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Editorial

The yeast genome at 30: a blueprint written by a collaborative and consilient community

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Abstract

Completion of the *Saccharomyces cerevisiae* genome sequence three decades ago marked a defining moment in eukaryotic genomics. Beyond a technical milestone, it established a shared reference that transformed how yeast biology is studied, interpreted, and extended across disciplines. This Editorial revisits the yeast genome sequencing project with a focus on the scientific culture that enabled it: an extraordinarily collaborative community willing to coordinate effort, share resources, and collectively tackle biological complexity. That consilient culture proved essential in converting a static DNA sequence into a dynamic framework for discovery, enabling systematic exploration of gene function, cellular organization, and genome-scale biology. As this Special Collection celebrates the 30th anniversary of the yeast genome sequence, we reflect on how shared infrastructure, and collective ambition turned the genome sequences of three related lab strains (S288c and its derivatives FY1679 and AB972) into a lasting platform for innovation. Apart from enabling the field of population genomics and access to the vast genetic diversity of the species, these foundations have facilitated the synthesis and assembly of all 16 chromosomes of the same laboratory strain of *S. cerevisiae*, bringing the Sc2.0 project within reach of creating the first eukaryotic cell with a fully synthetic genome. This transition—from genome *reading* to genome *writing*—positions yeasts as powerful systems for iterative *design–build–test–learn* cycles and for reimagining genomes of other *Saccharomyces* and non-*Saccharomyces* strains (including those used in industry) as highly modifiable biological platforms.

Keywords research collaboration, consilience, genome sequencing, genome engineering, *Saccharomyces cerevisiae*, functional genomics, synthetic genomics, yeast

A turning point in yeast genomics

Thirty years ago, the publication of the complete genome sequence of *Saccharomyces cerevisiae* (derived from related reference strains, S288c, FY1679 and AB972), marked a significant milestone in contemporary biology. For the first time, the entire genetic blueprint of a eukaryotic organism—an organism with a nucleus and complex internal organization—was revealed in full. The frontier-shifting achievement immediately transformed yeast research and profoundly influenced biology as a whole. Yet, three decades on, the most enduring legacy of the yeast genome sequencing project is not simply the sequence itself, nor even the astonishing scientific advances it enabled, but the way in which that sequence came to be: through a remarkable act of global collaboration, openness, generosity, and intellectual consilience.

The landmark 1996 *Science* publication by André Goffeau, Bernard Dujon, Stephen Oliver and colleagues, aptly titled "*Life with 6000 genes*", described a genome of just over 12 million base-pairs, distributed across 16 chromosomes, encoding 5885 predicted protein-coding genes, ∼140 ribosomal RNA genes, 40 small nuclear RNAs, and 275 transfer RNAs (Goffeau et al. 1996). The genome also revealed higher-order chromosomal organization, extensive gene duplication, and unexpected redundancy. Perhaps most strikingly, a substantial fraction of the predicted genes had no known biological function.

In a companion *Nature* article published the same year—"*From DNA sequence to biological function*"—Stephen Oliver captured the moment with characteristic clarity (Oliver 1996). Genome sequencing, he observed, was discovering genes at a rate 50–100 times faster than classical genetics, yet nearly half of those genes were biologically uncharacterized. The challenge facing yeast biology was no longer how to find genes, but how to understand them and elucidate their function (Oliver 1996). Implicit in both publications was a deeper truth: the era of in-

