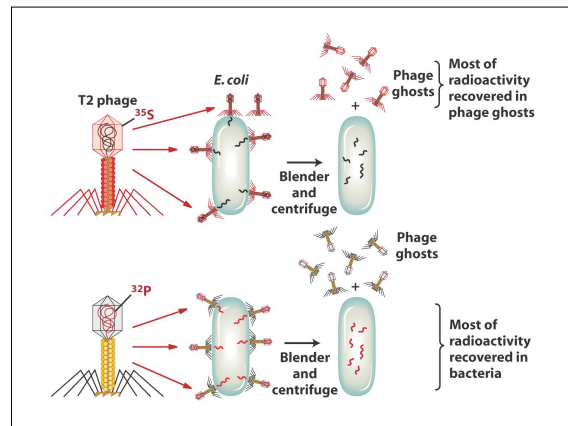
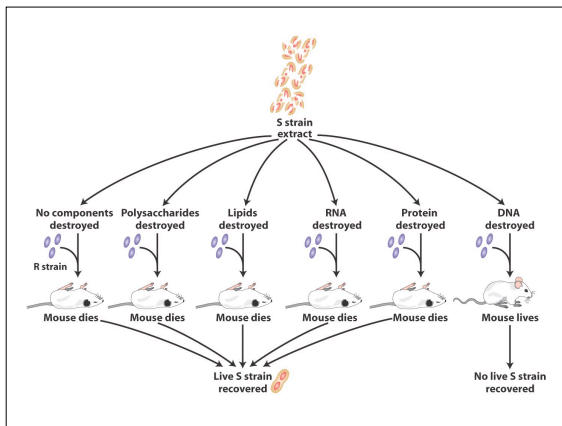
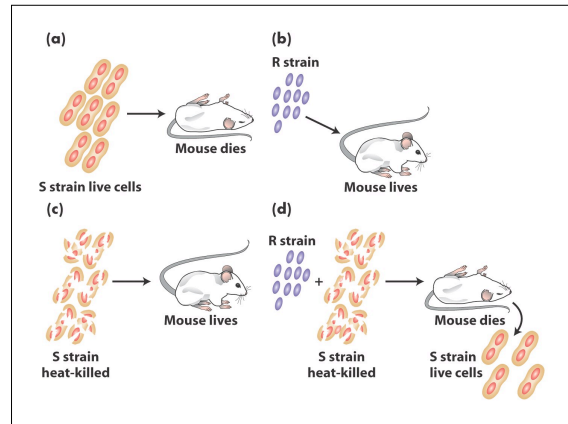


## DNA structure and replication

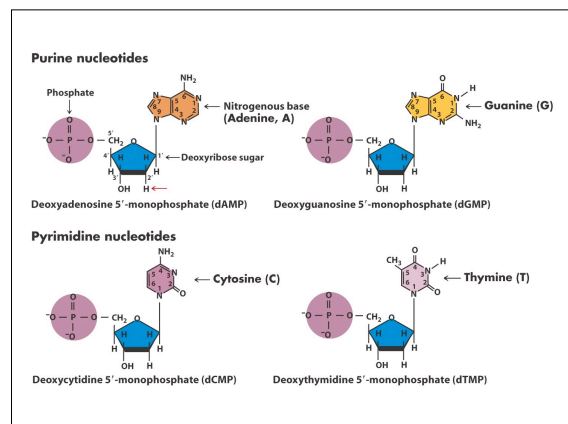
### What was known?

- 1) Hereditary factors were associated with specific traits
- 2) One-gene-one-protein model - from mapping genes for biosynthetic pathways
- 3) Genes are on chromosomes
- 4) Chromosomes are made up of DNA and protein



## Three key features needed for any model of DNA structure

- 1) Must allow for faithful replication
- 2) Must have information content
- 3) Must be able to change in order to explain mutations



**Table 7-1 Molar Properties of Bases\* in DNAs from Various Sources**

Organism	Tissue	Adenine	Thymine	Guanine	Cytosine	$\frac{A + T}{G + C}$
<i>Escherichia coli</i> (K12)	—	26.0	23.9	24.9	25.2	1.00
<i>Diplococcus pneumoniae</i>	—	29.8	31.6	20.5	18.0	1.59
<i>Mycobacterium tuberculosis</i>	—	15.1	14.6	34.9	35.4	0.42
Yeast	—	31.3	32.9	18.7	17.1	1.79
<i>Paracentrotus lividus</i> (sea urchin)	Sperm	32.8	32.1	17.7	18.4	1.85
Herring	Sperm	27.8	27.5	22.2	22.6	1.23
Rat	Bone marrow	28.6	28.4	21.4	21.5	1.33
Human	Thymus	30.9	29.4	19.9	19.8	1.52
Human	Liver	30.3	30.3	19.5	19.9	1.53
Human	Sperm	30.7	31.2	19.3	18.8	1.62

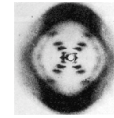
\*Defined as moles of nitrogenous constituents per 100 g-atoms phosphate in hydrolysate.  
Source: E. Chargaff and J. Davidson, eds., *The Nucleic Acids*, Academic Press, 1955.



