phate-resistant. From each drill site, two holes can be drilled in opposite directions along the trend of Adam's Bridge. If the holes are deviated to almost horizontal, one can place filters of several hundred metres length in the borehole, and inject waste sulphuric acid into the limestone. The depth of injection is in the order of 100 m, so the injection pressures are no more than 10 to 20 bars, not enough to cause hydrofracturing. From the description of the Jaffna limestone it appears that the limestone is well jointed, which means that the acid will rapidly move into the limestone up to some distance from the points of injection. Intergranular diffusion plays no major role; transport of acid is mainly along small, existing or newly created fissures.

The uplift that is caused by the transformation of calcite into gypsum will result in a more or less continuous land barrier. It will, of course, be necessary to leave one or more gaps for shipping. Because the normal tidal currents will be interrupted over most of the distance between India and Sri Lanka, the current through the remaining gaps will be stronger, which is favourable for the emplacement of hydro turbines. Fears about a reduction of strength of the rock are probably unfounded. From laboratory experiments with confined limestones that cannot expand sideways, it appears that lateral expansion translates into an upward creep of the limestone, but the rock does not lose its cohesion. Gypsum rocks can form sound foundations. It is well known that several medieval towns in Germany are situated on mounds that rise from the plain, and are underlain by a gypsum caprock on top of rising salt diapirs.

When the method was published around 1990, it attracted a good amount of public attention. Some members of the public, however, were worried about possible environmental effects. There will be no direct effect on flora and fauna, as the rock transformation takes place well below the surface of the earth, separated from the biosphere by a layer of unreacted limestone. Indirectly, of course, if one changes a sea bottom into a land surface, there is an obvious effect. A second objection concerned the fate of heavy metals if polluted waste acids are used. We have shown experimentally that these are immobilized at the reaction front between gypsum and limestone, where the pH sharply rises. In fact, this makes the process an attractive way of neutralizing waste acids and removing their heavy-metal content. The third type of objection is related to the release of CO_2, which would contribute to the greenhouse effect. Although the argument seems logical at first sight, it is a fallacy. The chemical rule 'a strong acid dislodges a weak acid from its salts', holds also for the relation between sulphuric acid (strong) and carbonic acid (weak). Any strong acid at the earth's surface will prevent an equivalent amount of CO_2 from being removed from the atmosphere and sequestered in mineral form. In the subsurface, this same amount of acid will produce an equivalent amount of carbonic acid, but as long as some of that remains in the subsurface, for example, dissolved in formation waters, the process is favourable as regards the greenhouse gas balance.

India has many industries that produce waste sulphuric acids or low-grade technical grade sulphuric acid. An example of a large producer is the TiO_2 plant of Travancore Titanium Products near Trivandrum, Kerala. By shipping such waste acids to Adam's Bridge an environmental problem can be solved, while at the same time a contribution to a significant and economically valuable construction is made.

1. Waring, F. J., Minutes Proc. Inst. Civ. Eng., 1916–1917, CCIII, 284.
2. Cathcart, R. B., *Curr. Sci.*, 2003, **85**, 430.
3. Cooray, P. G., *The Geology of Sri Lanka (Ceylon)*, Natl. Mus. Sri Lanka Publ., 1984, 2nd edn, p. 340.
4. Ramasamy, S. *et al.*, *Curr. Sci.*, 1998, **75**, 884–886.
5. Schuiling, R. D., Utrecht University, Dutch Patent Application no 8800838, 1988.
6. Schuiling, R. D., *Appl. Goechem.*, 1990, **5**, 251–262.
7. De Graaff, J. W. M., Speck, P. J. H. R. and Zijlstra, J. J. P., Final project report, The Netherlands Technology Foundation, 2000, p. 59.
8. O'Connor, K. M., Clark, R. J., Whitlatch, D. J. and Dowding, C. H., Real Time Monitoring of Subsidence Along I-70 in Washington, Pennsylvania. http://www.iti.northwestern.edu/publications/dowding/RT-MolSal70WaPa.pdf

