

# 第3章 基因的本质

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第1节 DNA是主要的遗传物质

第2节 DNA分子的结构

第3节 DNA的复制

第4节 基因是有遗传效应的DNA片段

# 第2节 DNA分子的结构

## 本节聚焦

- 1、沃森和克里克是怎样发现DNA分子的双螺旋结构的？
- 2、DNA分子的双螺旋结构有哪些主要特点？

# 一、问题探讨



DNA雕塑

坐落于北京中关村高科技园区的DNA雕塑，以它简洁而独特的双螺旋造型吸引着过往行人。你知道为什么将它作为高科技的标志吗？

2003年是DNA分子双螺旋结构发现50周年。上网查一查有关DNA的信息，收集你感兴趣的资料与同学交流共享。

## 二、DNA双螺旋结构模型的构建

DNA分子是以4中脱氧核苷酸为单位连接而成的长链，这4中脱氧核苷酸分别含有ATGC四种碱基。

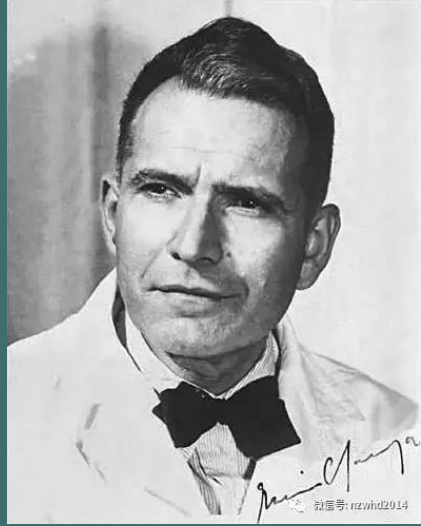
1951年春



DNA分子呈螺旋结构

尝试多种结构失败后，构建磷酸—核糖骨架在螺旋外部，碱基在螺旋内部的结构；

## 二、DNA双螺旋结构模型的构建



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A=T, G=C;

A与T配对，G与C配对，构建新的DNA模型；

相同碱基进行配对；

违反化学规律

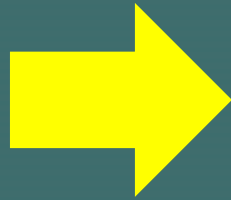
A-T碱基对，与G-C碱基对具有形同的形状和直径——DNA具有稳定的直径，能够解释碱基数量关系，也能解释DNA的复制；

# 二、DNA双螺旋结构模型的构建

1953年

1962年

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No. 4556 April 25, 1953 NATURE 737

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#### A Structure for Deoxyribonucleic Acid

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A structure for nucleic acid has already been proposed by Pauling and Corey<sup>1</sup>. 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:

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We wish to put forward a radically different structure for the salt of deoxyribonucleic 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 ester groups joining β-D-deoxyribofuranose residues with 2',5' linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow righthanded 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<sup>2</sup> 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<sup>3</sup>, 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. As the phosphates are on the outside, cations have easy access to them.

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 one chain being hydrogen-bonded to a single base from the other chain, so



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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.

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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<sup>5,6</sup> on deoxyribonucleic 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 stereo-chemical 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 Donnan 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.

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F. H. C. CRICK

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

<sup>1</sup> Pauling, L., and Corey, R. B., *Nature*, 71, 38 (1953); *Proc. U.S. Nat. Acad. Sci.*, 39, 84 (1953).

<sup>2</sup> Furberg, S., *Acta Chem. Scand.*, 6, 634 (1952).

<sup>3</sup> Chargaff, E., for references see Zamechoff, S., Hlawerman, G., and Chargaff, E., *Biochim. et Biophys. Acta*, 9, 402 (1952).

<sup>4</sup> Watson, G. R., *J. Gen. Physiol.*, 36, 201 (1952).

<sup>5</sup> Astbury, W. T., *Symp. Soc. Exp. Biol.*, 1, *Nucleic Acids*, 66 (*Camb. Univ. Press*, 1947).

<sup>6</sup> Wilkins, M. H. F., and Randall, J. T., *Biophys. Acta*, 10, 102 (1953).



