



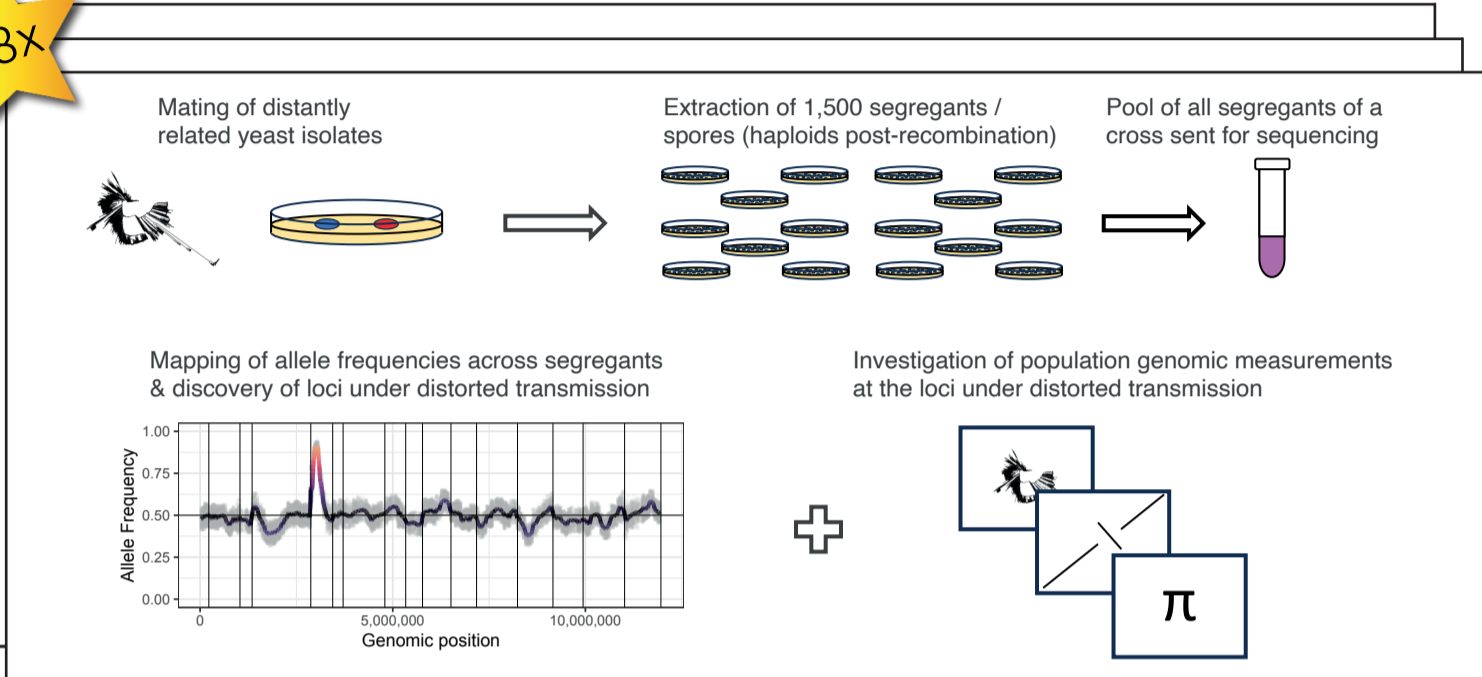
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High prevalence of transmission ratio distortion in species-wide yeast crosses



Methods

38x



BACKGROUND

- Deviations from expected allele frequencies in offspring are called transmission ratio distortion (TRD).
- They can be caused by genetic incompatibilities, lethal allele combinations, or selfish genetic elements that actively manipulate transmission.
- TRD causes evolutionary pressure, but its prevalence is unknown.
- TRD is difficult to discover, requiring large crossing experiments, often unfeasible.

METHODS

- Crossed maximally divergent yeast *S. cerevisiae* isolates.
- Aimed to extract 1,500 segregants per cross.
- Sequenced pooled segregants to derive allele frequencies.
- Identified TRD regions.
- Scanned a 2,500 strains genotype matrix for genomic signals associated with TRD.

