Schedule:

09.15 – 10.00 am
**Origin and evolution of Indian biota**
Praveen Karanth, IISc Bangalore

10.00 – 10.45 am
**Evolution of phenotypic plasticity**
Ullasa Kodandaramaiah, IISER Trivandrum

10.45 – 11.15 am: Tea/coffee break

11.15 am – 12.00 pm
**Heterogeneity, cooperation and metabolic interdependence in microbial communities**
Sandeep Krishna, NCBS Bangalore

12.00 – 12.45 pm
**Nature does not play dice with the genome**
Basant Tiwary, University of Pondicherry

02.30 – 03.15 pm
**Life with sex but no crossing-over in meiosis in the yeast species Sd.Ludwigii**
Michael Knop, University of Heidelberg

03.15 – 04.00 pm
**Fast-and-furious vs. slow-and-steady: resource use strategies in tropical trees**
Deepak Barua, IISER Pune

4.00 pm: Tea
ABSTRACTS

Origin and evolution of Indian biota
Praveen Karanth, IISc Bangalore

India is one of the 17 megadiverse countries in the world with two biodiversity hotspots. How was this rich biota of India assembled? i.e., was this diversity generated in-situ or was it derived from elsewhere, if so where did they come from? When and how? These are some of the questions that are very pertinent to our understanding of the origin and evolution of Indian biota. To address these issues we study species distributional patterns and try to understand the underlying historical processes (past geological and climatic events) that might have generated these patterns. To this end we study a range of taxonomic groups from across the tree of life use diverse tools and approaches including molecular phylogenetics, molecular dating, ancestral area reconstruction, diversification analysis and niche modelling. The Indian biota is broadly classified into ancient Gondwanan elements and the more recent intrusive elements that came into India post collision. Studies undertaken in the lab have revealed Southeast Asian origin of many intrusive elements. However there is very little evidence for Gondwanan origin hypothesis, instead most of the so-called Gondwanan elements appear to have dispersed into the drifting Indian plate post separation from Madagascar. Interestingly, many intrusive lineages underwent in-situ diversification resulting endemic radiations suggesting that India remained an insular landmass post collision at least for some taxa.

Evolution of phenotypic plasticity
Ullasa Kodandaramaiah, IISER Trivandrum

“...evolution is the control of development by ecology.’ - Van Valen, 1973

Phenotypic plasticity (or developmental plasticity) is the expression of more than one phenotype by a single genotype through the influence of differing environments during development. A common strategy in organisms that face variable environmental conditions is adaptive phenotypic plasticity, wherein the resulting phenotypes have higher fitness in their respective environments compared to that of the alternate phenotypes of the same genotype. Using examples from published literature and work in our lab, I will discuss a) the concept of adaptive phenotypic plasticity b) the distinction between reversible and irreversible plasticity c) the central role of phenotypic plasticity vis-a-vis genetic polymorphisms in adaptation and diversification of life forms d) various approaches which researchers use to understand this phenomenon, and e) exciting challenges and avenues of research in this field.

Nature does not play dice with the genome
Basant Tiwary, Pondicherry University

The genome evolution is shaped by a complex interplay of stochastic processes such as mutation and genetic drift and the deterministic force of natural selection to maintain the fitness of an organism under ever changing environment. The stochastic processes of mutation and genetic drift can turn an evolutionary trajectory towards alternative directions even when population starts from the same state.
On the other hand, natural selection is a powerful deterministic force which is likely to give repeatable outcomes either from same state or different states at the level of genes if the adaptive landscape offers few alternatives. The convergent evolution in nature has led to an argument that evolution is predictable and that contingencies of history have a limited control over the direction of evolution. The endocrine system in higher organisms is endowed with multiple organs, cross-talk between various ligand-signal transduction systems and functional redundancy. The neuroendocrine genes showed very similar expression profiles and local network properties across a wide range of tissues consistent with the physiological roles of their proteins. Moreover, the coordinated evolution of 10 neuroendocrine genes involved in mammalian reproduction and homeostasis was observed using several evolutionary analyses such as correlated evolution, relative-rate test, relative-rate test and codon usage bias. The neuroendocrine genes are subjected to evolve predominantly under similar selective strengths and regimes of purifying selection estimated in their evolutionary fingerprints. Thus, a key role of natural selection in creating and maintaining a well-designed neuroendocrine system at the genomic level is empirically demonstrated for the first time. Further work in this direction will lead to a better understanding of how fate and chance decide the evolutionary trajectory of the genome.

**Life with sex but no crossingover in meiosis in the yeast species Sd.Ludwigii**
Michael Knop, University of Heidelberg

The ubiquity of eukaryotic sex despite its significant costs has been a persistent conundrum. Its paradoxical evolutionary success is largely attributed to meiotic crossing over, which is thought to handle mutational load whilst ensuring faithful chromosome segregation in meiosis.

The yeast species Sd. ludwigii has been reported to be capable of undergoing a full sexual cycle; however, no recombination of its genome during meiosis I could be detected by classical genetic analysis. It thus constitutes an ideal model to address the impact of sexual recombination on a sexual species.

To approach this we used genome sequencing and comparative genomics analyses of meiotic gene content as well as many different genomic structure elements with 100 sequenced Saccharomycetes and other fungi; high-resolution DNA variant segregation analysis in meiosis; functional study of important meiotic genes and experimental characterisation of selected mutants and genetic elements.

Crossing over was confirmed to be absent from meiosis in S. ludwigii, despite a nearly full complement of meiotic genes, and an experimentally validated dependence of meiosis I on Spo11 and the meiotic DNA repair pathway. Comparative sequence analysis detected a high degeneracy of the genome, consistent with the predicted impact of the absence of recombination on genome evolution. We furthermore detected several new non-Mendelian heritable genetic elements, some of which we validated experimentally.

Altogether, our data enables us to phrase and discuss hypotheses on strategies developed by this species to compensate for the loss of meiotic recombination.
Fast-and-furious vs. slow-and-steady: resource use strategies in tropical trees
Deepak Barua, IISER Pune

Tropical systems may be particularly vulnerable to extreme climatic conditions, and understanding theresponses of tropical forests to increased drought and heat is a major limitation in predicting globalresponses to future climate change. In my research I use an integrated approach to understand and predict responses of tropical systems to changing environmental conditions. This integrates information from anatomical, morphological and physiological traits to understand plant performance under controlled environmental conditions. These experimental approaches are complemented with data from the behaviour of species in the field, and finally used to test growth, mortality and regeneration of species over longer term scales, and distribution of species over environmental gradients. I highlight this with an example of a study that examined water-use strategies in tropical trees. Here we examined water uptake under well watered conditions, and drought tolerance when water was limited. We asked if these were related to stem xylem anatomical traits, and tested the relationship between water transport efficiency and safety. Xylem size was positively related to water uptake, but negatively related to drought tolerance, resulting in a tradeoff where water uptake and growth under well watered conditions was negatively related to drought tolerance when water was limiting. These results suggest that tropical trees with acquisitive water use strategies may be more sensitive to drought and future climates may favour slower growing species with conservative strategies that are more tolerant to drought. From these results I speculate on possibilities of whole plant strategies that include tolerance to drought and high temperature and acquisition of multiple resource including light and nutrients.