University of Birmingham

Dr Aditi Kanhere PhD

School of Biosciences (/schools/biosciences/index.aspx)

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About

Dr Aditi Kanhere's research focuses on understanding how non-coding RNA, transcription factors and epigenetic modifications regulate gene expression changes in normal and diseased conditions. Her laboratory integrates cutting-edge genomics technologies with computational methods to understand mechanisms of transcription regulation in cancer.

Kanhere lab website: https://sites.google.com/site/kanherelab (https://sites.google.com/site/kanherelab/)

Qualifications

PhD (Indian Institute of Science, India)

BSc (University of Mumbai)

Biography

Dr Kanhere's research interest in transcription regulation stems from work during her PhD where she analysed common structural themes in bacterial promoters and proposed a novel methodology for promoter prediction in prokaryotes. Wishing to understand whether such rules apply to transcription regulation in eukaryotic genomes, she carried out research at Max Planck Institute for Molecular Genetics, Berlin and University College London. During this period, she worked on next-generation techniques like ChIP-seq and RNA-seq. Here, she combined her computational biology expertise as well as molecular biology techniques, which led to discovery of a new class of short non-coding RNA and other gene regulatory elements with important role in cell development. In mid-2012 she joined University of Birmingham to start her own group.

Teaching

Dr Kanhere will be involved in tutoring undergraduates and hosting lab-based projects for master students.

Postgraduate supervision

Students looking for Summer Work Experience Placements and potential PhD students interested in Dr Kanhere's research should contact via email: **a.kanhere@bham.ac.uk (mailto:a.kanhere@bham.ac.uk)** .
Research council funded PhD studentships are awarded each year competitively within the School of Biosciences.
International students with own funding and Postdoctoral fellows interested in applying for fellowships are encouraged to contact.

Research

Understanding regulation of protein-coding genes is fundamental to understanding mechanisms of cell development as well as diseases. Various non-coding elements and epigenetic modifications play important roles in regulating expression of coding genes. These regulatory non-coding elements include non-coding RNAs (ncRNA), transcription factor binding sites and non-coding DNA elements like enhancers. Dysregulation of non-coding elements is a source of many diseases including many types of cancers and developmental disorders.

However, the exact mechanism by which these non-coding genetic variations play a role in diseases is not clear. This lack of knowledge is due in part to the fact that identification, annotation and functional characterisation of these elements is still incomplete. Therefore, in-depth study of non-coding elements is necessary to understand their role in diseases and also to utilise as novel biomarkers and drug targets.

Currently Dr Kanhere's group is working on

- Identifying and characterising novel RNAs in various cancers.
- Building regulatory networks involving epigenetic modifications and ncRNAs in the normal and diseased cells.
- Novel mechanisms of transcription factor interactions and their role in gene regulation.

Publications

For a full list of publications visit PubMed.

Selected publications:

Noncoding RNA localisation mechanisms in chromatin regulation.
Kanhere A, Jenner RG.
Silence. 2012 3:2.

Short RNAs are transcribed from repressed polycomb target genes and interact with polycomb repressive complex-2.
Kanhere A, Viiri K, Araújo CC, Rasaiyaah J, Bouwman RD, Whyte WA, Pereira CF, Brookes E, Walker K, Bell GW, Pombo A, Fisher AG, Young RA, Jenner RG.
Mol Cell. 2010 38:675-88.

CpG-depleted promoters harbor tissue-specific transcription factor binding signals--implications for motif overrepresentation analyses.
Roider HG, Lenhard B, **Kanhere A**, Haas SA, Vingron M.
Nucleic Acids Res. 2009 37:6305-15.

Predicting transcription factor affinities to DNA from a biophysical model.
Roider HG, **Kanhere A**, Manke T, Vingron M.
Bioinformatics. 2007 23:134-41.

Structural properties of promoters: similarities and differences between prokaryotes and eukaryotes.
Kanhere A, Bansal M.
Nucleic Acids Res. 2005 33:3165-75.

A novel method for prokaryotic promoter prediction based on DNA stability.
Kanhere A, Bansal M.
BMC Bioinformatics. 2005 6:1.

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