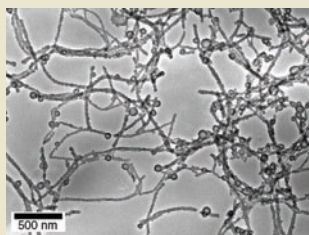


## Viruses for the electronics toolkit

The nascent field of nanobiotechnology continues to invent new ways of exploiting biological entities for bottom-up assembly of diverse structures and devices, often involving hybrids of organic and inorganic components. In a clever recent example, Belcher and colleagues have used viruses to fabricate batteries. The M13 virus is a long, cylindrical structure made of ~2,700 copies of the major coat protein wrapped around a single strand of DNA, with minor coat proteins forming the virus ends. Previously, Belcher's group had shown that the properties of M13 could be altered by mutagenizing the coat proteins and that the virus crystallizes into nanowires. The next step was to fashion the nanowires into a device. The authors added four glutamate residues, which bind metal ions, to the N terminus of the major coat protein. The mutated M13 was used to produce cobalt oxide nanowires, which were then mixed with other materials to form the electrode of a lithium battery. The M13 nanowires showed superior electrochemical performance compared with cobalt oxide nanoparticles produced by standard methods. Even better results were obtained with a cobalt-gold M13 virus generated by incorporating two different peptide motifs into the major coat protein. By taking advantage of the propensity of M13 to form liquid crystalline layers on polyelectrolyte films, the authors succeeded in producing thin, flexible batteries at the 10-cm scale. (*Scienceexpress*, 6 April 2006 10.1126/science.1122716) KA



## Customized plant miRNAs

The use of small interfering RNAs to downregulate plant genes has been hampered by off-target effects and may cause systemic spread of gene silencing. Now, two studies, from the laboratories of Yuval Eshed and Detlef Weigel, show how artificial versions of native micro (mi) RNAs can silence plant genes of choice, including targets not normally associated with RISC-mediated control. Microarray analysis indicates that these synthetic miRNAs act with very high specificity. Moreover, although their effects are apparently not completely cell autonomous, there is no evidence of significant transmission of miRNA-mediated silencing. The custom-made miRNAs described thus far target genes for which there are conventional *Arabidopsis thaliana* mutants with clear phenotypes, and they mediate comparable defects when expressed in tomato and tobacco. The availability of a web-based tool for automated design of synthetic plant miRNAs should facilitate the adoption of the approach for targeting genes of agricultural importance. (*Plant Cell*, published online 7 April 2006; 10.1105/tpc.105.040725; *Plant Cell*, published online 10 March 2006; 10.1105/tpc.105.039834) PH

## Improving on daptomycin

Heterologous expression of mixed-and-matched enzymatic domains has been shown to be feasible for polyketide antibiotics. Researchers have now exploited the approach to generate new analogs of daptomycin, a cyclic lipopeptide antibiotic synthesized by *Streptomyces roseosporus*

and approved by the Food and Drug Administration in 2003 for use against Gram-positive pathogens, including several enterococci and methicillin- and vancomycin-resistant *Staphylococcus aureus*. Baltz and colleagues achieved this by substituting entire subunits of the daptomycin nonribosomal peptide synthetase (NRPS) with NRPS subunits from lipopeptide pathways in two related bacteria, *Streptomyces coelicolor* and *Streptomyces fradiae*. They suggest that the efficient production of daptomycin analogs observed in *S. roseosporus* is most likely a result of the exquisite complementarity of the pathways chosen, as exemplified by the high conservation among 'docking' sequences of the different subunits, which ensures good integration of these elements. Besides successfully generating new analogs of daptomycin, the work lays the groundwork for further rational engineering of lipopeptide antibiotics. (*Chem. Biol.* 13, 269–276, 2006) GTO

## Wastewater genome

Publication of the sequence of an anaerobic, ammonium-oxidizing (anammox) bacterium, *Kuenenia stuttgartiensis*, promises to provide new insights into the role of bacteria in purifying wastewater and ultimately could suggest ways of improving sewage treatment. Anammox bacteria, which were only isolated in the past decade, short-circuit the traditional nitrogen cycle and have a major role in fixing nitrogen from ammonia and nitrites in marine environments and sewage. Because these bacteria are hard to culture, the authors recreated a microbial community in the laboratory by inoculating a bioreactor with sludge from a wastewater treatment plant. After one year of growth, this culture was enriched to ~73% with *K. stuttgartiensis*. Using an environmental genomics approach—reconstructing the genome directly from the bioreactor—the authors assembled the bacterium's 4.2-Mb genome. The genome contains 200 genes involved in catabolism and respiration, far more than most other bacteria, suggesting extraordinary metabolic versatility. In fact, *K. stuttgartiensis* was shown to respire both iron and manganese oxides in addition to ammonium. Genes likely to be involved in the metabolism of hydrazine, a highly toxic molecule, and ladderane biolipids, which impart great density and impermeability to the membrane, were also identified. (*Nature* 440, 790–794, 2006) TM

## Libraries expand the silence

New short hairpin RNA (shRNA) library designs promise to advance the utility of the technology for cancer genomics and to enable it to be applied in primary and nondividing cells. In a recent paper, Ngo *et al.* describe an inducible retroviral shRNA library capable of high-throughput identification of oncogenes. Traditionally, retroviral shRNA libraries have been restricted to identifying tumor-suppressor genes. But in the inducible shRNA library, any shRNA vector that reduces expression of a gene essential for cancer cell proliferation or survival is selectively eliminated after induction of shRNA expression. Abundance of each shRNA vector in the cancer cell population before and after induction of shRNA expression is measured by microarray quantification of a unique sequence in each vector. After introducing the inducible shRNA library into cell lines representing two distinct B-cell lymphomas, the authors successfully identified 17 shRNA vectors targeting 15 genes that were significantly depleted after induction of shRNA expression. In a related study, Moffat *et al.* substituted a lentiviral vector for the traditional retroviral vector and created an shRNA library targeting 22,000 human and mouse genes. In contrast to retroviruses, lentiviruses efficiently infect a wider range of cell types, including nondividing cell lines and primary cells. (*Nature* published online 29 March 2006, DOI: 10.1038/nature04687; *Cell* 124, 1283–1298, 2006) JWT

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