Gene therapy of hair follicles has has potential for treating disorders of the hair and skin, however, achieving high levels of gene expression remains a serious obstacle to therapeutic applications. In this issue, Cotsarelis and colleagues (p. 420) describe a new method that strikingly increases transfection efficiency of hair follicle cells. They grafted skin from a human scalp onto mice to create a model that faithfully recapitulates the characteristics of human follicle structure and hair cycle, and used this system to test the feasibility of topical liposomes for delivering DNA to the hair follicles. By monitoring the expression of β-galactosidase, they defined the parameters important for transfection, such as liposome composition, timing of application, and pre-treatment with depilation and retinoic acid. They found that their method targets hair progenitor cells, and so has the potential to affect the characteristics of the hair follicle should provide a valuable tool in the testing of genes for treatment of hair and skin disorders.

Accessorizing biomaterials

Fibrin is a natural biomaterial that has found uses in surgery and tissue engineering as a tissue sealant and matrix for cellular ingrowth. An important feature is its ability to be remodeled and replaced by the protease activities associated with cells during their migration and invasion. In this issue, Hubbell and coworkers (p. 415) confer additional morphoregulatory signals into fibrin by incorporating exogenous bioactive peptides into the matrix during its coagulation in vitro. Using the enzymatic activity of Factor XIIIa, they incorporated peptides from laminin and N-cadherin and showed that the modified matrices enhanced neurite extension and axon regeneration in a rat model of nerve

Cellular magnetism

By tracking cells' movements in whole organisms, scientists hope to learn how cellular migration contributes to processes such as immune response, angiogenesis, and embryogenesis. Magnetic resonance imaging (MRI) provides a way of doing this non-invasively and with cellular resolution. However, current methods require attaching magnetic beads to the cells' surface, which leads to rapid clearance of the labeled cell. Lewin and colleagues have overcome this obstacle, using the Tat peptide of HIV, which has been shown to mediate efficient internalization of proteins into cells. Reasoning that it might also mediate internalization of iron particles used as magnetic labels, they attached the peptide to a triple magnetic, fluorescent, and isotopic label, and showed that the label was efficiently taken up by cells including $CD34^+$ and neural progenitor cells. After injection into mice, the magnetic $CD34^+$ cells homed to bone marrow, and once the bone marrow was harvested, the cells could be detected by MRI at single cell resolution, and then recaptured with magentic separation columns. (See p. 282 and 410.)

Unleashing a killer protein

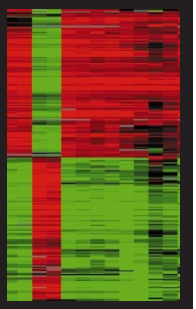
In this issue, Sautter and colleagues use a new approach for improving crop resistance to fungal infections. They took advantage of a so-called "killing protein" produced by a virus that infects the fungi, which can inhibit growth of fungal strains other than the host strain. They showed that expression of a *Ustilago* killing protein in wheat provided resistance to smut fungi responsible for large crop yields in economically important crops like wheat, maize, and oat (see p. 446).

Identifying DNA targets of chromatin proteins

DNA-binding proteins control many essential cellular processes such as transcription, DNA repair, and DNA replication, to name a few. Identifying the DNA sequences that bind such proteins can provide considerable insight to these processes, however, methods for doing so are cumbersome and prone to artifacts. Now on page 424, van Steensel and Henikoff describe a new way of identifying DNA sequences that interact in vivo with specific proteins. They tethered the *Escherichia coli* Dam protein, which mediates adenine methylation, to GAL4, a well-studied DNA binding protein, and expressed the fusion in *Drosophila*. When the GAL4 binds to DNA, it brings Dam along, which leads to an increase of adenine methylation in the region—all in vivo. By monitoring the methylation of different genetic loci, it is possible to determine which ones are targets for GAL4 binding. Combining this approach with microarray technology could allow genome wide screens to find the target genes of DNA-binding proteins.

Technical Reports

The completion of the Human Genome Project has made possible the comprehensive analysis of gene expression using DNA microarrays. A limiting factor for these studies is the amount of RNA available, particularly if the sample is derived from a surgical specimen. In this issue, Marincola and colleagues (p. 457) have devised a procedure that optimizes amplification of low abundance RNA samples by combining the template switching effect with antisense RNA amplification. Their results define the operational parameters of RNA amplification and should facilitate the use of DNA microarrays for applications where starting material is limiting, such as clinical samples from fine-needle aspirates or microdissection.



Chemical mutagenesis has not been used widely for reverse genetic strategies for the analysis of gene function due to the difficulty in detecting lesions, which are primarily point mutations. In this issue, McCallum et al. (p. 455) demonstrate that mutations induced by ethyl methanesulfonate (EMS) in *Aridopsis thaliana* can be easily identified by a denaturing high-performance liquid chromatography (DHPLC) single nucleotide point mutations by heteroduplex analysis. The method is efficient and automatable and should be applicable to any organism that can be chemically mutagenized.

Review

With the increasing application of systematic approaches to biology, new formats are needed for rapidly analyzing protein function on a large-scale. Increasingly, novel types of array are allowing thousands of peptides and proteins to be screened in one experiment, enabling researchers to carry out hypothesis-generating, as well as hypothesis-driven, experiments. In their review on p. 393, Emili and Cagney compare the strength and weaknesses of current array approaches with functional screening of libraries, describe the different ways of arraying peptides, proteins and living cells, contrast the particular strengths of each system, and suggest some potential future applications for the technology. While arrays are unlikely to replace traditional case-by-case studies of protein function, they are likely to prove extremely useful for facilitating the dissection of protein networks.