

confined in a closed volume (a cylindrical vessel).

This universality is just the beginning of the story presented by Bramwell *et al.* They also consider a two-dimensional magnetic system at a critical point near the second-order phase transition between magnetically ordered and disordered phases. In such systems the magnetic moment $m(\mathbf{r}, t)$ strongly fluctuates, on a scale with the same probability distribution as velocity fluctuations in developed turbulence. The fluctuations of the total moment $M(t)$ may also be characterized by the probability distribution function Q_M and the authors observe that the functions Q_M and Q_P are amazingly close (see their Fig. 1c on page 553).

Magnetic systems near the second-order phase transition and developed turbulence are microscopically very different physical systems. Moreover, the first one enjoys thermodynamic equilibrium; the second, energy-flux equilibrium. Most surprisingly, however, Bramwell *et al.* show that there are similarities in statistical behaviour between these systems. These results may well serve as a starting point for further theoretical and experimental work to understand the underlying reasons behind such similarities, and their consequences. □

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Ocean geochemistry

Carbon dioxide uptake at sea

Alain Poisson

o what extent will the world's oceans be able to take up carbon dioxide and reduce its rate of increase in the atmosphere? Numerical modellers^{1,2} have tried to give a provisional answer. But their estimates of the main parameters differ considerably — particularly in the Southern Ocean and the tropics, where the flux of anthropogenic CO₂ across the air–sea interface seems to be largest. On page 560 of this issue³, however, Peng *et al.* claim that it is now possible to make a direct and reliable determination of anthropogenic CO₂ penetration into the ocean. Their approach is based on the temporal variation of measurements of the total dissolved inorganic carbon concentration in seawater.

Before the beginning of the industrial era (around 1850), the global CO₂ cycle was in steady state on a decadal timescale. Since then, the atmospheric concentration of CO₂ has risen increasingly rapidly; now, about

one-half of the CO₂ emitted by the combustion of fossil carbon remains in the atmosphere, the rest being partly dissolved in the oceans and partly stored by the terrestrial biosphere. Researchers have long tried to measure the flux of anthropogenic CO₂ at the air–sea interface and through the oceans' water column, to determine the geographical distribution and rate of CO₂ penetration into deep waters. This is no easy task — data are scarce on the time scales required, and the annual increase of the signal is small relative to the local temporal variability in the oceans' dissolved inorganic carbon.

Twenty years ago, a direct method^{4,5} was devised for estimating the total anthropogenic CO₂ inventory in the ocean. It was based on a simple concept. The total concentration of dissolved inorganic carbon in oceanic deepwater is the result of its original carbon content when it was at the surface, and the changes that the water has subse-

quently undergone. When a parcel of seawater sinks from the surface, its salinity and temperature alter because it becomes mixed with seawater from other origins, implying alteration also of its content of dissolved carbon. Moreover, phytoplankton and zooplankton in the surface layers create organic matter and carbonate skeletons that sink in the water column, are oxidized or dissolved, and produce more dissolved carbon in deep seawater. These changes are respectively estimated by the difference in oxygen content and alkalinity between surface and deep water, and are subtracted from the total inorganic carbon of deep water to obtain the original carbon content of that water when it was at the surface. It was claimed that comparing this original, 'preformed' carbon content with that of the present carbon content of surface water gives the anthropogenic CO₂ signal. But this is only true if the deep water was at the surface in preindustrial times; if it was at the surface after that, only the increase in the signal can be estimated.

This method was criticized for several reasons, mainly the way of estimating the composition of the preindustrial waters which mix together to form the deep waters, and that of correcting for the changes that occur as they sink. Nevertheless, the profiles of the anthropogenic signal obtained by this simple method are more or less similar to those of chlorofluorocarbons — CFCs, transient tracers whose penetration into the ocean is close to that of anthropogenic CO₂; this approach was later improved by using an exponential distribution of CFCs (ref. 6).

