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COVER The olfactory bulb of a mouse (image width, 0.5 mm). Axons of olfactory sensory neurons terminate in globose structures, glomeruli, of which there are 1800 per bulb. The vomeronasal nerve carrying pheromone information terminates separately in a diffuse structure, the accessory olfactory bulb (top). Olfactory neurons can be stained blue in this strain of genetically manipulated mice. For recent advances in olfaction, see the special section beginning on p. 703. [Photo: P. Mombaerts]

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THIS WEEK IN SCIENCE

edited by PHIL SZUROMI

SEMICONDUCTOR LASERS: TWO IN ONE

Unipolar devices have an advantage over bipolar ones in that they can be operated independent of the polarity of the applied voltage—they are bidirectional. Gmachl *et al.* (p. 749) have now designed quantum cascade lasers that can be operated bidirectionally. Moreover, through careful design of the series of quantum wells that make up the injection region of the laser, they show that a tailored asymmetry can produce lasing at two different wavelengths, depending on the polarity.

AMYLOID SECRET (ASE) REVEALED

Alzheimer's disease is characterized by the progressive formation in the brain of insoluble deposits containing the amyloid β peptide (A β). This peptide is generated when the amyloid



precursor protein (APP) is cleaved by two distinct and long-sought proteases, the β - and γ -secretases. Vassar *et al.* (p. 735; see the news story by Pennisi) have identified a transmembrane aspartic protease, beta-site APP cleaving enzyme, or BACE, that has all of the known characteristics of the β secretase. Future development of BACE-specific inhibitors will allow testing in animal models of A β 's role in Alzheimer's disease and may lead to new treatments for the disease.

INORGANIC ELECTRONICS FROM SOLUTION

The majority of inorganic electronic devices used today are fabricated in a series of steps that require deposition of inorganic species from the gas phase. These processes are performed at relatively high temperatures and are often rather expensive. Ridley *et al.* (p. 746) introduce an alternative, and potentially cheaper, all-solution route that takes advantage of the

reduced melting point of nanocrystals. Cadmium selenide (CdSe) nanoparticles, formed by mixing cadmium iodide and sodium selinide, were suspended in pyridine. The resulting solution was then printed onto a substrate, and a subsequent low-temperature annealing process drives off the pyridine to leave behind a thin film of CdSe. The authors demonstrate the potential of such a process by fabricating thin film transistors with good electrical characteristics.

ICED SEAS

Repeated abrupt climate changes occurred during the long buildup of ice sheets toward the Last Glacial Maximum (LGM). Detailed oceanic records of these events and their effects on sea surface temperatures (SSTs) are scarce, yet important for understanding the mechanisms and extent of abrupt climate change. Sachs and Lehman (p. 756) now provide a high-resolution marine record from the Bermuda Rise of SSTs spanning the period from 30,000 to 60,000 years ago. The record shows several cases where SSTs increased abruptly by 2° to 5°C, which is comparable to the change observed from the LGM to the Holocene. These events parallel those seen in Greenland records. The periods of warming appeared to have been unstable and were followed by either abrupt or continued gradual cooling. Thus, the abrupt climate changes seen in the ice core records affected tropical oceans.

SLOWING GETTING MORE COMPLEX

The issue of complexity in evolution has generated interest in biology, but it has been notoriously difficult to measure the dynamics of complexity in the fossil record. Saunders et al. (p. 760) describe the evolution of complexity in the septal sutures of an extinct group of mollusks—ammonoids—in more than 500 genera during the 140 million years from the Devonian to the Triassic, a period that includes three mass extinctions. Although mass extinctions tended to eliminate more complex structures, the largescale evolutionary trend was toward increased complexity. Thus, they show that two non-random evolutionary trends acted in opposition—a withinlineage-driven bias for increased suture complexity and an among-lineage differential extinction of more complex forms during times of biotic crisis.

OLDEST DINOSAURS?

The Middle to Late Triassic (about 225 to 230 million years ago) was a crucial period in the early evolution of dinosaurs, yet little has been known about the faunal composition at that time. Flynn et al. (p. 763) now report the discovery of a fossil fauna in Madagascar that contains newly identified dinosaur and eucynodont (mammallike reptiles) taxa. Their discovery represents a major new source of terrestrial vertebrate fossils for a time period that is sampled poorly elsewhere in the world; the dinosaurs may be more ancient than any others worldwide; and the recovery of the eucynodont fills in a 170-million-year gap in the fossil record of the region.

STABILITY WITH MATURITY

Signaling through the transmembrane protein Notch occurs in a variety of tissues in order to determine cell fates during development. Šestan *et al.* (p. 741; see the Perspective by Chenn and Walsh) show that Notch signaling is also important in the already differentiated neurons of the mature cerebral cortex. The various protein components of the signaling pathway are found in dendrites and control dendrite extension.

