EDITORS' CHOICE

edited by Gilbert Chin

BIOCHEMISTRY

RNA Structure Conservation

Telomere length is maintained by the ribonucleoprotein enzyme telomerase, which contains a reverse transcriptase activity that adds sequence repeats onto the ends of chromosomes. These tandem repeats help to stabilize the double-stranded DNA ends of chromosomes.

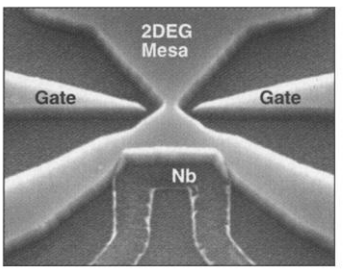
Chen *et al.* construct a secondary structure model for the RNA component of vertebrate telomerase based on phylogenetic comparisons. To do this they cloned and sequenced 32 new telomerase RNA gene sequences from five different classes of vertebrates. Sequence alignment revealed eight conserved regions, and aligned sequences were analyzed for nucleotide covariation in order to identify residues likely to form double helical base pairs. One of the conserved regions is the template that specifies synthesis of the telomere repeats. Immediately adjacent is a domain predicted to adopt a pseudoknot structure. This pseudoknot region is known to be essential for activity of human telomerase, and another conserved secondary structure, the Box H/ACA domain, may contribute to RNA stability and nucleolar localization. The vertebrate structure has a similar overall topology to that of ciliate telomerase RNA despite extensive sequence divergence and evolutionary distance, suggesting that these structural motifs are critical for telomerase function. — VV

Cell **100**, 503 (2000).

PHYSICS

Upon (Andreev) Reflection

Transistor devices containing a semiconductor-superconductor interface would combine the facile control of carrier concentration in the semiconductor with the low-dissipation and low-noise properties of the superconductor. As an electron passes from the semiconductor into the superconductor, it must form a Cooper pair with another electron. A hole, which is created to maintain charge-neutrality, is then retroreflected back along the path of the incoming electron in a process known as Andreev reflection. However, interfaces are not perfect, and most of the incident electrons are specularly reflected, which makes the magnitude of the induced supercurrent difficult to control and limits potential device applications.



At the semiconductor (2DEG)-superconductor (Nb) interface, holes are retroreflected through the gate.

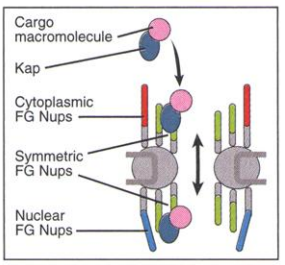
Jakob *et al.* have directly determined the probability of Andreev reflection. They use a point contact to inject a known current of ballistic electrons toward the interface region. The geometry of their device is such that only the retroreflected holes have a high probability of making it back to the point contact region for detection. With this technique, they determine an Andreev reflection probability of 20%. The quantification of Andreev reflection at the semiconductor-superconductor interface raises the prospect of designing and fabricating well-characterized integrated semiconductor-superconductor devices. — ISO

Appl. Phys. Lett. **76**, 1152 (2000).

CELL BIOLOGY

Nuclear Pore Mapped

The nucleus of eukaryotic cells is surrounded by a double membrane punctuated by pores through which proteins and RNAs travel. Rout *et al.* have conducted a systematic proteomics study of the yeast nuclear pore complex: separating protein components by chromatography and electrophoresis; identifying molecules by peptide sequencing and mass spectrometry; and localizing them by subcellular fractionation and immunofluorescence.



Side view of the nuclear pore.

The pore complex is composed of approximately 30 different proteins, which are assembled in a repeated motif to form two stacked rings. Filaments (FG Nups—nucleoporin proteins containing the phe-gly motif) extend from the pore complex towards the cytosol where they are thought to usher incoming nuclear proteins into the pore. On the nucleoplasmic side of the pore, similar filaments form a basket-like structure through which imported proteins enter the nucleus. The structure is remarkably symmetrical, given the vectorial nature of traffic across the pore. The authors suggest that the pore mediates transport by providing multiple high-affinity binding sites for karyopherins (Kap) on one side, which promote diffusion through the pore, after which the high-affinity interactions are inactivated and the cargo macromolecules released. — SMH

J. Cell Biol. **148**, 635 (2000).

GEOCHEMISTRY

Getting an Iron Grip

Earth's iron core creates our planet's magnetic field; the geodynamo is driven by convection in the liquid outer core that surrounds the solid inner core. The properties of iron at extreme pressures and temperatures, and particularly the structure of iron that is present in the core and its melting temperature, have been the focus of much study, as these data would limit the temperature of Earth's interior and would allow seismic observations of features in the core to be interpreted more reliably. Several papers in a special issue of *American Mineralogist* tackle these questions. In particular, Anderson and Isaak summarize some of the recent results (and debate) that surround the iron phase diagram, including the possible presence of a new fifth phase of iron that might be present at core conditions. They conclude that a fifth iron phase is likely but that its melting temperature is still uncertain. — BH

