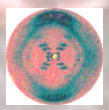
FiberNet Fiber Diffraction Workshop
Fall Creek Falls State Park, TN, August 6-9, 2006

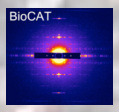
sponsored by

FiberNet **(a NSF-sponsored research coordination network in fiber diffraction from biological polymers and assemblies)**



www.fiberdiffraction.org

BioCAT **(the Biophysics Collaborative Access Team at the APS, Argonne National Laboratory, a NIH-supported research center for the study of the structure and dynamics of partially ordered biological systems)**



FiberNet Fiber Diffraction Workshop Program
Fall Creek Falls State Park, TN, August 6-9, 2006

Sunday, 6 August

transport leaves Nashville Airport 12:30 pm

3:30 Introduction (Gerald Stubbs, chairman, *FiberNet*)
3:45 Kenn Gardner (University of Delaware)
Workshop: Introduction to fiber diffraction
5:15 welcome and meeting information (Gerald Stubbs)

Steering Committee meeting 5:30 – 6:30

Monday, 7 August

8:00 Tom Irving and Joseph Orgel (Illinois Institute of Technology)
BioCAT
8:30 R. Chandrasekaran (Purdue University)
Polysaccharides: Paradigms or Puzzles?
9:10 Joseph Orgel (Illinois Institute of Technology)
Crystallographic approaches to studying biological fibers
9:50 panel workshop: John Squire, Ganeshalingam Rajkumar
CCP13 software

10:50 break

11:05 Tim Wess (Cardiff University)
Changing order and disorder in fibrous macromolecules
11:50 Amy Kendall (Vanderbilt University)
Oriented sols for fiber diffraction from limited quantities or hazardous materials
12:05 Olga Antipova (Illinois Institute of Technology)
The molecular structure of collagen type II

12:20 lunch

Afternoon free: enjoy Fall Creek Falls!

7:00 Paul Langan (Los Alamos National Laboratory)
Neutron fiber diffraction

8:00 posters

Tuesday, 8 August

8:15 Jianpeng Ma (Baylor College of Medicine)
Protein structural modeling guided by low-resolution experimental data
8:55 Kenn Gardner (University of Delaware)
New insights into the structure of poly(p-phenylene terephthalamide) from neutron fiber diffraction studies
9:15 panel workshop: Gerald Stubbs, Wen Bian, Alex Borovinskiy
FiberNet software

10:15 break

10:30 John Squire (Imperial College, London)
Fibre diffraction studies in muscle research
11:10 Dean Myles (Oak Ridge National Laboratory)
New opportunities for neutron structural biology at ORNL

11:45 lunch

1:00 leave for Oak Ridge to visit the Spallation Neutron Source & High Flux Isotope Reactor
return by about 6:00

7:00 posters (continued)

Wednesday, 6 August

9:00 Tom Irving (Illinois Institute of Technology)
Towards an understanding of stretch activation in insect flight muscle
9:35 Rick Millane (University of Canterbury, New Zealand)
Accounting for disorder in fiber diffraction analysis

10:15 break

10:35 Michele McDonald (Vanderbilt University)
Microchambers: fibers in an enclosed cell
10:50 Holger Wille (UCSF)
Studying the structure of infectious prions by fiber diffraction
11:05 Gerald Stubbs (Vanderbilt University)
A tale of two viruses
11:45 closing remarks (Gerald Stubbs)

checkout by 11:00 am

transport leaves for Nashville Airport approximately 12:45 pm

Workshop Participants

Olga Antipova, Illinois Institute of Technology, Chicago, IL	antiolg@iit.edu
Diana Bedolla, SISSA, Trieste, Italy	bedolla@sissa.it
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Holger Wille, University of California, San Francisco, CA	wille@cgl.ucsf.edu

FiberNet Steering Committee

Gerald Stubbs (chairman and ACA SIG chairman)
R. Chandrasekaran
Joseph Orgel
Tom Irving (BioCAT director)
Kenn Gardner
Dan Kirschner
Jianpeng Ma
Trevor Forsyth
John Squire (editor, Fibre Diffraction Review)
Tim Wess (CCP13 chairman)

We gratefully thank Amy Kendall for a major part of the organization of this meeting and Rebecca Stubbs for putting this abstract collection together.