R. D. SCHUILING

Department of Earth Sciences – Geochemistry,
Faculty of Geosciences,
Utrecht University,
P.O. Box 80.021; 3508 TA Utrecht
The Netherlands
e-mail: schuiling@geo.uu.nl

Variety in DNA secondary structure

I wish to point out serious errors in the review article by Delmonte and Mann[1]. Without sufficient new ideas or any new experimental evidence, the article seeks to reopen a 20-year-old controversy that arose from the proposal by a couple of groups of a 'side-by-side' model of DNA structure[2,3]. The chief point of this model was that it sought to address the presumed topological and energetic problems that could arise when the Watson–Crick double helix, an interwound 'plectonaemic' structure was unwound during transcription and replication. The side-by-side model was a 'paranaemic' model with two strands and Watson–Crick base pairs, but without the interwinding. Several ingenious, but ultimately untenable suggestions were then made to explain the X-ray diffraction patterns, and the other experimental evidence available. However, the discovery of topoisomerases took the sting out of the topological objection to the plectonaemic double helix. And the more recent solution of the single crystal X-ray structure of the nucleosome core particle[4] showed nearly 150 base pairs of the DNA (i.e. about 15 complete turns), with a structure that is in all essential respects the same as the Watson–Crick model. This dealt a death blow to the idea that other forms of DNA, particularly double helical DNA, exist as anything other than local or transient structures.

The authors of the above review have stubbornly refused to accept this, going so far as to call into question some of the foundational principles of X-ray crystal-

lography. For example, consider the following statement: 'Though . . . [the structure of the nucleosome particle] . . . is claimed to show a double-helix structure for DNA *in vivo*, all the heavy atoms, offering the most intense diffraction reflections, are placed in the histones and none lie in the DNA'. The authors obviously are trying to discredit the crystal structure by claiming that the data used to obtain it does not pertain to the DNA. But, as everyone knows, heavy atoms in crystals are used to phase *all* the measured reflections. In any case, even if only a subset of the reflections is used, the structure that is revealed is for the entire asymmetric unit. Thus, if Delmonte and Mann wish to say that the structure of the DNA in the nucleosome core is wrong, they need to find some way of proving the entire structure wrong. Given the high resolution (1.9 Å) of the current version of the structure[5], this is an impossible task.

Delmonte and Mann also take arms against some of the structures deposited in what they incorrectly call the 'Rutgers Protein Database'. (The correct name is PDB or Protein DataBank. But in fact, the structure IDs given in the article refer to the NDB or the Nucleic Acid Database.) They claim that the structures 'show patterns of systematic absence in a hexagonal net which would allow the choice of transformed, smaller unit cells . . .'. In the first place, as we have shown a few years ago[6], DNA, being a cylindrical molecule, packs in ways that offer alternate ways of indexing the X-ray reflections. However, it is the symmetry of the entire reflection set that decides the unit cell and space group, not a few reflections that may be absent due to, perhaps, the data collection geometry. There is no reason at all to suspect that the authors of the structures committed such elementary mistakes as suggested by Delmonte and Mann. Quite to the contrary, the structures are all at high resolution and well refined. Secondly, even if it were the case that the reflections are better indexed in a smaller unit cell, this says nothing about DNA being a paranaemic rather than plectonaemic structure. Again, the impression is that authors of the review are out of their crystallographic depth.

The article abounds in quotations out of context, which it would be tedious to catalogue. As just one example, there is reference to just one independent supportive commentary on the side-by-side models. Even that, unfortunately, is of doubtful scientific value, as it apparently addresses the sociological aspects of the controversy and was published in a journal of social science and a book on the politics of science.