Am. Mineral. **85**, 376 (2000)

CHEMISTRY

Polymer Dynamics in a Pore

Unlike ion channels, which usually are specific for cations or anions and are gated by voltage or small molecules, the α-hemolysin from *Staphylococcus* assembles to form relatively large transmembrane pores (tens of angstroms) that allow many types of molecules to pass freely across the lipid bilayer of a cell. Howorka *et al.* have derivatized the hemolysin monomer with synthetic polymers in an attempt to modify and control their porosity. When polyethylene glycol (PEG, of 5000 daltons) was attached to the inside of a single subunit, the heptameric pore

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SOURCE: ROUT *ET AL.*, *J. CELL BIOL.* **148**, 635 (2000); JAKOB *ET AL.*, *APPL. PHYS. LETT.* **76**, 1152 (2000).

could readily accommodate only one such subunit along with six of the wild type—additional PEG molecules apparently exceeded the volume of the pore's vestibule and interfered with assembly. Single-channel recordings showed fluctuations in low conductance states (with lifetimes of tens of seconds) that were attributed to occupancy of the vestibule by the polymer chain. High-amplitude conductance fluctuations (millisecond duration) were observed and attributed to the movement of the polymer chain into the narrower transmembrane channel. These modified pores could find use for studies of polymer dynamics and may find applications in biosensing. — PDS

J. Am. Chem. Soc., in press.

OCEANOGRAPHY

Reconsidering Coral Paleothermometers

One method of estimating sea surface temperatures across glacial cycles during the Quaternary relies on the measurement of the ratio of Sr to Ca in the aragonite skeletons of coral. Studies of modern corals have shown that this ratio has a simple thermodynamic dependence. The accuracy of this proxy for temperature depends on the assumption that the Sr/Ca of sea water has been constant over the relatively short time scales of these cycles, which is based on the oceanic residence times of Ca and Sr of about one and five million years, respectively.

This assumption may not be correct—Martin *et al.* have found coincident variations in the Sr/Ca of planktonic and benthic foraminifera from the Pacific and Atlantic basins over the past three hundred thousand years. They suggest these variations were caused by changes in the Sr/Ca of sea water, and not by temperature. This would mean that coral Sr paleothermometry has overestimated the temperature increase of the surface ocean during glacial to interglacial transitions. — HJS

Geochem. Geophys. Geosys. **1**, paper 1999GC000006 (1999).

BIOPHYSICS

Controlling Turbocharged Glycolysis

Metabolism of glucose requires an initial investment of two ATPs, used to doubly phosphorylate the six-carbon skeleton, in order to reap a harvest of four ATPs on the way to two molecules of pyruvate. This arrangement runs the risk of creating a positive feedback loop unless the hexose kinase enzymes are allosterically regulated, as they are in most organisms. There is, however, no such regulation of these enzymes in trypanosomes (the causative agent of sleeping sickness), although they do contain an unusual organelle known as the glycosome that compartmentalizes the enzymes of glycolysis.

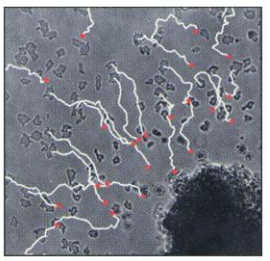
Using quantitative models of metabolism based on experimentally determined kinetic parameters, Bakker *et al.* now suggest that the presence of this organelle serves to regulate ATP and hexose phosphate concentrations. Within the glycosome, total phosphate is fixed, which functions to brake the initial glycolytic steps as hexose phosphate accumulates. Furthermore, these pools of phosphorylated intermediates provide a primed start for the organism to recover from a period of glucose starvation. Neither of these regulatory mechanisms were observed in a trypanosome modeled with the same enzyme parameters but lacking the glycosomal compartment. — GJC

Proc. Natl. Acad. Sci. U.S.A. **97**, 2087 (2000).

Science's stke

Shedding Light on Phototaxis

Under starvation conditions, the unicellular slime mold *Dictyostelium discoideum* aggregates into a multicellular mass referred to as a slug. Aggregation occurs as a chemotactic response to periodic cAMP signals initiated at the center of accretion. Although these cAMP waves coordinate chemotaxis, how light produces phototaxis has been unclear. Miura and Siegert demonstrate that light directly induces the release of cAMP from severed slug tips in culture, and that this is followed by migration of single slime mold cells toward the slug tip aggregate. As expected, this chemotactic response was specifically dependent on the presence of cAMP receptors; in addition, light increased the frequency of cAMP waves in *Dictyostelium* aggregates. Thus, phototaxis and light perception are mediated in the multicellular slug by the anterior tip. — JN



White tracks and red dots indicate movement and final positions of single cells.

SOURCE: MIURA AND SIEGERT, *PROC. NATL. ACAD. SCI. U.S.A.* **97**, 2111 (2000).

Proc. Natl. Acad. Sci. U.S.A. **97**, 2111 (2000).