ABSTRACTS

Polysaccharides: Paradigms or Puzzles?

R. Chandrasekaran

Purdue University

The molecular architecture of polysaccharides of biological importance and/or industrial utilization is well known from x-ray fiber diffraction studies. Among neutral polysaccharides, cellulose, mannan and chitin adopt canonical ribbon structures that lead to stacks of sheets commensurate with their water insoluble properties. However, surprisingly, sheet-forming guaran displays high viscosity in aqueous solution. Chitosan, the solitary cationic polysaccharide, often departs from the chitin-like structure. While anionic polysaccharides containing carboxylate groups (such as alginate, pectin, gellan family and hyaluronan) have robust helical structures and crystalline arrangements, those with sulfate groups (carrageenans) have flexible surface conformations on rigid cores and more complex packing modes. Binary systems involving anionic and neutral polysaccharides also exhibit novel features. Ionic and hydration effects account for some of these oddities.

Crystallographic approaches to studying biological fibers

Joseph P.R.O. Orgel[*], Shiamalee Perumal[*], Olga Antipova[*], Raul Barrea[*], Thomas C. Irving[*], Hélène Miller-Auer[†], Godfrey S. Getz[†], Kristi L. Lazar[†], and Stephen C. Meredith[†]

*Illinois Institute of Technology, †University of Chicago

A major focus of the research group based at Illinois Institute of Technology is the development of “Fiber Crystallography”, a term used for the application of single crystal associated techniques to fiber diffraction problems, as well as the development of new capabilities at BioCAT to facilitate the study of fibrous samples. Our work towards determining the structure of type I collagen is helping to drive these developments. This presentation will cover details of the structure of type I collagen and one of the development projects that involves the study of amyloid associated peptides and fibers.

Changing order and disorder in fibrous macromolecules

Tim Wess

School of Optometry and Vision Science, Cardiff University

Fibre diffraction affords the possibility of observing structural changes in dynamic systems where the lattice and ordering of systems can be challenged by a number of factors. In the presentation I will show changed induced in molecular structure by mechanical testing, radiation damage, heating, drying and cooling. Each case corresponds to phenomena required to be understood in a physiological process, or the modification of a structure as a function of attempting to examine it.

Examples of molecular hierarchies studied are from collagen (mechanical testing, radiation damage, cooling), fibrillin (mechanical testing) and cellulose (drying). The experimental observations will be complemented by the work in progress that is attempting to explain each of the observed effects.

Oriented sols for fiber diffraction from limited quantities or hazardous materials

Amy Kendall and Gerald Stubbs

Center for Structural Biology, Vanderbilt University

Specimens for fiber diffraction have traditionally been made either by orienting concentrated sample solutions or by drying fibers. We describe a new method for making oriented sols for fiber diffraction. Samples are made by centrifuging dilute solutions of filamentous assemblies in thin-walled glass X-ray capillaries for several days at low speeds. Orientation is improved by exposure to high magnetic fields. We have demonstrated this method for tobacco mosaic virus and potato virus X, and have shown the resulting orientation to be comparable with that achieved by conventional methods of specimen preparation. The method requires much smaller quantities than conventional methods, and is better suited for use with hazardous materials and labile assemblies. Supported by NSF MCB-0235653.

The molecular structure of collagen type II

Olga Antipova, Shiamalee Perumal, and Joseph P.R.O. Orgel

Illinois Institute of Technology

Collagen type II is the major structural component of extracellular matrices (ECM) of cartilages, invertebral discs, vitreous humour, dermis and notochord. Its interaction with other molecules is necessary for proper ECM functioning. Knowledge of the specific conformation of the collagen type II fibril is crucial, if the binding of ligands to collagen is to be understood.