Only recently, however, has the issue of estimating a reliable CO₂ anthropogenic signal been taken up again, largely due to intensification of the collection of carbon data by the World Ocean Circulation Experiment (WOCE) and the Joint Global Ocean Flux Study (JGOFS). The main difficulties are elimination of the nonlinear effects of mixing, and determination of the preindustrial carbon

Palaeontology

The face of Cinderella

The discovery of a complete skull of the hominid *Australopithecus*, associated with abundant limb bone material, is announced this week. The picture shows the exposed left side of the skull. The jaws, with a complete set of teeth in occlusion, can clearly be seen. As R. J. Clarke of the University of the Witwatersrand Medical School in Johannesburg reports (*South African Journal of Science* 94, 460–463; 1998), the skull is still embedded in the Member 2 breccia in the Silberberg Grotto of the Sterkfontein Caves near Krugersdorp, South Africa, and more finds are likely. The taxonomic status of the fossil has yet to be determined, although it is believed to



be more than three million years old.

In 1994, Clarke found four articulating foot bones of *Australopithecus* in rocks from the same site. Eight more foot and

lower leg bones turned up last year, all from the same individual. This discovery prompted Clarke to send his colleagues Nkwane Molefe and Stephen Motsumi into the Silberberg Grotto — like Prince Charming, looking for the girl whose foot would fit a glass slipper — to search for *in situ* remains that would fit neatly onto fragments already found. Cinderella duly turned up, in the form of two lower legs arranged side by side, as if the individual had been buried face-down in the breccia. Further work produced parts of an upper arm and the skull as illustrated. Clarke speculates that the rest of the skeleton is still buried under breccia. **Henry Gee**

concentration in the original surface waters that contribute to the composition of deep waters. One technique⁷ is based on a quasi-conservative carbon tracer, which reflects the anthropogenic signal, and the disequilibrium of the CO₂ concentration between the atmosphere and the surface water when the water sinks; it is corrected by using the water age estimated by the transient tracers tritium and helium-3. But this method can be applied only locally to specified water layers, and still involves questionable assumptions on the corrections that have to be applied.

Peng *et al.*³ have taken advantage of the high precision of new measurements of the total concentration of dissolved carbon in seawater, and have developed a method for determining the anthropogenic signal on a similar model of variation of the total concentration of dissolved carbon in the ocean. But instead of directly estimating the global inventory of that signal, they calculate its temporal variation at several depths between time periods 17 years apart. This is a good way to eliminate the principal drawbacks of the inventory methods.

This technique is however only valid if the concentration of natural total dissolved carbon and the changes in deep waters due to biological processes do not vary with time. This should be the case, or nearly so, on the decadal time scale. Nonetheless, significant increase of temperature and salinity, correlated with oxygen decrease, has been described for the period 1981–92 in intermediate water in the Atlantic Ocean⁸. So we

cannot be sure whether such variations will affect the calculations.

That apart, the approach of Peng *et al.* gives only the increase of the anthropogenic signal on a decadal scale at specified layers of seawater in specified parts of the ocean. But the high-quality, worldwide data stemming from the WOCE and JGOFS programmes will provide a good basis for extension of that approach, or for use of another new technique⁹ (one which takes the fundamentals of water-source mixing), to produce a direct and reliable global inventory of CO₂. The results will provide powerful constraints on and validation of models of oceanic carbon which aim to estimate the temporal evolution of ocean uptake of anthropogenic CO₂, an essential component for predicting how global climate will change. □

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1. Tans, P. P., Fung, I. Y. & Takahashi, T. *Science* **247**, 1431–1438 (1990).
2. Ciais, P., Tans, P. P., Trolier, M., White, J. W. C. & Francey, R. J. *Science* **269**, 1017–1188 (1995).
3. Peng, T.-H., Wanninkhof, R., Bullister, J. L., Feely, R. A. & Takahashi, T. *Nature* **396**, 560–563 (1998).
4. Brewer, P. G. *Geophys. Res. Lett.* **5**, 997–1000 (1978).
5. Chen, C.-T. A. & Millero, F. K. *Nature* **277**, 205–206 (1979).
6. Papaud, A. & Poisson, A. *J. Mar. Res.* **44**, 385–402 (1986).
7. Gruber, N., Sarmiento, J. L. & Stocker, T. F. *Glob. Biogeochem. Cycles* **10**, 809–837 (1996).
8. Garcia, H., Cruzado, A., Gordon, L. & Escanez, J. *J. Geophys. Res.* **103**, 2817–2830 (1998).
9. Goyet, C. *et al.* *J. Mar. Res.* **57**, 1–30 (1999).

