



**Post-Doctoral Researcher(2017-2018)**  
University of Angers, Research  
Institute of Horticulture and Seeds,  
INRA, France

Mob: +91 8899158260  
Email: lakhwanideepika@gmail.com

**Specialization: Bioinformatics**

**Education:**

- PhD in Biological Science,  
AcSIR,CSIR-NBRI, 2017
- Post-Graduation in  
Bioinformatics from  
Banasthali University,  
Jaipur, Rajasthan– Marks  
68%
- Bachelor of Science  
(Biotechnology), C. S. J.  
M. University, Kanpur –  
Marks 72%

**Language:**

Hindi, English and Sindhi.

**Address:**

Flat no. 302, Wing A, Tulsi Aura  
Society, Sector 8, Ghansoli, Navi  
Mumbai, 400701

## Objective

Desire to Work in Challenging and rewarding position in field that will allow me to utilize my skills, energy and talent in providing quality services.

## Work Experience

- Post-Doctoral Researcher, University of Angers, Research Institute of Horticulture and Seeds, INRA, France (2017-2018).
- Visiting fellow, Tata Institute of Fundamental Research, Mumbai (Feb 2019 to April 2019).

## Specialization

- Strong knowledge to analyses Next generation sequencing datasets
- Differential gene expression analysis
- In-silico identification of MiRNAs and LncRNAs in plants.
- Long range chromatin interaction analysis in plants.
- Gene family analysis
- Strong knowledge of Assembler tools.
- Experienced in using various bioinformatics tools to identify and annotate genes.

## Skills

- Good knowledge about parallel Computation.
- Gained sufficient knowledge of Perl, R language, Python, Linux, and Macro.
- Excellent ability to deal with Linux workstation, Windows XP.
- Quick Learner and self- directed and good analytical power.
- An efficient key player in challenging and creative environment with excellent capacity to adapt to new technologies and skills.

## Major Interest

- Transcriptome and Genome analysis, Epigenetic, Alternative Splicing, MiRNAs, LncRNAs, Functional genomics.

## Publications

### Book chapter

1. **D. Lakhwani (2020).** ‘Databases and tools for long noncoding RNAs’ in Long Non-coding RNAs in Plants: Roles in development and stress. Pp.35-45.

### Research articles

1. Lakhwani D, Pandey A, Sharma D, Asif MH, Trivedi PK: Novel microRNAs regulating ripening-associated processes in banana fruit. *Plant Growth Regulation* 2020, 90(2):223-235. (**Impact factor: 2.388**) (**First author**)
2. Lakhwani D, Pandey A, Dhar YV, Bag SK, Trivedi PK, Asif MH: Genome-wide analysis of the AP2/ERF family in Musa species reveals divergence and neofunctionalisation during evolution. *Scientific reports* 2016, 6:18878. (**Impact factor: 4.12**) (**First author**)
3. Saint-Oyant LH, Ruttink T, Hamama L, Kirov I, Lakhwani D, Zhou N-N, Bourke PM, Daccord N, Leus L, Schulz D: A high-quality genome sequence of

- Rosa chinensis to elucidate ornamental traits. *Nature plants* 2018, 4(7):473-484. **(Impact factor: 13.29)**
4. Shivhare R, Lakhwani D, Asif MH, Chauhan PS, Lata C: De novo assembly and comparative transcriptome analysis of contrasting pearl millet (*Pennisetum glaucum* L.) genotypes under terminal drought stress using illumina sequencing. *The Nucleus* 2020, 63(3):341-352. **(Impact factor: 0.56)**
  5. Menz I, Lakhwani D, Clotault Jrm, Linde M, Foucher F, Debener T: Analysis of the Rdr1 gene family in different Rosaceae genomes reveals an origin of an R-gene cluster after the split of Rubeae within the Rosoideae subfamily. *PloS one* 2020, 15(1):e0227428. **(Impact factor: 2.776)**
  6. Dhar YV, Lakhwani D, Pandey A, Singh S, Trivedi PK, Asif MH: Genome-wide identification and interactome analysis of members of two-component system in Banana. *BMC genomics* 2020, 20(1):1-15. **(Impact factor: 3.73)**
  7. Shukla T, Khare R, Kumar S, Lakhwani D, Sharma D, Asif MH, Trivedi PK: Differential transcriptome modulation leads to variation in arsenic stress response in Arabidopsis thaliana accessions. *Journal of hazardous materials* 2018, 351:1-10. **(Impact factor: 8)**
  8. Pandey SP, Srivastava S, Goel R, Lakhwani D, Singh P, Asif MH, Sane AP: Simulated herbivory in chickpea causes rapid changes in defense pathways and hormonal transcription networks of JA/ethylene/GA/auxin within minutes of wounding. *Scientific reports* 2017, 7(1):1-14. **(Impact factor: 4.12)**
  9. Bhambhani S, Lakhwani D, Shukla T, Pandey A, Dhar YV, Asif MH, Trivedi PK: Genes encoding members of 3-hydroxy-3-methylglutaryl coenzyme A reductase (HMGR) gene family from Azadirachta indica and correlation with azadirachtin biosynthesis. *Acta Physiologiae Plantarum* 2017, 39(2):65. **(Impact factor: 1.19)**
  10. Bhambhani S, Lakhwani D, Gupta P, Pandey A, Dhar YV, Bag SK, Asif MH, Trivedi PK: Transcriptome and metabolite analyses in Azadirachta indica: Identification of genes involved in biosynthesis of bioactive triterpenoids. *Scientific reports* 2017, 7(1):1-12. **(Impact factor: 4.12)**
  11. Pandey A, Misra P, Alok A, Kaur N, Sharma S, Lakhwani D, Asif MH, Tiwari S, Trivedi PK: Genome-wide identification and expression analysis of homeodomain leucine zipper subfamily IV (HDZ IV) gene family from Musa accuminata. *Frontiers in plant science* 2016, 7:20. **(Impact factor: 4.298)**
  12. Pandey A, Alok A, Lakhwani D, Singh J, Asif MH, Trivedi PK: Genome-wide expression analysis and metabolite profiling elucidate transcriptional regulation of flavonoid biosynthesis and modulation under abiotic stresses in banana. *Scientific reports* 2016, 6:31361. **(Impact factor: 4.12)**
  13. Agarwal P, Pathak S, Lakhwani D, Gupta P, Asif MH, Trivedi PK: Comparative analysis of transcription factor gene families from Papaver somniferum: identification of regulatory factors involved in benzyloquinoline alkaloid biosynthesis. *Protoplasma* 2016, 253(3):857-871. **(Impact factor: 2.80)**
  14. Sharma D, Tiwari M, Lakhwani D, Tripathi RD, Trivedi PK: Differential expression of microRNAs by arsenate and arsenite stress in natural accessions of rice. *Metallomics* 2015, 7(1):174-187. **(Impact factor: 4.069)**
  15. Dubey S, Shri M, Misra P, Lakhwani D, Bag SK, Asif MH, Trivedi PK, Tripathi RD, Chakrabarty D: Heavy metals induce oxidative stress and genome-wide modulation in transcriptome of rice root. *Functional & integrative genomics*

