Virology

Probing Neurodegeneration

Although great strides have been made toward the global eradication of poliovirus, this pathogen continues to be studied intensely in research labs, in part because history has shown that identification of the cellular pathways disrupted by viruses can provide fundamentally important insights into disease. One mystery yet to be solved is how poliovirus causes the motor neuron degeneration that leads to the muscle weakness and paralysis typical of poliomylitits.

A tantalizing clue has emerged from the work of Almstead and Sarnow, who have identified a potentially unifying molecular feature of poliomylitits and spinal muscular atrophy, an inherited neurodegenerative disease. Spinal muscular atrophy arises from loss or mutational inactivation of the gene encoding the survival of motor neurons (SMN) protein. Together with eight other proteins called Gemins, SMN is part of a dynamic macromolecular complex that facilitates the assembly of ribonucleoprotein complexes implicated in pre-mRNA splicing. The splicing complexes are built around a so-called Sm core of RNA-binding proteins, and patients with spinal muscular atrophy show reduced levels of Sm core assembly. The authors show that poliovirus infection inhibits Sm core assembly through viral-mediated proteolysis of Gemin3, a critical component of the SMN complex. The downstream effects of reduced Sm core formation on motor neuron survival have been contentious, but poliovirus may serve as a useful research tool for exploring this issue. — PAK

Chemistry

Aligned for Speed

In purple photosynthetic bacteria, a ring of bacteriochlorophyll molecules assembles through noncovalent interactions to form the light-harvesting antenna complex. The ultrafast energy transfer rates of such complexes can be approached in mimic complexes with covalently linked chromophores, but complexes more efficiently synthesized through self-assembly have exhibited slower rates because of nonoptimal alignment of the molecular dipoles. Kelley et al. prepared a zinc chlorophyll derivative and established through small-angle x-ray scattering (SAXS) that it self-assembles into tetramers (shown above) in toluene solution. Transient absorption spectra reveal a much faster Förster energy transfer rate in this complex than in prior porphyrin tetramers; however, the rate was still 10 times slower than in the fastest photosynthetic proteins, suggesting that the dipole alignment could be optimized further. — PDS


Ecology/Evolution

Hunting in Forests

The killing of large vertebrates by humans can have ramifications beyond the immediate effects on the prey populations themselves. There is growing evidence that harvesting of animals from tropical forests affects the entire ecological community. In particular, the dispersal of plant seeds is altered when their animal sowers are depleted by hunting; this in turn has long-term consequences for tree species composition in the forest. The outcomes may be unexpected: in some cases, hunting can actually increase the relative abundance of large-seeded plant species because it reduces seed predation pressure, as described by Beckman and Muller-Landau. The hunting of vertebrates can also affect invertebrate populations. For example, a reduction in the amount of dung directly stresses the populations of dung beetles. These and other sequelae of hunting in tropical forests, and the steps that might be taken to reduce hunting pressure, are discussed in 10 papers in a special section edited by Wright and Stoner. — AMS

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Applied Physics

To Know a Tortured Flow

When stresses induce flow of non-Newtonian fluids, such as paint or whipped cream, the fluid viscosity may depend on the shear strain rate and/or the length of time that the stress is applied. Common industrial processes in which polymer or surfactant solutions move through porous media also involve non-Newtonian flows. In these cases, the fluid properties depend on the local velocity gradients and hence the local pore structure; modeling based on macroscopic approximations tends to fail.

Sullivan et al. have developed a hydrodynamic lattice Boltzmann (LB) method for quantitative three-dimensional simulations of non-Newtonian flow through disordered porous media. The key to their method is the use of ³H magnetic resonance imaging to accurately model the porous media. The authors examined four fluids: two Newtonian and two that showed a reduction in viscosity with increasing strain rate. For the flow profile across a transverse two-dimensional slice, the difference between the experimental and simulated flow values was small (~4% of the average velocity). In comparisons between two fluids with similar overall flow rates, the more shear-thinning fluid showed increased dispersion, with more high-velocity

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channels as well as more stagnant ones, consistent with macroscopic observations. — MSL


CLIMATE SCIENCE

Melting Faster

Observations of the extent of Arctic sea ice in September—at the end of the melt season, when ice coverage is at its annual minimum—have shown a large decline over the past several decades, consistent with current qualitative understanding of natural variability and the effects of a warming climate. Nearly all climate models predict that September Arctic sea ice extent will continue to decline through the 21st century, largely in response to rising concentrations of atmospheric greenhouse gases. How well do observations and models agree, though? To answer that question, Stroeve et al. compared the output of the more than a dozen models participating in the Intergovernmental Panel on Climate Change Fourth Assessment Report that calculated sea ice. They found that nearly all of the models overestimated annual minimum Arctic sea ice area, in many cases by large amounts. These findings have two important implications: first, that the effect of rising greenhouse gases may have been more important than has been believed; and second, that future loss of Arctic sea ice may be more rapid and extensive than predicted. — HJS


VIROLOGY

Shifting Landscapes

Influenza epidemics are thought to emerge as a result of escape from host immunity as the viral genome mutates along a trajectory of antigenic drift. However, a puzzle for influenza epidemiologists is the limited diversity of observed antigenic types. Recker et al. present a model in which successive antigenic types emerge independently of the mode or tempo of mutation in a cyclical manner. The model is consistent with data from hemagglutination inhibition assays of H3N2. The authors suggest that rather than virus mutation driving the epidemiology of influenza, the changing landscape of host population immunity governs whether and when epidemics emerge. Much of the epidemiology of influenza, such as the re-emergence of an antigenic type, is probably missed in routine clinical data based on detection of symptoms. For instance, data from poultry workers chronically exposed to avian influenza suggest that they enjoy a significant degree of cross-protection against the lethal effects of H5N1. This shift in perspective could have important implications for the way we monitor influenza virus for epidemic prediction and vaccine design. — CA


<< Who You Are Versus Where You Are

The ability to identify essential components by network analysis may provide one means of ranking targets for disrupting specific cellular processes. Yu et al. have assessed the relative importance of being a hub (that is, being a highly connected node) in comparison to being a bottleneck, a node that serves as a conduit for nonredundant paths through the network. These attributes do overlap, but they were able to find all four types of nodes in large-scale protein-protein interaction maps: hub-bottleneck, nonhub-bottleneck, hub-nonbottleneck, and nonhub-nonbottleneck. For instance, in signaling networks, hub-bottlenecks and nonhub-bottlenecks were likely to be encoded by essential genes, whereas hub-nonbottlenecks were not. Thus, being a bottleneck may be a better indicator of necessity than the degree of connectedness. A refinement of the nonhub-bottleneck nodes was achieved by dividing them into those that participate in permanent interactions, such as those that hold multisubunit complexes together, versus those that mediate transient protein-protein interactions. Not surprisingly, permanent nodes were more likely to be encoded by an essential gene than were the transients. Furthermore, the authors suggest that nonhub-bottlenecks are key to pathway crosstalk. Cak1p, which is encoded by an essential gene in yeast and is a cyclin-dependent protein kinase–activating kinase, is offered as an example of a nonhub-bottleneck that is the critical link between two signaling pathways: regulation of the cell cycle and sporulation. — NRG

Shifting Landscapes
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