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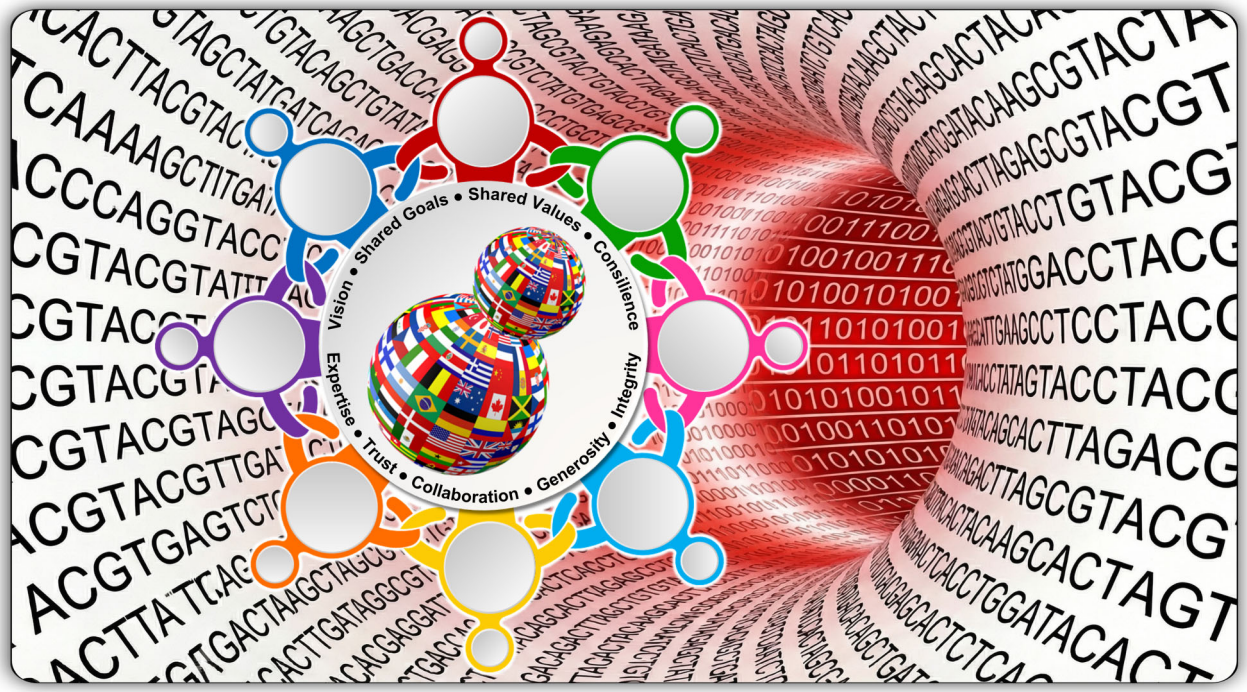

Figure 1 Global collaboration underpinning the sequencing of the *Saccharomyces cerevisiae* genome. The diagram illustrates the highly decentralized, international effort of the early 1990s, in which more than 100 laboratories across 19 countries coordinated the sequencing of individual chromosomal regions. Despite the absence of centralized infrastructure or uniform pipelines, the project succeeded through shared goals, open data exchange, and a strong culture of trust, cooperation and consilience. This collective ambition and collaboration culminated in the completion of the first fully sequenced eukaryotic genome in 1996.

dividual laboratories working in isolation was drawing to a close.

A genome written by brilliant minds and built by many hands

The genome sequencing project was unprecedented in both ambition and organization. Conducted in the early 1990s, long before next-generation sequencing, high-throughput automation, or cloud-based data sharing, it demanded technical ingenuity, organizational courage, and a collaborative mindset. Sequencing was labour-intensive, expensive, and slow. No single laboratory, institution, or nation could realistically undertake the task alone. The solution was collaboration on a scale rarely seen at the time (Fig. 1).

The *Saccharomyces Genome Database* (SGD) was established in 1993 as a community resource to collect, organize, and disseminate information about the *S. cerevisiae* genome and its gene products. It was initially created by David Botstein and colleagues at Stanford University, with Michael Cherry playing a leading role in its development and early curation. The database began as a set of spreadsheets, was migrated to an early biological database system (ACEDB), and then became publicly accessible via the World Wide Web in 1994. SGD has since grown into the principal curated knowledgebase for budding yeast genetics and genomics, serving as a central repository for sequence data, functional annotations, and nomenclature that supports researchers worldwide (Engel et al. 2025).

During this time, an international consortium involving researchers from 19 countries and over 100 laboratories came together to sequence the genome, chromosome by chromosome. Coordination was led largely from Europe, with André Goffeau playing a pivotal role in shaping the vision, organizing contributions, and sustaining momentum. European laboratories completed more than half of the genome sequence, supported by major efforts at the Wellcome Sanger Institute in England, Washington University in St. Louis, Stanford University, McGill University in Montreal, and RIKEN in Japan, among many others.

Each participating group took responsibility for defined chromosomal regions, generating sequence data that were rapidly deposited in public databases and assembled into a coherent whole. The project began in the early 1990s and reached completion with the release of the full genome sequence in April 1996—a remarkably short timeframe of roughly six years, given the technological constraints of the time.