James Watson Francis Crick



Rosalind Franklin



X-ray diffraction  
Photograph of B-DNA



Maurice Wilkins



Linus Pauling

*Nature* 171, 737-738 (1953) © Macmillan Publishers Ltd.

**Molecular structure of Nucleic Acids**  
WATSON, J. D. & CRICK, F. H. C.

**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.....

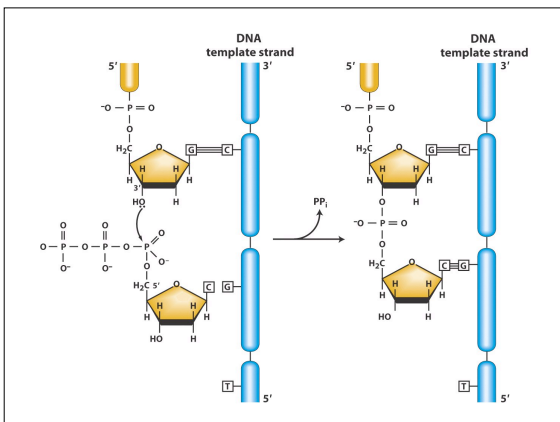
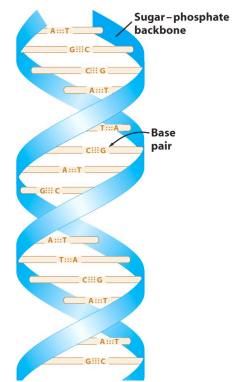


**Figure 1.** This figure is purely diagrammatic. The two ribbons symbolize the two phosphate-sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis.

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

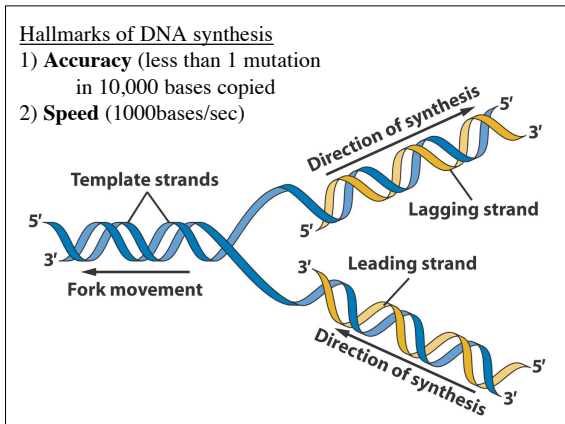
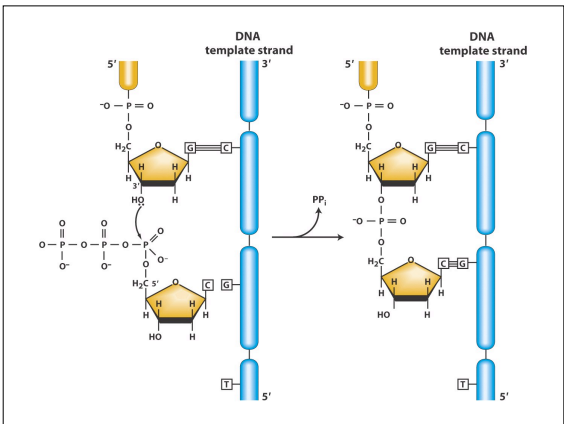
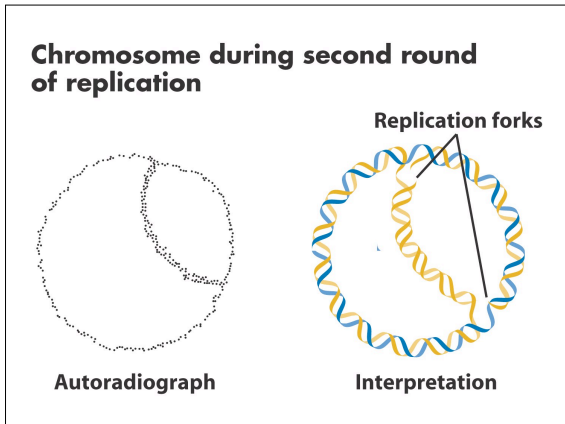
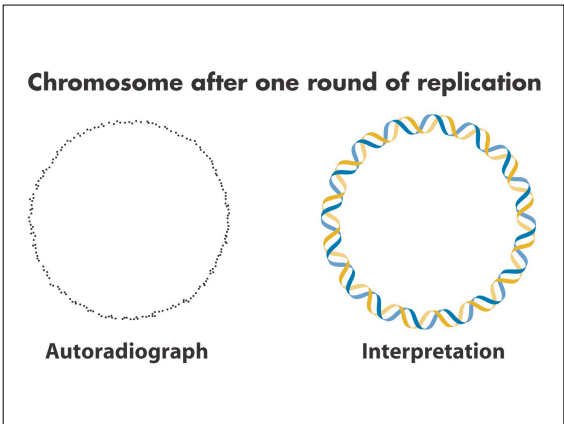
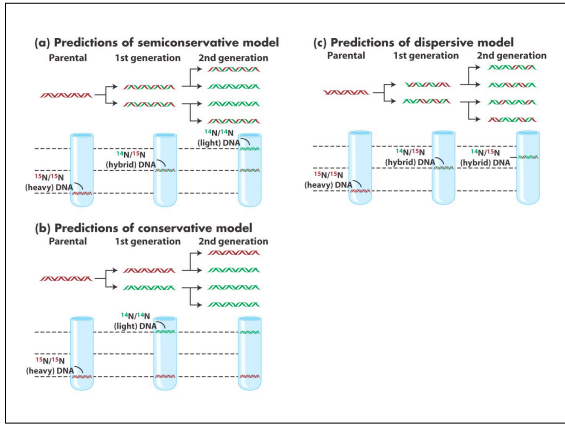
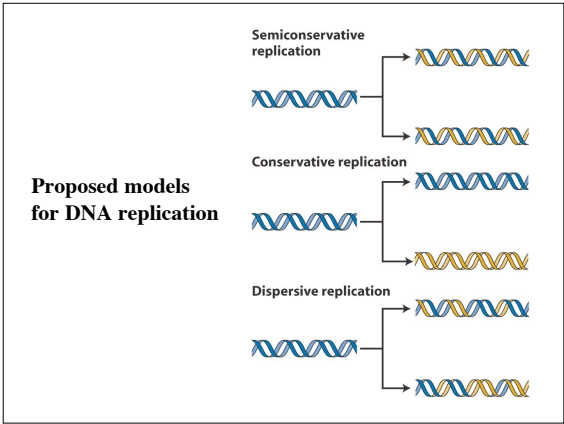
**Features of the double helix**

