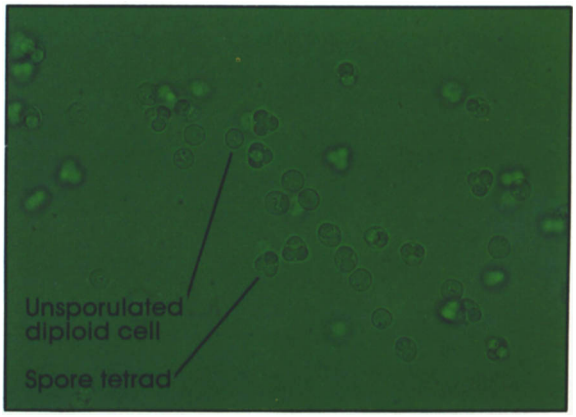
tuitously combining many of the best traits of their parents. Again, time is a problem. It takes time for characteristics of the bole, branches, and wood to develop to a point where evaluation is appropriate. Each year, some clones are disqualified, while the rest are used with increasing confidence.

A fourth option is now becoming possible. Tissues from outstanding mature trees may be cultured in nutrient medium, becoming undifferentiated masses of cells (callus). Fragments of the callus can be induced to differentiate into small plants resembling seedlings, and when these have become large enough, juvenile cuttings can be taken from them. An important aspect of this method is manipulation of the developmental, or maturation, state of a clone. Early promising results in rejuvenating redwood clones have become available from the tissue-culture laboratories of Professor E. Ball and Professor T. Murashige, at the University of California's Santa Cruz, Irvine, and Riverside campuses, and from France.

There is one report of a hybrid between coast redwood and giant sequoia. We and others have not been able to repeat it by normal controlled-pollination crosses. Interspecific hybrids with giant sequoia or other species may someday be created by cell fusion in culture, followed by recovery and cloning of the hybrid plants.

As a general principle, the more the newly selected redwoods are like previously tested trees, the quicker they can be used for large-scale reforestation. Conversely, if the new trees are radically different genetically, they must properly be tested in many conditions for many decades before their widespread use is appropriate. Some new techniques will be immediately valuable, for example, in rejuvenating tested trees or clones, or rapidly expanding clones of known families. But the great promise of the new techniques for producing radically new trees must be tempered by the need to be sure those trees can survive and perform well, for many decades, in the varied and uncertain environments of our forests.

William J. Libby, Professor, Genetics, U.C., Berkeley.



Microphotograph of sporulated wine yeast strain shows unsporulated diploid vegetative cells and sporulated cells, which contain four ascospores. The diploid cells have two sets of chromosomes in each nucleus; the ascospores have only one. The spores result from meiotic divisions similar to those occurring in nearly all higher plants and animals.

Genetic alteration of yeast

Richard Snow

Yeast is one of the major industrial microorganisms, used in the brewing, baking, and wine industries. Most improvements in wine making have resulted from better grape varieties (such as Ruby Cabernet developed at University of California, Davis) or from improvements in fermentation practices. Not much attention has been given to planned improvement of the other organism on which the wine industry is based, the wine yeast. Yeast has many favorable characteristics making it one of the best organisms to use for basic genetics research, and as a result, our genetic understanding of it has reached an extremely high level.

Yeast is classified scientifically with the fungi, the same group to which the common mushroom and many plant disease organisms belong. Baker's, brewer's, and wine yeasts belong to the same species, *Saccharomyces cerevisiae*. Surveys of many wine yeast strains have been made for characteristics of interest to the wine maker, and in every case they have uncovered a great deal of variability, indicating considerable genetic heterogeneity that could be exploited by appropriate breeding programs.

The standard breeding method of crossing strains and selecting desirable recombinant progeny can be applied to yeast, just as it can to most other agriculturally important plants and animals. But one of the most attractive features of yeast is that the new techniques of transformation with foreign DNA and protoplast fusion also can be applied. These techniques open the door to the use of genetic engineering methods in yeast improvement. In my laboratory we are working on one such project, the introduction of a gene from a bacterial strain into a wine yeast strain.

This gene codes for the structure of an enzyme that converts malic acid (the principal grape acid) into lactic acid—the process of malolactic fermentation. This conversion is of importance in preventing wine spoilage and in cases where the grape must is too acid. To cause malolactic fermentation, wine makers either hold the must under conditions that encourage the bacteria naturally present to multiply, or they inoculate with a starter culture of the desired bacteria. It would be desirable to have a yeast strain that could carry out both the malolactic and the alcoholic fermentations at the same time.

We have been able to isolate the malolactic gene from a species of lactic acid bacteria by cloning it on a plasmid. A plasmid carrying the gene has been put into the bacterium *Escherichia coli* (a widely used genetic organism) and into a laboratory yeast strain. In both cases, the recipient organisms acquired the malolactic function, indicating that the gene is working in its new hosts. At present its expression in yeast is too low to be of use to wine makers, but we expect to be able to increase its activity greatly.

The selective introduction of genes from one organism into another will be important in future plant breeding, and in many cases will circumvent laborious (or impossible) breeding programs. The malolactic case is one example: yeast and bacteria cannot be crossed directly. What we learn about increasing the expression of our bacterial gene in yeast should also have direct application to many other cases of agricultural importance.

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