Astronomy

The legacy of a lonely life

Neutron stars are extremely dense, compact stars consisting mostly of neutrons. They are thought to be the hot remains of a supernova explosion — when an old massive star collapses in on itself. Most known neutron stars are either pulsating (pulsars) or have a close companion.

There are supposed to be as many as a billion lone neutron stars zooming about the Milky Way, but the first isolated, non-pulsating neutron star was discovered just five years ago by Fred Walter of the State University of New York at Stony Brook (*Nature* **379**, 233–235; 1996). The initial X-ray discovery was confirmed by optical data from the Hubble Space Telescope (*Nature* **389**, 358–360; 1997). Last week, at a meeting of the American Astronomical Society in

Honolulu, Hawaii, Walter revealed the latest Hubble observations of this extraordinary object (*The Astrophysical Journal*, in the press).

The extreme densities of neutron stars offer a natural laboratory for exploring the 'equation of state' of nuclear matter — the relationship between pressure, temperature and radius in the atomic nucleus. Although the first optical measurements of the neutron star gave Walter a fairly good idea of its radius and distance, he needed to know its parallax to be sure. Parallax is the apparent motion of nearby objects, when seen against the background of more distant ones. As the Earth orbits the Sun, the positions of nearby stars shift slightly, with a maximum every six months.

From observations over three years (see image), Walter calculated a distance of 200 light years for the star, making it the closest known neutron star to Earth. He found its radius to be just 11 km; together with the mass this places constraints on the nuclear equation of state. Walter's results also show that the star is speeding away (at about 108 km s^{-1}) from a group of stars known

as the Upper Sco OB association, from which it was probably ejected a million or so years ago. When combined with the X-ray and optical observations, this date allows us to estimate how quickly neutron stars cool, which for this star seems to be faster than theoretical expectations. Quite a legacy for what was once just another mystery X-ray source.

Leslie Sage

NASA/E. M. WALTER

On page 354 of this issue, Adams *et al.*³ pose the question, "During the evolution of a particular eukaryotic lineage, how many times and how often has a given mitochondrial gene been relocated from organelle to nucleus?". In the case of angiosperms (flowering plants), the answer is, "Very many times and very often, indeed".

Even the most gene-rich mtDNAs encode at least ten times fewer genes than the smallest bacterial genomes. So most of the reduction in mitochondrial genome size and gene content is assumed to have occurred early in mtDNA evolution. However, the extremely variable gene content of contemporary mitochondrial genomes implies that mitochondrial gene loss has been an on-going process. By mapping gene losses onto phylogenetic trees, we can infer that the same mitochondrial gene has been transferred to the nucleus in separate events in different eukaryotic lineages⁴. Individual instances of mitochondrion-to-nucleus gene transfer have been well documented⁵. Up to now, however, we have had little appreciation of the overall frequency and timing of such gene relocations during mtDNA evolution.

Adams *et al.*³ report the remarkably frequent loss from angiosperm mtDNA of the gene encoding ribosomal protein S10 (a component of the mitochondrial ribosome) and the transfer of this gene (*rps10*) to the nucleus. Their results conjure up a picture of an evolutionary rapid-transit system, in which *rps10* is being continually and frequently transported from the mitochondrial to the nuclear genome in different groups of

angiosperms — and at a dizzying pace in evolutionary terms.

The authors used part of the *rps10* gene as a hybridization probe to score the presence or absence of this gene in DNA extracted from 277 angiosperms representing 169 families. The lab concerned has creatively exploited this valuable resource in other studies^{6,7}. The approach works well in plants for two reasons. First, there are many copies of the mitochondrial genome. Second, angiosperm mitochondrial genes evolve very slowly compared with single-copy nuclear genes — not to mention their counterparts in the mitochondria of animals, fungi and protists.

When plotted onto a phylogenetic tree of the angiosperms examined, the hybridization results indicated a loss of *rps10* on 26 separate occasions. In 16 of these cases, the authors amplified a nuclear *rps10* counterpart (not detectable by hybridization) using the polymerase chain reaction. Because a single mitochondrion-to-nucleus transfer of *rps10* could conceivably be followed by many independent losses of this gene from the mitochondrial genome, several of the nuclear *rps10* genes were characterized in more detail to see how many separate *rps10* transfers these 16 losses may represent.

To become active in the nucleus, a gene acquired from mtDNA must be inserted into the nuclear genome in such a way that a mature, translatable messenger RNA can be produced. Moreover, the resulting protein (made outside the nucleus, in the cell's cytosol) must be targeted to and imported into mitochondria. What emerges from the

analysis of such transferred mitochondrial *rps10* genes is an intriguing diversity in the mechanism of functional activation in different angiosperms.

In some cases, pre-existing copies of other nuclear genes have been parasitized, with the *rps10* coding sequence being inserted into the host gene. In several instances, a mitochondrial targeting sequence (pre-sequence) has been effectively co-opted to provide entry for the RPS10 protein back into the mitochondrion; however, different nuclear genes are used as the source of the presequence in different plants. In other cases, the nucleus-encoded RPS10 protein appears to be imported into mitochondria despite the absence of an obvious pre-sequence. From these results and other published data, the authors infer that there have been at least seven separate transfers of *rps10* to the nucleus in angiosperms, and probably many more.

