**Trends in Genetics** | Genome of the Month

# *Saccharomyces cerevisiae*

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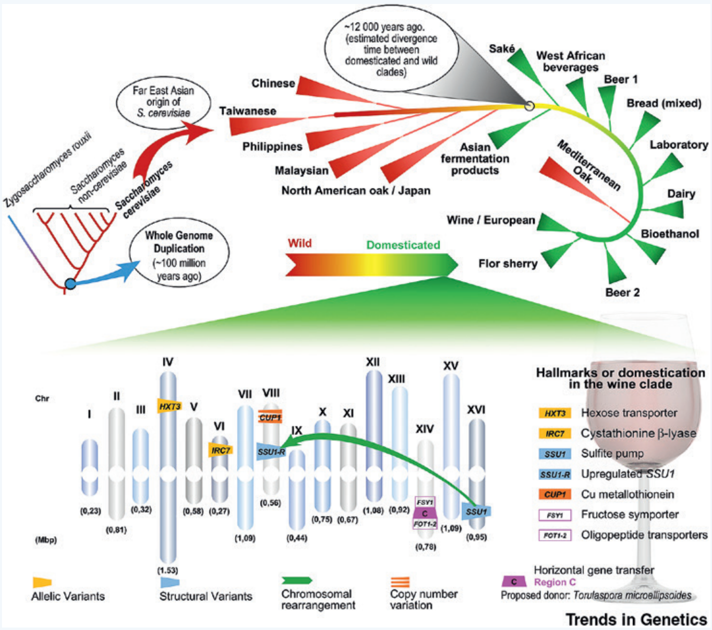

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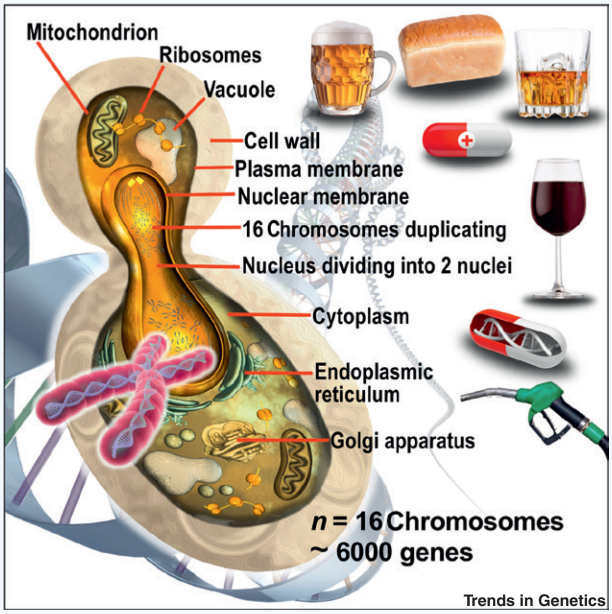
*Saccharomyces cerevisiae* (*S. cerevisiae*) is a food-grade budding yeast with ‘generally regarded as safe’ status. It has been used in the production of fermentative foods (bread), beverages (beer, wine, spirits), and biofuels. It is also used as a cell factory for the production of pharmaceutical and other important biochemical compounds. Harnessed as a workhorse in the fermentation industry and a study model organism in the laboratory, the *S. cerevisiae* genome has been molded for millennia through different anthropogenic domestication events. The *S. cerevisiae* genome was the first eukaryotic genome to be sequenced (1996; and updated in 2010). A synthetic version (Sc2.0) of the genome of the BY lineage of the S288c reference strain is currently being constructed by a large-scale international Yeast 2.0 consortium and will be the world’s first synthetic eukaryotic genome (www.syntheticyeast.org).



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**TAXONOMY AND CLASSIFICATION:**
**KINGDOM:** Fungi
**DIVISION:** Ascomycota
**ORDER:** Saccharomycetales
**FAMILY:** Saccharomycetaceae
**GENUS:** *Saccharomyces*
**SPECIES:** *Saccharomyces cerevisiae*

**GENOME FACTS:**
The genome of the haploid laboratory-bred reference strain (S288c), *S. cerevisiae*, comprises 16 linear chromosomes, varying from ~200 to ~2000 kb. The total genome size includes 12.07 Mb of chromosomal DNA, 85 kb of mitochondrial DNA, and 6.3 kb episomal plasmids (2μ).

The genome contains 6604 open reading frames (ORFs), with 79% of them verified, 11% uncharacterized, and 10% regarded as dubious, and 1786 of the ORFs still annotated to unknown function. The genome carries 428 RNA genes [299 tRNA, 77 small nucleolar (snoRNA), 27 rRNA, 18 noncoding (nc) RNA, 6 small nuclear (sn)RNA] and one telomerase RNA.

At least 55 genes found in other ‘well-studied’ *S. cerevisiae* genomes are absent in S288c. There are more than 500 sets of paralogs.

The Saccharomyces Genome Database provides comprehensive genomic information with online search and analysis software for analysis of the yeast genome (www.yeastgenome.org).

**SPECIES FACTS:**
Although difficult to isolate outside of anthropic environments, where fermentation can occur, *S. cerevisiae* is recognized as a ubiquitous fungus with natural strains found on plants, animals, soils, and aquatic environments.

A major event in the genetic evolution of the *S. cerevisiae* lineage was a whole-genome duplication (WGD) event (8 to 16 chromosomes). This fact has likely permitted *S. cerevisiae* to show an increased glycolytic flux, the Crabtree effect and a diauxic shift [the ‘make-accumulate-consume’ (MAC) strategy], all of which allow for a more fermentative life style.

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**Fun fact about the Genome:**

The speciation process in the *Saccharomyces* clade started with a WGD event approximately 100 million years ago. *Saccharomyces*' MAC strategy emerged after the WGD event, determining the niche specialization for *S. cerevisiae* to sugar-rich environments. The MAC strategy arose from: (i) genomic changes, which increase the flux from hexose to ethanol and allows the later consumption of ethanol (i.e., duplication of alcohol dehydrogenase (ADH)1 and ADH2); and (ii) a WGD-linked promoter rewiring resulting in the loss of regulatory elements from genes involved in respiration.

## Literature

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