

Race for the Double Helix

This Assignment consists of 3 parts

Part I: QUESTIONS (answer while watching movie) **(due February 2, 2004)**
(see below for questions)

Part II: COMMENTARY (due February 3, 2004)

Part III: ASSESSMENT (in class February 6, 2003)

Part II COMMENTARY

Read and comment on the Nobel Prize Winning paper from Nature-[April 1953](http://biocrs.biomed.brown.edu/Books/Chapters/Ch_8/DH-Paper.html) on DNA structure.
http://biocrs.biomed.brown.edu/Books/Chapters/Ch_8/DH-Paper.html

Please include the answers to the following questions in the commentary

1. Describe the major significance of this specific structure?
2. Explain why a triple helix model didn't work to explain DNA structure
3. What is the novel feature of the Watson-Crick Model?
4. How does the sequence of one side of DNA determine the other side?

Please cite any reference source you used in the proper manner

This commentary on the [1953 Nature](http://www.accessexcellence.org/AB/BC/casestudy2.html) article may help
<http://www.accessexcellence.org/AB/BC/casestudy2.html>

Part III ASSESSMENT

This will be an **in-class ASSESSMENT**

Please prepare your answers ahead of time. You may use your own notes, outlines, etc during the assessment.

ANSWER BOTH QUESTIONS.....THIS MEANS YOU HAVE TO BE PREPARED!!!!

1. Many biologists feel that the discovery of DNA structure is the most significant biological discovery of the 20th century. In a well-written paragraph, please discuss why scientists think this way and what you think about DNA as the most significant biological discovery. Also, comment on whether or not you think they deserved the Nobel Prize
2. Select one of the characters in the **RACE** (Crick, Franklin, Watson, or Wilkins) and comment on his or her motivation in science. Use specific quotes or scenes from the film to support your answer. This answer should be at least 2 paragraphs long.



Name _____ Period _____ Date _____

Part I Questions

1. Who is one of the "believers"?
2. Name the bright hope.
3. What is the gossip?
4. What are the goals, and who is goal oriented?
5. What is the "buried treasure"? Who possesses it?
6. What is the "A" form of DNA? Who is working on it?
7. What is the "B" form of DNA? Who is working on it?
8. How do the scientists look at the structure of DNA?
9. What are the little problems?
10. Who are the " little boys"?
11. What didn't she see?
12. How did they pair the bonds? Were the paper cutouts of any value?
13. What is beautiful?
14. What benefits would have been achieved if everyone would have shared information



Film Synopsis

<http://www.skidmore.edu/~mmarx/LS12000/helixintro.htm>

The film opens in 1951, when the young American biologist James D. Watson (1928-), attending a conference in Italy, is jolted into active pursuit of the structure of DNA by an X-ray diffraction image of a DNA sample presented by the English biophysicist Maurice Wilkins. Since Wilkins's image reveals the regularity of a crystal, Watson is convinced that DNA might be analyzed by straightforward methods that have previously succeeded in solving the structure of other types of crystals. This conviction carries Watson to England, where the technique of X-ray crystallography is most advanced. However, since various attempts (including an introduction to Watson's sister) have failed to impress Wilkins, Watson does not join Wilkins at King's College, London, but instead goes to Cambridge University, where he teams up with Francis Crick (1916-), another physicist who has turned his attention to problems in biology. The Cavendish Laboratory at Cambridge, where Watson and Crick work, is headed by Sir Lawrence Bragg (1890-1971), who shared a Nobel Prize in physics with his father in 1915 for their research in X-ray crystallography. The crucial steps in applying the technique of X-ray diffraction to DNA research, however, take place at King's College, London, through the expertise of Rosalind Franklin (1920-1958)-- an expertise she acquired through the study of coal. Although Franklin and Wilkins find it difficult to work together, the possibility of their collaboration heats up the race to discovery, as Watson and Crick see it. They are already worried that the American chemist Linus Pauling (1901-1994) is closing in on a solution.

By the first week of March 1953, Watson and Crick have won the race. In the model they construct that week, DNA (deoxyribonucleic acid) takes the shape of a spiral staircase (a "double helix," in geometrical terms), with the steps composed of pairs of molecules known as bases, and the formed by chains of sugar and phosphate molecules. Because the same types of bases always pair together (adenine with thymine, guanine with cytosine), one half of the DNA staircase (the sequence of bases attached to either sugar-phosphate chain) contains enough information to reproduce the entire structure (the basis for biological reproduction). Moreover, the sequence of bases along the sugar-phosphate chain makes up a code of genetic information. An alphabet of only four letters, A, T, G, C (the initial letters of the names of the bases), produces enough variations in genetic information to account for the great diversity of all living things, including human beings.

Although he did not win the race for the double helix, Linus Pauling won a Nobel Prize in chemistry in 1954 for his work on the nature of chemical bonding. In 1962 (the same year Pauling won the Nobel peace prize for his advocacy of nuclear weapons control), Watson, Crick and Wilkins shared the Nobel Prize in physiology or medicine for their work on the structure of DNA. Rosalind Franklin was not considered for that prize because the rules require that recipients be living at the time of the award, and Franklin had died four years earlier.



A Structure for Deoxyribose Nucleic Acid

<http://biocrs.biomed.brown.edu/Books/Chapters/Ch%208/DH-Paper.html>

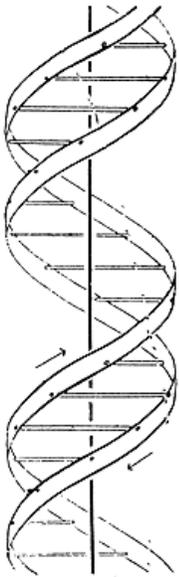
The year 1953 could be said to mark, in biology at least, the end of history. Here is James Watson and Francis Crick's paper on the structure of DNA, which ushered in the new era with the celebrated understatement near the end. (as published in NATURE magazine)

2 April 1953

MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

We wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.



A structure for nucleic acid has already been proposed by Pauling and Corey (1). They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this 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.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This structure as described is rather ill-defined, and for this reason we shall not comment on it.

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate diester groups joining β -D-deoxyribofuranose residues with 3',5' linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre 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 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 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. As the phosphates are on the outside, cations have easy access to them.

This figure is purely diagrammatic. The two ribbons symbolize the two phosphate-sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

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 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 specific pairs of bases can bond together. These pairs are : adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must 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 specific 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.

It has been found experimentally (3,4) that the ratio of the amounts of adenine to thymine, and the ration of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact. The previously published X-ray data (5,6) on deoxyribose nucleic acid are insufficient for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the following communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereochemical arguments.

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 much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on interatomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at King's College, London. One of us (J. D. W.) has been aided by a fellowship from the National Foundation for Infantile Paralysis.

J. D. WATSON F. H. C. CRICK

Medical Research Council Unit for the Study of Molecular Structure of Biological Systems, Cavendish Laboratory, Cambridge. April 2.

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