

/THE LAST WORD

The Diverse Potential of Yeast

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The biotechnology, food, and pharmaceutical industries have had a long and profitable association with the yeasts. Brewing and breadmaking yeasts have been used in foods and beverages for thousands of years. More recently, a wider range of yeast species have found application in biotransformation, bioremediation, chiral compound production, flavor production, the fats and oils industry, pharmaceutical screens, and heterologous protein production.

The budding yeast, or baker's yeast, *Saccharomyces cerevisiae*, will soon become the first higher organism for which the DNA sequence of the entire genome is available, initiating a new era of research in the cellular engineering and analysis of genes of unknown function. The resulting identification of new genes and gene families will provide a rich source of genetic diversity for potential industrial exploitation.

It is curious, therefore, that so little is known about the biological diversity of the yeasts. To date, some 600 species of yeast have been described, but these are likely to represent only a fraction of those existing.

The Biodiversity Convention has given impetus to attempts to preserve species diversity on a global scale; as plant and animal species disappear at unprecedented rates, a proportion of the associated microflora disappears with them. The problem is how to measure this diversity and to develop approaches to characterize and preserve those species that remain, particularly those that are likely to be of commercial value.

The many rapid and highly discriminatory molecular techniques now available for characterization of yeasts provide one solution to this problem. The utility of these techniques for a particular purpose can easily be evaluated by reference to the large collections of well-characterized yeasts preserved in genebanks throughout the world.

In many cases, there is no obvious direct relationship between genetic variation and the distribution of commercially important traits. While techniques such as ribosomal RNA phylogeny provide a rapid taxonomic framework for understanding species interrelationships, frequently only one isolate from a given species or group of species displays properties of commercial interest. Techniques such as karyotype analysis and genetic fingerprinting provide extremely fine discrimination between isolates, but have yet to be correlated with commercial yeast data, or to be used to indicate ways of changing characteristics in industrially useful ways.

In the near future, it is possible to envisage molecular probes that will detect the presence of yeasts in any environment and rapidly identify commercial potential independent of laboratory screening and ease of culture (wild yeasts appear able to survive for long periods in unculturable form). Such probes will accelerate collection and characterization of yeast biodiversity, including that from threatened and extreme environments. Novel species of potential biotechnological utility are likely to be identified using such approaches. For example, an isolate of *S. cerevisiae* from seawater with the favorable properties of salt tolerance and high maltose-fermentation has been commercialized for bread production in Japan. A more accurate assessment of the environmental role of yeasts will also be possible, perhaps indicating further applications, for example, in bioremediation. An even more extensive scientific and industrial exploitation of these versatile and safe microorganisms, which grow at low pH with consequently few problems of contamination, can clearly be anticipated.

Partnerships need to be forged between taxonomists and the industries that exploit yeasts and that accumulate data concerning their phenotypic variation. For example, in the same way that algorithms have been developed to compare vast gene sequence databases, data mining tools are now becoming available for examining the enormous amounts of data produced from high-throughput screens in the pharmaceutical industry.

This kind of comparative analysis, in which both evolutionary genetics and phenotypic variation are taken into account, will become increasingly important as a means to preserve and exploit biological diversity. It will enable us not only to target further exploitation of yeasts, but also to define best approaches to fingerprinting important traits in other organisms.

Mathematical models of biodiversity might also be tested using simple yeast systems. Such information will be of value to all yeast-utilizing industries, whether in the search for new enzymes, pathways, flavor compounds, brewing properties, or indeed pharmaceuticals. Yeasts are proving to be of greater metabolic complexity than hitherto realized, and compounds such as polyketides and phalates have recently been shown to be produced by some species. In this context, it is worth noting that some 50% of the genes identified by the Yeast Genome Project have yet to be ascribed a function; even the humble baker's yeast clearly has some hidden potential. ///