Francis Harry Compton Crick (1916-2004)

诺贝尔  
生理学  
或  
医学奖



James Dewey Watson (1928 - )



Maurice Hugh Frederick Wilkins (1916-2004)

## 二、DNA双螺旋结构模型的构建

### 思考与讨论

1、请根据资料回答有关DNA结构方面的问题：

1) DNA是由几条链构成的？它具有怎样的立体结构？

**1) DNA由2条链构成，盘旋成双螺旋结构；**

2) DNA的基本骨架是由哪些物质组成的？它们分别位于DNA的什么部位？

**2) DNA的基本骨架由磷酸和脱氧核糖组成，位于DNA的螺旋外部；**



## 二、DNA双螺旋结构模型的构建

### 思考与讨论

3) DNA中的碱基是如何配对的？它们位于DNA的什么部位？

1) A与T配对，G与C配对，分布在螺旋的内部；

## 二、DNA双螺旋结构模型的构建

### 思考与讨论

2、上述资料中涉及到哪些学科的知识和方法？这对你理解生物科学的发展有什么启示？

2) 主要涉及物理学（主要是晶体学）、生物化学、数学和分子生物学等学科的知识。涉及的方法主要有：X射线衍射结构分析方法，其中包括数学计算法；建构模型的方法等。现代科学技术中许多成果的取得，都是多学科交叉运用的结果；反过来，多学科交叉的运用，又会促进学科的发展，诞生新的边缘学科，如生物化学、生物物理学等。