Fiber diffraction methods are used to reveal the molecular structure of fibrils. This information can help us to understand ECM assembly during tissue development and turnover. The samples for our experiments were prepared from lamprey notochord, the best known source of highly organized collagen type II. We are also trying the approach of microfocus diffraction to improve spatial resolution of the Bragg reflections.

Determining tertiary topology of proteins from small angle X-ray scattering (SAXS) profiles

Jianpeng Ma and Yinghao Wu

Department of Biochemistry and Molecular Biology, Baylor College of Medicine

We report novel computational results for determining tertiary topology of small proteins or protein domains. A new multi-scale Monte Carlo simulation protocol was developed to enhance the sampling. In addition to the knowledge-based potential functions, small angle x-ray scattering (SAXS) profile was used as a weak constraint for guiding the folding. The results show that the method can consistently deliver structural models that are better than 5 ~ 6 Å cryo-EM maps by using SAXS data. The success of this computational method could enable the SAXS technique to be a fast and inexpensive solution-phase experimental method that could bridge a long-standing gap between x-ray crystallography and electron cryomicroscopy (cryo-EM) in determining structures of small, soluble, but noncrystallizable, proteins. This is because x-ray crystallography requires crystals and cryo-EM only works for very large complexes, while SAXS doesn't have any of these constraints. We hope that this will add a valuable tool for the community of structural genomics.

New insights into the structure of poly(*p*-phenylene terephthalamide) from neutron fiber diffraction studies

K. H. Gardner, A. D. English, and V. T. Forsyth

Department of Materials Science and Engineering, University of Delaware, DuPont Central Research and Development, Experimental Station Institut Laue Langevin, Lennard Jones Laboratory, School of Chemistry and Physics, Keele University

Poly(*p*-phenylene terephthalamide), PPTA, is a highly crystalline polymer that can be spun into fibers that exhibit exceptional thermal and mechanical properties. It has numerous commercial applications and is sold under the trade names of Kevlar and Twaron. In some respects the structure of PPTA is well-known - the unit cell parameters, chain conformation, and the hydrogen bonding of neighboring chains (between amide groups) to form sheets are all well established. However, the relative displacement of the chains and the nature of the intersheet interactions are still in question.

The aim of the current study is to resolve the issue of the structure of PPTA in a way that is compatible with the available neutron fiber diffraction data. It is clear that previous X-ray fiber diffraction work has suffered from the fact that the terephthaloyl and diamine groups differ only slightly in their overall scattering of X-rays. As a result, it has proved difficult to distinguish between a number of competing models. A key aspect of this study has been the use of selectively deuterated PPTA fibers in which the terephthaloyl residues were selectively deuterated, so that the terephthaloyl and diamine groups make markedly different contributions observed neutron diffraction patterns.

This study highlights a number of issues relating to the use of neutron fiber diffraction for the study of polymer conformation and the complementarity of such work with X-ray diffraction studies.

Fibre diffraction studies in muscle research

John Squire[*] Hind AL-Khayat[*] Carlo Knupp[+], Felicity Eakins[*], and Ganeshalingam Rajkumar[*]

*Imperial College London, UK [+]University of Cardiff, UK

Two kinds of muscle are sufficiently well ordered in 3D to allow rigorous analysis of their low-angle X-ray fibre diffraction patterns. These muscles are the skeletal muscles from bony fish and the flight muscles from insects. This talk will discuss structural analysis of bony fish muscle diffraction data, what has been achieved so far and what kinds of developments are in the pipeline. It will also describe new software, apart from FibreFix for data reduction, which is helping to analyse the observed diffraction patterns. Muscle diffraction patterns are immensely rich and can yield vital information about muscle structure and the force-producing mechanism, but without careful analysis they can be misleading.

Towards an understanding of stretch activation in insect flight muscle.

