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Current Research Activities

(A) **Regulatory system analysis** with respect to non-coding regions of genome, considering combined role of transcription factors as well as microRNAs in gene regulation.

Through this project it is being tried to chalk out the principle of microRNA formation, their binding to their target sites and finally to assess the weighted impact of this system in regulatory network. Various related softwares are being developed under this project.

As a part of this project I have finished a module to refine the microRNA target prediction methodology via pattern encoding and target RNA folding features modeled into Machine Learning models claiming accuracy level as high as 91%. For plant system we have developed first ever machine learning based and parallel coded software to detect targets with highest ever accuracy, where translational repression in plants is also detected.

Besides this we have discovered an entirely previously unknown property of miRNA and their biogenesis process, which suggests that merely discovering and predicting miRNA would not be of much use till we incorporate the regulatory information at all possible level, from chromatin to nuclear export and localization as well as target detection.

A highly accurate miRNA identification tool, miR-BAG was developed by my team, under this research objective.

(B) **Transcriptional regulation by non-codings, computational epigenomics and regulomics.**

The science has evolved a very beautiful way. We would get contended with finding one gene in our labs after working for years. There came cloning, amplification and sequencing methods. Reductionist approach towards the metabolic disorders or diseases took the limelight till the realization of genomic level studies occurred opening new areas of genomics, proteomics and whole genome SNP studies. A huge realization toward TFBS based studies was sensed thereafter resulting into new softwares to detect TFBS and new promoter models. Now in present couple of years many studies have proved that alone genome, proteome sequencing and SNP mappings don't give enough information to elucidate the behavior of cell and development. Here comes the epigenetic control, which does not change nucleotide but methylation and related modification in DNA and histones determine the chromatin and DNA response to binding proteins. A combination of TFBS alongwith methylation pattern of DNA and histones decide the age, age stage and behavior of the regulatory system.

(C) Computational issues with Next Generation Sequencing.

The cyclic sequencing methodology is the new flavor for whole genome sequence through which whole genome sequencing has become easier, faster and cheaper. Its called next generation sequencing. However the new challenges made by this approach are in majority computational in nature. It requires handling of massive data, handling of issues arising due to very short length of sequence reads and errors in base calling. De novo sequence assembling and validity of new sequence is another challenge. The present study is all about these issues and finding solutions to them.

Under this project we are performing next generation sequencing and associated studies for plant species like Picrorhiza kurroa, Podophyllum, Vinca, Tea and other species. Besides this, we are also working over miRNA and other non-coding elements discovery using Next Generation Sequencing and developing tools.

(D) The Mythology of miRNAs: Re-understanding the “micro” of regulatory RNAs.

Will not reveal much at this time, as my excitement with our latest findings suggests that let our paper speak about it! Will just say that this work may change the way you approach miRNAs and systems affected by them.

PhD Research Work

The title of my PhD research was: “ Significance of Alu repeats in human genome”. The research objective was met through completely in-silico and Bioinformatics study.

The research work included:

- 1) Identification of functionally significant Alu repeats.
- 2) Understanding Alu expansion and effect over gene regulation.
- 3) Alu Evolution
- 4) Significance of Alu repeats with respect to primate evolution as well as their functional evolution.
- 5) Development of study related Bio-Computational tools and softwares.

Work Experience

- Finished **Post Graduate Advanced Diploma in Bioinformatics** from Centre for Computational Biology and Bioinformatics (CCBB), **Jawaharlal Nehru University**, N. Delhi, year 2001.
- **Worked over protein trial structure development with Professor B. Jayaram**, Department of Chemistry and BioComputing Facility, **Indian Institute of Technology, New Delhi (2000-2001)**.
- **Joined IGIB, as a Knowledge Center Fellow** as well as **Junior Research Fellow**, in GNR Genome Informatics Lab & Functional Genomics Unit, **IGIB, CSIR under Prof. Samir Brahmachari**. Worked over various parts of my PhD projects, under supervision of **Dr. Mitali Mukerji. (2002-2006)**

- **Designed and carried out an international project over** Human and Chimpanzee divergence, with Dr. Alexander Kel & Dmitry Chekmenev, Biobase International, Germany, and Evgeny Cheremushkin, EHS, Russia, as international collaborators, year 2005.
- **Finished PhD work** in September 2006 and joined GIRI with **Dr. Jerzy Jurka, President GIRI, CA** in October 2006.
- **Researcher** at Genetic Information Research Institute(GIRI), Mountain View, California (October, 2006 to February, 2007).
- **Bioinformatician at BIOBASE International(Transfac fame)**, (2007 to 2008). Carried pathways related research.
- **Faculty**, Department of Bioinformatics and Structural Biology, **IAR**, Gandhinagar (2008 to 2010)).
- **Group Leader**, Studio of Computational Biology & Bioinformatics, CSIR-IHBT (2010 to present).

