

Mutation spectrum variation in *Saccharomyces cerevisiae*

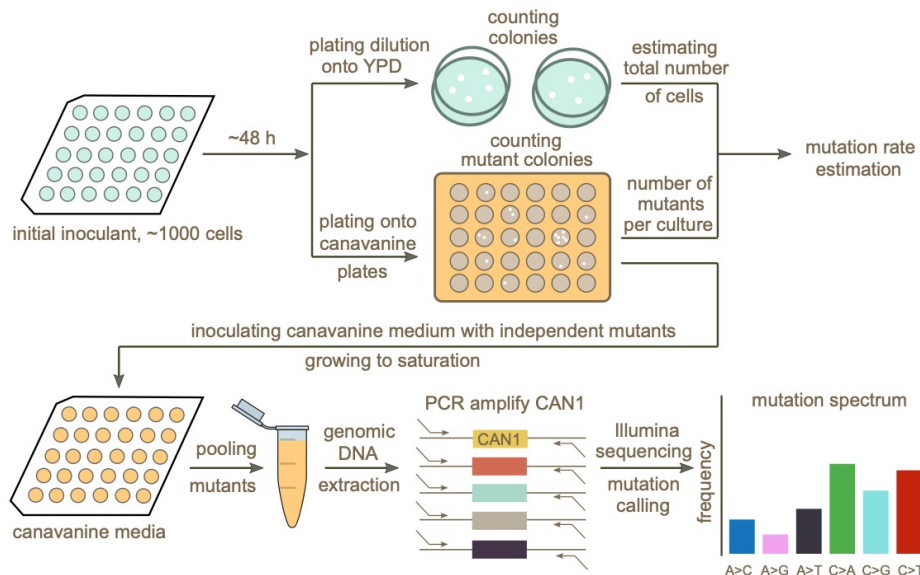
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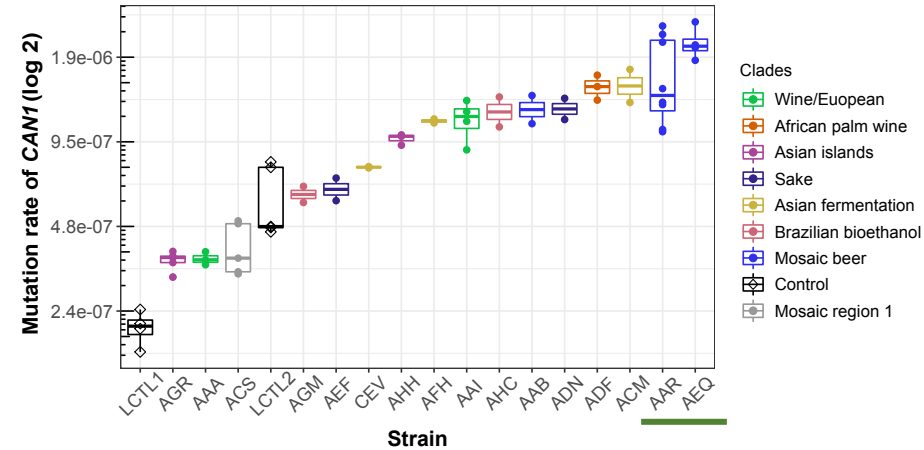
Introduction

Mutation, the ultimate source molecular variation, is a process can be affected by both genetic variation in DNA repair genes and environmental stressors. Little is known about the extent of mutation process variation that exist among individuals. Recently, the 1002 Yeast Genomes Project surveyed 1011 strains from natural populations of *Saccharomyces cerevisiae* in diverse environments across five continents [1], providing an ideal resource for a mutation analysis. In this work, we surveyed 16 haploid *S. cerevisiae* natural isolates from diverse environmental conditions of their *de novo* mutation rate and spectrum.

Experimental pipeline

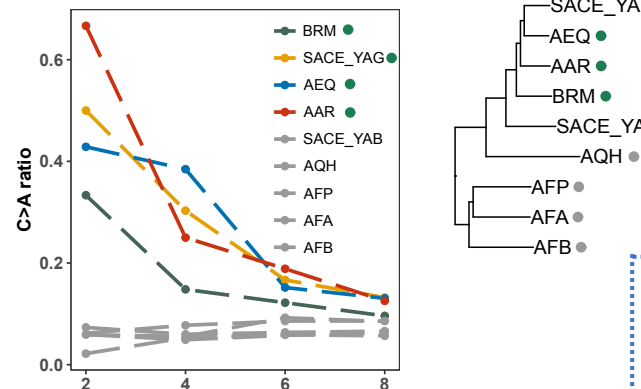


Mutation rates variation (*de novo*)



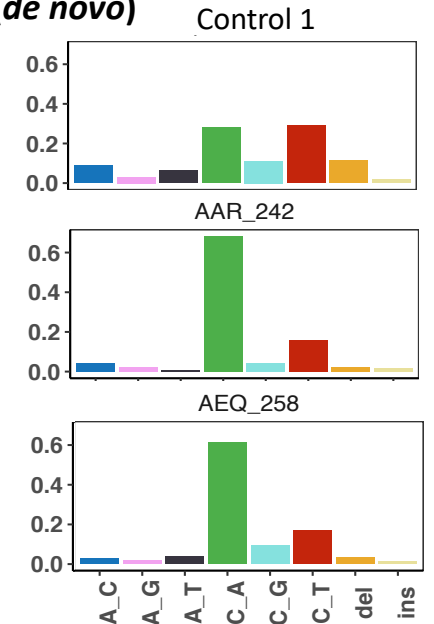
Mutation rates vary in roughly 10 folds in the haploid natural isolates using *CAN1* as the reporter.

Enrichment of C>A mutations in rare natural variants



Enrichment of C>A mutations in AAR and AEQ are observed in rare natural variants.

Mutation spectrum variation (*de novo*)



Many strains do not show a difference in mutation spectrum, while some show significant differences. AAR and AEQ show strong bias in the enrichment of C>A mutations (chi-square test, $p < 2e-10$).

Future directions

Map the underlying genetic loci that are responsible for the mutator phenotype using QTL.

Acknowledgement

This work is supported by Burroughs Wellcome Fund career award at the scientific interface to Kelley Harris.