Astronomy

Light-bending reveals stellar mass

Astrophys. J. (in the press); preprint at http://arXiv.org/abs/astro-ph/0405124 (2004)

It's not easy to deduce a star's mass. At present, it is usually done indirectly, by using spectroscopic measurements to determine the star's radius and surface gravity. Direct mass measurements are possible for binary stars via their orbital parameters, but the only single star for which a truly direct mass measurement has been made is the Sun. That was done by looking at how the Sun bends light coming from a distant source: essentially the same measurement that Eddington made in 1919 during a solar eclipse, confirming Einstein's general theory of relativity.

Andrew Gould *et al.* have now used this same principle to measure the mass of a star 2,000 light years away in our Galaxy. This star acted as the lens for a microlensing event in 1993, denoted MACHO-LMC-5, when it crossed the path of a more distant star and focused that star's light. This observation, part of a project to look for dark-matter candidate objects called MACHOs by their gravitational-lensing effect, has only now been analysed in detail. The MACHO-LMC-5 lens is a dim red star with an apparent mass about one-tenth that of the Sun (±17%). **Philip Ball**

Evolution

Dark prospects

Biol. J. Linn. Soc. **82,** 359–366 (2004)

With the realization that the sooty consequences of Europe's industrial revolution favoured the dark form of the peppered moth (*Biston betularia*) over its light-coloured counterpart (pictured side by side), the insect entered the textbooks as a stalwart example of natural selection. But it now seems that the dark form, called *carbonaria*, is nearing the end of the line.

L. M. Cook and colleagues analysed surveys of the frequencies of the pigmented and original typical forms, and of an intermediate form called *insularia*. The surveys were carried out in Britain during the later years of the twentieth century, when numbers of *carbonaria* were declining in response to falling pollution levels. Cook *et al.* brought mathematics to bear on the surveys, to estimate the changing prospects of the different forms in various times and places.

The *carbonaria* form is in terminal decline, they conclude. But the same cannot be said for *insularia*, which should continue to be viable even in the post-industrial environment. What's more, although it has been suggested that heavy pigmentation can be triggered by metal salts in the larval diet, the authors believe that the results indicate that the origin of the different pigment patterns is entirely genetic. **Michael Hopkin**

Analytical chemistry

How low can you go?

Anal. Chem. doi:10.1021/ac049657j (2004)

A sensitivity record for detecting trace amounts of molecules in extremely dilute solution has been shattered. Sunia A. Trauger *et al.* report that their mass-spectrometry approach can detect 800 yoctomoles (800×10^{-24} moles) of des-Arg^9-bradykinin, a peptide commonly used as a sensitivity standard. That's equivalent to only 480 molecules, and represents a 50-fold greater sensitivity than previously obtained by mass spectrometry.

Using the technique known as desorption/ionization on silicon, or DIOS, the molecules are first adsorbed onto a porous silicon wafer, then desorbed and ionized by a laser pulse. This detaches the molecules from the silicon surface without breaking the complex structure apart. The charged peptide then flies through a conventional mass spectrometer, which calculates the mass of the molecule based on its 'time of flight'.

The authors' key breakthrough is the addition of fluorinated 'chemical tethers' to the silicon surface which help grab even the most elusive molecules from solution. The authors claim that this system could detect tiny amounts of compounds from a complex mixture by tailoring the tether to bind selectively to the desired target molecule. **Mark Peplow**

J. MASON/ARDEA

Genetics

First aid for flies

PLoS Biol. **2,** e239 (2004)

Wound healing is essential for an organism's survival, but the genetic signals that control the process are unclear. Michael J. Galko and Mark A. Krasnow have developed a fly model of larval wound healing and used it to elucidate key regulatory genes.

The duo stabbed fruitfly larvae with needles to create non-fatal puncture wounds. Normally, a scab forms and neighbouring epidermal cells spread across the wound to regenerate the skin. But when the JNK (for c-Jun N-terminal kinase) signalling pathway is inactivated, although scabs form, epithelial migration is blocked. Moreover, larvae with defects in a gene needed for the generation of crystal cells — a type of blood cell — could not form scabs properly.

The study hints that cellular aspects of wound healing are coordinated by multiple, separate genetic signals. Cellular and genetic parallels exist between wound healing in flies and in mammals, so the researchers speculate that the process might be an ancient response that diversified during evolution. **Helen Pilcher**

Biological chemistry

Kinase connections

J. Am. Chem. Soc. doi:10.1021/ja048659i (2004)

Protein phosphorylation is a major mechanism for signalling within a cell. But it's no easy matter to trace the biochemical pathway back from a known phosphorylation site to the kinase enzyme that catalyses the phosphate transfer. Dustin J. Maly and colleagues have tackled this problem, and come up with a new method for identifying upstream kinases.

The authors set out to develop a way of linking biologically relevant substrate–kinase pairs. To ensure specificity for the desired phosphorylation site, the 'phosphoacceptor' amino acid (serine or threonine) is replaced with cysteine. The crosslinking reagent is an ATP analogue, which is designed to form a link in a kinase-catalysed reaction with both a lysine amino acid at the enzyme's active site and the cysteine of the modified substrate. As a proof of principle, Maly *et al.* demonstrate specific crosslinking of kinase and peptide partners, and reactivity of the crosslinker with a range of serine/threonine kinases.

The next steps will be to identify previously unknown kinase–substrate pairs, and to extend the method for use *in vivo*. **Joanne Kotz**