Tom Irving

Illinois Institute of Technology

Stretch dependent activation is a property of all striated muscles. It may be particularly important in cardiac muscle where the contraction of one region stretch activates neighboring regions adding ejection during the heart-beat. The indirect flight muscles (IFM's) of insects are ideal model systems to study mechanisms of length-dependent activation not only because the phenomenon of stretch activation is particularly strong in these muscles but also because of their high degree of structural order. Dickinson *et al.*, 2006, Nature 433:330-333, on the basis of their time resolved fiber diffraction study of living *Drosophila* during tethered flight, proposed a model for stretch activation where strain in the thick filaments is transmitted to the thin filaments via bond myosin cross-bridges. This model will be discussed in the context of new analyses of fiber diffraction data from IFM's from *Drosophila* and the giant waterbug Lethocerus.

Accounting for disorder in fiber diffraction analysis

Rick Millane

University of Canterbury, NZ

Fiber specimens are by their nature disordered. They always exhibit some degree of disorientation, they often lack crystallinity, and even polycrystalline fibers have a limited crystallite size. These effects are generally taken into account when processing and interpreting diffraction data. However, polycrystalline specimens can also exhibit various forms of packing disorder within the crystallites which has more complex effects on diffraction patterns. I will discuss various characteristics of the packing disorders which can occur, the effect on diffraction patterns, and how these might be accounted for in structure determination.

Microchambers: fibers in an enclosed cell

Michele McDonald, Sarah Tiggelaar, Amy Kendall, and Gerald Stubbs

Center for Structural Biology, Vanderbilt University

Humidity control is used in fiber diffraction to slow the drying process of fibers. We have designed a cell that effectively controls humidity of a fiber even while mounted on a synchrotron beamline. The microchamber is manufactured from inexpensive materials, is easily mass produced, and requires relatively small amounts of sample material. It is also suitable for magnetic alignment and stretching fibers. The microchamber does not interfere with diffraction patterns and is adaptable to a range of resolutions. Supported by NSF MCB-0235653 and NIH P01 AG010770.

Studying the structure of infectious prions by fiber diffraction

Holger Wille[2,3], Alexander Borovinskiy[1], Michele McDonald[4], Amy Kendall[4], Gerald Stubbs[4], Fred E. Cohen[1,3,5], and Stanley B. Prusiner[2,3,5]

Departments of [1]Cellular and Molecular Pharmacology, [2]Neurology, [5]Biochemistry and Biophysics, and [3]Institute for Neurodegenerative Diseases, University of California, San Francisco, and [4]Center for Structural Biology, Vanderbilt University

Prion diseases are associated with conversion of the cellular, non-infectious prion protein (PrP^{C}) to the infectious, scrapie isoform (PrP^{Sc}). A conformational change in the prion protein gives rise to a large increase in beta-sheet content, which is also considered a key feature for the formation of fibrillar assemblies. Recently, we obtained a partially oriented X-ray diffraction pattern of infectious prion rods (N-terminally truncated PrP^{Sc}, or PrP 27-30) that were extracted from scrapie-infected Syrian hamster brains. The diffraction pattern demonstrated the cross-beta structure typical for amyloid and also showed a number of peaks in the equatorial region. An initial analysis of the pattern suggests that the trimeric left-handed beta-helical model of Govaerts et al. (PNAS, 2004) satisfies most of the constraints provided by the diffraction pattern. We refined this structural model in order to accommodate the experimental data.

A tale of two viruses

Gerald Stubbs, Amy Kendall, and Michele McDonald

Center for Structural Biology, Vanderbilt University

Filamentous plant viruses make up almost half of plant virus genera, with hundreds of individual species recognized. Two of the largest families, the *Potyviridae* and the *Flexiviridae*, have some morphological similarities, but are significantly different chemically and biologically. We have obtained fiber diffraction data from a number of viruses from these two families, particularly from narcissus mosaic virus, a *Potexvirus* from the *Flexiviridae*, and soybean mosaic virus, a *Potyvirus* from the *Potyviridae*. Potexvirus data are from oriented sols; potyvirus data are from fibers dried under high humidity. The data include the first well-ordered data ever obtained for the potyviruses, and considerably illuminate the relationship between the two families.
Supported by NSF MCB-0235653 and USDA 2003-01178.