Throughout the article, there is no clear description of the structure proposed by the authors. Figure 3, presumably a stereo representation of the model, is uninterpretable as a stereochemically reasonable structure. Other than this, to know what the new paranaemic model is, we are referred to a British company(!) and two websites. One of the websites is maintained by K. Biegeleisen, who describes his unrelenting, but so far unsuccessful attempts to prove the Watson–Crick double helix wrong. Biegeleisen's explanation for his failure appears to postulate a grand world-wide conspiracy and reads like a Robert Ludlum thriller. There a single reference, but no details, in this website to the work of 'Clive Delmonte', presumably one of the authors of the *Current Science* review article. The other website says it is 'under construction'.

With all these errors, and many more not mentioned here, it is surprising and disappointing that *Current Science* should see it fit to lend its prestige to the ideas expressed in the article and to the manner in which this has been done.

1. Delmonte, C. S. and Mann, L. R. B., *Curr. Sci.*, 2003, **85**, 1564.
2. Rodley, G. A., Scobie, R. S., Bates, R. H. T. and Lewitt, R. M., *Proc. Natl. Acad. Sci. USA*, 1976, **73**, 2959.
3. Sasisekharan, V. and Pattabhiraman, N., *Curr. Sci.*, 1976, **45**, 779.
4. Luger, K., Mader, A., Richmond, R. K., Sargent, D. F. and Richmond, T. J., *Nature*, 1997, **389**, 251.
5. Davey, C. A., Sargent, D. F., Luger, K., Maeder, A. W. and Richmond, T. J., *J. Mol. Biol.*, 2002, **319**, 1097.
6. Sadasivan, C., Karthe, P. and Gautham, N., *Acta Crystallogr.*, 1994, **D50**, 192.

N. GAUTHAM

Department of Crystallography and Biophysics,
University of Madras,
Guindy Campus,
Chennai 600 025, India
e-mail: gautham@unom.ac.in

Reply:

Our briefest comment is that Gautham promises to 'point out serious errors' but this drastic claim is not supported by anything in his letter.

The evidence we review suffices to show that the controversy was never closed, and we therefore deny that it could be 'reopened'.

Gautham says 'the discovery of topoisomerases took the sting out the topological objection to the plectonaemic double helix'.

The invocation of topoisomerases and similar proteins to explain the strand-separation of DNA *in vivo* would in any case leave unexplained, as our review pointed out and Gautham ignores, the observation that duplex DNA denatures rapidly without heat in enzyme-free solutions.

Gautham contends that X-ray diffraction of crystalline nucleosome core particles 'dealt a death blow to the idea that other forms of DNA, particularly double helical DNA, exist as anything other than local or transient structures'. It is a disappointment to us that Gautham, while indulging in a lengthy complaint about minutiae, often with unsupported allegations, has foregone this opportunity to provide any explanation of the wide-ranging experimental results which we drew together in our paper, none of which relate to a transient state for duplex DNA.

Many model building/refinement programs (LALS, NUCLSQ, etc.) incorporate a double helix within their logic and are incapable of furnishing an *ab initio* structural solution but could only provide a double-helical outcome.

We are not asserting that any paranaemic model is the only correct structure of duplex DNA. What we are asserting is that the published experimental data across the many diverse methods deployed in molecular biology cannot exclude the wide variety of the several structures we describe, none of which are topologically interlinked in their secondary structures.

We do not claim the W–C structure does not exist. It may well exist in some parts of DNA, and the relatively tiny, approx. 150-bp DNA of the nucleosome core particle, unusual in size and in function, may well be an example. Gautham accuses us of 'trying to discredit the crystal structure by claiming that the data used to obtain it does not pertain to the

DNA'. We made no such extreme claim. It is the DNA structure which is under review, not the histone structure, and it would have been better if the heavy atoms had been in the DNA. But our objection to the work of the Klug/Richmond/Luger group on the nucleosome core particle was more fundamental: the algorithms insisted upon by that group cannot regress on any model except the double helix.

Further, there was no demonstration in the Luger *et al.*[1] paper that the resolution that was attained, while a major improvement over earlier work in that field, was sufficient to distinguish a W–C double helix from a both-senses helical duplex having the topologically non-wound structure developed by the research groups of Sasisekharan and Rodley.

