Tata Institute of Fundamental Research
Survey No. 36/P, Gopanpally Village, Serilingampally, Ranga Reddy Dist., Hyderabad - 500107

TIFR-UoH (Life Sciences) Seminar Series

Decoding the transcriptional control of B cell differentiation

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The transcription factor EBF1 promotes B cell fate choice of hematopoietic multipotent progenitors, MPPs, by restricting their alternate cell fate options. We have employed high-throughput molecular strategies to determine the downstream components, which act in concert with EBF1 in a feed-forward manner, promoting B cell fate commitment. These molecular analyses demonstrate that EBF1 activates early B lineage genes that are important for B cell specification and suppresses several key factors that are crucial to the development of T, NK, and myeloid lineages. Accordingly, deep-sequence analysis of small-RNA libraries followed by integration of EBF1 expression analysis revealed that B lineage gene expression pattern coincides with attendant changes in activation or repression of a number of miRNAs. Furthermore, HiC analyses, a powerful high-throughput approach that captures long-range chromatin interactions indicating that EBF1 induces several novel higher-order chromatin interactions impinging on the expression of B lineage genes. Analysis of chromatin modifications within these interacting domains has led to the identification of a distinct set of cis-elements whose functions appear to be closely associated with the EBF1 activity. Collectively, our molecular analyses demonstrate that EBF1 is the first B cell architectural factor that controls lineage and developmental stage-specific gene expression program.

Monday, Aug 20th 2018

11:30 AM (Tea/Coffee at 11:00 AM)

Auditorium, TIFR-H