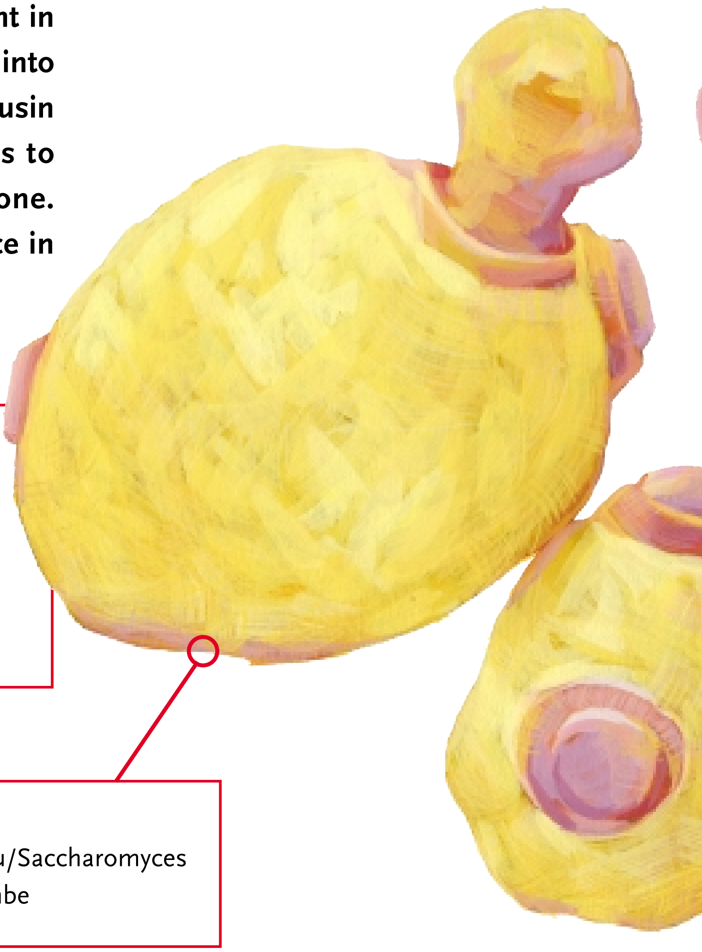
“Blues is

The Yeast

(Saccharomyces cerevisiae and Schizosaccharomyces pombe)

Despite being only one-tenth the size of a white blood cell, many of the cellular functions of higher species are present in unicellular yeast. Two species of yeast have been pressed into service as model organisms: *S. cerevisiae* and its distant cousin *S. pombe*. Each one has nearly 200 genes homologous to human genes involved in disease, with 23 for cancer alone. Used since Ancient Egypt, yeast has economic importance in beer and bread making.