POSTER ABSTRACTS

The *in situ* structure and arrangement of collagen type I

Olga Antipova[*], Shiamalee Perumal[*], Tim J. Wess[†], Andrew Miller[‡], Thomas C. Irving[*], and Joseph P.R.O. Orgel[*]

*Illinois Institute of Technology, †Cardiff University, ‡University of Stirling

The fibrous collagens are ubiquitous in animals and form the structural basis of all mammalian connective tissues including those of the heart, vasculature, skin, bones, cartilages and tendons. But in comparison with what is known of their production, turnover and physiological structure, very little is understood regarding the three-dimensional arrangement of collagen molecules in naturally occurring fibrils. This knowledge may provide insight into key biological processes such as fibrillogenesis and tissue remodeling and into diseases such as heart disease, arthritis and cancer. Here we show recent progress in determining the structure of collagen type I, and investigations into the significance of this structure to the mammalian ECM.

Thick filaments in *Dipteran* indirect flight muscle are not in axial register

Tanya I. Bekyarova[2], John M. Squire[1], Mary C. Reedy[3], Gerrie P. Farman[4], Michael H. Dickinson[5], Mark A. Frye[6], David W. Maughan[7], Michael K. Reedy[3] and Tom C. Irving[2]

[1]Imperial College, London, United Kingdom, [2]Illinois Institute of Technology, Chicago, IL ,USA, [3]Duke University, Durham, NC, USA, [4]University of Illinois at Chicago, Chicago, IL, USA, [5]Caltech, Pasadena, CA, USA, [6]UCLA, Los Angeles, CA, USA, [7]University of Vermont, Burlington, VT, USA.

The indirect flight muscles of insects have been an important model system for structural studies of crossbridge arrangements in striated muscles because of their high degree of crystalline order. While most of this work to date has been on IFM from the giant waterbug *Lethocerus sp.*, IFM from the fruit fly (*Drosophila sp.*) is becoming of increasing importance. Low-angle X-ray diffraction patterns from relaxed Drosophila flight muscle show many features similar to such patterns from *Lethocerus*, but there is a characteristically different pattern of sampling of the myosin filament layer-lines that indicates the presence of a superlattice structure for the myosin filaments in the *Drosophila* A-band. We show from analysis of the structure factor for this lattice that the sampling pattern is exactly as expected if adjacent 4-stranded myosin filaments, of repeat 1160 Å, are axially shifted in the hexagonal A-band lattice by one-third of the 145 Å axial spacing between crowns of myosin heads. Thin filaments in electron micrographs of longitudinal sections of Drosophila IFM have been observed that show periodic labeling by myosin heads in a perpendicular orientation on one side of the filament with the heads on the other side at an oblique angle consistent with our proposed axial stagger between thick filaments on either side of a given thin filament. In addition, electron micrographs of the Blowfly (*Sarcophaga*), suggest that the same A-band superlattice occurs here as found in *Drosophila*. This different A-band organization in flies compared with *Lethocerus*, which operates at a much lower wing beat frequency (~30 Hz), may offer a way of optimizing the myosin and actin filament geometry needed for stretch activation and for rapid continuous force application to the higher wingbeat frequencies (200 Hz) found in flies.

