Flowers of solanaceous species.

DEVELOPMENT

When MADS, Don't Throw Tomatoes

Two types of MADS-box *APETALA3* (*AP3*) genes are found in members of the tomato family of plants: the *euAP3* group, which is critical for the proper development of the petals and stamens in angiosperms, and the less well-understood *TM6* group. *Petunia hybrida* and tomato (*Solanum lycopersicum*) each have a *euAP3* gene (*PhDEF* and *TAP3*, respectively) and a *TM6* gene (*PhTM6* and *TM6*). The *euAP3* and *TM6* lineages are hypothesized to have originated through a gene duplication event before the diversification of the major core eudicot lineages approximately 125 million years ago.

Rijpkema *et al.* and de Martino *et al.* have analyzed petunia and tomato mutants and found that in both species, *euAP3* genes maintain petal and stamen identity, whereas *TM6* genes function redundantly with *euAP3* genes in stamen development. Ectopic expression of *TM6* genes in *euAP3* lack-of-function mutants demonstrates that *TM6* genes are functionally redundant in both petal and stamen development. Rijpkema *et al.* also examined the promoter regions of *euAP3* and *TM6* regulatory sequences and found distinct yet highly conserved regions among *euAP3* core eudicot genes as well as in tomato and petunia *TM6* genes. Despite these similarities, the differences in expression and function between tomato and petunia *TM6* genes suggest that these genes have diversified functionally over a relatively short evolutionary time of 40 million years. — LMZ

Plant Cell **18**, 10.1105/tpc.106.042937; 10.1105/tpc.106.042978 (2006).

MOLECULAR BIOLOGY

Regulating the Regulators

MicroRNAs are small noncoding RNAs that regulate gene expression in eukaryotes by targeting homologous sequences in messenger RNAs, but less is known about how the synthesis of miRNAs is regulated. To begin with, miRNA genes are transcribed by RNA polymerase II. After transcription, miRNAs undergo a complex maturation process: (i) the primary miRNA, or pri-miRNA, is cleaved by the nuclear enzyme Drosha into a stem-loop precursor called a pre-miRNA, and (ii) the pre-miRNA is exported to the cytoplasm and cleaved by Dicer into the mature 22-nucleotide miRNA.

Mouse let-7 miRNAs are strongly induced during embryonic development, and the levels of pre-miRNA and mature miRNA change coordinately. In contrast, Thompson *et al.* show that for several of these same let-7 miRNAs, the levels of pri-miRNAs are constant during embryogenesis, suggesting that pri-miRNA maturation is being regulated at the Drosha processing step, and that this is also true for a number of other developmentally regulated mouse miRNAs. Intriguingly, the generalized down-regulation of miRNAs in cancer may be due to a block at the Drosha processing step. Together with previous evidence that miRNA levels can be controlled at the stage of Dicer cleavage, regulating pri/pre-miRNA processing provides a further mechanism for tightly constraining the expression of developmentally potent (and thus potentially dangerous) miRNAs. — GR

Genes Dev. **20**, 2202 (2006).

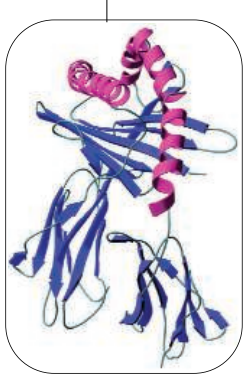
CREDITS (TOP TO BOTTOM): RUPKEMA *ET AL.*, *PLANT CELL* **18**, 10.1105/TPC.106.042937 (2006); ZENG *ET AL.*, *SCIENCE* **277**, 339 (1997)

VIROLOGY

Now You See It, Now You Don't

When a cell is infected with a virus, it can alert the host immune system by expressing telltale markers on its surface. Natural killer T cells recognize these markers and kill the infected cell, preventing viral replication and stopping infection. Yuan *et al.* studied cells infected with herpes simplex virus 1 (HSV-1) and found that the virus reduced the surface expression of CD1d molecules, the proteins that bind viral lipids and present them to natural killer T cells during antiviral defense. It did this not by reducing synthesis levels nor by promoting endocytosis from the cell surface, but instead by preventing the recycling of internalized CD1d to the cell surface and diverting CD1d to the lysosomal membrane. Reducing the levels of CD1d at the cell surface reduces the ability of the infected cells to stimulate natural killer cells and helps HSV-1 to evade the immune surveillance machinery, particularly during latent infections. — SMH

Nat. Immunol. **7**, 835 (2006).



Structure of CD1d.

CHEMISTRY

Cope in a Capsule

One goal of self-assembly research is to prepare synthetic structures of sufficient complexity to achieve the remarkable catalytic rate accelerations and selectivities characteristic of enzymes. Fiedler *et al.* explore the capacity of self-assembled tetrahedral capsules to catalyze a unimolecular reaction—the 3-aza Cope rearrangement of allyl enammonium cations. Each capsule is composed of four gallium centers bridged by catecholamide ligands and bears a 12-negative charge that attracts the cationic reagent to the interior but reduces affinity for the neutral hydrolyzed product.

