

VINESH VINAYACHANDRAN

Center for Eukaryotic Gene Regulation
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RESEARCH INTEREST

My laboratory will undertake genomic approaches for querying transcriptional dynamics in perturbed eukaryotic systems. I will be focusing on (packaged DNA) chromatin; its unpackers the chromatin remodelers, and cis as well as the trans modifiers of transcriptional epigenetics. Laboratory will be intercalating multidisciplinary approaches of biochemistry, molecular biology, and cell biology, along with next generation sequencing and bioinformatics. My research will be directed to identify the interplay between and within chromatin remodelers, and its sub modules, the epigenetic modifier subunits, under physiological perturbations. This involves genome-wide the near base pair resolution mapping of transcriptionally involved factors, under Dis-Ease conditions. The outcomes will be followed up with functional genomic approaches to dissect the roles of these regulatory factors. The preliminary analysis of this data can shed knowledge about the probable genomic regulators its co-operativity and target for therapeutic searches.

EDUCATION

Ph.D. in Life Sciences, Center for Cellular and Molecular Biology (CCMB), Hyderabad, India	2005-2011
M.Sc in Plant Physiology, University of Agricultural Sciences (UAS), Bengaluru, India	2002-2004
B.Sc in Agricultural Sciences, Kerala agricultural University (KAU), Vellayani, India	1997-2001

RESEARCH EXPERIENCE

Post Doctoral fellow, The Pennsylvania state university With Dr. Benjamin Franklin Pugh, CEGR, Dept. of Biochemistry and Molecular Biology.	2011-Present
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Transcriptional dynamics under physiological perturbations in yeast

Identified the mechanisms and the interplay between transcription factors during heat shock using the near base pair resolution ChIP-Exo assay. The fine grain mapping of PIC forming rulers, SAGA and TFIID provided us with a comprehensive and specific binding map of these factors genome wide and elucidate the mechanism of transcriptional regulation during heat shock.

Graduate research, Center for cellular and molecular biology With Dr. Purnima Bhargava, CCMB, Hyderabad, India	2005-2011
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Role of chromatin and terminator in transcription of Yeast SNR6

Discovered that in a gene locus, multiple nucleosome positions are directed by DNA sequences. These provide a pool of nucleosomal positional possibilities, from which the preferred nucleosome statuses are selected by the specific chromatin remodelers and transcription factors depending on the physiological status of the organism.

Masters research, University of Agricultural Sciences 2002-2004
With Dr. M Udayakumar, UAS, Bengaluru, India

Transcriptome analysis in salt stressed roots of Eleusine coracana

Using fundamental molecular biology and biochemical techniques made a cDNA library of salinity stressed Finger millet roots. From the cDNA library the differentially expressed genes in finger millet were identified using subtractive hybridization and sequencing, one of the first differential transcriptome in salt stress in *Eleusine coracana*.

Bachelors research, Kerala agricultural University 2001
With Dept. of agricultural extension

Rural Agricultural Work Experience (RAWE)

First hands-on experience as a scientist with farmers and farming. During RAWE, farms were visited and recommendations were made on various field crop pest and disease management, water shed management and rainwater harvesting.

HONORS AND AWARDS

Indian Counsel of Agricultural Research, junior research fellowship (ICAR)	2002-2004
Gold medalist for Masters in Plant Physiology	2004
Gold medalist for Best thesis in Masters	2004
Council of Scientific and Industrial Research (CSIR) and University Grant Commission (UGC), senior research fellowship	2005-2010

PUBLICATIONS

R-H Pusarla*, **Vinesh Vinayachandran**, Purnima Bhargava.2007. Nucleosome positioning in relation to nucleosome spacing and DNA sequence-specific binding of a protein. *FEBS Journal* 274:2396-2410. (*Authors equally contributed to work)

Vinesh Vinayachandran, R-H Pusarla, Purnima Bhargava.2009. Multiple sequence-directed possibilities provide a pool of nucleosome position choices in different states

of activity of a gene. *Epigenetics & Chromatin*, 2:4.

Yen K, **Vinayachandran Vinesh**, Batta K, Koerber RT, Pugh BF. 2012. Genome-wide nucleosome specificity and directionality of chromatin remodelers. *Cell* 149(7):1461-73.

Yen K*, **Vinayachandran Vinesh***, Pugh BF. 2013. SWR-C and INO80 chromatin remodelers recognize nucleosome-free regions near +1 nucleosomes. *Cell* 154(6):1246-56. (*Authors equally contributed to work)

Maren Schneider, Doris Hellerschmied, Tobias Schubert, Stefan Amlacher, **Vinesh Vinayachandran**, Rohit Reja, B. Franklin Pugh, Tim Clausen, Alwin Kohler. 2015. The Nuclear Pore-Associated TREX-2 Complex Employs Mediator to Regulate Gene Expression. *Cell* 162(5):1016-1028

Rohit Reja, **Vinesh Vinayachandran**, Sujana Ghosh, B. Franklin Pugh. 2015. Molecular mechanisms of ribosomal protein gene coregulation. *Genes & Dev* 29:1942-1954

Garam Celine Han, **Vinesh Vinayachandran**, Alain Bataille, Ka Yim Chan-Salis, Cheryl A Keller, Maria Long, Susan Magargee, Shaun Mahony, Ross C Hardison, B. Franklin Pugh. 2014. A High Resolution Genome-wide binding of GATA1 and TAL1 during Erythroid Development (manuscript accepted in MCB)

POSTER AND ORAL PRESENTATION

Vinesh Vinayachandran, Rama-Haritha P, and Bhargava P. "Nucleosome Positioning in relation to nucleosome spacing and DNA sequence-specific binding of a protein, November 26 to 29th, CCMB, Hyderabad, India

Vinesh Vinayachandran, Rama-Haritha P, Bhargava P, "Multiple sequence-directed possibilities provide a pool of nucleosome position choices in different states of activity of a gene", December 11 to 13th 2006, JNCASR, Bangalore, India.

Vinesh Vinayachandran, Kuangyu Yen, B. Franklin Pugh, " Genome-wide structural integration of Swr1-C and Ino80 Chromatin remodelers at +1 Nucleosome, Mechanism of eukaryotic transcription, August 27 to 31st 2013, CSHL, NY, USA.

Vinesh Vinayachandran, Rohit Reja and B. Franklin Pugh, "Genome-wide reprogramming of transcription machinery under physiological perturbation, Epigenetics and chromatin meeting, September 9-13th 2014 CSHL, NY, USA.