PROVIDING FEEDBACK

Further clues into the regulation of circadian clocks are the subject of two reports. In plants and insects, cryptochromes (CRYs) are activated by light, and in the fruit fly Drosophila, CRY blocks the negative feedback action of the PER-TIM complex. Griffin et al. (p. 768) show that CRY1 and CRY2 play a central role in the mammal clock, but in a light-independent fashion-they appear to regulate transcriptional cycling of *Per1* by contacting both the activator and its feedback inhibitors. In Drosophila, three of the critical clock genes, period (per), timeless (tim), and Drosophila Clock (dClk), are expressed rhythmically. In their study of the cycling of dClk, Glossop et al. (p. 766) have found that the molecular clock in Drosophila is composed of two interlocked negative feedback loops-the per-tim loop, which is activated by the dCLK and CYCLE proteins and repressed by PER-TIM, and the dClk loop, in which these proteins exert the opposite effect.

INTERFERING WITH TGF- β

Unregulated cell growth results in tumor production; therefore, it is important to identify developmental factors that regulate cell growth. Transforming growth fac-CONTINUED ON PAGE 643

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tor- β (TGF- β) regulates cell growth and differentiation through receptor-mediated phosphorylation of Smad proteins. These Smad proteins in turn form protein complexes and enter the cell's nucleus to activate the transcription of target genes. Stroschein et al. (p. 771; see the news story by Vogel) have identified a new player, SnoN, in TGF- β signaling. In the absence of TGF- β , the SnoN oncoprotein binds to a Smad2/Smad4 complex and recruits a transcription co-repressor, thus inhibiting transcription activation. When TGF- β is present, Smad3 triggers the degradation of SnoN and transcription activation resumes. Finally, a negative-feedback mechanism is present in which TGF- β stimulates SnoN production, which then represses the transcription activation function of the Smad complex once again. SnoN is found in various carcinomas. Hence, the transforming activity of SnoN may be explained by its interference with the role of TGF- β in inhibiting cell growth.

TO LIVE OR LET DIE

The release of intracellular calcium (Ca²⁺) can trigger signals that lead to cell survival or to cell death; two reports illustrate how the same transcription factor, MEF2, which functions in the differentiation of skeletal muscle, can play different roles in the survival of neurons and T cells. During development of the mammalian brain, neurons that make proper synaptic connections and receive signals from other cells experience an increase in the intracellular Ca2+. This Ca2+ influx promotes cell survival or resistance to cell death. Mao et al. (p. 785) present evidence that MEF2 mediates the pro-survival effects of Ca²⁺ in cultured neuronal cells from the rat cerebral cortex. The increase in Ca²⁺ apparently causes activation of the p38 mitogen-activated protein kinase, which may directly phosphorylate and activate MEF2. Neuronal survival thus appears to be modulated through transcriptional regulation by MEF2, as well as through posttranslational changes in components of the cell death machinery. Activation of mature T cells eventually leads to their demise. It is thought that expression of the Nur77 orphan steroid receptor, whose transcription is dependent on Ca2+, the phosphatase calcineurin, and the transcription factor MEF2, mediates this apoptosis. Youn et al. (p. 790) have begun to elucidate the regulation of Nur77 expression and T cell apoptosis. Endogenous MEF2 is bound by Cabin 1, an inhibitor of calcineurin. When intracellular Ca2+ increases, calmodulin

competes for binding to Cabin 1 at the same site as MEF2 and forces the release of MEF2, which makes it available for assembly into the transcriptional complex.

SOME DISASSEMBLY REQUIRED

The dynamics of the mitotic spindle is regulated in part by katanin, an enzyme that localizes to centrosomes. However, just how this AAA-type adenosine triphosphatase severs microtubles of the spindle has been unclear. Hartman and Vale (p. 782) now reveal the mechanism by which katanin forms a stable multimeric ring. Katanin oligomerization is driven by binding to its substrate, microtubules, and by binding to the nucleotide ATP. Hence, microtubules that comprise the mitotic spindle may assist their own disassembly by serving as a scaffold onto which katanin assembles.

ACCUMULATING DAMAGE WITH AGE

One hypothesis for the cause of aging is that mutations accumulate in mitochondrial DNA (mtDNA). However, previous searches, which have generally studied protein- or RNA-coding regions of mtDNA, have yielded numerous types of age-related mutations, but these occur only at low frequencies (a few percent). Michikawa et al. (p. 774; see the news story by Pennisi) have studied the main control region for replication of mtDNA and found frequent point mutations in normal older subjects that were not found in normal young subjects. In particular, a TG transversion was found in up to 50% of the mtDNA molecules from 8 of 14 older subjects that did not appear in mtDNA of 13 younger subjects. Longitudinal studies of three individuals help show that these mutations are not inherited.

STRUCTURAL PROBE INTO IRON METABOLISM

The transferrin receptor (TfR) delivers transferrin-associated iron into cells for use in a variety of physiological processes, including cell growth. The receptor also binds HFE, the protein that is defective in human hereditary hemochromatosis, an iron storage disease that affects 1 in 300 individuals of northern European origin. Lawrence et al. (p. 779) determined the three-dimensional crystal structure of the extracellular domain of TfR. The structure revealed a monomer of three domains, one of which resembles carboxy- and aminopeptidases. This work provides a structural foundation for future studies of how iron uptake and release are controlled in the cell.



