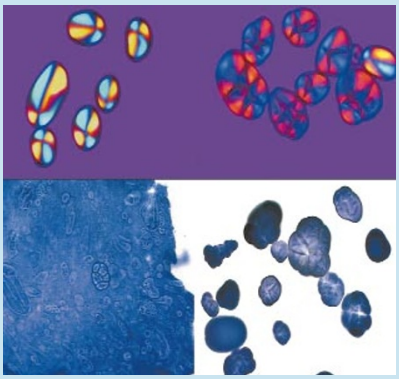


Finding ways to manipulate the ratio of amylose to amylopectin in starch is an important goal in the starch industry, as these two components strongly influence the biophysical properties of starch, and thus the range of applications. Recent attempts to modify the expression of starch synthases and branching enzymes (SBEs) have been moderately successful, but thus far no one had been able to produce a potato starch high in the essentially linear amylose. In their paper on page 551, Schwall et al. use antisense technology to generate transgenic potatoes capable of producing the first truly high-amylose potato starch. *JJ*

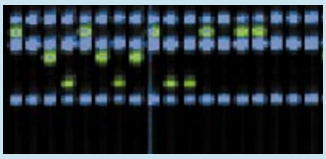
On page 555, Zhu et al. report the first application of oligonucleotide-mediated gene repair for crop improvement. Plant genetic engineering has historically relied on the introduction of transgenes by integration into random locations on the chromosomes. However, recently chimeric oligonucleotides—which have been used in mice to repair mutations like the one that causes sickle cell anemia—were shown to introduce a precise mutation in plant calli, thereby conferring resistance to herbicides. The current report extends that work by showing that the repaired trait can be stably inherited and expressed in progeny. The relative inefficiency of the method may hinder its wide application to crop engineering in the near term. However, as the technique avoids many problems inherent in transgene technology, such as introduction of vector sequences, silencing and position effects, it will likely make a useful addition to the plant scientists' toolbox of the future. *ND*

Tapping into tumor immunotherapy

The immune system can target tumor cells for destruction by recognizing tumor-associated antigens displayed on their surface. However, if the cellular machinery for antigen processing fails, the cancer cells will escape immunosurveillence. Such failure can be caused by downregulation of ER proteins called transporters associated with antigen processing (TAP), which pump antigenic peptides into the ER lumen where they bind to MHC class I for presentation on the cell surface. In this issue, Alimonti et al. test whether restoring TAP1 to TAP-deficient tumor cells makes them recognizable by the immune system. They show that TAP1 transfection restores antigen presentation to some MHC-defective cell lines, leading to better immune response recognition of tumors in vivo. Immunizing mice with TAP1-transfected cells protected mice against TAP-deficient tumor cells, suggesting that this approach could be applied to tumor therapies in humans (p. 515). *ND*

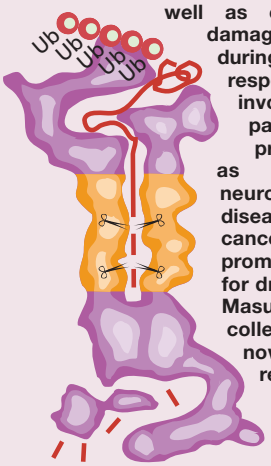
Technical Report

Microarray studies based on hybridization of target and probe have not proved useful for detecting insertion and deletion mutants. On page 561, Favis et al describe an alternate DNA array technology which uses a modified PCR reaction followed by ligase detection reaction (PCR/LDR), combined with "zip code" addressing to separate and identify the products on the microarray. Using the technique, they were able to detect small insertions and deletions in *BRCA1* and *BRCA2* genes from DNA samples of Ashkenazi Jewish individuals. *ND*



Review

Single nucleotide polymorphisms (SNPs), the most common form of human genetic variation, have been touted as useful markers for dissecting the genetic basis of complex diseases and predicting differences in drug response. It is hoped that disease profiling and chemopredictive testing will one day enable patients to be screened for disease and guide the therapeutic course of action—so-called pharmacogenomics. SNP discovery has now begun in earnest, with the US National Institutes of Health (Rockville, MD) starting work on a genome wide map of 100,000 markers and a consortium of 10 pharmaceutical companies and the Wellcome Trust planning to generate 300,000 publicly available SNPs within 2 years. While these efforts promise to rapidly collate SNP data, the feasibility of extensive SNP-based analysis of complex disease and drug response remains widely debated. On p. 505, McCarthy and Hilfiker discuss the practical issues in realizing the potential of SNPs for dissecting drug response and disease traits. Their review describes how patient sample size, SNP density and genome coverage, statistical significance, and data interpretation will be important in designing large-scale studies for the reliable identification fof genetic associations. *AM*



The ubiquitin/proteasome-dependent proteolytic pathway plays a role in diverse processes such as cell cycle progression, apoptosis, and antigen presentation by MHC class I, as well as clearance of damaged proteins during stress responses. Its involvement in pathological processes such as inflammation, neurodegenerative diseases, and cancer makes it a promising target for drug discovery. Masucci and colleagues (p. 538) now describe a reporter system for monitoring proteosome activity in living cells. They tagged GFP with sequences that target proteins for degradation by the proteosome. The tagged GFPs are normally degraded rapidly, but they accumulate in cells treated with proteosome inhibitors. These constructs should prove quite useful for designing high-throughput screens for identifying and optimizing novel inhibitors. *ND*