This was a profoundly decentralized enterprise. There was no single sequencing centre, no uniform pipeline, and no centralized control of data generation. What held the project together was a shared commitment to a common goal, mutual trust among collaborators, and an extraordinary willingness to place collective success above individual recognition.

Research collaboration before consortia were fashionable

In today's research environment, large international consortia are common, often driven by formal agreements, detailed governance structures, and mandated data-sharing policies (McLennan and Maslan, 2025). The yeast genome sequencing project predated much of this bureaucratic infrastructure. Its success rested less on contracts than on culture.

Authorship on the 1996 *Science* paper reflected this ethos (Goffeau et al. 1996). Credit was collective, inclusive, and deliberately broad. Progress depended on openness: laboratories shared clones, sequencing strategies, primers, vectors, strains, and hard-won technical insights. Problems encountered in one part of the genome were solved through expertise developed elsewhere. Competition, where it existed, was tempered by a strong sense that the real achievement lay in completing the genome, not in claiming individual pieces of it.

This spirit of generosity did not emerge overnight. It was rooted in the long-standing traditions of the global yeast research community, which had already developed shared strain collections, communal databases, and an expectation that materials and methods would circulate freely. The genome sequencing project amplified these norms and demonstrated their power at scale. In retrospect, it is hard to imagine the yeast genome sequence being completed in any other way.

This project originated in 1989 when Andre Goffeau coordinated a consortium of 35 European laboratories to secure funding from the European Community's Biotechnology Action Programme. The European Community is now the European Union, and its research funding operates under the *Horizon Europe* banner but the principle that 'funded research' must be transnational remains. This European ethos that linked 'the European (political) Project' with research collaboration served the yeast community very well. In an era of increasing focus on nationalism and 'sovereignty', the scientific community should always promulgate the message that the greatest advances do not come through isolationism.

A collegial culture of generosity and trust

The collaborative success of the genome sequencing project was inseparable from a deeper culture of generosity. Yeast researchers had long recognized that the organism's greatest strength lay not only in its experimental tractability, but in its ability to unite a diverse community around shared goals, tools and scientific questions.

Strains were exchanged without hesitation. Mutant collections were built explicitly for community use. Data were released early, often before publication. Databases such as the SGD were conceived as shared infrastructure rather than proprietary resources.

This generosity extended across disciplines. Molecular biologists, geneticists, biochemists, evolutionary biologists, physicists, mathematicians, and computational scientists all found a common reference point in the yeast genome. The sequence became a shared language, enabling ideas to flow between fields that had previously been separated by methods, terminology, and tradition.

The yeast genome sequencing project thus fostered not only collaboration, but trust—a commodity that is essential for large-scale science, yet increasingly fragile. As Stephen M.R. Covey observed in *The Speed of Trust*, "*when trust goes up, speed goes up and cost comes down*" (Covey 2008). This principle proved central to the success of the yeast genome sequencing project.

The glue that binds the yeast community

To understand the enduring culture of the yeast community it is necessary to delve deeper into the past, indeed to the origins of yeast genetics in the 1930s in Europe with the work of Øjvind Winge at the Carlsberg Laboratory, Denmark, and the 1940's and 50's in the USA by Carl and Gertrude Lindegren, Herschel Roman, and disciples (Hall and Lindner 1993). The third critical leg of this transatlantic community originated in Pavia, Italy, whence came luminaries such as Adriano Buzzati-Traverso, Luca Cavalli Sforza, Giovanni Magni, and Mario Polsinelli (Frontali 2016, Hartl 2026). The independent, yet interdependent, research of these early foci set the scene for what was to follow.

By 1961, this nascent community decided to co-ordinate and convene the first recognized meeting of the yeast genetics community at Carbondale, Illinois, USA. That very first meeting focused on a topic that was surely critical to all future efforts to study the yeast genome—yeast nomenclature and how to name genes! From a modest beginning with eleven attendees, this meeting series has grown and prospered, with the *32nd International Conference on Yeast Genetics and Molecular Biology* (ICYGMB), which took place in Paris, France in 2025, hosting well over five hundred delegates (Dujon and Cooper 2026). The success of the ICYGMB series of conferences is mirrored by many examples of yeast scientists coming together to share knowledge and collaborate.