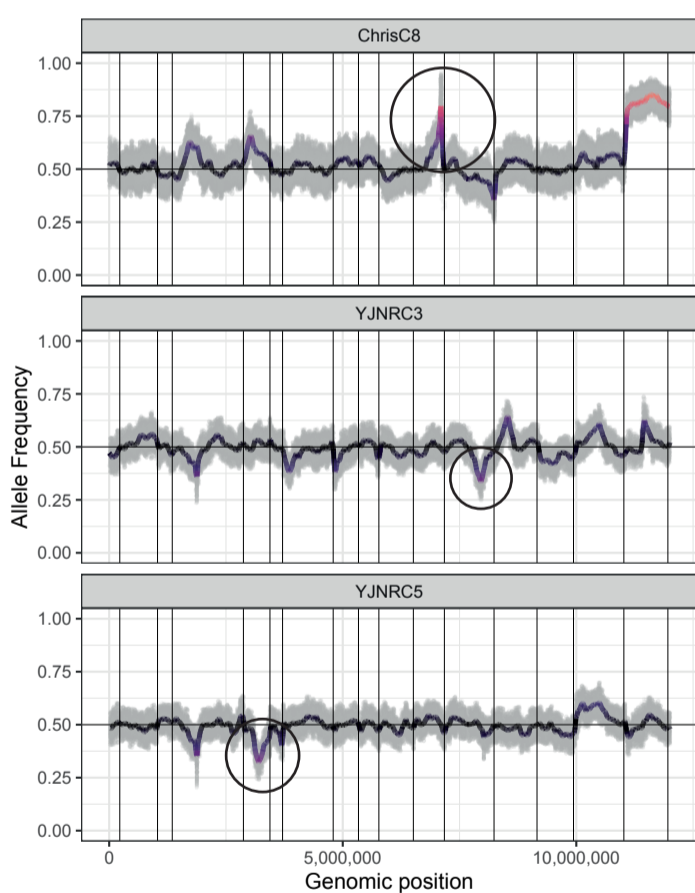
RESULTS

- High prevalence of TRD loci at unique positions.
- Diverse genomic signals associated with TRD, different in every cross.
- Overall, TRD loci are more distant to other strains than random loci on average.

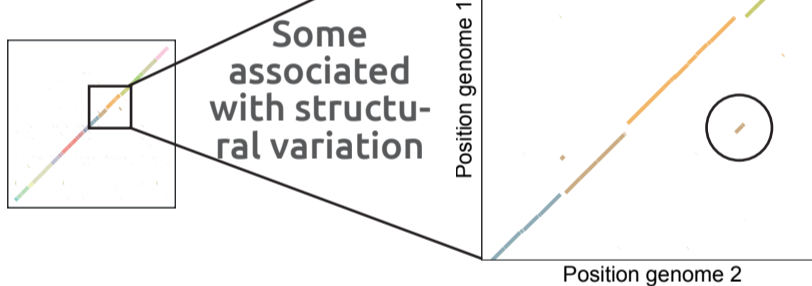
OUTLOOK

- First systematic species-wide search for TRD reveals an unexpectedly high prevalence of distortion.
- The TRD regions are diverse and likely have unique properties in all cases.
- Signals of diversification and selection were found so far.
- Will require further work to understand the mechanisms.

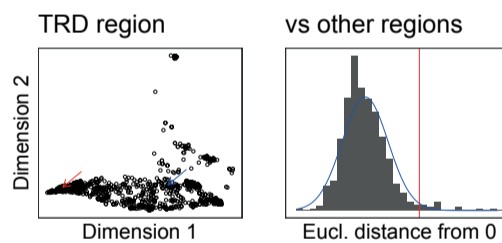
Results



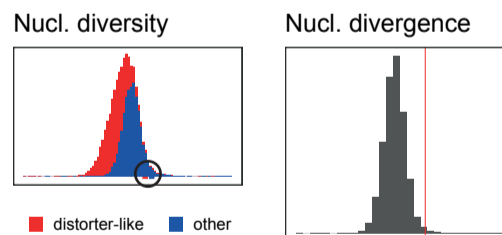
37-63% of crosses show TRD



Some show increased divergence of the region



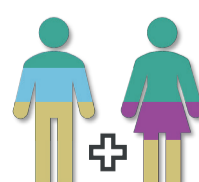
Some show extreme population genomic parameters



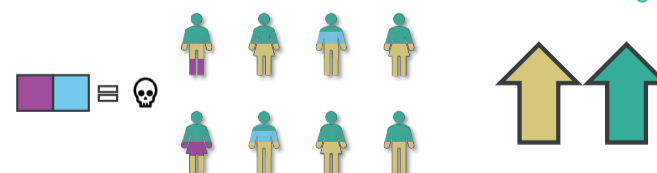
Background

What is TRD?

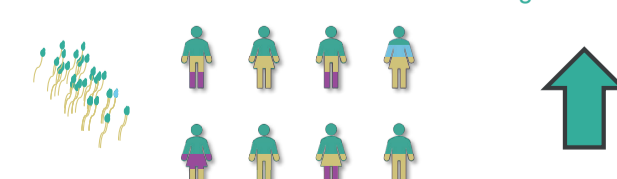
Two loci, alleles green/lightblue and khaki/purple



Scenario Genetic incompatibility: Lethality of individuals with purple+lightblue allele combinations
Outcome: Transmission distortion in favor of khaki and green



Scenario Selfish transmission manipulation: Production / survival of almost exclusively green-khaki sperm/spores
Outcome: Transmission distortion in favor of green



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