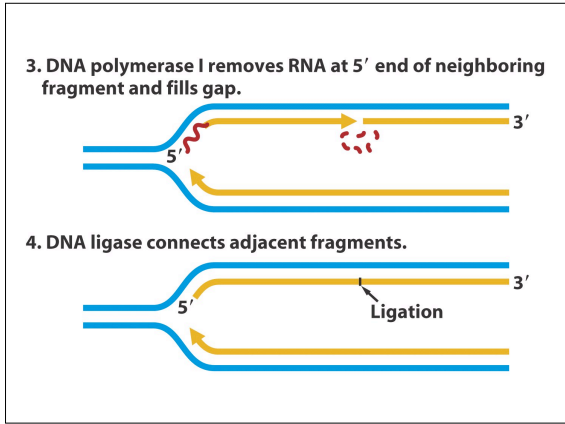
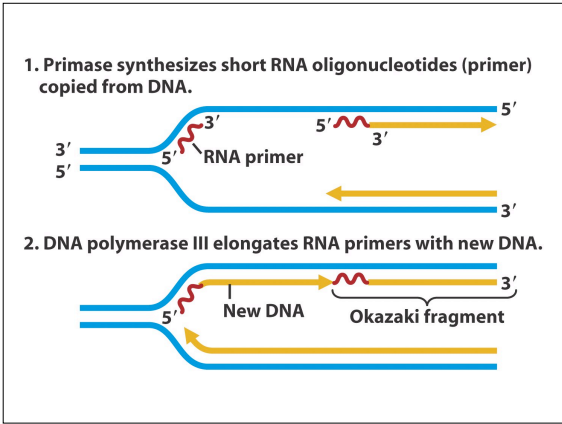
- 1) Two parallel strands
- 2) Bases held together by H-bonds
- 3) Phosphodiester backbone
- 4) The base is attached to the position 1 on the sugar
- 5) Base pair stack - provides stability
- 6) Contains a major and minor groove



**Three key features needed for any model of DNA structure**

- 1) Must allow for faithful replication - each strand of DNA serves as a template for replication
- 2) Must have information content - the sequence of bases predict the sequence of amino acids in proteins
- 3) Must be able to change in order to explain mutations - changes in DNA sequences result in changes in the amino acid sequence in proteins





**Players:**

- DNA gyrase** - a topoisomerase
- Primase** - RNA polymerase - synthesizes a primer
- Helicase** - unwinding enzyme - acts upstream of the replication fork
- Okazaki fragments** - DNA fragment synthesized on lagging strand
- SS binding proteins** - bind single stranded DNA around the replication fork
- DNA ligase** - links the okazaki fragments by making a phosphodiester bond
- DNA polymerase** - synthesizes the new DNA strands
- Sliding clamp** - DNA binding protein - keeps the DNA polymerase bound to DNA