Evolutionary biology

A plastic genome

Pierre Capy

views on the evolution of genome structure and function have changed dramatically over the past three decades. Once thought to be rather stable, except for occasional changes in chromosome structure brought about by translocations or inversions, the genome is now known to have a flexibility often referred to as plasticity. At the molecular level, the genome is like a puzzle made up of parts that can move from one position to another and, through exchange, deletion, insertion or amplification, generate new combinations of elements with different functions and expression patterns. Indeed, because of this modular construction, unrelated proteins often include similar functional domains.

A remarkable demonstration of plasticity in the *Drosophila* genome is described by Nurminsky *et al.*¹ on page 572 of this issue. They identify a gene that encodes a sperm-specific axonemal dynein intermediate chain, and show that it has evolved extremely rapidly in the lineage leading to *D.*

melanogaster — at least within the three million years or so since the species diverged from *D. simulans*. The new gene is called *Sdic* (for sperm-specific dynein intermediate chain), and it was created from different parts of two unrelated genes; one, *Annexin X* (*AnnX*), encoding a cell-adhesion protein,

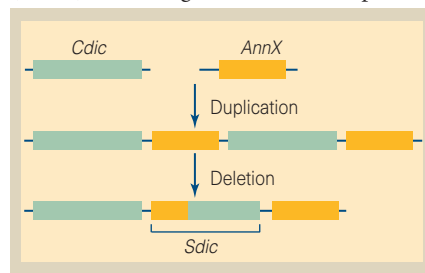


Figure 1 Evolution of the *Sdic* gene in *Drosophila melanogaster*. Nurminsky *et al.*¹ report that *Sdic* evolved recently (within the last three million years) from two unrelated genes. The *Sdic* promoter was created from a protein-coding region of *AnnX*, and its protein-coding exon comes from part of an intron in the *Cdic* gene.

and the other (*Cdic*) encoding a cytoplasmic dynein intermediate chain. In an odd exchange of genetic roles, a protein-coding region of the new gene, and part of an intron in the *Cdic* gene was refashioned into a new protein-coding exon (Fig. 1). The new gene emerged after a duplication and several deletions, and the resulting structure was amplified into a tandemly repeated block of about ten copies.

Sdic is unique among newly evolved genes in *Drosophila* because a putative function has been identified. Another chimaeric gene known as *jingwei* (*jgw*) has been described² in the related species *D. teissieri* and *D. yakuba*. This gene was created in the common ancestor of the two species when a transcript of the gene for alcohol dehydrogenase (*Adh*) was reverse-transcribed into DNA and inserted into the third intron of an unrelated gene called *yande* (*ynd*). Although its function remains unknown, *jgw* is expressed differently in the two species, possibly indicating some divergence in function. Both *Sdic* and *jgw* exemplify 'exon shuffling' in the origin of new genes^{3,4}, but *Sdic* also shows the *de novo* origin of a protein-coding exon from a previously non-coding sequence.

Any new molecular rearrangement will probably be eliminated by deletion unless it is maintained by some sort of selective constraint⁵. Intense selection for modifications in the coding or regulatory regions may lead to one or more 'selective sweeps'. These reduce genetic variability in the new gene itself and, because of 'genetic hitchhiking', also reduce variability around that gene⁶. Indeed, Nurminsky *et al.*¹ analysed the chromosomal region near the newly evolved *Sdic* gene and found an extremely low level of genetic variation. This finding is also consistent with a model of background selection in which the selective elimination of deleterious mutations also eliminates linked neutral variants^{7,8}. Ordinarily there is no way to distinguish between a selective sweep and background selection because the target of the selective sweep is not known⁹. But in the case of *Sdic*, the inference of a selective sweep is reasonably strong in view of independent evidence for large, selectively driven changes in the gene.

Although both *Sdic* and *jgw* were created through genome rearrangements, transposable elements — regions of DNA that can hop around the genome — are not implicated in the origin of either gene. I believe this may be because transposable elements affect genome evolution at a different level. They represent from 5–50% of total genomic DNA, depending on the species, and cause mutations because of their ability to move. Insertion of a transposable element can inactivate a gene, or can change its spatial and temporal expression. Transposition is