ABSTRACT

Title: The Yeast Saga: Breakthroughs That Shaped Modern Life Sciences and Arts

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Abstract content:

The history of modern yeast research closely parallels the development of molecular biology, biotechnology, genomics, and systems biology. Long before 1966, yeasts were already central to baking, brewing, winemaking, and industrial fermentation, while also serving as important experimental systems in studies of metabolism, enzymology, cytology, physiology, and microbial taxonomy. European schools of fermentation science and yeast taxonomy — particularly in Western and Central Europe — established much of the conceptual and methodological foundation upon which modern yeast biology was built. Following the establishment of the International Conference on Yeast Genetics and Molecular Biology in Carbondale in 1961 and the activities of the International Commission on Yeasts beginning in Bratislava in 1966, yeast evolved from a fermentation organism into one of the most influential eukaryotic model systems in modern science. One of the defining milestones in this yeast saga was in 1996 the completion of the first fully sequenced eukaryotic genome, Saccharomyces cerevisiae, coordinated through a broad international consortium with major European participation. This phase culminated in the 1996 publication of the first fully sequenced eukaryotic genome, an achievement that fundamentally transformed genomics, systems biology, and computational life sciences. Based on this we can address yeast penetration from nature to science via food in decades, which correspond well with human advancement in science and culture.

Before 1966: Yeast–the quiet herald of the invisible microcosm: Yeasts were mainly recognized for their roles in baking, brewing, winemaking, and industrial fermentation. They slowly penetrated into scientific focus and with their help many new scientific fields were established.

1966–1975: Foundations of Modern Yeast Genetics and Cell Biology: During this decade, advances in genetics, cytology, taxonomy, mating-type analysis, and recombination established key principles of eukaryotic inheritance and cellular regulation. Sacch. cerevisiae emerged as a tractable experimental system for studying gene regulation, mating pheromones, mitochondrial genetics, and cell-cycle organization.

1976–1985: Recombinant DNA and the Rise of Modern Biotechnology: The emergence of recombinant DNA technology transformed yeast into a central platform for molecular biology and industrial biotechnology. Yeast cloning vectors, shuttle plasmids, and heterologous gene-expression systems enabled the production of recombinant proteins and expanded the

possibilities of experimental genetics. Consequently, yeast became a preferred eukaryotic host for biotechnology and industrial fermentation research.

1986–1995: Cell-Cycle Control and the Pre-Genome Molecular Revolution: Studies of yeast cell-cycle regulation identified highly conserved molecular mechanisms controlling eukaryotic cell division, discoveries that profoundly influenced cancer biology and biomedical research. During this period, molecular genetics, gene mapping, and early large-scale sequencing efforts developed the technological and conceptual foundations required for genome-scale biology. This phase was characterized by the transition from classical molecular genetics to systematic biological analysis. It culminated in the establishment of international genome initiatives and collaborative sequencing strategies that enabled the completion of the first fully sequenced eukaryotic genome in the following period. Yeast became firmly established as the reference system for eukaryotic cell biology and molecular genetics.

1996–2005: Post-Genome Functional Genomics and Systems Biology: Following the completion of the first fully sequenced eukaryotic genome in 1996, Sacch. cerevisiae, yeast research entered a new phase in which the genome became the central reference framework for all cellular processes. This period marked a transition from individual gene studies to systematic, genome-wide analysis of biological function. High-throughput approaches including transcriptomics, proteomics, interaction mapping, deletion libraries, and computational modeling enabled functional annotation of genes at genome scale. Systems-level analysis revealed the modular and networked architecture of the eukaryotic cell, establishing yeast as the leading model organism for integrative and quantitative biology and laying the foundations of systems biology.

2006–2015: Synthetic Biology, Metabolic Engineering, and Bioart: Synthetic biology and metabolic engineering transformed yeast into a programmable cellular factory for the production of pharmaceuticals, biofuels, fine chemicals, flavors, fragrances, and recombinant biomolecules. Genome engineering, pathway optimization, and evolutionary engineering expanded industrial applications. In parallel, artists, architects, and designers increasingly incorporated microbial systems, including yeasts, into experimental cultural practices and bioart.

2016–2026: CRISPR, Biodiversity, Ecology, and Medical Mycology: This decade has been characterized by the widespread adoption of CRISPR-based genome engineering, expanded exploration of global yeast biodiversity, and growing recognition of the ecological roles of yeasts within natural and host-associated microbial communities. Research on emerging pathogenic yeasts, antifungal resistance, and multidrug-resistant species such as Candida auris underscored the medical importance of yeast biology. Simultaneously, advances in precision fermentation and sustainable biomanufacturing further broadened the industrial applications of yeasts.

Beyond 2026: Sustainable Biotechnology and Living Systems: Looking beyond 2026, yeast research is expected to remain central to sustainable biotechnology, synthetic ecosystems, precision fermentation, alternative food systems, and environmentally responsive biomaterials. Future developments will likely integrate artificial intelligence, automation, evolutionary design, and ecological engineering with synthetic genomics and systems biology. Yeast will continue to serve as a unifying experimental system demonstrating how microbial model organisms can profoundly shape both science and culture.

Yeast Researcher view: Modern yeast research was shaped by several influential scientific schools: the Carlsberg and Delft traditions of fermentation physiology and industrial microbiology; the CBS/Dutch and Central European schools of yeast taxonomy and biodiversity; the American schools of molecular genetics and recombinant DNA research; the British fission-yeast cell-cycle tradition; and the European genome-consortium model that culminated in the first complete eukaryotic genome sequence in 1996. All this would not be possible without culture collections. The first public microbial culture collection was established in Prague in 1890 by František Král. Since then, culture collections evolved into a global infrastructure comprising nearly 800 registered microbial culture collections in more than 70 countries, preserving more than three million microbial strains, including numerous specialized yeast repositories located in 78 countries and regions as listed by the World Data Centre for Microorganisms (WDCM).

The yeast view: At the time of the completion of the first fully sequenced eukaryotic genome in 1996, yeast taxonomy recognized approximately 100 genera comprising more than 700 described species, according to the fourth edition of The Yeasts: A Taxonomic Study edited by Kurtzman and Fell (1998). By 2026, advances in molecular phylogeny, environmental sequencing, and global biodiversity exploration had expanded the recognized diversity to nearly 2,000 species distributed among more than 242 genera, reflecting a profound transformation in our understanding of yeast evolution and ecology (theyeasts.org).

Holistic view: Across more than six decades, yeast research has linked fundamental biology, technological innovation, ecology, medicine, industry, and culture, while also inspiring interdisciplinary collaborations with design, architecture, and bioart. Dedicated yeast research groups expanded from only a few dozen laboratories worldwide in the 1960s to several hundred by the time of the yeast genome sequencing in 1996. In the post-genomic era, yeast research became increasingly distributed across molecular biology, biotechnology, and systems biology laboratories, resulting today in approximately 150–250 core yeast-focused groups, embedded within a much larger global network of several thousand laboratories using yeast as a model system.