Talks and Poster Presentations Delivered

“**The HMM**”. Informatics. at **Informatics, N. Delhi** . 2002

“**Motif Finding and Statistics**”. at **Informatics N. Delhi**.-2002

“**Strategies in Regulatory Elements Finding**” at CeBiTech, The Bioinformatics Graduate School, Bielefeld, Germany. **Research work presented on invitation from Bielefeld University, Germany (2003).**

“**Alu repeats as a caravan to regulatory house**”, A presentation during Celebration of 50 years of Triple Helix. **Vigyan Bhawan, New Delhi**. 2004. (**Presentation given before Honorable President of India, Dr. APJ Kalam**)

“**Alu repeats as a caravan to regulatory house**”. BioTech 2004, **India International Center, N. Delhi**, 2004

“**AF-1: Finding Alus in Primate Genomes**”. Lecture Delivered at Faculty of Technology and Applied Mathematics, MS University, Baroda, Gujarat. 2008.

“**A MicroRNA target refinement method and tool**” , Indian Institute of Integrative Medicine, Jammu, June 26, 2009.

“**MiRNA: The “Little Master” of Gene Regulation**”, Indian Institute of Technology (IIT), Mandi. April 8, 2011.

“Novel to Reference Free miRNA Discovery: NGS powered miRNA discovery with miR-BAG and miReader”, 35th Lorne Genome Conference, Victoria, Australia, 2014.

“In the pursuit of small RNAs: A journey since 2010”: At the retreat function of EMBL Director's lab and Preiss Lab, ANU, Retreat, 2014, at ANU Kiola Beach Campus, New South Wales, Australia. 2014.

Publications (<http://scholar.google.co.in/citations?hl=en&user=6oxMtu0AAAAAJ>)

***Corresponding author**

miRNAting control of DNA methylation.

A Jha, R Shankar*

Journal of Biosciences 39 (3), 365-380, 2014

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

A Paul, A Jha, S Bhardwaj, S Singh, R Shankar*, S Kumar*

Nature's Scientific reports 4, 2014, 5932 doi:10.1038/srep0593

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

Comprehensive Transcriptomic Study on horse gram (*Macrotyloma uniflorum*): De novo Assembly, Functional Characterization and Comparative Analysis in Relation to Drought Stress

Jyoti Bhardwaj^{1†}, Rohit Chauhan^{2†}, Mohit Swarnkar¹, Rakesh Kumar Chahota³, Ravi Shankar^{2*} and Sudesh Kumar Yadav^{1*}.

BMC Genomics 14 (doi:10.1186/1471-2164-14-647), 647, 2013

miReader: Discovering novel miRNAs in species without sequenced genome.

Ashwani Jha[†] and Ravi Shankar*

PLoS ONE 8 (6), e66857, 2013

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 , 2013

miR-BAG: Bagging Based Identification of MicroRNA Precursors.

Ashwani Jha†, Rohit Chauhan†, Mrigaya Mehra†, Heikham Russiachand Singh, **Ravi Shankar***

PLoS ONE 7(9): e45782. doi:10.1371/journal.pone.0045782, 2012

De novo sequencing and characterization of *Picrorhiza kurroa* transcriptome at two temperatures showed major transcriptome adjustments

Parul Gahlan†, Heikham Russiachand Singh†, **Ravi Shankar***, Niharika Sharma, Anita Kumari, Vandna Chawla, Paramvir Singh Ahuja, Sanjay Kumar*.

***BMC Genomics*, 13:126, 2012**

Employing Machine Learning for Reliable miRNA Target Identification in Plants.

Ashwani Jha and **Ravi Shankar***

***BMC Genomics* 2011, 12:636**

The Regulatory Epicenter of miRNAs.