Is this just the tip of the iceberg? Apparently it is. Adams *et al.*³ point out that their study encompasses only about 2% of living angiosperm genera, so that *rps10* may have been "independently transferred hundreds of times during angiosperm evolution". Other genes that encode ribosomal proteins also seem to have been lost frequently from angiosperm mitochondrial genomes. Individual examples of such transfers have been characterized, again illuminating the myriad mechanisms that seem to be employed for functional activation. In grasses, for instance, a relocated *rps14* gene has ended up within a nuclear gene (*sdhB*) that encodes a subunit of the mitochondrial enzyme succi-

nate dehydrogenase. Co-expression of the *sdhB* and *rps14* coding sequences, followed by alternative splicing of the resulting mRNA, gives rise to two different proteins having the same mitochondrial targeting signal^{8,9}.

Further studies have yielded evidence of comparably high and variable rates of loss of a majority of 13 other mtDNA-encoded ribosomal protein genes during angiosperm evolution (K. Adams, Y.-L. Qiu and J. D. Palmer, personal communication). In contrast, only two of a sample of 13 genes involved in energy generation showed a similarly high rate of loss from angiosperm mtDNA. A particularly striking point is that in many plants the relative rate of ribosomal-protein gene loss actually exceeds the rate of nucleotide substitution at a single silent site (a site at which a mutation does not result in an amino-acid change): this is a conclusion that Adams *et al.* (and I) find astonishing.

In other eukaryotes (animals, for instance), further transfer of genes from mitochondria to the nucleus has effectively been blocked by changes in the mitochondrial genetic code: essentially, mitochondrial gene content has been frozen. In plants, mitochondrion-to-nucleus gene relocation is undoubtedly facilitated by the fact that there is no genetic code

barrier to such transfer: the systems for translating RNA into protein use the same genetic code in both mitochondria and the cytosol. Even so, we could hardly have imagined the relative ease with which angiosperms seem to be able to shuttle mitochondrial genes into the nucleus and activate them there. Unravelling the genetic and biochemical workings of this highly efficient rapid-transit system will undoubtedly provide further surprises down the road. ■

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Neural engineering

Real brains for real robots

Sandro Mussa-Ivaldi

Neural signals from the brains of monkeys have been used to drive the movement of robotic arms. The ultimate objective of such work is to design controllable prosthetic limbs.

The idea of driving robotic limbs with what effectively amounts to the mere 'power of thought' was once in the realm of science fiction. But this goal is edging closer to reality, thanks in part to two decades of studies that have revealed a close match between the activity of neurons in the brain's cerebral cortex and the movements of the hand¹. Now, writing on page 361 of this issue², Wessberg and colleagues describe how they have used electrical signals from five regions in the cerebral cortex of monkeys to drive the movement of robotic arms.

Such 'brain-computer interfacing'³ has clear-cut clinical aims. The ambitious goal is to provide amputees and patients suffering from a variety of severe motor disorders — such as paralysis and amyotrophic lateral sclerosis — with the means to act and communicate by replacing the control of muscles with the control of artificial devices by brain activity.

The idea of using signals from the cerebral cortex to drive artificial limbs was pioneered 30 years ago⁴, when these signals were

used to predict the movement of the wrist in real time. But only since the motor cortex region of the brain has been studied in detail⁵ have researchers begun to explore the possibility of reproducing the full complexity of arm movements⁶. To do so one requires the ability to extract — in real time — the information concerning arm movements that is hidden within the activities of large groups of neurons⁷.

Researchers are gradually developing the hardware and software needed to connect brains to robotic limbs. The hardware includes 'conic electrodes'⁸, an innovative development based on the idea of inducing nerve growth within small, hollow electrodes containing nerve growth factor. This technique establishes stable, long-lasting electrical contacts between brain cells and electrodes.

Wessberg *et al.*², meanwhile, have been working on the software. They provide a simple solution to the problem of extracting 'movement information' from neural signals detected by microelectrodes implanted in

100 YEARS AGO

A simple method of recording the speed of motor cars and other vehicles has been devised by M. L. Gaumont, and accounts of the device appear in *Cosmos* and *La Nature* of November 3. The instrument consists simply of a camera with a double shutter, by which two exposures are made of the same plate, separated by a known interval of time. On developing the photograph, two images are obtained of the moving object, and, by measuring the distance between them, the dimensions of the car being supposed known and also measured on the plate, it is easy to calculate the speed of the car at the instant when the photograph was taken. The object is to assist the authorities in regulating the speed of these vehicles and checking furious driving.

From *Nature* 15 November 1900.

50 YEARS AGO

In 1925, Prof. Dart announced the discovery of a new type of higher primate that seemed to be somewhat intermediate between ape and man. This was the skull of the Taungs child which he called *Australopithecus africanus*. For some years there was considerable dispute between those of us who regarded the little skull as that of a being closely allied to the ancestor of man, and those who considered it only a variety of ape, allied to the chimpanzee, which by parallelism had come to resemble man in many characters. Since 1936 we have made a large number of new discoveries, and this group of higher primates is now known by many skulls and skeletal remains of adults of a considerable variety of forms which we think should be placed in different genera and species. In the past two years we have discovered a number of nearly complete skulls which give us a new picture of the origin of man. When the only known skulls of our so-called 'ape-men' had brains of between 450 and 650 c.c., those who said they were only apes and had no close relationship to man seemed to have some case. But now that we have skulls with brains of 750, 800 and possibly 1,000 c.c., we seem to be dealing with beings that have some claim to be human...Possibly we are correct in assuming that there lived in South Africa a million or perhaps two million years ago a family of higher primates, not closely related to the living anthropoids, but perhaps evolved from a very early anthropoid or even a pre-anthropoid by a different line...

From *Nature* 18 November 1950.