

**Sheetal Ambardar**

**Post-doctoral fellow**, TransDisciplinary University, Bangalore

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**Key achievements:**

- 2017- Organising Secretary, National Symposium on Future of Functional Genomics (TransDisciplinary Genomics – I) conducted on October 13-14, 2017 at TransDisciplinary University, Bangalore. (<http://tdu.edu.in/tdu-genomics-symposium-2017/>)
- 2016- Selected for **National Post-doctoral fellowship (N-PDF)** in life sciences under SERB, DST, Government of India
- 2010 - Qualified **INSPIRE-AORC** fellowships in Microbiology under DST, GoI
- 2009 - Qualified NET **CSIR-JRF** in life sciences, Government of India.
- 2007 - Qualified **NET-LS** in life sciences under CSIR, government of India.
- (2006-2008) - Secured **1<sup>st</sup> position** in M.Sc Microbiology (Gold medalist).
- Distinction throughout the academic carrier

**Positions held:**

- 2016- onwards National Post-doctoral fellow (DST-SERB-NPDF) at The Institute of Trans Disciplinary Health Sciences and Technology, TDU, Bangalore 560064
- 2015-2016 Senior research scientist, InterpretOmics Center for Next Generation Sequencing, Bangalore 560008
- 2014-2015 Research Associate, Next Generation Sequencing facility, Center of Cellular and Molecular Platform, National Center of Biological Sciences, Bangalore 560065

**Education:**

Exam. Passed	Year	% Marks	University / Board	Remarks
Ph.D (Microbiology) (NET-CSIR- JRF)	2015	Awarded	University of Jammu	Title of The thesis : “Mining microbial diversity of <i>Crocus sativus</i> rhizosphere by metagenomic approach”
M.Sc. (Microbiology)	(2006-2008)	77.6 %	University of Jammu	<b>(Gold medalist)</b> Distinction
B.Sc. (Biotechnology)	(2003-2006)	77.5 %	Bangalore University	Distinction

**Research Experience in Genomics:**

- Eight year experience (2009-till date) in genomics, microbiology and molecular biology.
- Three and half year experience in second and third generation sequencing technology and Bioinformatics analysis.
  - **Illumina Sequencing Platform** -Whole genome, transcriptome, exome and restricted site associated DNA marker sequencing using Illumina sequencing platform
  - **Ion proton Sequencing Platform** - Whole transcriptome and small RNA sequencing using Ion Proton sequencing platform and its analysis
  - **454 pyrosequencing Platform** -Amplification of ITS genes from Saffron metagenome by PCR, Pyrosequencing of ITS gene from different samples, Analysis of 454 Roche data using bioinformatics software
  - **PacBio Sequencing Platform-** Library construction of Human Leucocytes Antigen (HLA) gene and sequencing using PacBio sequencing platform and data analysis

- Post-doctoral research experience on Human genomics and worked on HLA typing using third generation (PacBio SMRT) sequencing.
- 2014 - One month training on 454 pyrosequencing data analysis using bioinformatics in Next Generation Genomic Facility, C-Camp, May-June 2014
- 2012 - Two weeks training on sequence analysis of 16S rRNA metagenomic library Bioinformatics softwares in Department of Zoology, DU- South Campus, 15th Aug-30th Aug 2012
- 2011 - 3 months training on Metagenomic Library construction and analysis in Madurai Kamraj University, TamilNadu as NRCBS visiting Fellow. September- December, 2011.

#### Key Research Achievements (Deliverables):

- **2012** - Best paper award, in IV International Saffron Symposium Advances in Saffron Biology, technology and trade. 22- 25<sup>th</sup> October 2012 SKAUST-K, Kashmir
- **2012** - **2<sup>nd</sup> prize in 3<sup>rd</sup> Global conference on Plant pathology for food security**. Organized by Indian society of Mycology and Plant pathology and Maharana Pratap University of Agriculture & technology, Udaipur January 10-13, **2012**
- **2011** - **2<sup>nd</sup> prize in poster presentation** in Symposium on Microbial Diversity and Bio-prospecting held at Department of Botany, University of Jammu on 28-30 October **2011**.
- **2011** -**Selected for UGC-MKU-NRCBS** visiting Fellowship programme at Madurai Kamraj University, Madurai, Tamil Nadu, India
- **2010** - **Best paper award** in National conference National seminar on technological innovations in Saffron 25-26 November 2011 SKAUST Kashmir

#### PUBLISHED WORK:

1. **Ambardar S**, Heikham RS, Gowda M and Vakhlu J (**2016**) Temporal and spatial changes in the fungal community associated with belowground parts of *Crocus sativus* during flowering and dormant growth stages. **PLOSone**. 11(9): e0163300. doi:10.1371/journal.pone.0163300. **Impact factor: 3.234**
2. **Ambardar S**, Gupta R, Trakroo D, Lal R and Vakhlu J (**2016**) High Throughput Sequencing: An overview of sequencing chemistry **Indian Journal of Microbiology**. DOI 10.1007/s12088-016-0606-4. pp 1-11. **Impact factor: 1.143**
3. Gowda M, **Ambardar S**, Dighe N, Manjunath A, Shankaralingu C, Hallappa P, Harting J, Ranade S, Jagannathan L, Krishna S (2016) Comparative analyses of low, medium and high-resolution HLA typing technologies. **Journal of Clinical & Cellular Immunology**. Vol 7 issue 2 <http://dx.doi.org/10.4172/2155-9899.1000399>. **Impact factor: 2.240**
4. **Ambardar S**, Sangwan N, Manjula A, Rajendhran J, Gunasekaran P, Lal R and jyoti Vakhlu (**2014**). Bacteria associated with underground parts of *Crocus sativus* by 16S rRNA gene targeted metagenic approach. **World Journal of microbiology and biotechnology**. Volume 30, Issue 10 page 2701-2709. **Impact factor: 1.532**
5. **Ambardar S** and Vakhlu J. (**2013**) Plant growth promoting bacteria from *Crocus sativus* rhizosphere. **World Journal of microbiology and biotechnology**. Volume 29, Issue 12 (2013), Page 2271-2279 **Impact factor: 1.532**
6. Vakhlu J, **Ambardar S** and Johri B.N (**2012**). Metagenomics – a relief road to novel microbial genes and genomes. In Editor/s T. Satyanarayana, Bhavdish Narain Johri, Anil Prakash. *Microorganisms in Sustainable Agriculture and Biotechnology*, 263-294 Springer.