Whether for specialized congresses like *SMYTE*, *The Small Meeting on Yeast Transport and Energetics* (Hoefer and Cooper 2026), or for broad-topic gatherings like *Annual Conferences on Yeasts in Smolinece Castle*, Slovakia, yeast researchers love to congregate. And these are not transient, easily dispersed clusters—we mention these two specifically as they host their 40th and 50th meetings, respectively in 2026! And globally, the sister organization to ICYGMB, the *International Commission on Yeasts*, established in 1966, continues to organize annual yeast symposia and congresses all over the world (https://www.icy-yeast.org/).

What sustains all these workshops, symposia, conferences and congresses? First of course, it is the chief protagonist with its multiple personas: *S. cerevisiae* is the ideal organism for fundamental studies on genetics, cell biology, biochemistry and evolution; it is an excellent model of human diseases and medicine; there is no better workhorse for modern biotechnology; and its fermentative metabolism has given rise to staples of human diet for thousands of years. In this latter trait, there may lie a clue to the success and longevity of yeast conference series, which distinguish themselves by their conviviality. The observation by Sy Fogel at the closing of the 5th ICYGMB in Chalk River, Ontario, Canada that he had developed a better appreciation of the advertising billboards "*Drink Canada Dry*" may point to the glue that binds yeast researchers?

It runs much deeper than this, however. From the earliest days, the founders of the field of yeast genetics understood that competing for new discoveries and collaborating for the greater good were not mutually exclusive concepts. While nobody would suggest that yeast research is immune from the cut-throat competition that exists is all scientific fields, in the yeast community that has never come at the expense of adhering to the true values of scientific endeavour. That is exemplified in the story of the yeast genome sequencing project, and of its legacy, which is described in this article and in others in the special collection. It is also evident in the contributions that yeast researchers make to their community. This is seen is the work in scientific societies, including the conference organization already mentioned, and the support for specialized scientific journals, notably *Yeast* (Wiley) and *FEMS Yeast Research*, the journal of the yeast community. For example, the voluntary work that editors, editorial boards, and reviewers make to the work of *FEMS Yeast Research* enables FEMS (the *Federation of European Microbiology Societies*) to support the community through meeting grants, fellowships, and other activities. It may be said that the strongest glue binding the yeast community is a love of yeast and a set of shared values.

Consilience in practice

The yeast genome sequencing project exemplified consilience long before the concept gained prominence in contemporary research strategy documents. The term itself was coined in the 19th Century by the philosopher William Whewell (who also coined the term "scientist") to describe the "consilience of inductions"—the moment when evidence from independent lines of inquiry converges to form a unified explanation. More than a century later, the biologist Edward O. Wilson popularized and expanded this idea in his 1998 book *Consilience: The Unity of Knowledge* (Wilson 1998), arguing that the deepest understanding of complex phenomena emerges when insights from different disciplines are linked rather than siloed. Rather than being limited to interdisciplinary work, consilience represents a deliberate and sustained process of integrating knowledge across diverse boundaries—disciplinary, sectoral, and geographic—through common problem definitions, shared frameworks, bridging roles, translation processes, and enabling governance arrangements.

In practice, the yeast genome sequencing project embodied this philosophy intuitively and organically. Sequencing the genome required the integration of classical genetics, recombinant DNA technology, molecular biology, systems biology, physical mapping, enzymology, and emerging computational approaches. Making sense of the sequence demanded even more: evolutionary theory to interpret gene duplication and divergence, systems thinking to understand networks and pathways, structural biology to infer molecular function, and quantitative modelling to grasp emergent behaviour. No single discipline could claim ownership of the genome, nor could any single perspective fully explain it.

As a result, disciplinary boundaries became permeable. Classical and molecular geneticists were compelled to move beyond single-gene analyses toward pathway- and network-level thinking. Computational scientists were drawn deeply into the biological complexity of a living eukaryotic cell, while evolutionary biologists found in the genome a richly annotated record of adaptation, redundancy, and historical contingency. This convergence did not dilute disciplinary expertise; it sharpened and deepened it.

The yeast research community, shaped by this shared intellectual endeavour, became unusually fluent at disciplinary interfaces. That fluency positioned yeast research at the forefront of systems biology, functional genomics, and later synthetic biology, and helped establish *S. cerevisiae* not merely as a model organism, but as a model system for how integrative, consilient science can be practized.

From sequence to function—together

One of the most enduring messages of the original genome sequencing publications was how much remained unknown (Oliver 1996, 1998). Nearly half of the predicted genes lacked any functional annotation. Rather than being framed as a limitation, this was presented as an invitation—and the yeast community responded collectively.

