



The April 25 1953 issue of the journal *Nature* carried three classic papers collectively entitled 'Molecular Structure of Nucleic Acids' published back to back. The paper by Rosalind Franklin and R G Gosling was preceded by the paper of Watson and Crick that announced their famous model of DNA and one from the Wilkins group. For most biologists, the paper by Watson and Crick is very lucid, as it is not constrained by hard data and interpretations, whereas the one by Franklin and Gosling is elegant but technical. All the same, among the three, only Franklin's had real data relevant to the model, her beautiful X-ray photograph of B-DNA and the parameters of the double helix calculated from it. Yet, it is ironic that the paper gives the impression of being just an afterthought, with the statement "Thus, our general ideas are not inconsistent with the model proposed by Watson and Crick in the preceding communication". With her insight and original data, Rosalind Franklin would have been the most likely person who would have solved the structure of DNA if Watson and Crick had not seen her data and come up with the model first. But her approach would have been more formal, deducing it from first principles using Fourier transforms, as she was not in favour of short-cut methods such as model building. The full text of her classic paper is reproduced below.

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Molecular Configuration in Sodium Thymonucleate

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Sodium thymonucleate fibres give two distinct types of X-ray diagram. The first corresponds to a crystalline form, structure *A*, obtained at about 75 per cent relative humidity; a study of this is described in detail elsewhere [1]. At higher humidities a different structure, structure *B*, showing a lower degree of order, appears and persists over a wide range of ambient humidity. The change from *A* to *B* is reversible. The water content of structure *B* fibres which undergo this reversible change may vary from 40-50

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per cent to several hundred per cent of the dry weight. Moreover, some fibres never show structure *A*, and in the structure *B* can be obtained with an even lower water content.

The X-ray diagram of structure *B* (see photograph⁺) shows in striking manner the features characteristic of helical structures, first worked out in this laboratory by Stokes (unpublished) and by Crick, Cochran and Vand [2]. Stokes and Wilkins were the first to propose such structures for nucleic acid as a result of direct studies of nucleic acid fibres, although a helical structure had been previously suggested by Furberg (thesis, London, 1949) on the basis of X-ray studies of nucleosides and nucleotides.

While the X-ray evidence cannot, at present, be taken as direct proof that the structure is helical, other considerations discussed below make the existence of a helical structure highly probable.

Structure *B* is derived from the crystalline structure *A* when the sodium thymonucleate fibres take up quantities of water in excess of about 40 per cent of their weight. The change is accompanied by an increase of about 30 per cent in the length of the fibre, and by a substantial re-arrangement of the molecule. It therefore seems reasonable to suppose that in structure *B* the structural units of sodium thymonucleate (molecules or groups of molecules) are relatively free from the influence of neighbouring molecules, each unit being shielded by a sheath of water. Each unit is then free to take up its least-energy configuration independently of its neighbours and, in view of the nature of the long-chain molecules involved, it is highly likely that the general form will be helical [3]. If we adopt the hypothesis of a helical structure, it is immediately possible, from the X-ray diagram of structure *B*, to make certain deductions as to the nature and dimensions of the helix.

The innermost maxima on the first, second, third and fifth layer lines lie approximately on straight lines radiating from the origin. For a smooth single-strand helix the structure factor on the *n*th layer line is given by:

$$F_n = J_n(2\pi r R) \exp i n (\psi + 1/2 \pi),$$

where $J_n(u)$ is the *n*th-order Bessel function of *u*, *r* is the radius of the helix, and *R* and ψ are the radial and azimuthal co-ordinates in reciprocal space [2]; this expression leads

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