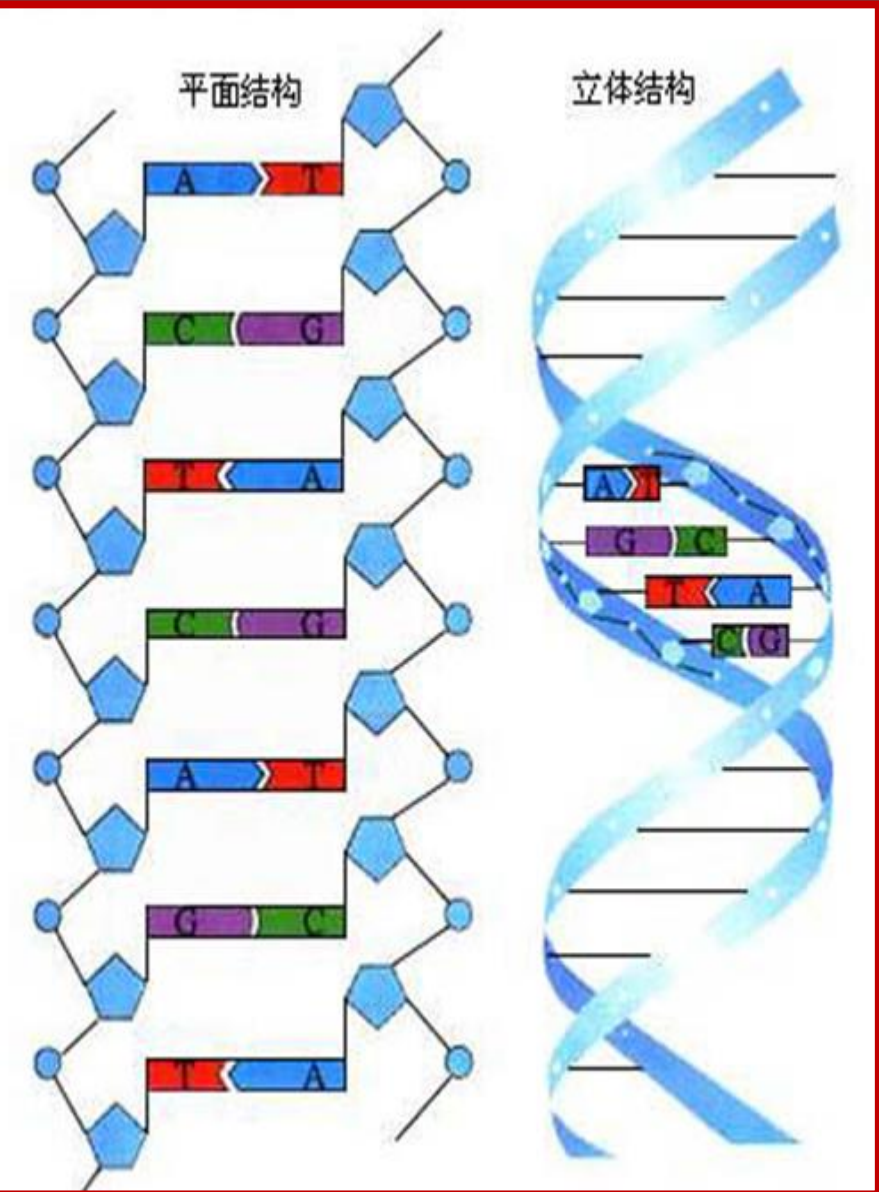
## 二、DNA双螺旋结构模型的构建

### 思考与讨论

3、沃森和克里克默契配合，发现DNA双螺旋结构的过程，作为科学家合作的典范，在科学界传为佳话。他们的这种工作方式给予你哪些启示？

3) 要善于利用他人的研究成果和经验；要善于与他人交流和沟通，闪光的思想是在交流与撞击中获得的；研究小组成员在知识背景上最好是互补的，对所从事的研究要有兴趣和激情等。