Over the following decades, systematic gene deletion collections, genome-wide expression profiling, protein–protein interaction maps, and large-scale phenotypic screens were developed, often explicitly as shared resources. These efforts again relied on collaboration, replication across laboratories, and open dissemination of data and materials. Some of these are highlighted below, and more are discussed in other articles in this Special Collection. It must also be recognized, of course, that the original description of the blueprint was based on the state of knowledge thirty years ago. Back then, the emphasis was on protein-coding genes and known stable (mostly short) non-coding RNA (ncRNA) molecules, such rRNA, tRNA and splicing associated RNAs. Long non-coding RNA had not yet been discovered—but now at least eleven families of long ncRNA have been described in yeast and it is estimated that over half of the transcriptional activity of the cell may be devoted to these (Qi et al. 2025). Future systematic approaches will consider the genome blueprint from both the protein coding and the non-protein-coding perspectives.

Crucially, recognition accrued not only to those who made headline discoveries, but also to those who built the tools, datasets, and frameworks that enabled discovery by others. The yeast sequencing genome project thus helped normalize the idea that contribution to communal infrastructure is itself a fundamental form of scientific leadership.

Population genomics—closing the circle

The *S. cerevisiae* genome that was published in 1996 was actually generated from three related strains, S288c, FY1679 and AB972 (Engel et al. 2014, Dujon and Cooper 2026). Because strains FY1679 and AB972 were derived from strain S288c, it is often said that the genome sequence is that of strain S288c. Thus, while it is probably fair to say that the genome sequence is very close to that of S288c, technically, that is not correct, and there is some minor variation with S288c. Going back further into strain history, a virtual reconstruction of the genealogy of lab strains of *S. cerevisiae* concluded that strain S288c itself is about 88% derived from EM93, a wild strain isolated in California from rotting figs in

1938, with contributions from five other strains, including some domesticated ones (Mortimer and Johnston 1986). S228c was selected through multiple crosses by Mortimer to have characteristics that made it amenable to laboratory research, and the other derivatives were also lab-derived for favourable traits. Based on this history, the general consensus that the original genome sequence was of a "lab strain" is certainly valid. Even before genome sequences were available, it was evident that strain S288c does not represent the full genetic potential of *S. cerevisiae* as it lacks features found in industrial strains used in brewing, baking and winemaking.

With genome sequencing, it became possible to sequence the genomes of many domesticated and wild isolates of *S. cerevisiae,* and the field of yeast population genomics was born. Initial studies focusing on strains from anthropogenic environments led to the finding that all wine strains shared a common origin, with Mediterranean oak harbouring the ancestors of these strains (Almedia et al. 2015). This line of research was extended by Kevin Verstrepen's group who established that all industrial strains cluster in a small number of domesticated sub-lineages that are distinct from wild ancestors (Gallone et al. 2016). The 1002 yeast genomes project addressed the problem that domesticated strains are overrepresented in these studies by sequencing a large number of wild isolates from across the globe. This work led to the remarkable finding that the largest diversity of wild *S. cerevisiae* is found in East Asia, leading to the "out of China" hypothesis for the origins of the species (Peter et al. 2018). This has been supported by the most recent compilation and analysis of $>$ 3000 strains, which identified 39 distinct clades of domesticated and wild isolates of *S. cerevisiae,* and which confirmed several distinct and independent domestication events (Loegler et al. 2024). Interestingly, strain EM93 sits in the "lab strain clade", demonstrating that while the S228c genome sequence is as "representative" as any other single strain that could have been chosen, it still just provides a small snapshot of the total diversity of the species (Figure 2). Without it, however, the *S. cerevisiae* pan-genome with almost two million SNPs could not have been determined, and the myriads of studies that now seek to understand evolutionary processes such as domestication, or to exploit the diversity for biotechnological applications, would not be possible.

It is interesting to reflect on how technological advances connect to the philosophy of the early seminal figures in yeast genetics. While the US-school led by the Lindegrens, Hershel Roman and colleagues emphasized the importance of well-characterized "model" strains, in Florence, Polsinelli established a large collection of natural isolates associated with grapes and wine and can be considered a founder of yeast population genetics. Armed with the knowledge, genome sequence, and technological know-how that was gained with the model S228c and derivatives, it has become possible to move from population genetics to population genomics: the circle has been closed.

