which is then flushed along the channel. The channel is narrowed at its outlet end by an amount determined by the size of the particles, such that particles that arrive at the outlet become stuck there, preventing themselves and any others from flowing out of the channel (this phenomenon is known in the art as the keystone effect). As a result, the continued flushing with the slurry causes the channel to become packed with the particles.

This work was done by Wilbur W. Wilson and Carlos D. Garcia of Mississippi State University and Charles S. Henry of Colorado State University for **Marshall Space Flight Center**.

In accordance with Public Law 96-517, the contractor has elected to retain title to this invention. Inquiries concerning rights for its commercial use should be addressed to:

Mississippi State University
Office of Intellectual Property and Technology Licensing
P.O. Box 5282
Mississippi State, MS 39762
Phone: (662) 325-9263

Refer to MFS-31978-1, volume and number of this NASA Tech Briefs *issue, and the page number.*

Studying Functions of All Yeast Genes Simultaneously

This method could accelerate research on treatment of some diseases.

Ames Research Center, Moffett Field, California

A method of studying the functions of all the genes of a given species of microorganism simultaneously has been developed in experiments on *Saccharomyces cerevisiae* (commonly known as baker's or brewer's yeast). It is already known that many yeast genes perform functions similar to those of corresponding human genes; therefore, by facilitating understanding of yeast genes, the method may ultimately also contribute to the knowledge needed to treat some diseases in humans.

Because of the complexity of the method and the highly specialized nature of the underlying knowledge, it is possible to give only a brief and sketchy summary here. The method involves the use of unique synthetic deoxyribonucleic acid (DNA) sequences that are denoted as DNA bar codes because of their utility as molecular labels. The method also involves the disruption of gene functions through deletion of genes. *Saccharomyces cerevisiae* is a particularly powerful experimental system in that multiple deletion strains easily can be pooled for parallel growth assays. Individual deletion strains recently have been created for 5,918 open reading frames, representing nearly all of the estimated 6,000 genetic loci of *Saccharomyces cerevisiae*.

Tagging of each deletion strain with one or two unique 20-nucleotide sequences enables identification of genes affected by specific growth conditions, without prior knowledge of gene functions. Hybridization of bar-code DNA to oligonucleotide arrays can be used to measure the growth rate of each strain over several cell-division generations. The growth rate thus measured serves as an index of the fitness of the strain.

This work was done by Viktor Stolc of **Ames Research Center***; Robert G. Eason, Nader Pourmand, Zelek S. Herman, and Ronald W. Davis of Stanford Genome Technology Center; Waraporn Tongprasit of ELORET Corp.; and Kevin Anthony and Olufisayo Jejelowo of Texas Southern University. Further information is contained in a TSP (see page 1).*.

Inquiries concerning rights for the commercial use of this invention should be addressed to the Innovative Partnerships Office, Ames Research Center, (650) 604-2954. Refer to ARC-15345-1.