A Brief Curriculum Vitae of Dr Ravi Shankar, CSIR-IHBT (March 2016)

Name: Ravi Shankar	Date of birth: 18/09/1977
Affiliation: CSIR-IHBT	
Telephone:	Designation: Scientist Coordinator, Bioinformatics Program AcSIR Group Leader, SCBB
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Education:

S.No.	Degree	Institution	Year
1	BSc	University of Delhi	1997
2	MSc(Biochemistry)	Jamia Hamdard University, New Delln 99	
3	PGAD(Bioinformatics)	JNU, New Delhi	2001
	(Now MTech)		
4	PhD	CSIR-IGIB and Pune University	2006(Thesis submitted)
			2008 (Degree awarded)

Professional Experience:

S.No	Position and Organisation	Nature of Job	Period
1	Researcher, Genetic Information Research Institute, Mountain View, California	It was H1B visa based employment in the USA. Major work included non-coding elements and repeats oriented research and supervision of Repbase.	2006-2007
2	Main Bioinformatician, BIOBASE, Bangalore	To look after bio informatics research activities in its India office. Included network analysingene regulation.	2007-2008 is and
3	Faculty in Bioinformatics, Indian Institute of Advanced Research Gandhinagar, Gujarat.	To carry out Bioinformatics research and teaching.	2008-2009
4	Scientist Bioinformatics, CSIR-IHBT	To start Bioinformatics research	12:03:12:01 to present

activities with major areas like NGS, noncoding biology, epigenomics and
computational regulomics,
microRNAs

Current research interests:

Noncoding biology, NGS, Computational regulomics and Epigenomics. HPC

Honors and awards:

NIH, USA Research Fellow.

CSIR-NET-2000 qualified.

GATE-2000 qualified.

DBT fellowship for PGAD Bioifnormatics from JNU.

DST INSA Indo-Australia fellowship (2012).

DST/SERB Young Scientist Fast track grant award(2012).

University Exams Topper for all the three years of BSc at University of Delhi (1994-97 batch).

Details of externally funded projects being implemented

1) Profiling and characterization of early phase differential miRNA(s) responsible for downstream development of insulin resistance in hMSC derived adipocytes.

Funding agency: DBT; BT/PR8721/AFR/36/775/2013

Amount Sanctioned: Rs 68,15000/-Period: 2015-2018. Status: Started.

Description: To identify DM-2 with respect to miRNA responses in adipocytes. Whole regulatory network with respect to important miRNAs has to be developed. Experimental part is being looked upon by CDRI PI.

2) Epigenetic and transcriptional regulation by small RNAs: A computational approach. Funding agency: DST under Young Scientist Fast Track grant award.; SR/FT/LS-97/2010 Amount Sanctioned: Rs 19,60,000.

Period: 2012- 2015. Status: Completed.

Description: Under this project the roles of sRNA are being studied, how they influence DNA methylation in plants, as well as indirect regulation of epigenetic system without RdDM and their association with repetitive elements.

3) Regulatory System Analysis with respect to microRNA and development of related tools and servers.

Funding agency: DBT; BT/PR-11098/BID/07/261/2008

Amount sanctioned: 16.334 Lakhs

Period: 2010-2013. Status: Completed.

Description: This project has been completed. Novel algorithms, tools and servers were developed to identify novel miRNAs and their targets and establishment of miRNA mediated regulatory networks.

- 4) National 12th FYP Project in Computational Biology (GENESIS): PI at IHBT
- 5) National 12th FYP Project in Epigenetics (EpiHED): PI at IHBT.
- 6) CSIR-EMPOWER Grant to study ncRNAs in Human Brain.

Five important publications in past five years:

S. No.	Authors	Title	Journal Volume, Page	Year
1	Ashwani Jha and Ravi Shankar *	Employing machine learning for reliable miRNA target identification in plants.	BMC Genomics	2011
2	A Pault, A Jhat, S Bhardwaj, S Singh, R Shankar*, S Kumar*	RNA-seq-mediate d transcriptome analysis of actively growing and winter dormant shoots identifies non-deciduous habit of evergreen tree tea during winters	Nature Scientific reports 4, 2014, 5932 doi:10.1038/srep 0593	2014
3	Ashwani Jha and Ravi Shankar *	miReader: Discovering novel miRNAs in species without sequenced genome.	Plos One	2013
4	Ashwani Jha, Mrigaya Mehra and Ravi Shankar*	The Regulatory Epicenter of miRNAs.	Journal of Biosciences	2011
5	Ashwani Jha, Ganesh Panzade, Rajesh Pandey, Ravi Shankar*	A legion of regulatory sRNAs exists beyond the typical microRNAs microcosm.	Nucleic Acids Research	2015

^{*}Corresponding authors. †Equally contributed.

Publications: (Full updated list available at Google Scholar link: Updated Publication)

* Corresponding Author

1.A legion of potential regulatory sRNAs exists beyond the typical microRNAs microcosm. Ashwani Jha, Ganesh Panzade, Rajesh Pandey and **Ravi Shankar*. Nucleic Acids Research**, 2015, doi: 10.1093/nar/gkv871

2.A Deluge of Complex Repeats: The Solanum Genome. Mrigaya Mehra, Indu Gangwar, **Ravi Shankar***. **PLoS ONE** 10(8): e0133962. doi:10.1371/journal.pone.0133962

3.Expression of SOD and APX genes positively regulates secondary cell wall biosynthesis and promotes plant growth and yield in Arabidopsis under salt stress. Amrina Shafi, Rohit Chauhan, Tejpal Gill, Mohit K. Swarnkar, Yelam Sreenivasulu, Sanjay Kumar, Neeraj Kumar, Ravi Shankar, Paramvir Singh Ahuja, Anil Kumar Singh. Plant Mol. Biol., 2015, Volume 87, Issue 6, pp 615-631

4.RNA-seq-mediated transcriptome analysis of actively growing and winter dormant shoots identifies non-deciduous habit of evergreen tree tea during winters.

