pieces of RNA are introduced into a cell, where they bind to a target RNA sequence, decreasing the expresion of that sequence and of its encoded protein. Xiao-Ya Chen and colleagues at the Shanghai Institutes for Biological Sciences in China used this technique to target an enzyme in cotton bollworms that confers resistance to the cotton plant's chemical defences. When plant leaves containing a trigger RNA were fed to the cotton bollworms, the worms were unable to make as much of their defensive enzyme against the cotton toxin, and their growth was stunted.

James Roberts of Monsanto Company in Chesterfield, Missouri, led a team that took its experiments all the way to the field. The group engineered corn plants that express short RNAs targeted against an essential enzyme found in the western corn rootworm. They then allowed corn rootworm larvae to dine on engineered and non-engineered plants for three weeks, and found that the engineered plants had much less root damage (pictured below, right) than their unprotected counterparts (left).

CHEMISTRY

Green cleaver

Science **318,** 783–787 (2007)

An iron compound that can selectively break carbon–hydrogen bonds in organic compounds looks set to pave the way for easier — and greener — syntheses.

The carbon–hydrogen bond is ubiquitous in organic molecules. Breaking it open to add other chemical groups generally requires a catalyst. Often, in more complex molecules, the bond has to be made more reactive and other parts of the molecule need to be shielded from activity before the catalyst can do its job. Both these steps involve potentially toxic reagents.

Christina White and Mark Chen at the University of Illinois in Urbana have unveiled an iron catalyst that can oxidize carbon–hydrogen bonds using only hydrogen peroxide, which is relatively benign. The catalyst can target specific bonds, even in complicated molecules. For each molecule, this selectivity is based largely on the inherent reactivity of the bonds and how accessible the bonds are to the catalyst.

GENETICS

Light release

Nature Chem. Biol. doi10.1038/nchembio.2007.44 (2007)

Manipulation of the genetic code has allowed researchers in San Diego, California, to produce proteins in which the amino acid serine is 'photocaged'. Changes to the genetic coding and translational mechanisms in the yeast *Saccharomyces cerevisiae* can be used to produce proteins in which an extra chemical group masks a specific serine residue, report Peter Schultz and his colleagues at the Scripps Research Institute and the Novartis Research Foundation. The masking group can later be removed by exposure to visible light.

By selectively illuminating such cells, and thus choosing when to expose the serine residues, the researchers were able to study the circumstances under which Pho4, a transcription factor, is phosphorylated. They suggest that this means of exerting fine control over protein function *in vivo* could have wide applicability, and expect in time to apply it to other amino acids and cell types.

MICROBIOLOGY

Divide and conquer

Chem. Biol. **14,** 1119–1127 (2007)

Researchers have found a new treatment that fights *Staphylococcus aureus* infections in mice by shutting down lines of communication among bacterial cells.

Antibiotic-resistant forms of *S. aureus* pose an escalating public health threat. Kim Janda and his colleagues at the Scripps Research Institute in La Jolla, California, report a new type of antibiotic: an antibody that binds to a signalling molecule *S. aureus* use to communicate with each other. This communication, known as quorum sensing, regulates the production of some proteins associated with virulence.

The antibody reduced production of one such protein, α-haemolysin, and inhibited the breaking apart of red blood cells in bacterial cultures. It also prevented *S. aureus*-induced skin lesions in mice, and fully protected mice against lethal doses of the bacterium.

JOURNAL CLUB

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An ecologist wonders how biotic feedback matters to global-change research.

I have increasingly been drawn to the question of how the biotic world responds to climatic change. In the face of environmental change, biology responds — organisms often compensate, adapt and change the nature of their ecologies. But exactly how important is this biological feedback to how ecosystems respond to a warmer world?

My colleagues and I have called for a need to focus on quantifying the importance of what we call the three As — acclimation, adaptation and assembly — on ecosystem-level processes such as carbon flux.

Acclimation is a plastic response by an organism to a change in the environment, whereas adaptation is the end result of natural selection in populations. Assembly is how species come to dominate a local environment and is the result of ecological interactions. We know that all these processes are affected by changes in climate. The end result of the three As is a group of species that live in a given location and control the flow of resources and energy.

These processes operate on differing time scales and have mostly been studied in isolation. However, two fascinating papers (K. Ishikawa *et al. New Phytol.* **176,** 356–364; 2007, and C. Campbell *et al. New Phytol.* **176,** 375–389; 2007) assess the role of both acclimation processes and between-species adaptation in the responses of photosynthesis and respiration to changing temperature. Remarkably, they find that acclimation and adaptative responses seem to compensate for temperature-driven changes in carbon flux.

Putting these two As together with how species assemble in ecological communities will probably reveal generalities in how evolutionary biology and plant-community ecology matters in global change.

Discuss these papers at **http://blogs.nature.com/nature/journalclub**