Modeling the structure of mammalian prions based on fiber diffraction data

Alexander Borovinskiy[1], Holger Wille[2,3], Michele McDonald[4], Amy Kendall[4], Gerald Stubbs[4], Stanley B. Prusiner[2,3,5], and Fred E. Cohen[1,3,5]

Departments of [1]Cellular and Molecular Pharmacology, [2]Neurology, [5]Biochemistry and Biophysics, and [3]Institute for Neurodegenerative Diseases, University of California, San Francisco, and [4]Center for Structural Biology, Vanderbilt University

Prion diseases are associated with conversion of the cellular, non-infectious prion protein (PrP^{C}) to the infectious, scrapie isoform (PrP^{Sc}). A conformational change in the prion protein gives rise to a large increase in beta-sheet content, which is also considered a key feature for the formation of fibrillar assemblies. Recently, we obtained a partially oriented X-ray diffraction pattern of infectious prion rods (N-terminally truncated PrP^{Sc}, or PrP 27-30) that were extracted from scrapie-infected Syrian hamster brains. The diffraction pattern demonstrated the cross-beta structure typical for amyloid and also showed a number of peaks in the equatorial region. An initial analysis of the pattern suggests that the trimeric left-handed beta-helical model of Govaerts et al. (PNAS, 2004) satisfies most of the constraints provided by the diffraction pattern. We refined this structural model in order to accommodate the experimental data. We also describe results on modeling the structure of a prion peptide [PrP(89–143,P101L)] based on earlier diffraction data (Inouye et al., JMB, 2000), and how this model relates to that for PrP 27-30.

Polymorphic and pseudopolymorphic behavior of the sodium salt of iota-carrageenan

S. Janaswamy and R. Chandrasekaran

Purdue University

X-ray fiber diffraction patterns of the sodium salt of ι-carrageenan are diagnostic of three (I, II, and III) distinct packing arrangements. Surprisingly, the helical repeat (*c*-axis 13.0 to 13.2 Å) of the polymer is nearly the same, but there are dissimilarities in the basal net dimensions. Two of them crystallize in similar trigonal nets with a = 24.02 for I and 21.8 Å for III. But, II favors an orthogonal net with a = 13.70, b = 20.08 Å. Previous structure analysis on polymorph I has shown that three half-staggered double helices in the unit cell, each pair at 13.9 Å apart, are able to interact through their 2-sulfate and 4-sulfate groups with the aid of sodium ions and ordered water molecules [Janaswamy, S.; Chandrasekaran, R. *Carbohydr. Res.* 2001, *335*, 181–194]. However, the present observation of two more crystalline structures for the same salt form, in which the helix-helix separations are considerably shorter, suggest that the sulfate group orientations as well as inter helical interactions are unique to each polymorph. This novel finding reflects the ramifications to the practical applications of ι-carrageenan in food and pharmaceutical industries.

Sheet formation from arabinan association: results from powder diffraction data

S. Janaswamy and R. Chandrasekaran

Purdue University

X-ray fiber diffraction is a powerful technique for unraveling the helix-forming biopolymer structures. This experimental tool combined with computer modeling is instrumental in providing the molecular details and hence insights on several polysaccharides of biological and industrial importance. However, some of them fail to yield good quality fiber patterns and, instead, render powder patterns. The debranched arabinan (a plant polysaccharide), branched bacterial S-657 (a polysaccharide in the gellan family) and κ-carrageenan (a gel forming seaweed) are three known paradigms. X-ray powder diffraction data from debranched arabinan suggest that all the observed peaks index on a monoclinic cell with a = 5.444(7), b = 6.395(10), c = 8.680(5) Å, and γ = 99.6(3)º. The unit cell can accommodate one 2-fold helix along the c-axis. Compatible molecular and packing models have been developed by LALS and refined against powder intensities using the Rietveld analysis. Results reveal that in the best model, arabinan helices associate along the b-axis through inter-chain O3–H···O2 bonds leading to a continuous stack of arabinan sheets separated by the cell edge a.