### 三、DNA分子的结构



1) DNA分子由反向平行的双链组成，盘旋成双螺旋结构；

2) DNA分子的基本骨架由磷酸和脱氧核糖交替连接而成，排在外侧；碱基成对排在内侧；

3) DNA两条链上的碱基通过氢键进行互补配对：A—T，G—C；  
——**碱基互补配对原则**；

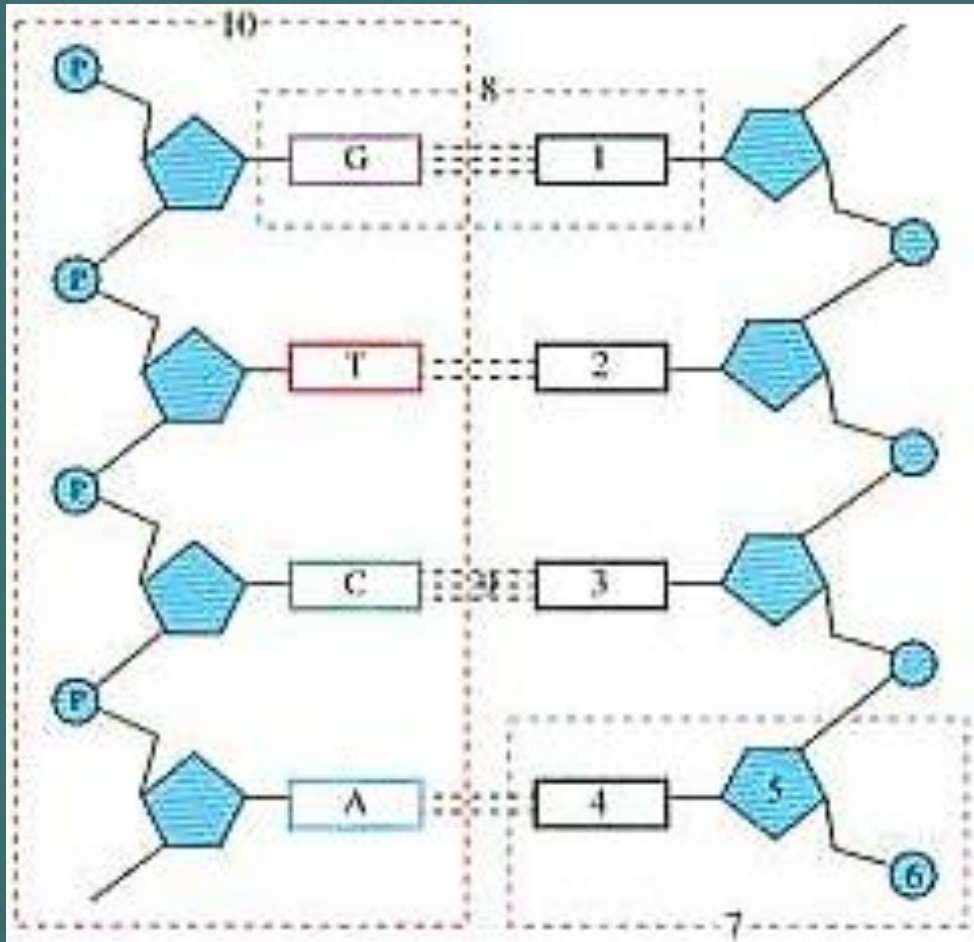
# 三、DNA分子的结构

模型构建

## 制作DNA双螺旋结构模型

## 四、DNA分子的结构——课后练习

1、下面是DNA分子的结构模式图，请用文字写出图中1—10的名称；



1、 \_\_\_\_\_

2、 \_\_\_\_\_

3、 \_\_\_\_\_

4、 \_\_\_\_\_

5、 \_\_\_\_\_

6、 \_\_\_\_\_

7、 \_\_\_\_\_

8、 \_\_\_\_\_

9、 \_\_\_\_\_

10、 \_\_\_\_\_

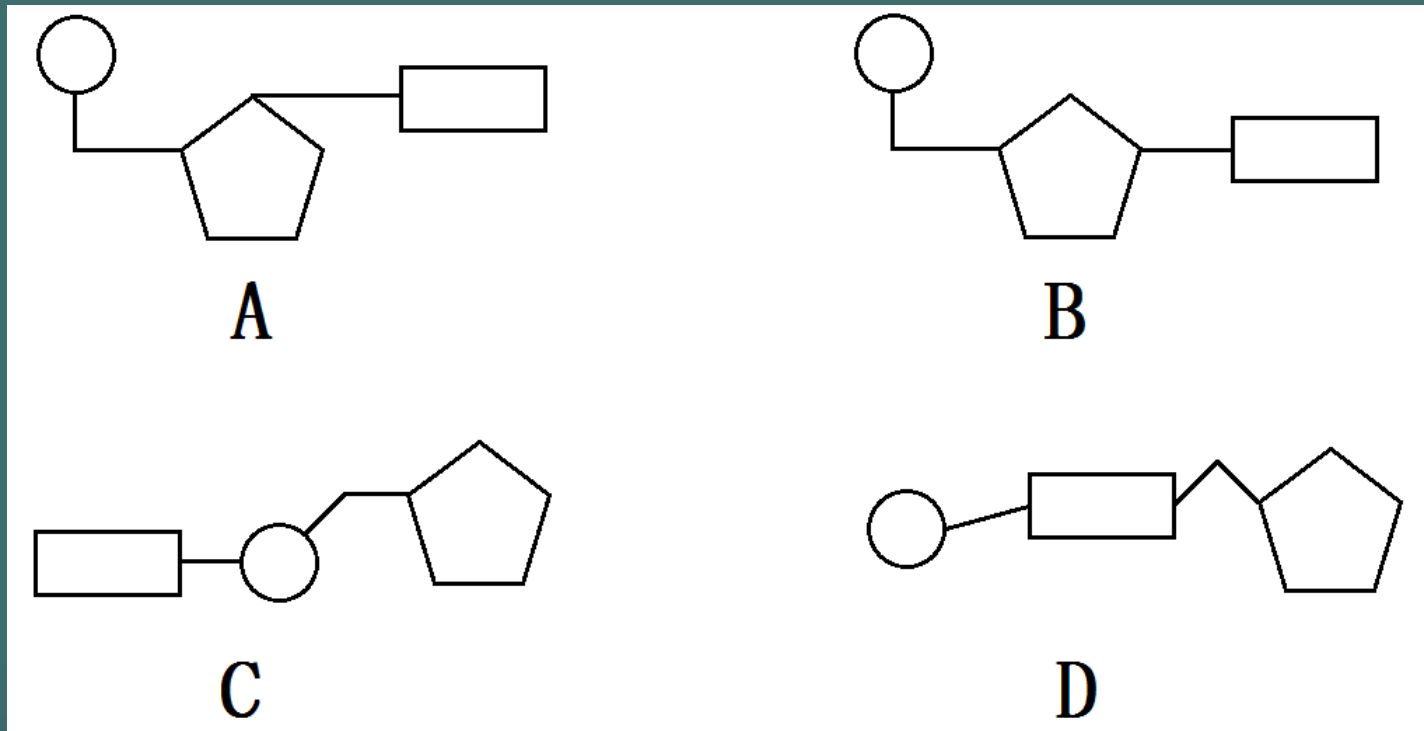
## 四、DNA分子的结构——课后练习

2、已知1个DNA分子中有4000个碱基对，其中胞嘧啶有2200个，这个DNA分子中应含有脱氧核苷酸的数目和腺嘌呤的数目分别是：

- A、4000个和900个