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detected simultaneously with the gammaray emissions; for a brief moment, this optical emission became as bright as 10 million type Ia supernovae (7).

The ability to determine the location of and distance to a GRB and observe its burst and decay in detail at a variety of different wavelengths has allowed astronomers to test GRB models. An early model, developed long before the present observations, proposed that GRBs were caused by a shock

wave emerging from the photosphere of a supernova (3). However, this model was soon discarded, as the GRB discovery paper already showed that there was no known correlation of GRBs with observed supernovae. Now after detailed studies of several GRBs in the late 1990s have revealed more information, theorists propose a connection between GRBs and supernovae.

There are at present two main models for GRBs. In the first, two compact stars (such as a neutron star and a black hole) coalesce (8). In the second, the core of a presumably very massive star collapses, leaving behind a black hole surrounded by a solar mass accretion disk (9). In this second, so-called collapsar model, the GRB is produced by a relativistic jet that pierces through the exploding star along its rotational axis. In addition to the fast GRB, a much slower (~10⁴

km/s) outflow is produced, giving rise to thermal emission from an expanding photosphere, that is, a supernova. If this model is correct, one would thus expect a (relatively weak) supernova to be apparent in the afterglow light curve of GRBs.

The first direct evidence for a connection between GRBs and supernovae came from observations of GRB980425, which occurred on 25 April 1998 (see figure on previous page). The BeppoSAX satellite determines an area called the error box, in which a GRB must have occurred. The error box for GRB980425 also contained a supernova, SN1998bw, located in a spiral arm of galaxy ESO 184-G82 (10). This galaxy lies at a distance of ~40 megaparsecs from Earth, cosmologically speaking just around the corner from the Milky Way. GRB980425's energy budget was quite small, a factor of $\sim 10^5$ smaller than that of normal GRBs. The probabili- $\frac{1}{2}$ ty of finding a supernova as bright as SN1998bw that would explode within a day of the burst inside the error box of GRB980425 is on the order of 10^{-4} , and day of the burst inside the error box of

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thus a physical association between the two seemed likely (10). Some researchers have rejected the association, because of the presence of a faint x-ray source in the GRB error box (which does not coincide with the supernova) that could be the GRB afterglow. But a recent analysis of this xray source by Pian et al. (11) shows that it is unlikely to be a GRB afterglow.

Independent of its association with the GRB, SN1998bw was a remarkable event.



Afterglow. R-band light emission of GRB980326 as measured by various sources superimposed on a relatively faint supernova light curve (red) at a redshift of about 1, which fits the data well.

It is by far the most luminous supernova observed to date at radio wavelengths, and its properties indicated the presence of a mildly relativistic outflow at about 90% the speed of light (12). It has been classified as a type Ic supernovae; that is, hydrogen and helium are absent in its spectra. Such supernovae are believed to have lost their hvdrogen- and helium-rich envelope in a strong stellar wind or as a result of mass transfer in a binary star. The optical light curve and spectra of SN1998bw indicate that the exploding star was a CO star of about 10 solar masses, whose core collapse probably left a black hole. The amount of radioactive ⁵⁶Ni produced in the event has been estimated to be ~ 0.75 solar masses, an order of magnitude higher than that of typical type Ic supernovae, with a total explosion energy of several 1052 ergs (13).

A recent study (14) has been able to fit the decay properties of GRB980425 and SN1998bw with a model similar to the collapsar model.

Recently, evidence for a second GRB coinciding with a supernova was found in

the case of GRB980326 (14). Several weeks after the burst, the afterglow brightened by a factor of 60, compared with the extrapolation of the early power law decay (see figure on this page). Afterward, the flux decay continued, showing that the flattening of the light curve does not reflect the steady light of a host galaxy. Bloom et al. (14) successfully modeled the light curve of GRB980326 with a combination of a power law afterglow and the light curve of SN1998bw, redshifted to about 1. The very steep afterglow decay of GRB980326 can be explained by a blast wave propagating in the wind of a massive star.

A similar connection between GRBs and supernovae was recently suggested (15) for the optical light curve of GRB970228, the first GRB to be optically identified. In this case, the redshift is known, and the only free parameter in the fit to the light curve is the exponent of the power law component. Chevalier and Li (16) have shown that after subtraction of the supernova contribution, the light curve of GRB970228 is also steep and best explained by an explosion in a massive stellar wind, lending further support to the association between GRBs and supernovae.

The exciting consequence of these recent studies is that at least some GRBs, and perhaps all of them, originate from the core collapse of very massive stars. The supernova connection provides a direct link between GRBs and crucial events in the evolution of massive stars and galaxies. This framework for describing GRBs promises a rapid increase in our understanding of this violent phenomenon.

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