‘Omics

S. cerevisiae; S. pombe

Genome size: 12 Mb; 13.8 Mb

Chromosomes: 16; 3

Number of genes: ~6,000; 4,900

Genes with introns: 5%; 43%

Average gene: 1.5 kb, ~1 exon; 3 kb, ~3 exons

Proteins: 6,217; 5,002

Web Sites

Yeast Resource Center: depts.washington.edu/~yeastrc

***Saccharomyces* Genome Database:** genome-www.stanford.edu/Saccharomyces

***S. pombe* Genome Project:** www.sanger.ac.uk/Projects/S_pombe

1857
Louis Pasteur identifies *S. cerevisiae* as responsible for fermentation

1893
P. Lindner describes *S. pombe*, isolated from East African beer

1907
Eduard Buchner receives Nobel Prize in chemistry for demonstrating yeast fermentation

1935
First genetic analysis of yeast

1943
Heterothallism (obligate outcrossing) reported

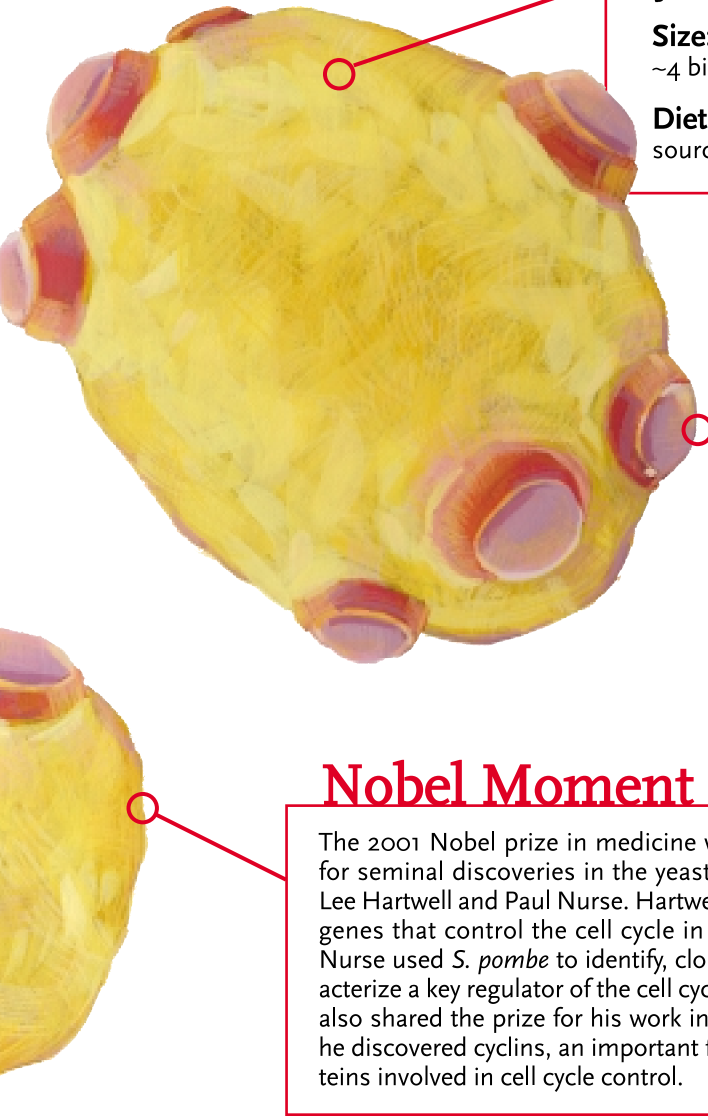
1949, 1952
First genetic maps of *S. cerevisiae* published

1953
Wallace Coulter awarded patent for Coulter Counter, predecessor of flow cytometer

1960s
Methods developed for synchronous culture of yeast

1967
Lee Hartwell publishes on 400 temperature-sensitive mutants

> *to jazz what yeast is to bread*
> *—without it, it's flat."*
>
> —Carmen McRae (1920–1994)



Stats

(for S. cerevisiae, shown at left)

Size: 2 microns; ~4 billion fill a teaspoon

Diet: A fermentable carbon source and a nitrogen source

Cell cycle: 90 minutes; 38 hours from first division to senescence

Reproduction: Sexual and asexual

Feature Technology

Molecular Bar Codes: Many yeast genes function in similar ways to their more complex, metazoan counterparts, and a new technique using molecular bar codes is now available to aid functional genomicists. Researchers have individually knocked out almost 96% of *S. cerevisiae* genes. That's nearly 6,000 gene-disruption mutants made available to the scientific community for functional analysis of the yeast genome. Each strain has a unique tag, or molecular bar code, which makes it possible to do phenotypic analysis either on a single gene or on a genome-wide scale.

Nobel Moment

The 2001 Nobel prize in medicine was awarded for seminal discoveries in the yeast cell cycle to Lee Hartwell and Paul Nurse. Hartwell discovered genes that control the cell cycle in *S. cerevisiae*; Nurse used *S. pombe* to identify, clone, and characterize a key regulator of the cell cycle. Tim Hunt also shared the prize for his work in sea urchins; he discovered cyclins, an important family of proteins involved in cell cycle control.

Illustration: Tammy Irvine, Rear View Illustration

1976 Paul Nurse et al. describe cell cycle mutants in fission yeast

1976 Gene conversion described

1978 Publication on *Wee* alleles of *cdc2*, with altered cell division

1982 Hepatitis B surface antigen produced using yeast-based expression system

1987 Yeast artificial chromosomes (YACS) invented as expression vectors

1989 Two-hybrid screen for protein-protein interactions developed

1996 First eukaryotic genome, *S. cerevisiae*, sequenced

2001 Hartwell and Nurse share Nobel Prize for work on yeast cell cycle

2002 Sequence of *S. pombe* published

2002 Collection of 5,916 gene-deletion mutants made available