We pointed out, and Gautham ignores Bates' showing that B-DNA X-ray diffraction is more consistent with SBS than DH, when examined by the Patterson method which does not assume a helix or any other shape.

We cannot let pass Gautham's remark '[t]he article abounds in quotations out of context, which it would be tedious to catalogue'. Having wasted so much time on pseudo-corrections, he now grandly waives all duty to stipulate what is wrong with our paper.

We agree of course that *Current Science* has on this occasion – in a context of protracted important controversy and attempted suppression – taken the bold step of allowing citation of unrefereed works. One reason why this could be permissible in this context is the persistent blocking of non-DH theories by many journals unwilling to test the early work of Nobel Laureates against later, competent work by others we cite in that field.

The crystallographic community must adjust its cultural predeliction to ignore competent work using other methods of physical chemistry and prepare itself both to explain such results and to allow the inferences drawn from them to inform its own crystallographic work. Oligodeoxyribonucleotide crystallography really cannot be pursued successfully in scientific isolation.

1. Luger, K., Mader, A., Richmond, R. K., Sargent, D. F. and Richmond, T. J., *Nature*, 1997, **389**, 251.

C. S. DELMONTE[1]
L. R. B. MANN[2,*]

[1]*Open University,*
Clarendon Park,
Nottingham NG5 1AH, UK
[2]*P.O. Box. 28878 Remuera,*
Auckland 1005, New Zealand,
**For correspondence.*
e-mail: robtm@maxnet.co.nz

NEWS

2004: Year of Scientific Awareness

Science is a way of understanding the world, a perspective and a pattern of thinking that begins early in one's life. Scientific advances over the last fifty years have led to revolutionary changes in health, nutrition and communication, and generally enhancing socio-economic development and the quality of our lives. The role of science promises to be greater in the future because of the ever-more-rapid scientific progress. Our society is becoming increasingly dependent on science and technology. It is essential for the well being of our society that all citizens develop 'science literacy', an appreciation of science, the benefits of technology, and the potential risks associated with advances in both.

Science literacy does not imply detailed knowledge of any of the basic sciences like physics, chemistry or biology, but rather a broad understanding and appreciation of what science is capable of achieving and, equally important, what science cannot accomplish. Science literacy enables the public to make informed choices and to reject superstitions, blind-belief, unproven conjectures, and to avoid being mystified into making wrong decisions, where matters of science and technology are concerned (Box 1).

Science literacy aims to develop two broad goals: to promote literacy in science, mathematics and technology among the general public and to attract future generations to careers as researchers, entrepreneurs and teachers on whom the nation's continuing economic health and national security will depend.

Society makes progress in addressing critical issues by having both a skilled, creative, and productive workforce and a citizenry able to judge the risks and enjoy the benefits of advances in science and technology. Common people are unable to appreciate beauty in science, which is quite different from their capability to appreciate artwork, a piece of good music or beauty of a poem. This illiteracy of the general public on scientific subjects (sometimes even amongst politicians and decision-makers) reflects poor activity in science popularization and mystification of scientific work and data. In spite of this, people are still fascinated with complex scientific problems such as how large the universe is, what life and death are, and so on. The community of scientists has an important task for enhancement of science literacy in the society.

To push forward awareness within the scientific community itself, mainly among young graduate and postgraduate students that will make up the future generations of scientists, discussions should frequently be held during Ph D training, engaging young scientists on concrete projects and actions to promote scientific education.

Secondly, science education should be targetted at teachers, science communicators, journalists, and the general public, to popularize scientific information and the scientific method. New academic course materials may have to be produced in this direction. Scientists and the scientific community can contribute to narrow down the present gap between accumulated knowledge on one hand, and the quantity and quality of what the public knows on the other. Science is everywhere and one slowly recognizes the influence of science in everyday life.

Thirdly, scientists should engage themselves in active production of tools for science popularization. They should contribute to general publications for the