Selection for mitonuclear interactions revealed through mtDNA exchanges between *Saccharomyces cerevisiae* yeasts

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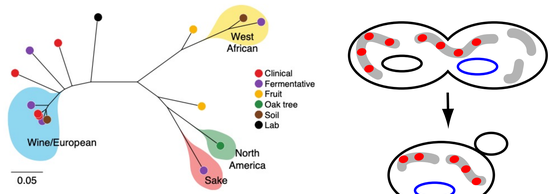
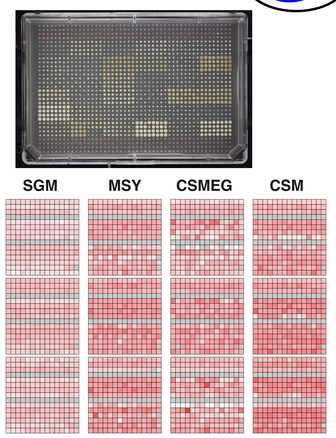
MITOCHONDRIA: Genetic interactions between mitochondrial and nuclear genes are essential for eukaryotic life. Coevolution between mtDNA and nuclear genomes must occur, but it can be difficult to document.

Here, we used *S. cerevisiae* to look for coadaptation of mitonuclear genotypes.

METHODS: mtDNAs were exchanged between wild isolates of *S. cerevisiae.*
15 mtDNA x 15 nDNA =
225 unique mitonuclear genotypes

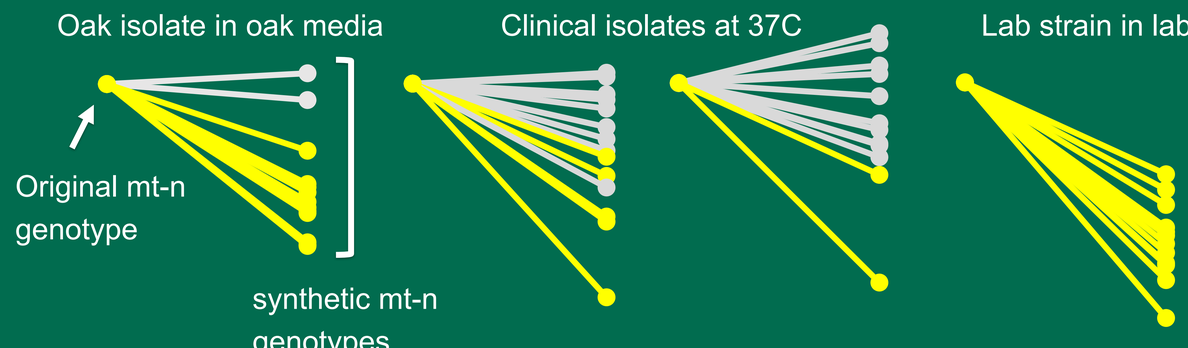
- controlled independent matings, selection, screening, and genotype verification used to create ~450 strains (2 replicates of each genotype)
- growth rates were quantified from solid media



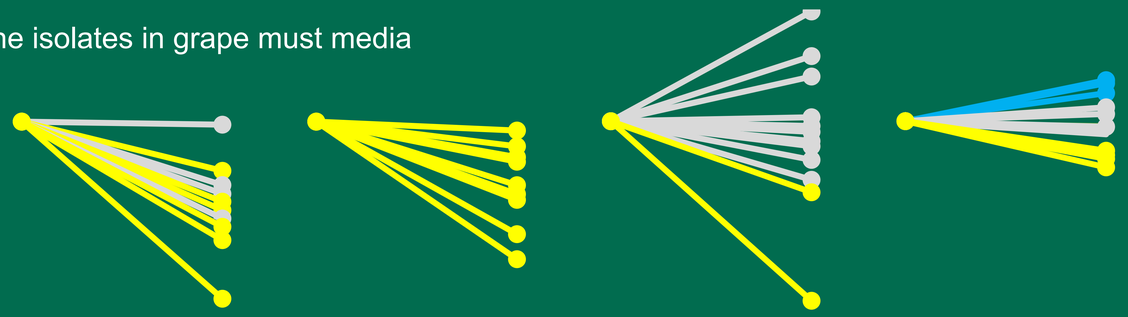


Evidence for **coadapted mitonuclear genotypes** in *S. cerevisiae*

yeast isolates prefer their own mtDNA



Wine isolates in grape must media



When grown in media emulating their isolation habitat, nuclear backgrounds paired with their original mtDNAs tended to grow better than when paired with a different mtDNA.
(significant differences in growth are indicated in yellow and blue)

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HOW DO MITONUCLEAR INTERACTIONS AFFECT PHENOTYPES?

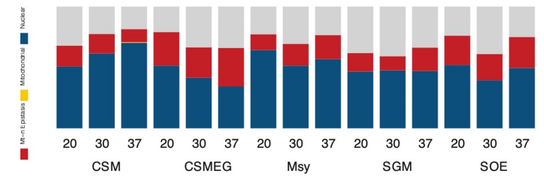
ANOVAs and VCA revealed that

mitonuclear interactions are:

observed in every condition
(mt x n, P <.001) with no independent mtDNA effects

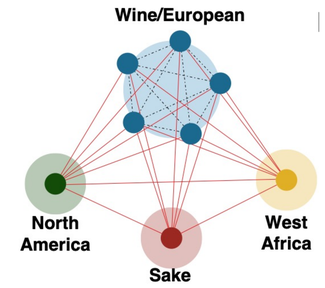
sensitive to environment
(mt x n x e, P <.001)

explain large proportions of phenotypic variances (10-32%)



That's a lot of potential for **coevolution!**

DO MITONUCLEAR INTERACTIONS FOLLOW POPULATION STRUCTURE?



mtxn interactions were observed when mtDNAs were exchanged both within and between clades but

mitonuclear effect sizes were greater when mtDNAs were exchanged between clades