A seven-residue peptide from the yeast prion protein Sup35 as a model for amyloids

Michele McDonald[1], Sarah Tiggelaar[1], Alexander Borovinskiy[2], Amy Kendall[1], and Gerald Stubbs[1]

[1]Center for Structural Biology, Vanderbilt University and [2]Department of Cellular and Molecular Pharmacology, University of California, San Francisco

The yeast prion protein Sup35 demonstrates many of the physical and biological properties of mammalian prions and other amyloids. The seven-residue sequence GNNQQNY from Sup35 forms amyloid fibrils; the peptide has also been crystallized and the crystal structure determined (Nelson *et al*., 2005, *Nature* **435**, 773). We have obtained highly detailed fiber diffraction patterns from oriented dried fibers of GNNQQNY, which show the cross-β meridional features typical of amyloids. We have developed a model for the fibril based on the published crystal structure, wide- and low-angle diffraction patterns, and electron micrographs of the fibrils.
Supported by NIH P01 AG010770.

Fiber crystallography at the BioCAT facility at the Advanced Photon Source

Joseph P.R.O. Orgel, Raul Barrea, Shiamalee Perumal, Olga Antipova, and Thomas C. Irving

Illinois Institute of Technology

The BioCAT facility is a NIH Biotechnology Research Resource dedicated the study of non-crystalline biological materials located at the Advanced Photon Source, Argonne National Laboratory. Supported techniques are fiber diffraction, small-angle scattering from macromolecules in solution and micro-emission and micro-absorption X-ray spectroscopic imaging of biological tissues. There is a large class of fibrous biological materials that can be subjected to crystallographic analysis. These include biological materials that naturally possess a relatively high degree of order (muscle, collagens type I and II in certain fibrillar tissues) and others that may be oriented by flow or the use of strong magnetic fields (actin, microtubules, filamentous viruses, complex carbohydrates, amyloids and other peptide fibrils). Here we report on recent developments to allow high-resolution fiber crystallography on such systems. We have also done preliminary micro-diffraction experiments that show the promise of micron-scale fiber diffraction to examine the distribution of locally ordered structures in tissues. Applications to neuro-degenerative disease, heart disease and cancer are discussed. Supported by NIH P41 RR008630.

The structure of crystalline natural rubber

Ganeshalingam Rajkumar, Struther Arnott, and John M. Squire

Biological Structure & Function Section, Imperial College London

Natural rubber is an elastic solid obtained from latex and is one of the most important and unusual polymers naturally produced by plants. The basic structural unit of natural rubber is cis-polyisoprene $(-CH_2-CCH_3=CH-CH_2-)_n$. Rubber is crystallised either by cooling it to below 0°C, when it remains disoriented, or by stretching a specimen to several times its original length when uniaxial orientation is obtained. The difficulty in modelling oriented polyisoprene is that alternative molecular structures consist of polyisoprene chains that are very similar to one another at the resolution of the available X-ray diffraction data. Even though many researchers including Bunn [1] and Nyburg [2] have studied possible molecular conformations and packing, no definitive structure for crystalline rubber has yet been defined.

In the present study we have found a satisfactory structure for crystalline natural rubber that overcomes the problems with the Bunn and Nyburg models. The structure analysis was carried out using the Linked Atoms Least Squares (LALS) program [3] under the auspices of the CCP13 project [4]. The best model had an orthorhombic unit cell of dimensions **a** = 12.58 Å, **b** = 8.98 Å and **c** = 8.20 Å and a $P2_12_12_1$ space group. Our structure is more satisfactory than Bunn's in its stereochemical orthodoxy and gives a much better fit with the X-ray data. It shares common features with the Nyburg model, namely that it is a 'statistical' model and has orthorhombic symmetry, but the space group is different.

[1] Bunn, C. W. Proc. R. Soc. London 1942, 180, 40.

[2] Nyburg, S. C. Acta Crystallogr. 1954, 7, 385.

[3] Kenji Okada, Keiichi Noguchi, Kenji Okuyama, Struther Arnott, Computational Biology and Chemistry 2003,27 265-285.

[4] www.ccp13.ac.uk (BBSRC Project #25/B15281).