

Colloquium

‘The benefits of being Single’: Single cell exploration of cell cycle

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Our body is composed of ~37 trillion cells of incredible variety, complexity and organization. Remarkably, the starting point of this dynamic organization is a single cell, which over the course of development grows, divides and increases in cell number (Cell cycle) alongside acquiring specialization. Self-renewing Pluripotent embryonic stem cells (ESCs) from blastocyst stage of embryonic development ultimately differentiate into all lineages of the embryo and adult organism. The ESCs have a distinct cell cycle program and gene regulatory network that governs their state, differentiation and cell-fate decisions.

Single-cell transcriptomics serves as a powerful tool to identify cell-states within populations of cells and to dissect underlying heterogeneity at high resolution. Singlecell transcriptomics on pluripotent stem cells has provided new insights into cellular variation, subpopulation structures and the interplay of cell cycle with pluripotency. I will present an overview of single-cell RNA-sequencing (scRNA-seq) approaches and our significant findings from application of single-cell technologies on pluripotent stem cells. I will also present an outline of computational approaches for scRNA-seq and outline for proposed multidisciplinary to elucidate the functional interplay between cell cycle and gene expression.

Wednesday, Jan 3rd 2018

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

Auditorium, TIFR-H