BOSE INSTITUTE COLLOQUIUM

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Main Auditorium, Unified Academic Campus
Bose Institute

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Title and Abstract :

The Centromere Code Hypothesis: Lessons Learned from Fungi

The fungal kingdom has been estimated to have more than 3 million species and one of the most well-studied groups to understand the evolutionary trajectory of fundamental cellular processes. One such process is chromosome segregation mediated by dynamic interactions between spindle microtubules and chromosomes. The chromosomal attachment site of the mitotic spindle is the centromere/kinetochore complex. In most organisms, centromeres are localized to a defined region as observed in monocentric chromosomes. In certain animals and plants, mitotic spindle fibers bind across the length of a chromosome on a holocentric chromosome. Centromeres of varying lengths in monocentric chromosomes were identified and mapped in more than 60 fungal species making it possible to find both conserved and unique species-specific centromere features (Guin et al., 2020, Ann Rev Microbiol). While centromeres are recognized genetically by exclusive centromere DNA sequence-specific binding of certain proteins in a few budding yeast species, centromeres are non-genetically/epigenetically defined in most other species. Thus, it is a paradox that there is no common DNA sequence signature that determines the centromere identity across fungal species. During the presentation, I intend to propose the centromere code hypothesis by providing evidence that a set of non-genetic factors together may determine centromere identity across fungal species. These factors include replication timing of centromeres and clustering of centromeric loci that shape the 3D genome assembly and the Rabl configuration of chromosomes. I will also discuss and provide evidence that centromere clustering and the Rabl-configuration facilitate the rapid evolution of centromeres and make centromeres a hotspot for genomic rearrangements that may play a role in speciation in fungi.