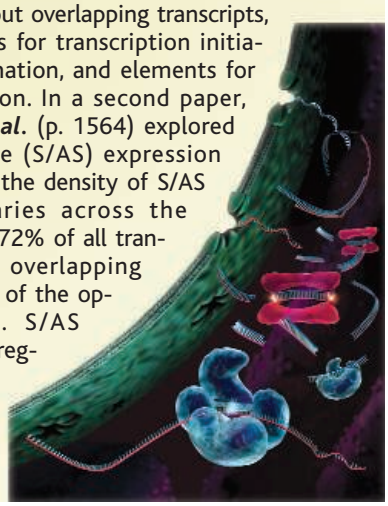
## Lapse in Understanding

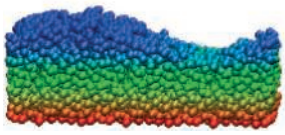
Some reconstructions of recent warming in the troposphere based on satellite data have indicated that the troposphere has warmed since 1979 (when the data were initially collected) at a rate considerably less than that, which should be expected from surface temperature measurements. Three studies (all published online 11 August 2005) reassess these data and reconstructions in favor of the surface temperature trends. **Mears and Wentz** (p. 1548) identify an error in the diurnal correction that has been applied to the satellite data, and derive a physically consistent one of the opposite sign, whose application brings into agreement a newer reconstruction of tropospheric warming, model calculations, and surface temperature measurements. **Sherwood *et al.*** (p. 1556) show that a spurious temporal trend was introduced into tropospheric temperature profiles recorded by radiosondes through changes in instrumentation made over time that involved solar heating of the instrument above ambient temperature. Correction for this bias brings many of the radiosonde data into better agreement with models and the surface temperature record, particularly in the tropics, where the disagreement between surface and expected tropospheric temperatures was most pronounced. **Santer *et al.*** (p. 1551) examined patterns of the amplification of surface temperature trends in the tropical troposphere using 19 different models. They show that the reconstructions used to argue that the troposphere was not warming are inconsistent with our understanding of the physical processes that control the vertical temperature structure of the atmosphere (the lapse rate).

## Mining the Mammalian Genome and Transcriptome

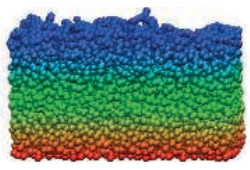
Analyses of the mammalian genome sequence and its corresponding transcriptome have revealed a complex assembly of information that provides great diversity through its varied sequence elements. **Hayashizaki *et al.*** (p. 1559) use a combination of approaches [complementary DNA (cDNA) isolation, 5′ and 3′-end sequencing of cDNAs, and ditag sequencing] to reveal a large number of novel cDNAs, noncoding RNAs, and proteins, as well as information about overlapping transcripts, alternative sites for transcription initiation and termination, and elements for splicing variation. In a second paper, **Hayashizaki *et al.*** (p. 1564) explored sense/antisense (S/AS) expression and found that the density of S/AS transcripts varies across the genome; about 72% of all transcription units overlapping with expression of the opposite strand. S/AS pairs can be coregulated or can be reciprocally or discordantly regulated.



## Hard but Smooth



High-energy carbon atoms can be deposited onto a substrate to form a hard diamondlike coating that can provide wear resistance in applications ranging from hard drive to hip joints. Despite the energetic conditions of their formation, these films are extremely smooth—the roughness can be as low as 0.1 nanometers on a lateral area of 1 square micrometer (equivalent of millimeter-scale bumps on a soccer field). Using a combination of atomistic and continuum modeling, **Moseler *et al.*** (p. 1545) show that when the carbon atoms are implanted, they generate particle currents that smooth out neighboring hills and valleys.



CREDITS (TOP TO BOTTOM): HAYASHIZAKI *ET AL.*; MOSELER *ET AL.*

## Twisting a Fine Wire

By linking a single-walled carbon nanotube to a macroscale metal block, **Meyer *et al.*** (p. 1539) have created a torsional pendulum whose end is visible in an optical microscope that rotates about a single molecule. When placed in a transmission electron microscope, the pendulum twists because of charging of the metal block. Oscillations set up by thermal effects can also be discerned. This experimental setup can also be used to determine the helicity of the carbon nanotube in diffraction experiments.

## Cut and Couple

In the Kondo effect, localized spins, such as magnetic impurities in nonmagnetic metal, can couple to conduction electrons and cause resistivity to increase with decreasing temperature. **Zhao *et al.*** (p. 1542; see the Perspective by **Crommie**) show that the effect of the magnetic moment of a single adsorbed magnetic atom can be changed by altering its chemical environment. Using a scanning tunneling microscope (STM) as a probe, they observed no Kondo effects when cobalt phthalocyanine (CoPc) was adsorbed on the (111) surface of gold. However, when they used the STM tip to dehydrogenate the Pc ligand, the local magnetic moment of the Co ion interacted with surface Au electrons to produce a Kondo effect with a high Kondo temperature (~200 kelvin).