Ashwani Jha, Mrigaya Mehra and **Ravi Shankar***

***J Biosci.* 2011, 36(4):621-38.**

“The Bioinformatics of Next Generation Sequencing”: Meeting Report

Ravi Shankar* *J. Mol. Cell Biol.* (Oxford Journal), 2011, 3 (3): 147-150.

Flanking region sequence information to improve microRNA target prediction.

Russiachand Heikham and Ravi Shankar* *Journal of Biosciences*, 35(1), 2010, 105–118

Finding Alu in Primate Genomes with AF-1.

Shankar R*, Kataria B and Mukerji M.

Bioinformation 3(7): 287-288 (2009)

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* (Springer)2007 Apr;277(4):441-55.**

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**

Rebase Reports. 2006, Vol. 6, Issue 10.

Shankar R & Jerzy Jurka.

Rebase Reports. 2006, Vol.6, Issue 11.

Shankar R & Jurka,J.

Rebase Reports. 2006, Vol.6, Issue 12.
Shankar R & Jerzy,J.

Rebase Reports. 2007, Vol.7, Issue 1.
Shankar R & Jerzy,J.

Peer Reviewer of Journals/Publishers

RNA (a Cold Spring Harbour Lab's published Journal)
BMC Genomics /Biomed Central
Bioinformatics /Oxford
BMC Bioinformatics /Biomed Central
Genomics, Proteomics & Bioinformatics/ Elsevier
Genome
CRC Press
PLOS ONE
Plant Molecular Biology

Academic awards, achievements and distinctions

- **DST Indo-Australia visiting scientist fellowship** by INSA & Australian Academy of Science (AAS), Year 2012-13.
- **DST Young Scientist Fast Track Grant Awardee**, 2010.
- Certified for project management training at BIOBASE, India, 2007.
- **NIH, USA project fellow** during the period of Oct. 2006 to Feb. 2007 at GIRI.
- Qualified **CSIR-National Eligibility Test (NET)** conducted by CSIR.
- Availed Hewlett Packard fellowship during PhD.
- **DBT fellowship** during PGAD Bioinformatics from JNU (2000-2001).
- Qualified Graduate Aptitude Test in Engineering (**GATE-2000**), conducted by India Institutes of technology(IITs) and Indian Institute of Science (IISc), Bangalore.
- B.Sc. Topped all of the university annual examinations for all the consecutive 3 years. University of Delhi. Year 1994-1997.

Teaching Experience:

- Taking classes of Msc Bioinformatics at Central University of Himachal Pradesh (India) as well as coordinating MSc classes(Bioinformatics and Statistics) with Central University staffs.
- Taking classes of PhD students for Bioinformatics course, for Academy of Scientific &

Innovative Research, AcSIR, at IHBT Palampur.

- Coordinator, Bioinformatics course of PhD, AcSIR at CSIR-IHBT, Palampur.
- Supervising 5 PhD candidates.

Grants & Funding attracted as a PI

Heading two Mega(network) Project funding for 12th Five Year Plan of CSIR, Govt of India in the field of Computational Epigenomics(EpiHed) and Computational Biology(Genesis), with total fund amount of ~ INR 40.00 millions. (Year 2012-17).

Research grant approved by DST, Govt. of India for Project entitled: “Epigenetics & Transcriptional regulation by small RNAs: A computational approach. Year 2012-15.

Research Grant approved from DBT, Govt. of India, for project titled as “Regulatory system analysis with respect to microRNA target prediction and development of related tools and servers” , **year 2010-13.**

CSIR EMPOWER Project “Identification of de novo non-coding transcripts in human brain”. Year 2010-12.

Multi Institutional collaborative project, to be funded by Indian Council of Agricultural Research (ICAR) ” **Understanding plant-nematode interaction: Identification of plant and nematode genes involved in disease development ”, year 2012-15.**

Course Director & Coordinator: National Bioinformatics workshop “The Bioinformatics of next generations sequencing”, 17-18, June, 2010, funded by Department of Biotechnology(DBT), India.

Education

B.Sc. in Agrochemistry, University of Delhi, 1997.

M.Sc. In Biochemistry, Jamia Hamdard University, New Delhi,1999.

Post Graduate Advanced Diploma In Bioinformatics, CCBB, JNU, N. Delhi, 2001

PhD from Department of Biotechnology, University of Pune, under supervision **Dr. Mitali Mukerji**, at IGIB, CSIR, Delhi.

PhD work finished and thesis submitted in September 2006. Degree awarded on January 14, 2008.