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## Metabolic engineering, synthetic biology and systems biology

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## Metabolic engineering, synthetic biology and systems biology

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The completion, in 1996, of the genome sequence of the *Saccharomyces cerevisiae* laboratory strain S288C represents a watershed in yeast research. In their historic Science publication marking this milestone, Goffeau and colleagues commented that ‘new graduate students are already wondering how we all managed in the “dark ages” before the sequence was completed’.

The words ‘the sequence’ in the above-mentioned quote illustrate how fast yeast research continues to develop today. Costs of whole-genome sequencing have decreased so spectacularly that it is now an integral part of the yeast research toolkit, and annotated genome sequences are available for many *S. cerevisiae* strains. Improvements in high-throughput, automated screening of mutant libraries as well as new developments in transcriptomics, proteomics and metabolomics further expand our analytical access to *S. cerevisiae*.

Increases in quality, scope and throughput of analytical platforms are complemented by similar developments in genetic modification. Automated strain construction, high-fidelity DNA synthesis and clever exploitation of *S. cerevisiae*’s homologous recombination mechanisms for *in vivo* assembly of large DNA constructs now enable genetic interventions that would have been unthinkable 10 years ago. Exploration of natural biodiversity, laboratory evolution and random mutagenesis provide additional means to investigate the impact of genetic changes on yeast biology.

Even unrestricted experimental access is of little value in the absence of methods to extract knowledge from information. Fortunately, bioinformatics and systems biology continue to provide yeast researchers with essential new databases, algorithms and mathematical models that enable interpretation of data and guide the design of experiments.

How do science and society profit from this concentration of analytical power, experimental access and mathematical modelling on a single eukaryotic microorganism?

In its role of a eukaryotic laboratory model system, *S. cerevisiae* generates important insights into the biology

of eukaryotic life, including processes that are of direct relevance to human biology and medicine such as ageing and apoptosis. Moreover, engineered ‘humanized’ yeast cells provide attractive platforms to study human disease and explore possible therapies.

In industrial biotechnology, its experimental accessibility, a large and rapidly growing body of biological knowledge and its proven robustness under industrial conditions make *S. cerevisiae* a popular platform for metabolic engineering of existing and novel product pathways. Today, the rapidly growing range of products produced with engineered *S. cerevisiae* strains already range from biofuels and bulk chemicals to food ingredients and life-saving pharmaceuticals, while many other yeast-based products are subject of intensive academic and industrial research.

Ten minireviews in this special issue of *FEMS Yeast Research* provide an overview of the rapid developments in Metabolic Engineering, Synthetic Biology and Systems Biology of *S. cerevisiae*. We thank the authors of the minireviews for their contributions and hope these will provide a useful and enjoyable reference and source of inspiration for new and established yeast researchers.

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