## Small RNA Assay of *Arabidopsis*

Small noncoding RNAs, in the form of small interfering RNAs (siRNAs, intermediates in RNA interference) and microRNAs (miRNAs), play vital roles in eukaryotes' cell biology, but are by their very nature difficult to detect. **Lu *et al.*** (p. 1567) have now thoroughly characterized small RNAs in the plant *Arabidopsis* through a massively parallel signal sequencing of more than 2 million such RNAs. Although they identify many siRNAs, particularly from transposons, centromeric regions, and other repeats, few are associated with overlapping antisense transcripts, which suggests that antisense transcription may regulate gene expression mainly through transcriptional interference. They also identify a significant number of new miRNAs but generally do not find evidence for miRNA transitivity.

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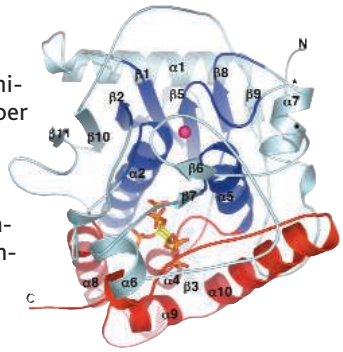
## Noncoding RNAs at Work

One type of the small noncoding RNAs (ncRNAs), microRNAs (miRNAs), are about 21 nucleotides in length and are believed to regulate gene expression either through messenger RNA (mRNA) cleavage or by translational repression. **Pillai *et al.*** (p. 1573, published online 4 August 2005) show that in human cells, the miRNA let-7 represses gene expression by inhibiting translation initiation of capped mRNAs, rather than through a degradation mechanism. This repressive machinery appears to be localized to cytoplasmic processing (P) bodies, where mRNAs are stored or degraded. A large fraction of eukaryotic genomes are transcribed into ncRNAs, some of which, such as miRNAs or the much larger Xist ncRNA, have known functions. However, the great majority of ncRNAs are of unknown functional significance. **Willingham *et al.*** (p. 1570) have developed a method for identifying functional ncRNAs—looking for evolutionary conservation and using a battery of cell-based RNA-interference assays—and have characterized the noncoding repressor of NFAT (NRON) that represses the transcription factor NFAT (nuclear factor of regulated T cells), probably though modulation of NFAT's cellular localization.

## Trapped by an Editor




A family of RNA editing enzymes, adenosine deaminases that act on RNA (ADARs), is important for proper neuronal function and are implicated in the regulation of RNA interference. **Macbeth *et al.*** (p. 1534) determined the crystal structure of human ADAR2 at 1.7 angstrom resolution. Surprisingly, inositol hexakisphosphate ($IP_6$) is buried within the fold of the enzyme core. Activity assays show that $IP_6$ is required for hADAR2 activity and for the activity of a yeast RNA editing enzyme, ADAT1.

## Small Takeover, Big Gain

Viruses exploit host functions in many ways in order to replicate. Identified functions now include taking over host-encoded microRNAs (miRNAs) that play a crucial role in RNA interference, a recently discovered mechanism of gene regulation. Studying the human pathogen hepatitis C virus (HCV), **Jopling *et al.*** (p. 1577) show that a host miRNA that is abundantly expressed in the liver, where the virus replicates, interacts with the 5′ noncoding region of the viral RNA. This interaction leads to an increase in HCV RNA and possibly contributes to viral persistence in the liver. Inactivation of this miRNA could be a useful therapeutic strategy for HCV, which is estimated to affect 170 million people worldwide.

## Similarities in Splicing

Group I self-splicing introns have been thought to be distinct from their group II cousins and messenger RNA (mRNA) splicing reactions in not generating a lariat (looped) intermediate that is subsequently removed from the spliced product. **Nielsen *et al.*** (p. 1584) show a group I–like ribozyme from the slime mold *Didymium iridis* also produces a lariat. The DiGIR1 ribozyme cleaves its RNA target to form a microlariat at the extreme 5′ end of its parent homing endonuclease mRNA. The lariat might function in an analogous manner to the cap found on regular polymerase II mRNAs. The evolution of the GIR1 ribozyme might parallel a possible step in the evolution of mRNA splicing. Biochemical studies of group 1 intron splicing have shown that both of its chemical steps require divalent metal ions, and several metal ligands have been identified. Mechanisms involving either two or three metal ions have been proposed. **Stahley and Strobel** (p. 1587) have determined the structure of an intron splicing intermediate that is active in catalyzing exon ligation. The active site contains two $Mg^{2+}$ ions that coordinate all six of the biochemically identified ligands. Thus, an RNA phosphotransferase can function through a two-metal-ion mechanism.

CREDIT: MACBETH *ET AL.*



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