The authors previously found that the capsules induced ~100-fold to ~1000-fold rate increases relative to the uncatalyzed reaction; temperature-dependent kinetic studies of an ethyl-bearing substrate suggested that the acceleration was due purely to decreased entropy of activation. Extending the kinetic studies to additional substrates reveals that although entropy factors continue to play a major role, in some cases the capsules reduce activation enthalpy as well. Analysis of nuclear

Continued on page 737

Continued from page 735

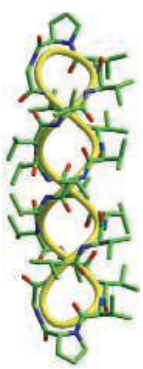
Overhauser effects in nuclear magnetic resonance spectra supports a mechanism in which the capsule binds substrates in particularly reactive conformations. Additional kinetic studies at variable hydroxide concentration suggest that the hydrolysis step takes place outside the capsule, through the intermediacy of a tight ion pair. Because the capsules are chiral, the authors suggest that further refinement may allow efficient diastereoselection or enantioselection in reactions of substrates that lack binding sites for more traditional molecular catalysts. — JSY

J. Am. Chem. Soc. **128**, 10.1021/ja062329b (2006).

CHEMISTRY

Pinning Down β Helices

The β-helical motif, which is formed by alternating D and L amino acids, has been pursued less often in small-peptide design than the more familiar α and 3_{10} helices, in part because the peptide can remain single-stranded or produce a mixture of parallel and antiparallel forms. Sastry *et al*. have designed and chemically synthesized β hairpin/β helix cyclic peptides with 5.6 residues per turn that form antiparallel helices in organic solvent. In the two peptides, two strands of either Val or Leu residues of alternating handedness are joined by two Pro-Gly hairpins and stabilized by 16 hydrogen bonds; circular dichroism spectroscopy confirmed that the sequences chosen create a left-handed Leu helix and a right-handed Val helix. Analysis of nuclear magnetic resonance spectra and amide vibrations in the infrared absorption spectrum indicated that the antiparallel helices are quite stable in solution, but that a variant with only one β hairpin exists in multiple conformations. The authors suggest that derivatives with more hydrophilic amino acids should exhibit similar stability in aqueous media. — PDS



β hairpin/ β helix motif.

CREDIT: SASTRY *ET AL., J. AM. CHEM. SOC.* **128**, 10.1021/JA062737F (2006)

J. Am. Chem. Soc. **128**, 10.1021/ja062737f (2006).

BIOPHYSICS

Spacing Out the Doughnuts

Recent innovations in fluorescence microscopy have brought within reach the goal of being able to image the internal workings of live cells at a resolution of 10 nm (see, for example, Betzig *et al.*, *Science* Express, Reports, 10 August 2006). Donnert *et al.* report the latest improvement in their approach, called stimulated emission depletion (STED) microscopy, which relies on an annular pulse that de-excites fluorophores around a central spot. In order to de-excite molecules in the doughnut-shaped area thoroughly and rapidly, relatively high intensities were needed, which increased the danger of photobleaching. They have now developed a paired-pulse delivery schedule (0.25 MHz) of the excitation (100 ps) and de-excitation (280 ps) beams, where the pulse duration is long enough to return excited molecules in higher singlet states to S_0 and the pulse frequency is low enough so that triplet states relax before the next pulse arrives. The reduction in data acquisition time is largely compensated for by a higher intensity de-excitation beam and an increase in fluorescence yield, with roughly one-sixth of all fluorophores in the spot being excited to S_1. — GJC

Proc. Natl. Acad. Sci. U.S.A. **103**, 11440 (2006).

COMPUTER SCIENCE

iTunes Meets Wikipedia

The organizing efficiency offered by searchable electronic databases has long been among the most useful features of modern computers. Compared with organizing text files, however, assembling a searchable multimedia database of recorded music is a daunting task. A musicologist would like to be able to type in "Mozart" and "piano sonata" and get as output a list of recordings sorted by performing artist and a selection of stored musical scores. The researcher might then like to synchronize each recording with the score so that when replayed, the recording would follow the score precisely as shown on the screen. Ideally, playing a few notes on an interfaced musical keyboard would cause the system to zero in on a particular passage.

Dunn *et al.* explain that such a fully functional system may be a decade away from realization. Nonetheless, their work on a system called Variations2 is gradually leading to more powerful music storage and retrieval environments, in which nontextual objects such as sound recordings are linked with graphical objects such as musical scores (which may exist in numerous editions) and the underlying sequences of musical notes. The researchers say that the next version, Variations3, will improve content-based searching of musical works and add better support for non-Western music. Such research could also provide valuable general strategies for navigating a wide range of nontextual data. — DV

Commun. ACM **49**, 53 (2006).

Published by AAAS

iTunes Meets Wikipedia

Science **313** (5788), 737.
DOI: 10.1126/science.313.5788.737c