

examples listed above illustrate.

A second question concerns the kinds of novelty likely to arise in this way. Prokaryotes and fungi are good at metabolic tricks that animals and plants have lost, or never had — an obvious example is vitamin synthesis. Symbiosis with them may provide new metabolic abilities, but is less likely to be relevant in the evolution of new modes of locomotion or feeding, which is what palaeontologists tend to have in mind when they talk of macroevolution. I therefore doubt whether symbiosis has been important for the morphological evolution of plants and animals, except in so far as it may generate selection for morphological change, as in the example of luminescent organs in fish. Even if a symbiont induces a morphological change in its host (and examples of this were reported), the host response, if adaptively complex, has to evolve by natural selection.

A final problem concerns the selective mechanisms responsible for the origin of symbioses. Parasitic interactions present no special difficulty, but mutualism is more puzzling: why should a symbiont benefit its host if it could gain immediate advantage by injuring it? The decisive questions concern methods of transmission and multiplicity of infection. The bacterial endosymbionts of weevils and of plant-sucking bugs can live only in their hosts, and are transmitted in the host eggs. Hence a symbiont that damages its host reduces its own chances of leaving descendants. But most symbioses probably passed through a stage in which the

association had to be re-established in every generation. This is still the case for the other examples listed above. Larval Pogonophora have a mouth, and swallow their future symbionts. Young fish swallow luminescent bacteria, young termites must acquire their gut symbionts, usually through the rear end — this may be one reason why they become social — and seedling plants re-establish contact with mycorrhiza in every generation.

With this life history, the spread of selfish mutations, converting a mutualistic relation into a parasitic one, is always a possibility. Yet all the above examples are ancient. One possible explanation for their stability is that few selfish mutations are possible. For a fungus, a heather plant is an excellent supplier of fixed carbon, and it may be better to keep alive the goose that lays the golden eggs than to kill it. But this argument depends on the assumption that, if you do not kill the golden goose, no one else will either: that is, it assumes that the host is infected by a single clone of symbionts. The same argument applies to the evolution of parasites from greater to less virulence.

Further work is needed on the origin and maintenance of symbiosis, but it is already clear that, by bringing together genetic material from distantly related ancestors, symbiosis provides a source of evolutionary novelty that is additional to mutation and homologous genetic recombination. □

*John Maynard Smith is at the University of Sussex, Brighton, Sussex BN1 9QG, UK.*

## ASTROPHYSICAL MAGNETISM

# Stretch, twist and fold

*H.K. Moffatt*

DYNAMO action, in astrophysical contexts, is the spontaneous growth of magnetic fields caused by the motion of electrically conducting fluids. That fluid motion can sustain a magnetic field against its natural tendency to decay is well-established, but there are doubts about the rates at which magnetic fields grow when the conditions for dynamo action are satisfied. It appears still to be an open question whether there can be a smooth velocity field capable of generating a fast dynamo action, in the sense of the distinction<sup>1</sup> between 'fast' and 'slow' introduced by Vainshtein and Zeldovich<sup>2</sup> in 1972. That question, and the surprising connections that have emerged recently with the theory of iterated maps, were explored at a recent workshop\*.

Dynamo theory is important in planetary physics and astrophysics because of the ubiquity of magnetic fields. Nearest to

home, the Earth's magnetic field is sustained by dynamo action in the outer liquid core, and the magnetic fields of Jupiter and Saturn and possibly of other planets are believed also to originate from fluid dynamos. If it were otherwise, these fields would decay in times of the order of  $10^4$  years, which is short compared with the age of the Solar System, throughout which, on geological and other evidence, the fields have persisted.

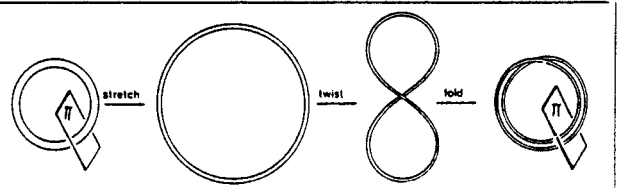
Stellar and, in particular, solar magnetism presents another problem. The natural decay time for a magnetic field may be  $10^9$  years, but there are systematic variations such as the 22-year solar sunspot cycle on much shorter timescales. Rapid changes such as these, involving global reversals of magnetic polarity, must be attributable to fluid motion deep in the

turbulent stellar convection zone. Whether galactic magnetic fields also originate in dynamos is another matter<sup>3</sup>.

The property of fluid motion crucial to dynamo action is helicity — in simple terms, the net imbalance between right-handed and left-handed helical motion. Surprisingly, it has recently been shown<sup>4</sup> that Ponomarenko's helical dynamo<sup>5</sup>, perhaps the simplest and purest of all, in which helical streamlines are confined to a cylinder, is a fast dynamo, but only when the velocity is discontinuous across the cylinder boundary. The other known model of fast dynamo action is that of Soward<sup>6</sup>, who has shown that certain spatially periodic velocity fields have the properties of a fast dynamo provided that there are mild singularities of vorticity at the stagnation points.