Looking forward by looking back

The lessons from earlier breakthroughs in yeast biology and the yeast genome sequencing project did not end with the completion of the sequence in 1996. Conceptually, technically, and culturally, they laid the groundwork for a new frontier in genome science. The same collaborative ethos that enabled researchers to *read* the genome is now enabling them to *write* it.

Perhaps the most striking embodiment of this transition is the international synthetic yeast genome sequencing project, Sc2.0—which is conducted with the "BY" lineage directly derived from the heterothallic, haploid S288c parental strain (Brachmann et al. 1998, Pretorius and Boeke 2018). Initiated nearly two decades after the publication of the original genome sequence, Sc2.0 represents one of the most ambitious undertakings in synthetic biology: the design and construction of a fully synthetic version of the *S. cerevisiae* BY genome (Fig. 3). Rather than simply reproducing the natural sequence, the project refactors it—removing unstable elements, introducing strategically placed recombination sites, and redesigning chromosomal architecture to make the genome more modular, evolvable, and experimentally tractable.

The scale of this effort mirrors that of the original genome sequencing project. Laboratories across multiple continents have collaborated to design, z, and assemble individual chromosomes of the yeast genome. With all sixteen chromosomes of that same haploid reference strain now successfully synthesized, the field stands on the threshold of constructing what may become the first eukaryotic cell with a completely synthetic genome (Erpf et al. 2025, 2026). This achievement reflects extraordinary advances in DNA synthesis, genome engineering, and computational design—but it also reflects the enduring strength of the global yeast research community.

The connection between the 1996 genome sequence and the current Sc2.0 project is therefore more than historical. The original genome provided the blueprint: a fully annotated, community-curated reference that enabled researchers to understand the organization, function, and evolution of a eukaryotic genome. Sc2.0 builds directly upon that foundation, transforming a static blueprint into a platform for iterative design–build–test–learn cycles in which genomes themselves can be redesigned to test biological hypotheses and explore new functionalities

In this sense, the trajectory of yeast genomics over the past three decades illustrates a profound shift in the life sciences. The initial era of genomics was concerned primarily with decoding life—reading DNA sequences and cataloguing genes. The emerging era of synthetic genomics moves beyond interpretation toward design and construction, allowing researchers to explore not only what genomes are, but what they could be (Archer et al. 2026, Erpf et al. 2026).

Yet the most important continuity between these two eras is cultural rather than technological. The Sc2.0 project, like the genome sequencing project before it, depends on open sharing of designs, strains, tools, and data; on coordinated efforts across institutions and nations; and on a community willing to pursue collective progress over individual acclaim. The transition from genome *reading* to genome *writing* is therefore not a departure from the original yeast genome sequencing project, but its natural continuation.

Thirty years ago, the phrase "*life with 6000 genes*" captured the excitement of revealing the genetic blueprint of a simple eukaryote. Three decades later, the yeast community is approaching another milestone: the construction of a fully synthetic version of that same genome, "*life with 16 constructed chromosomes*". If the first achievement transformed how we understand biological sys-

