A STRUCTURE FOR D.N.A.

Pauling and Corey[1] have recently proposed a structure for nucleic acid. They were kind enough to make their manuscript available to us in advance of publication. In our opinion their structure is unsatisfactory for two reasons:

1. We believe that the material which gives the X-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other.

2. Some of the van der Waals distances appear to be too small.

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has two helical chains each coiled round the same axis. The two chains (but not their bases) are related by a dyad perpendicular to this axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions. Each chain loosely resembles Furberg's[2] model No.1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's "standard configuration", the sugar being roughly perpendicular to the attached base. There is a residue on each chain every 3.4 Å in the z direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 Å. The distance of a

phosphorus atom from the fibre axis is 10 Å. The structure is an open one and its water content will therefore be rather high. As the phosphates are on the outside, cations have easy access to them.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so that the two lie side-by-side with identical z co-ordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows:

Purine position 1 to pyrimidine position 1

Purine position 6 to pyrimidine position 6

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms, (that is with the keto rather than the enol configurations) it is found that only <u>specific</u> pairs of bases can bond together. These pairs are:

Adenine (purine) with Thymine (pyrimidine)

Guanine (purine) with Cytosine (pyrimidine)

In other words, if an adenine forms one member of a pair, on either chain, then <u>on these assumptions</u> the other member <u>must</u> be thymine. Similarly for guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only <u>specific</u> pairs of bases can be formed it follows that if the sequence of bases on one chain is given, then the sequence on the other chain is automatically determined. ~~Even if the pairing is not~~

It has been found experimentally [3,4], that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine are always very close to unity for D.N.A.

It is probably impossible to build this structure with a ribose sugar in place of the desoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

The published X-ray data[5,6] on D.N.A. are inadequate. As far as we can tell, our structure is roughly compatible with the experimental data. It is known[7] that there is much unpublished experimental material. Until this has been used to test the structure it must be regarded as unproved.

It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material.

Full details of the structure, including the conditions assumed in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

We are heavily indebted to Dr. Jerry Donohue for constant advice and criticism, especially on inter-atomic distances. We have also been stimulated by the very beautiful experimental work of Dr. M. F. Wilkins and his co-workers at Kings College, London.

J. D. Watson

F. H. C. Crick.

MRC unit etc.

REFERENCES

1. Pauling, L. and Corey, R.B. Nature 171, 346, (1953): Proc. Nat. Acad. Sci. Wash. 39, 84 (1953)

2. Furberg, S. Acta Chem. Scand. 6, 634 (1952)

3. Chargaff, E. for references see Zamenhof, S., Lawerman, G. and Chargaff, E. Biochem. et Biophys. Act. 9, 402, (1952)

4. Wyatt, G. R. Jour. Gen. Phys. 36, 201, (1952)

5. Astbury, W.T. Symposium No. 1 of the Society for Experimental Biology, 66 (1947)

6. Wilkins, M.H.F. and Randall, J.T. Biochem et Biophys. Acta 10, 192 (1953).

7. Wilkins, M.H.F. - personal communication.

REFERENCES.

1. Pauling, L., and Corey, R.B., Nature, 171, 346 (1953): Proc. Nat. Acad. Sci. Wash. 39, 84 (1953).

2. Furberg, S., Acta Chem. Scand. 6, 634, (1952).

3. Chargaff, E., For references see Zamenhof, S., Brawerman, G. and Chargaff, E., Biochem. et Biophys. Acta, 9, 402, (1952)

4. Wyatt, G. R., Journ. Gen. Phys. 36, 201, (1952.)

5. Astbury, W.T., Symposium No.1 of the Society for Experimental Biology, 66 (1947).

6. Wilkins, M. H. F. and Randall, J.T. Biochem et Biophys. Acta 10, 192, (1953).

7, Wilkins

~~7. Wilkins, M. H. F. et al. (unpublished).~~

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