- 2014, 14(2):401-417. **(Impact factor: 2.74)**
16. Asif MH, Lakhwani D, Pathak S, Gupta P, Bag SK, Nath P, Trivedi PK: Transcriptome analysis of ripe and unripe fruit tissue of banana identifies major metabolic networks involved in fruit ripening process. *BMC plant biology* 2014, 14(1):316. **(Impact factor: 3.83)**
  17. Asif MH, Lakhwani D, Pathak S, Bhambhani S, Bag SK, Trivedi PK: Genome-wide identification and expression analysis of the mitogen-activated protein kinase gene family from banana suggest involvement of specific members in different stages of fruit ripening. *Functional & integrative genomics* 2014, 14(1):161-175. **(Impact factor: 2.74)**
  18. Singh AP, Dubey S, Lakhwani D, Pandey SP, Khan K, Dwivedi UN, Nath P, Sane AP: Differential expression of several xyloglucan endotransglucosylase/hydrolase genes regulates flower opening and petal abscission in roses. *AoB Plants* 2013, 5. **(Impact factor: 2.2)**
  19. Rai KM, Singh SK, Bhardwaj A, Kumar V, Lakhwani D, Srivastava A, Jena SN, Yadav HK, Bag SK, Sawant SV: Large-scale resource development in *Gossypium hirsutum* L. by 454 sequencing of genic-enriched libraries from six diverse genotypes. *Plant Biotechnology Journal* 2013, 11(8):953-963. **(Impact factor: 6.305)**
  20. Pathak S, Lakhwani D, Gupta P, Mishra BK, Shukla S, Asif MH, Trivedi PK: Comparative transcriptome analysis using high papaverine mutant of *Papaver somniferum* reveals pathway and uncharacterized steps of papaverine biosynthesis. *PloS one* 2013, 8(5):e65622. **(Impact factor: 2.776)**
  21. Ranjan, A., Pandey, N., **Lakhwani, D.**, Dubey, N.K., Pathre, U.V. and Sawant, S.V. (2012) Comparative transcriptomic analysis of roots of contrasting *Gossypium herbaceum* genotypes revealing adaptation to drought. *BMC Genomics*, 13, 680. **(Impact factor: 3.73).**

### Seminar/Workshop Attended

- Participated & presented poster titled ‘**Comparative transcriptome analysis using high papaverine mutant of *Papaver somniferum* reveals pathway and uncharacterized steps of papaverine biosynthesis**’ in the national symposium on "Accelerating Biology 2012: Computing to Decipher" in CDAC, Pune, Feb. 2012.
- Participated & presented poster titled ‘**Computational Prediction of candidate miRNAs and their targets from *Musa acuminata***’ in the Accelerating Biology 2012: in the national conference on "New trends in Bioinformatics" in IIT, Delhi, July. 2012.

### Extra-Curricular Activities and Achievements

- Best Research paper award for “Genome-wide analysis of the AP2/ERF family in *Musa* species reveals divergence and neofunctionalisation during evolution” in 2016 at CSIR-NBRI.
- Won CSIR 44th SSBMT indoor level tournament (Badminton) held in IIMT, Chandigarh, India, Feb. 13, 2013.
- Actively participated in Culture activities held at School and college.
- Qualified PhD CET state level exam, 2012.