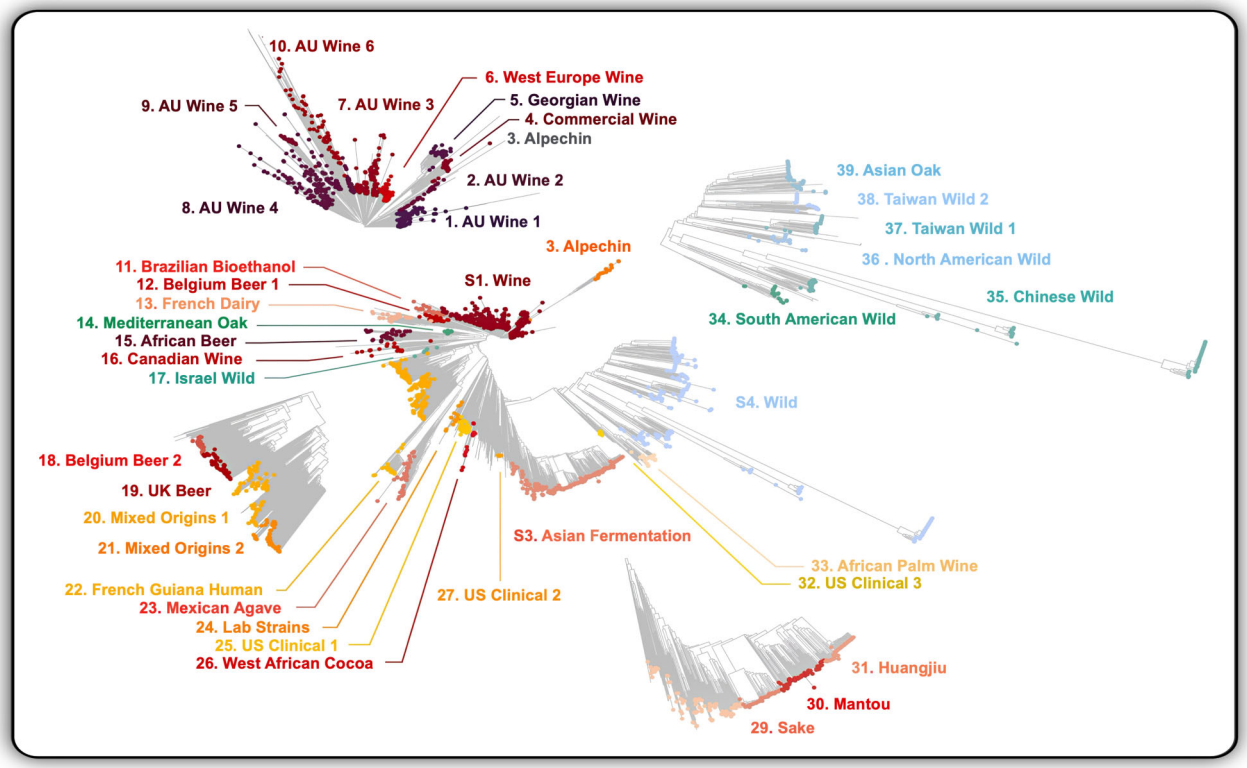

Figure 2 The *Saccharomyces cerevisiae* population structure through the lens of 3034 genomes. The Neighbour-joining tree built using 1 918 693 SNPs and shows the 39 clades and 4 superclades that were identified. Subtrees of the 4 superclades (designated S1–S4) are magnified (S1. Wine, S2. Beer, S3. Asian Fermentation, and S4. Wild). The tree shows that *S. cerevisiae* was independently domesticated from the wild multiple times. Strain EM93, which contributed about 88% of the S288c genome is located in clade 24–"lab strains". Figure reproduced from Loegler et al. (2024) under a creative commons licence (Loegler et al. 2024).

tems, the second promises to transform how we reframe and redesign them (Erpf et al. 2026).

Lessons that endure

This Editorial did not attempt to catalogue all the extraordinary scientific achievements enabled by the yeast genome over the past three decades. Those stories are told throughout this Special Collection and in countless studies that have drawn upon the sequence as a foundational reference. Instead, this reflection celebrates a different legacy: a model for how science can be done jointly.

As biology confronts global challenges that demand unprecedented cooperation—from human health and sustainable biomanufacturing to food security and climate resilience—the yeast genome sequencing project offers a timely reminder. Some of the most transformative advances arise not from competition, but from collaboration; not from secrecy, but from sharing; not from individual brilliance alone, but from collective endeavour. The international effort that decoded the genome of *S. cerevisiae* demonstrated that when a scientific community aligns around a shared goal and shared values, progress can accelerate in remarkable ways.

Thirty years on, genome sequencing has become routine. Thousands of eukaryotic genomes—including genomes from other *Saccharomyces* and non-*Saccharomyces* strains—have been decoded, often by individual laboratories or a handful of centres using industrial-scale technologies. These include industrial strains, such *Saccharomyces* wine yeast strains [e.g. AWR1631 (Borneman et al. 2008) and EC1118 (Novo et al. 2009)], and a non-*Saccharomyces* prevalent wine spoilage yeast, *Brettanomyces* (*Dekkera*) *bruxellensis* [e.g. AWR1499 (Curtin et al. 2012, Curtin and Pretorius 2014)]. This allowed for comparative genomics (Borneman et al. 2011, 2013, 2015), the construction of a pan-genome synthetic neo-chromosome in *S. cerevisiae* (Kutyna et al. 2022, 2026) and seeding the idea of an encapsulating representative synthetic metagenome in a single yeast cell (Belda et al. 2021).

