

## BITS :: Call for Abstracts 2021 - Oral communication

<i>Type</i>	Oral communication
<i>Session</i>	Molecular Evolution analysis
<i>Title</i>	A yeast living ancestor reveals the origin of genomic introgressions
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<i>Motivation</i>	Genome introgressions drive evolution across the animal, plant and fungal kingdoms. Introgressions of genomic material between populations and species often reflect key historical and demographical events of the species evolution. For example, non-African and Oceanian human populations contain approximately 2% Neanderthal and 2–4% of Denisovan DNA, respectively, as a consequence of archaic admixture with extinct hominid populations. Introgressions initiate from archaic admixtures followed by repeated backcrossing to one parental species. However, how introgressions arise in reproductively isolated species, such as yeast, has remained unclear.
<i>Methods</i>	We recently sequenced the genomes of more than 1,000 <i>S. cerevisiae</i> strains and described 26 well-defined lineages that represent specific ecological niches or geographical areas. Four of these lineages - Alpechin, Brazilian bioethanol, Mexican agave and French Guiana - present abundant introgressions of highly diverged (approximately 12%) sequence from the sister species <i>S. paradoxus</i> , derived from at least two ancient admixture events. The Alpechin lineage, associated with the production of olive oil, carries the largest amount of introgressed material, ranging from 4% to 5% in individual strains and combined covering 8% of the genome. Alpechin strains were mostly isolated from olive oil wastewater (Alpechin, in Spanish) in Spain.
<i>Results</i>	Here we report the discovery of a <i>S. cerevisiae</i> – <i>S. paradoxus</i> hybrid that is the direct clonal descendant of an ancient hybridization event that founded the Alpechin lineage by sexual reproduction and backcrossing to <i>S. cerevisiae</i> . For shorthand, we refer to this strain as the living ancestor, as it retains the genome structure of the ancestor—while noting that the present-day individual is separated from the actual ancestor by some evolutionary time. The ancestral hybrid genome was shaped by extensive genomic instability, resulting in mitotic recombination events that by loss of heterozygosity (LOH) generated over a hundred scattered blocks of homozygous DNA. We show that these LOH blocks restore recombination efficiency and gamete viability, explaining how the ancestral hybrid overcame the main barrier to introgression.
<i>Info</i>	-
<i>Figure</i>	-
<i>Availability</i>	<a href="https://www.nature.com/articles/s41586-020-2889-1">https://www.nature.com/articles/s41586-020-2889-1</a>
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