, Gupta AK, **Gupta V**, Khanuja SPS, Shasany AK (2013) Differentially expressed genes during contrasting growth stages of *Artemisia annua* for artemisinin content. *PLoS ONE* 8(4): e60375. (doi:10.1371/journal.pone.0060375.).
  17. The Tomato Genome Consortium (2012) The tomato genome sequence provides insights into fleshy fruit evolution. *Nature* 485: 635-641. (doi: 10.1038/nature11119.).
  18. **Gupta V**, Raghuvanshi S, Gupta A, Saini N, Gaur A, Khan MS, Gupta RS, Singh J, Duttamajumder SK, Srivastava S, Suman A, Khurana JP, Kapur R, Tyagi AK (2010) The water-deficit stress- and red rot-related genes in sugarcane. *Funct Integr Genomics* 10: 207-214.
  19. **Gupta V**, Mathur S, Solanke AU, Sharma MK, Kumar R, Vyas S, Khurana P, Khurana JP, Tyagi AK, Sharma AK (2009) Genome analysis and genetic enhancement of tomato. *Critical Reviews in Biotechnology* 29: 152-181.






20. The Tomato Genome Sequencing Consortium (2009) A snapshot of the emerging tomato genome sequence. *Plant Genome* 2: 78-92.
21. Mir RR, Banerjee S, Das M, **Gupta V**, Tyagi AK, Sinha MK, Balyan HS, Gupta PK (2009) Development and characterization of large-scale SSRs in Jute. *Crop Science* 49: 1687-1694. (doi.org/10.2135/cropsci2008.10.0599).
22. **Gupta V**, Khurana R, Tyagi AK (2007) Promoters of two anther-specific genes confer organ-specific gene expression in a stage-specific manner in transgenic systems. *Plant Cell Reports* 26: 1919-1931.
23. Vij S, **Gupta V**, Kumar D, Ravi V, Raghuvanshi S, Khurana P, Khurana JP, Tyagi AK (2006) Decoding the rice genome. *BioEssays* 28: 421-432.
24. The Rice Chromosomes 11 and 12 Sequencing Consortia (2005) The sequence of rice chromosomes 11 and 12, rich in disease resistance genes and recent gene duplications. *BMC Biology* 3: 20.
25. The International Rice Genome Sequencing Project (2005) The map-based sequence of the rice genome. *Nature* 436: 793-800.
26. Tyagi AK, Khurana JP, Khurana P, Raghuvanshi S, Gaur A, Kapur A, **Gupta V**, Kumar D, Ravi V, Vij S, Khurana P, Sharma S (2004) Structural and functional analysis of rice genome. *Journal of Genetics* 83: 79-99.
27. Singh NK, Raghuvanshi S, Srivastava SK, Gaur A, Pal AK, Dalal V, Singh A, Ghazi IA, Bhargav A, Yadav M, Dixit A, Batra K, Gaikwad K, Sharma TR, Mohanty A, Bharti AK, Kapur A, **Gupta V**, Kumar D, Vij S, Vydianathan R, Khurana P, Sharma S, McCombie WR, Messing J, Wing R, Sasaki T, Khurana P, Mohapatra T, Khurana JP, Tyagi AK (2004) Sequence analysis of the long arm of rice chromosome 11 for rice-wheat synteny. *Funct Integr Genomics* 4: 102-117. (doi: 10.1007/s10142-004-0109-y.).

## Book Chapters




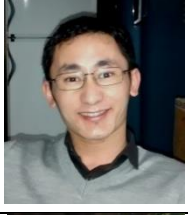

- Khan F, Qidwai T, Shukla RK, **Gupta V** (2013) Alkaloids Derived from Tyrosine: Modified Benzyltetrahydroisoquinoline Alkaloids. In: K.G. Ramawat, J.M. Merillon (eds.), *Handbook of Natural Products*, Springer-Verlag, Berlin Heidelberg, Article 0015. (doi: 10.1007/978-3-642-22144-6\_15.).
- Pandey D, Gupta A, **Gupta V** (2012) Genomics Technology. In: Kumar A, Pareek A, Gupta SM (eds.), *Biotechnology in Medicine and Agriculture - Principles and Practices*, I. K. International Publishing House Pvt. Ltd., New Delhi, India, pp. 142-163.
- Tyagi AK, Khurana JP, Khurana P, Kapoor S, Singh VP, Singh AK, Thakur JK, **Gupta V**, Anand S, Vij S, Jain M, Ray S, Agarwal P, Arora R, Sharma P, Mukherjee S, Nijhawan A, Giri J, Khurana R (2007) *Expression and functional analysis of rice genes involved in reproductive development and stress response*. In: Brar DS, Mackill DJ, Hardy B (eds.) *Rice Genetics V*, International Rice Research Institute, Philippines, pp. 313-330.
- Tyagi AK, Khurana JP, Sharma AK, Mohanty A, Dhingra A, Raghuvanshi S, Mukhopadhyay A, **Gupta V**, Anand S, Kathuria H, Bhushan S, Thakur J, Kumar D (2003) *Organ-specific gene expression and genetic transformation for improving rice*. In: Khush GS, Brar DS, Hardy B (eds). *Advances in Rice Genetics*. Pp. 552-555, IRRI, Manila.

## Research Scholars

### Present Ph.D. Students:

1	<b>Ms. Ranjana Soni</b> Senior Research Fellow (UGC) AcSIR-Ph.D. Scholar Enrollment No. 10BB16A10002	
2	<b>Ms. Arpita Singh</b> UGC Junior Research Fellow CIMAP-JNU Ph.D. Scholar Enrollment No. CIMAP/18/002	
3	<b>Mr. Rituraj Kumar</b> CSIR Junior Research Fellow AcSIR-Ph.D. Scholar Enrollment No. 10BB19J10008	
4	<b>Ms. Supriya Rana</b> CSIR Senior Research Fellow CIMAP-JNU Ph.D. Scholar Enrollment No. CIMAP/2019/015	
5	<b>Mr. Abhishek Kumar Shukla</b> UGC Senior Research Fellow AcSIR-Ph.D. Scholar Enrollment No. 10BB20A10023	

**Ph.D. Students Completed/Awarded (Alumini):**

1	<b>Dr. Alka Singh</b> CIMAP-JNU Ph.D. Scholar Ph.D. awarded (Sept 2013)	
2	<b>Dr. Pravin Prakash</b> CIMAP-JNU Ph.D. Scholar Ph.D. awarded (Dec 2015)	
3	<b>Dr. Sunita Jindal</b> CIMAP-JNU Ph.D. Scholar Ph.D. awarded (Nov 2017)	
4	<b>Dr. Bendangchuchang Longchar</b> CIMAP-JNU Ph.D. Scholar Ph.D. awarded (Dec 2017)	
5	<b>Ms. Dolly Ghosliya</b> CIMAP-JNU Ph.D. Scholar Ph.D. awarded (Feb 2021)	
6	<b>Mr. Raja R.</b> AcSIR-Ph.D. Scholar Ph.D. awarded (Nov 2021)	