Yet the 1996 yeast genome sequencing project remains distinctive, not because of its technical sophistication, but because of its social architecture. It offers enduring lessons. First, collaboration is most powerful when it is values-driven rather than compliance-driven. The yeast genome was completed not because researchers were required to collaborate, but because they chose to. Second, trust and generosity accelerate science. Open sharing of data, materials, and expertise did not diminish individual careers; it amplified collective impact. Third, consilience is not optional; the complexity revealed by genomes demands perspectives that no single discipline can provide. Finally, community matters. The yeast genome reminds us that trust, respect, and shared purpose are as essential to scientific progress as technology and funding.

The deeper lesson, however, remains unchanged. The yeast genome sequencing project showed that extraordinary science

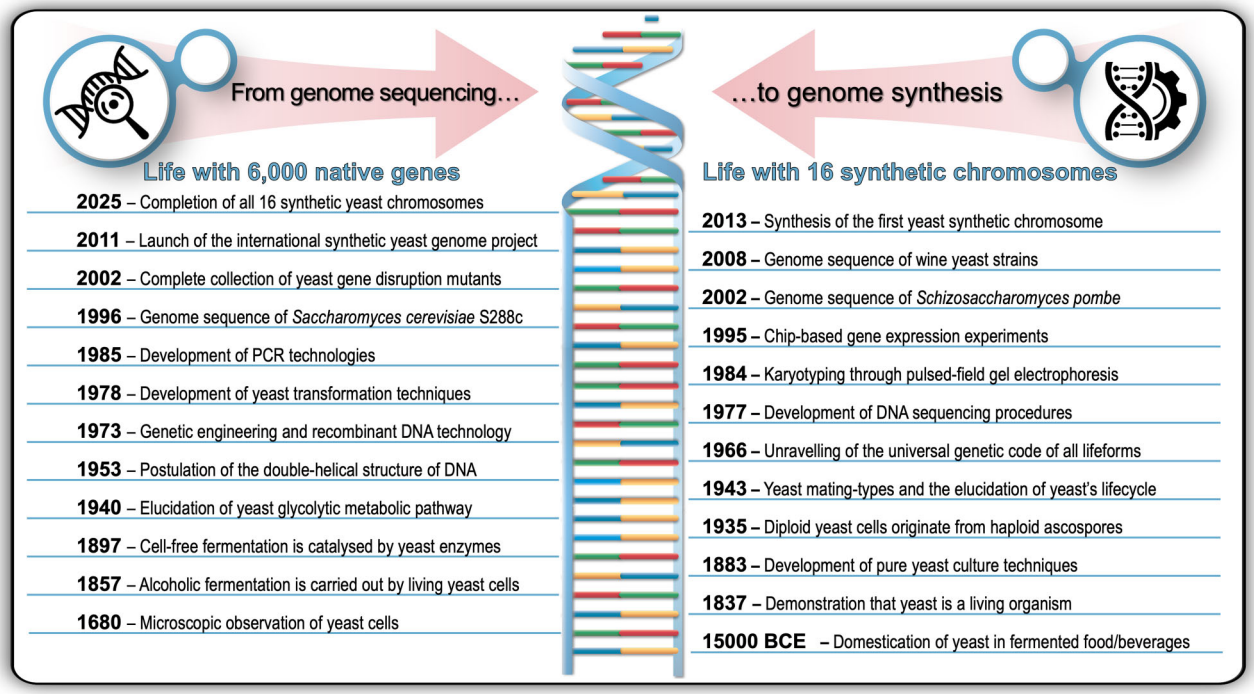

Figure 3 Building on breakthroughs spanning multiple centuries, yeast biology is poised to transition from genome *reading* to genome *writing*. The *Yeast Genome Sequencing Project* of the 1990s paved the way for the current international *Yeast Genome Synthesis Project* (Sc2.0). The diagram highlights the conceptual and technological progression from sequencing and annotation of the native *Saccharomyces cerevisiae* genome to the design, synthesis, and assembly of a fully synthetic, refactored genome. The latter entails the iterative *design–build–test–learn* cycle enabled by synthetic genomics, as well as the continuity of the collaborative, community-driven ethos that underpins both the original genome project and the ongoing construction of a synthetic eukaryotic cell.

can emerge when a community works together with openness, trust, and shared purpose. Thirty years later, that same spirit continues to propel yeast research forward—reminding us that life with 6000 genes was only the beginning, but life with thousands of collaborating scientists remains one of yeast biology's greatest strengths.

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