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Contribution of structural variations to the genetic and phenotypic diversity in *Saccharomyces cerevisiae*

LE JEUDI 28 JANVIER 2021 À 12 H 30

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There are mounting evidences that Structural Variations (SVs) of chromosomes play a major role in phenotypic variation. However, these genetic variants are the most difficult to identify and to interpret with respect to their functional consequences. We undertook a comprehensive mapping of natural SVs in *S. cerevisiae* using the Oxford Nanopore long-read single molecule sequencing technology. We generated high quality telomere-to-telomere genome assemblies for a large panel of strains selected to maximize the sampling of the species genetic diversity. We catalogued a large number of natural SV. In addition, in order to unequivocally determine the SVs contribution to phenotype variations, independently from the confounding effect of SNPs, we generated targeted and random SVs in a controlled genetic background by CRISPR/Cas9 genome editing to reveal their fitness impact and contribution to adaptation.

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