Asosii Paul[†], **Ashwani Jha**[†], Shruti Bhardwaj, Sewa Singh, **Ravi Shankar***, Sanjay Kumar*. **Nature Scientific Reports**, **2014**. **doi:10.1038/srep05932**

5.miRNAting control of DNA methylation. Ashwani JhaandRavi Shankar*. Journal of Biosciences, 39 365-380, 2014.

6.Comprehensive Transcriptomic Study on horse gram (*Macrotyloma uniflorum*): De novo Assembly, Functional Characterization and Comparative Analysis in Relation to Drought Stress. Jyoti Bhardwaj[†], **Rohit Chauhan**[†], Mohit Swarnkar, R Chahota, **R Shankar*** and S Yadav*. **BMC Genomics. 2013 14:647, 2013.**

7. Transcriptome sequencing of rhizome tissue of Sinopodophyllum hexandrum at two temperatures.

A Kumari † , HR Singh † , A Jha, MK Swarnkar, **R Shankar***, S Kumar*. **BMC Genomics**, **15** (1), **871**, **2014**.

8.miReader: Discovering novel miRNAs in species without sequenced genome. Ashwani Jha[†] and Ravi Shankar*[†] PLoS ONE 8(6): e66857. doi:10.1371/journal.pone.0066857

9.De-novo sequence assembly and transcriptome analysis of Venturia inaequalis, the deadly apple scab pathogen. Karnika Thakur[†], **Vandna Chawla**[†], Shammi Bhatti, Mohit Kumar Swarnkar, Jagdeep Kaur, **Ravi Shankar***, Gopaljee Jha*. **PLoS ONE** 8(1): e53937. doi:10.1371/journal.pone.0053937.

10.miR-BAG: Bagging Based Identification of MicroRNA Precursors.

Ashwani Jha[†], Rohit Chauhan[†], Mrigaya Mehra[†], Heikham Russiachand Singh, **Ravi Shankar* PLOS ONE** 2012 7(9): e45782. doi:10.1371/journal.pone.0045782.

11.De novo sequencing and characterization of *Picrorhiza kurrooa* transcriptome at two temperatures showed major transcriptome adjustments.

Parul Gahlan † , Heikham Russiachand Singh † , Ravi Shankar 1* , Niharika Sharma, Anita Kumari, Vandna Chawla, Paramvir Singh Ahuja, Sanjay Kumar 2* . BMC Genomics, 13:126, March, 2012.

12.Employing machine learning for reliable miRNA target identification in plants. Ashwani Jha and **Ravi Shankar***.

BMC Genomics, 12:636, December, 2011.

13. The Regulatory Epicenter of microRNAs. Ashwani Jha, Mrigaya Mehra, **Ravi Shankar***. **J Biosci.** 2011 Sep;36(4):621-38.

14."The Bioinformatics of Next Generation Sequencing": A meeting report. Ravi Shankar*. *Journal of Mol. Cell Biol.* doi: 10.1093/jmcb/mjq024, 2010.

15. Flanking region sequence information to improve microRNA target prediction. Russiachand Heikham and **Ravi Shankar***. *Journal of Biosciences*, 35(1), March 2010, 105-118

16.Finding Alu in Primate Genomes with AF-1. *Bioinformation* 3(7): 287-288 (2009) **Shankar R***, Kataria B and Mukerji M.

17.Involvement of repeats in non-random genomic divergence in 5' upstream regions of Human and Chimpanzee genes of different biological processes.

HUGO's 13th international meeting on the Human Genome. Chaurasia A, **Shankar R**, Mukerji M **The HUGO Journal (Genomic Medicine)** (2008) 2:401-413.

18.Non-random genomic divergence in repetitive sequences of human and chimpanzee in genes of different functional categories. **Shankar R,** Chaurasia A, Ghosh B, Chekmenev D, Cheremushkin E, Kel A, Mukerji M

Mol Genet Genomics. 2007 Apr; 277(4): 441-55.

19. Evolution and distribution of RNA polymerase II regulatory sites from RNA polymerase III dependant mobile Alu elements. **Shankar R,** Grover D, Brahmachari S K, Mukerji M. **BMC Evol Biol.** 2004 Oct 4;4(1):37

20.Repbase Reports. 2006, Vol. 6, Issue 10. **Shankar R** & Jerzy Jurka.

21.Repbase Reports. 2006, Vol.6, Issue 11. **Shankar R** & Jurka,J.

22.Repbase Reports. 2006, Vol.6, Issue 12. **Shankar R** & Jerzy,J.

23.Repbase Reports. 2007, Vol.7, Issue 1. **Shankar R** & Jerzy, J.

International Poster: Novel to Reference Free miRNA Discovery: NGS powered miRNA discovery with miR-BAG and miReader.

Ashwani Jha, Jennifer Clancy, Thomas Preiss, Ravi Shankar*.

35th Annual Lorne Genome Conference 2014 held in Lorne, Victoria, Australia, February 16–18, 2014