SCIENTIFIC SEMINAR

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From genotype to phenotype with 1,086 near telomere-to-telomere yeast genomes

Elucidating the underlying genetic causes of the astonishing phenotypic diversity observed in natural populations constitutes a challenge in biology. However, despite the efforts that have been made in that direction, no truly comprehensive atlas of genetic variants is available for any species. Here, we sought to obtain a comprehensive view of the genetic variants present in a species and how these variants contribute to its phenotypic landscape. We therefore took advantage of the genetic workhorse Saccharomyces cerevisiae, for which we sequenced a large population of natural isolates using long-read sequencing and obtained a total of 1,086 near telomere-to-telomere (T2T) assemblies. Our study delves into the comprehensive catalog of genetic variants, testing their associations with a wide range of 8,391 molecular and organismal traits. By including structural variants (SVs) and insertions/deletions (InDels) alongside single nucleotide polymorphisms (SNPs), we observed an increase in average heritability to 0.41, compared to 0.36 when only SNPs are considered. Notably, SVs emerged as more frequently associated with traits and exhibited higher pleiotropy, underscoring their significant role in phenotypic variation. Furthermore, our analysis revealed distinct genetic architecture between organismal and molecular traits, with different types of genetic variants contributing uniquely to each trait category. Lastly, to enhance our understanding of genetic variation, we constructed a graph-pangenome, highlighting 2.5 Mb of non-reference sequences. Overall, our study provides the first comprehensive dataset that accurately describes the effect of different genetic variants on phenotypic variation on a scale that would be nearly impossible in any other eukaryotic system.

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Tuesday
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12.00H

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