These examples are somewhat contrived, which may in part explain why the search for other more realistic examples has excited so much interest. The physical, rather than mathematical, prototype of a fast dynamo is that first discussed by Vainshtein and Zeldovich<sup>2</sup>, and may be likened to the process of stretching, twisting and folding a rubber band so as to double the tension. A similar procedure applied to a magnetic flux-tube in a perfectly conducting fluid (see figure) will double the magnetic field-strength, so that indefinite repetition of the stretch-twist-fold sequence will lead to exponential growth of the magnetic field on a time-scale determined by that of the motion, and independently of molecular diffusion. This example, of course, is also somewhat contrived: but insofar as stretching is invariably associated with turbulent flow, twisting with convection and folding with geometrical constraints thereon, the stretch-twist-fold sequence has some basis of reality in the turbulent convection zone of a rotating star.

How can one translate this physical argument into mathematical form? The stretch-twist-fold sequence can be represented as a three-dimensional time-dependent velocity field, but the resulting equation for the evolution of the magnetic field is so complex that it cannot be solved even with available computing power. But now there is an alternative procedure. The stretch-twist-fold sequence doubles the magnetic field-strength without increasing the cross-section of the flux-tube, which is tantamount to a mapping of the cross-section onto itself.



The stretch-twist-fold sequence, showing the plane of cross-section  $\Pi$  on which the associated mapping is constructed.

\*Workshop meeting at Observatoire de Nice, 25 - 30 June, 1989.

That observation alone links dynamo theory with the theory of iterated mappings, about which much is known. Several examples of iterated mappings, called dynamo maps, have now been found, notably by Bayly and Childress<sup>7</sup> and by Finn and Ott<sup>8</sup>, and were scrutinized at the workshop. It emerges that, although every time-periodic flow yields a map and every continuous map can be associated with a flow, it is not yet known whether these flows have the property of 'orientability' that would lead to reinforcement (rather than cancellation) of the convected magnetic field. That fundamental problem remains an obstacle in attempts to tackle dynamo theory with the theory of iterated maps.

There remains the sledge-hammer of the high-speed computer. The velocity field most likely to be tractable, is called the 'ABC' flow — essentially a superposition of three orthogonal circularly polarized velocity fields such that the velocity field  $\mathbf{u}$  has the components ( $B\cos ky + C\sin kz$ ,  $C\cos kz + A\sin kx$ ,  $A\cos kx + B\sin ky$ ). This flow is named after Arnol'd (who recognised that the particle paths may be chaotic), Beltrami (who first conceived of flows such as this in which the vorticity is everywhere parallel to the velocity) and Childress (who recognized the flow, through its property of maximal helicity, as a prime candidate for dynamo action).

Galloway and Frisch<sup>9</sup>, following Arnol'd and Korkina<sup>10</sup>, have computed the dynamo growth-rate as a function of the magnetic Reynolds number  $R_m$  (a dimensionless measure of electrical conductivity), and find two windows of dynamo action, in the ranges  $8 < R_m < 18$  and from  $R_m = 27$  up to  $R_m = 400$ , the present limit of reasonably accurate computation. The challenging question still outstanding is whether the ABC flow generates a fast or slow dynamo, or no dynamo at all, in the limit in which  $R_m$  tends to infinity.

A novel twist to this question was raised at the meeting by B.J. Bayly (University of Arizona, Tucson), following work by A.A. Ruzmaikin (Moscow). If the three ingredients of the ABC flow associated with the parameters  $A$ ,  $B$  and  $C$  are successively switched on and off at random, separated by periods when only diffusion operates, the result is a model reminiscent of the 'stasis' model of Backus<sup>11</sup>, who provided one of the first proofs of dynamo action — in the event, a slow dynamo. Bayly has now shown that fast dynamo action is also possible and, interestingly, that the wavelength of the growing magnetic field is exactly twice that of the underlying ABC ingredients of the flow. This behaviour has escaped attention in previous computations, which have concentrated on magnetic fields with the same periodicity as the velocity field.

Bayly's result, if confirmed, is certain to stimulate further computational attacks on the ABC problem.

An explicit fast-dynamo theory is potentially of the greatest importance in astrophysics because present accounts of stellar magnetism are based on insubstantial foundations. Most modern theories follow the mean-field formalism introduced by Steenbeck, Krause and Rädler<sup>12</sup> in which the effects of turbulence in convection zones are parameterized by a generation coefficient  $\alpha$  and a turbulent diffusivity  $\beta$ , which are usually related to the velocity and length scales of the turbulent convection by simple dimensional analysis. The resulting growth rates are determined by  $\alpha$ ,  $\beta$  and global properties such as differential and meridional circulation in the star, but do not depend on the magnetic diffusivity of the medium, so that the dynamos are intrinsically fast. Thus the whole theory of stellar magnetism hangs on the slender thread of dimensional analysis applied in a complex turbulent context. The mathematical difficulties inherent in fast dynamo theory are concealed in the mean-field theory which, in principle, determines  $\alpha$  and  $\beta$ , but there is a paradox: the molecular magnetic diffusivity seems to be essential to the production of an  $\alpha$ -effect even though the resulting value of  $\alpha$  is independent of the value of the diffusivity, which is in any case vanishingly small.

