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BSSE Seminar

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How do mitochondria drive genetic and phenotypic heterogeneity in a cell population?

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About the speaker:

Dr. Riddhiman Dhar obtained B. Tech and M. Tech degree in Biotechnology and Biochemical Engineering from Indian Institute of Technology Kharagpur in 2008. He then went on to do PhD at the University of Zurich, Switzerland where he worked on laboratory evolution of Biological systems. He obtained his PhD degree in 2013. He was a postdoctoral researcher in the Systems Biology Unit at the Centre for Genomic Regulation (CRG), Barcelona from 2013 to 2017. Since 2017, he has been an Assistant Professor in the Department of Biotechnology at IIT Kharagpur. His research interest lies in understanding the molecular origins of heterogeneity in biological processes and the consequences of such heterogeneity on cellular phenotypes including antibiotic and drug resistance.

Abstract:

Individual cells in a population often show distinct characteristics and phenotypes. However, population-wide measurements fail to capture these phenotypic variations. Only recently advances in technologies have allowed us to measure phenotypic heterogeneity among individual cells. Heterogeneity can originate from genetic and epigenetic variations. In addition, heterogeneity can have non-genetic origins such as from stochastic fluctuations in expression levels of genes, although specific contributions of these processes remain unclear. One phenotype that commonly show variations among individual cells is proliferation rate. Variations in this phenotype has been shown to have important implications in drug resistance in microbes and in cancer proliferation. Our earlier work showed that heterogeneity in proliferation rate in yeast is primarily driven by variations in copy number of mitochondrial genomes (mtGenomes) in individual cells. These variations in mtGenome copy number also have implications for stress tolerance and drug resistance. However, several aspects of the molecular origins of mtGenome copy variation remain unclear. Cell-cycle checkpoint genes control mtGenome copy number, but the underlying cellular pathway is not well-understood. Further, mtGenome copy number variations have been shown to induce DNA damage response, however the type and frequency of such damage is yet to be established. Variations in mtGenome copy number have been observed across several human diseases including

cancer. Thus, a comprehensive understanding of the role of mtGenome variations on genetic and phenotypic heterogeneity assumes great importance for human diseases.