

Members (Co-opted)

Dr Greg Diakun
Daresbury Laboratory, Daresbury, Warrington WA4 4AD,
Phone 01925 603343 **Email** g.diakun@dl.ac.uk

Dr Tom Irving
CSRRI, Dept BCPS, Illinois Institute of Technology, 3101 s. Dearborn, Chicago IL. 60616, USA.
Phone (312) 567-3489 **Fax** (312) 567-3494 **Email** irving@biocat1.iit.edu

Dr. K. H. Gardner
DuPont CR&D, P.O. Box 80228, Experimental Station, Wilmington, Delaware, DE 19880-0228, USA
Phone Tel: +1 302 695 2408 **Email** kenn.h.gardner@usa.dupont.com

Dr Geoff Mant
Daresbury Laboratory, Daresbury, Warrington WA4 4AD
Phone 01925 603169 **Email** g.r.mant@dl.ac.uk

Prof. Rick Millane
Dept of Electrical and Computer Engineering, University of Canterbury, Christchurch, New Zealand.
Email rick@elec.canterbury.ac.nz

Dr Keiichi Namba
Matsushita Electric Industrial Co. Ltd., 3-4 Hikaridai, Seika 619-0237, Japan.
Phone 81-774-98-2543 **Fax** 81-774-98-2575 **Email** keiichi@crl.mei.co.jp

Prof. Gerald Stubbs
Dept of Molecular Biology, Vanderbilt University, 2200 West End Avenue, Nashville, TN 37235
Phone (615) 322-7311 **Email** stubbsgj@ctrvax.vanderbilt.edu

Chairman's Message

This year above all others brings to us a palpable reminder of the power of fibre diffraction. Without the excellent X-ray diffraction patterns from DNA fibres produced by Rosalind Franklin in the laboratory of Maurice Wilkins at King's College London, the modelling studies of Francis Crick and Jim Watson at Cambridge 50 years ago would have had nothing concrete about the dimensions of the DNA molecule to go on apart from Astbury's earlier demonstration of the 3.4 Å repeat of the bases. The facts that the structure was helical, based on the helical diffraction theory of Cochran, Crick and Vand (1952: *Acta Cryst.* 5, 581), theory which also been developed (but not published) by Alec Stokes at King's College London, that the space group contained a dyad axis perpendicular to the fibre axis suggesting a pair of anti-parallel strands of polynucleotide, and that the axial repeat was 34 Å, all came from the fibre diffraction patterns of the King's College group. Without knowledge of these key experimental observations it is hard to see how the Watson-Crick double helix model for DNA could have been developed. Together with Watson's almost mystical discovery of base-pairing, following

Jerry Donohue's advice on the correct tautomeric forms of the bases, fibre diffraction led inevitably to the solution of probably the single most important question in biology 'how is the genetic information passed from parent to offspring?' (J.D.Watson & F.H.C. Crick, *Nature* 171, 737-738, 1953 and other papers in the same issue). An excellent insight into this story and the role of the Cavendish laboratory was recently given by Hugh Huxley (2003: *Physics World*, March 2003, 29-35), himself a pioneer in the application of fibre diffraction methods, this time to muscle.

Despite this initial flurry of activity on DNA structure, in fact it took the Wilkins group about another 10 years to prove that the Watson-Crick model was essentially correct by providing accurate coordinates of helical, base-paired duplexes that fitted improved fibre diffraction patterns very much better than the first Crick-Watson wire model. Nowadays of course there are many known DNA forms, almost all recognised first from fibre diffraction studies, and there are new structures still being discovered, such as the polyhexanucleotide

DNA duplex whose X-ray diffraction pattern appears on the front cover of this volume.

However, in the excitement about the double helix it is very easy to overlook the fact that fibre diffraction led the way in solving or at least confirming the structures of all of the known regular secondary folds of proteins. The correctness of Pauling and Corey's proposal about the α -helix was confirmed by the fibre diffraction studies by Perutz on keratin and poly-benzyl-glutamate, the β -sheet structure was first demonstrated in diffraction patterns from silks, and the characteristic collagen triple helical structure was first proposed based on diffraction patterns from tendon fibres and their relationship with data from some synthetic polypeptide fibres (e.g. poly-glycine and poly-proline).

Fibre diffraction has had a very long history of success and yet one still hears comments such as 'the structure of DNA was not really confirmed until oligonucleotides were crystallised and their structure solved by the methods of Macromolecular crystallography'. Why were the very good, earlier fibre diffraction results not in themselves compelling? One of the reasons for setting up CCP13 was the need to develop rigorous methods of stripping and modelling fibre diffraction data so that the quality of structural conclusions from fibre diffraction could be objectively assessed and so that the results would be believed by non-practitioners in the field. We are now well on the way to doing this. Excellent data extraction programs such as XFIX, FTOREC and LSQINT can now remap raw fibre patterns into reciprocal space, fit good backgrounds to the observed images and also model either Bragg peaks or continuous layer-lines with robust algorithms. Unfortunately these programs have been non-trivial to use, so a major challenge is to provide both better instruction manuals for their use and in the longer term a friendlier and more intuitive Graphical User Interface in Java (to be portable) from which all of the programs can be run. This Java GUI is currently in preparation. In addition to this we are in the process of developing a number of programs for modelling of either atomic arrangements in fibres based on high resolution fibre diffraction data (e.g. LALS and FX-PLOR), or the organisation of molecular domains based on low-angle fibre diffraction data (e.g. MOVIE). A full description and summary of the available CCP13 software with flow diagrams showing the logic of the processing procedure is given on pages 7-19 of this

volume.

The CCP13 website (www.ccp13.ac.uk) is now more informative and active than in the past and there are three live mirror websites; in the UK at Imperial College (www.ccp13.org), in the US at the APS in Chicago (www.bio.aps.anl.gov/biocat/mirror/www.ccp13.ac.uk/), and in France at the ILL (<http://www.ill.fr/ccp13>). The CCP13 bulletin board (ccp13bb@dl.ac.uk) is becoming more active and is an excellent place to exchange ideas or to get help. It is there for you to use - so please use it! Last year in June we had a memorable Workshop at Keele University and this year the Workshop will be held at Fitzwilliam College, Cambridge from July 2 to 4. In addition to some excellent talks, we plan to hold hands-on demonstrations of various kinds of CCP13 software, so why not come along and find out what can be done with your data.

Finally, I would like to record my thanks, surely reiterating your own feelings, for the enormous contributions to CCP13 that Trevor Forsyth made in his time as Chairman. This was a time when CCP13 saw considerable expansion and consolidation and Trevor's tremendous enthusiasm and ability were central to bringing this about. Fortunately, Trevor retains an active involvement in CCP13 as Vice Chairman of the Steering Committee. He also provides a strong connection to X-ray and neutron fibre diffraction facilities at the ESRF and the ILL in Grenoble - facilities which are of course of major importance to the CCP13 community. My only hope now, as Chairman again, is that I can help to sustain and further develop CCP13 into as good a core activity for a thriving international fibre diffraction community as it can possibly be. However, this can only be done with your help and support. Please come to the Workshop, make your views known, if you are not giving a talk bring a poster on your work, and above all let us know how the existing software can be developed to be more useful for you. CCP13 is there to help you to get the best out of your data, but it requires your input to make it really flourish.

John Squire - Imperial College - March 2003