If the solar dynamo is, indeed, a fast dynamo, then it is to be expected on dimensional grounds<sup>13</sup> that the field will nearly everywhere have a fine scale of the order of  $\sqrt{R_m}$  multiplied by  $L$ , the length-scale of the velocity field. Taking  $L$  to be of the order of 1,000 km from the observed granulation of the solar surface, and  $R_m$  to be of the order  $10^4$ , there should be variations of magnetic field on scales as small as 10 km, which is not incompatible with observation. Fast dynamo theory may therefore be of much more than merely academic interest. □

H. K. Moffatt is Professor of Mathematical Physics and a Fellow of Trinity College, University of Cambridge, Cambridge CB2 1TQ, UK.

1. Zeldovich, Ya.B., Ruzmaikin, A.A. & Sokoloff, D.D. *Magnetic Fields in Astrophysics*. (Gordon and Breach, London, 1983).
2. Vainshtein, S.I. & Zeldovich, Ya.B. *Sov. Phys. Usp.* **15**, 159–172 (1972).
3. Trimble, V. *Nature* **340**, 506–507 (1989).
4. Gilbert, A.D. *Geophys. Astrophys. Fluid Dyn.* **44**, 241–258 (1988).
5. Ponomarenko, Y.B. *Zh. Prikl. mech. tech. Fiz. (USSR)* **6**, 47–51 (1973).
6. Soward, A.M. *J. Fluid Mech.* **180**, 267–295 (1987).
7. Bayly, B.J. & Childress, S. *Phys. Rev. Lett.* **59**, 1573–1576 (1987).
8. Finn, J.M. & Ott, E. *Phys. Fluids* **31**, 2992–3011 (1988).
9. Galloway, D. & Frisch, U. *Geophys. Astrophys. Fluid Dyn.* **38**, 53–83 (1986).
10. Arnol'd, V.I. & Korkina, E.I. *Vest. Mosk. Un. Ta. Ser. 1. Mat. Mec.* **3**, 43–46 (1983).
11. Backus, G.E. *Ann. Phys.* **4**, 372–447 (1958).
12. Steenbeck, M., Krause, F. & Rädler, K.-H. *Z. Naturforsch.* **21a**, 369–376 (1966).
13. Moffatt, H.K. & Proctor, M.R.E. *J. Fluid Mech.* **154**, 493–507 (1985).

## PROTEIN STRUCTURE

# One enzyme from two genes?

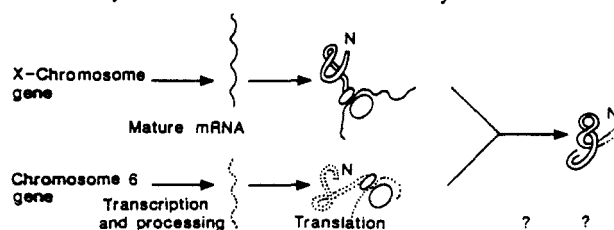
Lucio Luzzatto

GLUCOSE-6-PHOSPHATE dehydrogenase (G6PD) has long been a favoured system in human biochemical genetics. It was one of the first mammalian enzymes to be characterized<sup>1</sup>, it is one of the most polymorphic genes in the human genome<sup>2</sup> and, because it maps to the X-chromosome (Xq28)<sup>3</sup>, it has served as a wonderful marker to study X-chromosome inactivation<sup>4</sup>, the consequent mosaicism of somatic cells in females<sup>5</sup>, and the clonality of tumours<sup>6</sup>. In addition, this mosaicism is probably responsible for the biological advantage of G6PD deficiency with respect to malaria<sup>7</sup>. Now, an entirely unexpected development, of potentially general significance, arises from a study of G6PD just published in *Cell*<sup>8</sup>. If the work is confirmed, we shall have to adjust to a new way of thinking about how proteins can be assembled.

Briefly, Yoshida and his colleagues find that whereas one form of G6PD in red cells has an amino-acid sequence that conforms to

that predicted by the cDNA sequence first published by Persico *et al.*<sup>9</sup>, another form differs upstream of amino acid 36. By the use of two synthetic oligonucleotides corresponding to portions of the divergent sequence, they have isolated human genomic and reticulocyte cDNA clones that encode this sequence as part of a protein of 345 amino acids, the gene for which maps to chromosome 6 rather than the X chromosome.

They must, of course, have considered the possibility that the G6PD preparation used for protein sequencing was contaminated. But the remarkable result, on which the rest of the paper depends, is that the authors have actually isolated from a



Can a hybrid protein be formed during or after the translation of separate gene transcripts? And, if so, how?