Cologne Evolution Colloquium

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Population genomics and complex traits in yeast

Understanding the genetic mechaniss underlying complex traits is one of the next frontiers in biology. The budding yeast *Saccharomyces cerevisiae* has become an important model for elucidating the mechanisms that govern natural genetic and phenotypic variation. In the past decade, we assebled one of the world largest collection of natural isolates of *S. cerevisiae* and its closest relative *S. paradoxus* strains and characterized them at te genomic and phenotypic levels. These data provide a comprehensive view of genomic diversity in budding yeast and expose surprising and prononced differences between the variation within *S. cerevisiae* and that within *S. paradoxus*. Recently, we generated artificially outbred populations of yeast segregants to understand the genotype-phenotype relationship. In this talk, I will discuss how the previously unappreciated level of yeast natural variation can be useful in understanding fundamental principles of genetics.

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Hosted by Michael Lässig