

Department of Biological Sciences

Speaker: Dr. Nagarjun Vijay,

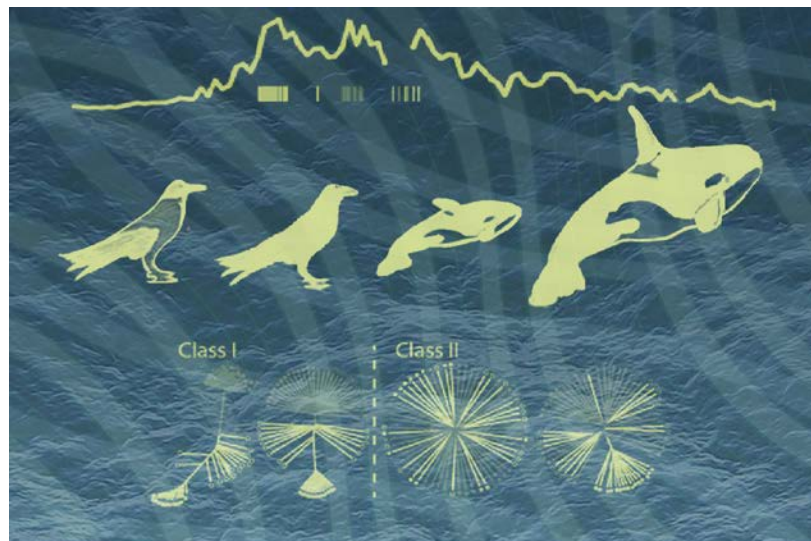
University of Michigan, Ann Arbor, MI, USA

Date/Time: Friday, November 25, 2016 at 10:00 am

Venue: L3, LHC

Title: Speciation genomics-understanding the evolutionary genetic processes generating diversity

Closely related species that are phenotypically different are an ideal system to study the genetic basis of these phenotypes. Since, most of the genome is extremely similar between closely related species, the genetic changes that are observed can be linked to phenotypic changes. We used whole genome sequencing and RNA-seq data from multiple crow and killer whale species to quantify the processes that are important in different stages of species divergence. Species of the genus *Saccharomyces*, with high quality genome assemblies provide a system ripe for investigation of the dynamics involved in these processes. These results spanning multiple study systems are of crucial importance to understand the genotype-phenotype map.



Speciation genomics
understanding the evolutionary genetic processes generating diversity

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