- B、4000个和1800个
- C、8000个和1800个
- D、8000个和3600个

## 四、DNA分子的结构——课后练习

3、下列各图中，图形● 五边形 长方形 分别代表磷酸、脱氧核糖和碱基，在制作脱氧核苷酸模型时，各部件之间需要连接，下列连接中正确的是：





## 四、DNA分子的结构——课后练习

**拓展题：**你能根据碱基互补配对原则，推导出相关的数学公式吗？推导后，尝试进一步总结这些公式，从中概括出一些规律。

$$\because A=T, G=C$$

$$\therefore A+G=T+C$$

$$\therefore (A+G) / ( \quad ) = (T+C) / ( \quad ) = 50\%$$

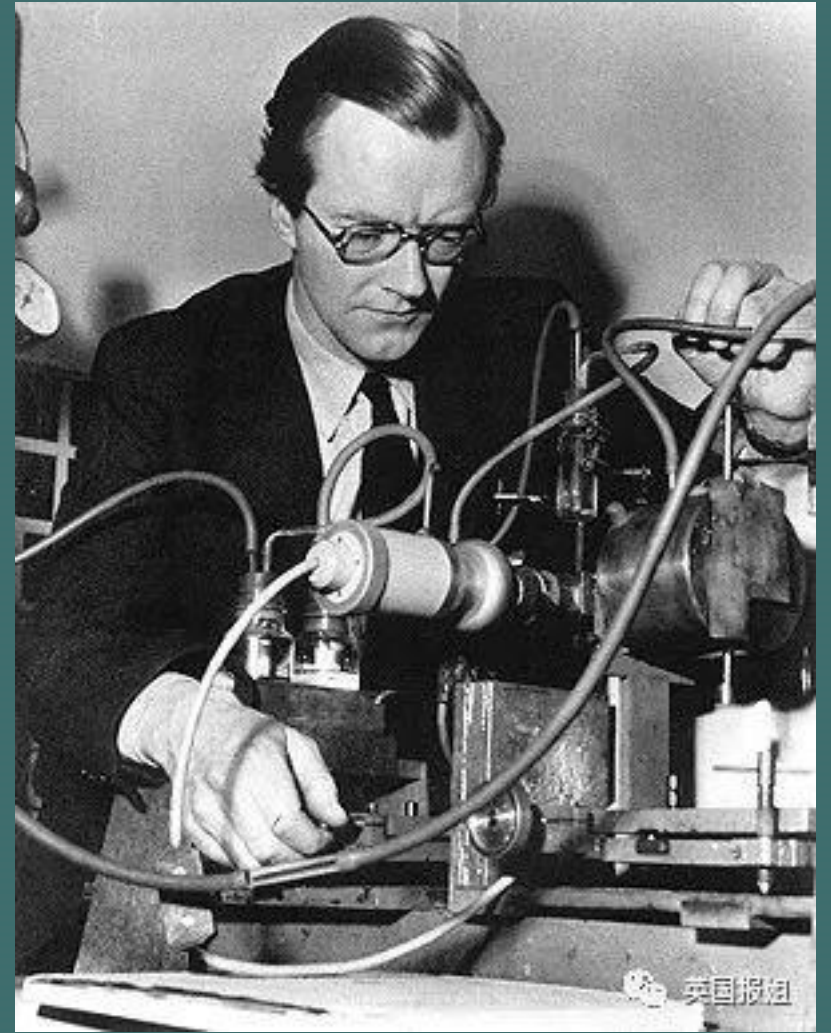
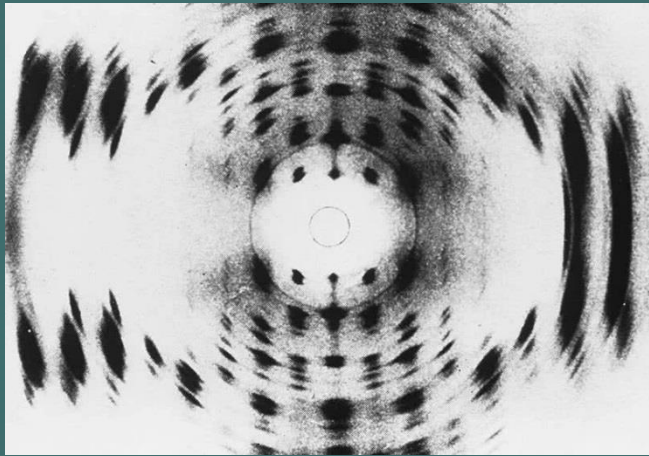
也可以写成以下形式：

$$\frac{A+G}{T+C} = \frac{( \quad )}{( \quad )} = \frac{( \quad )}{( \quad )} \dots\dots = 1$$

**规律概括：**在DNA双链中，任意两个不互补碱基之和\_\_\_\_\_，并为碱基总数的\_\_\_\_\_；

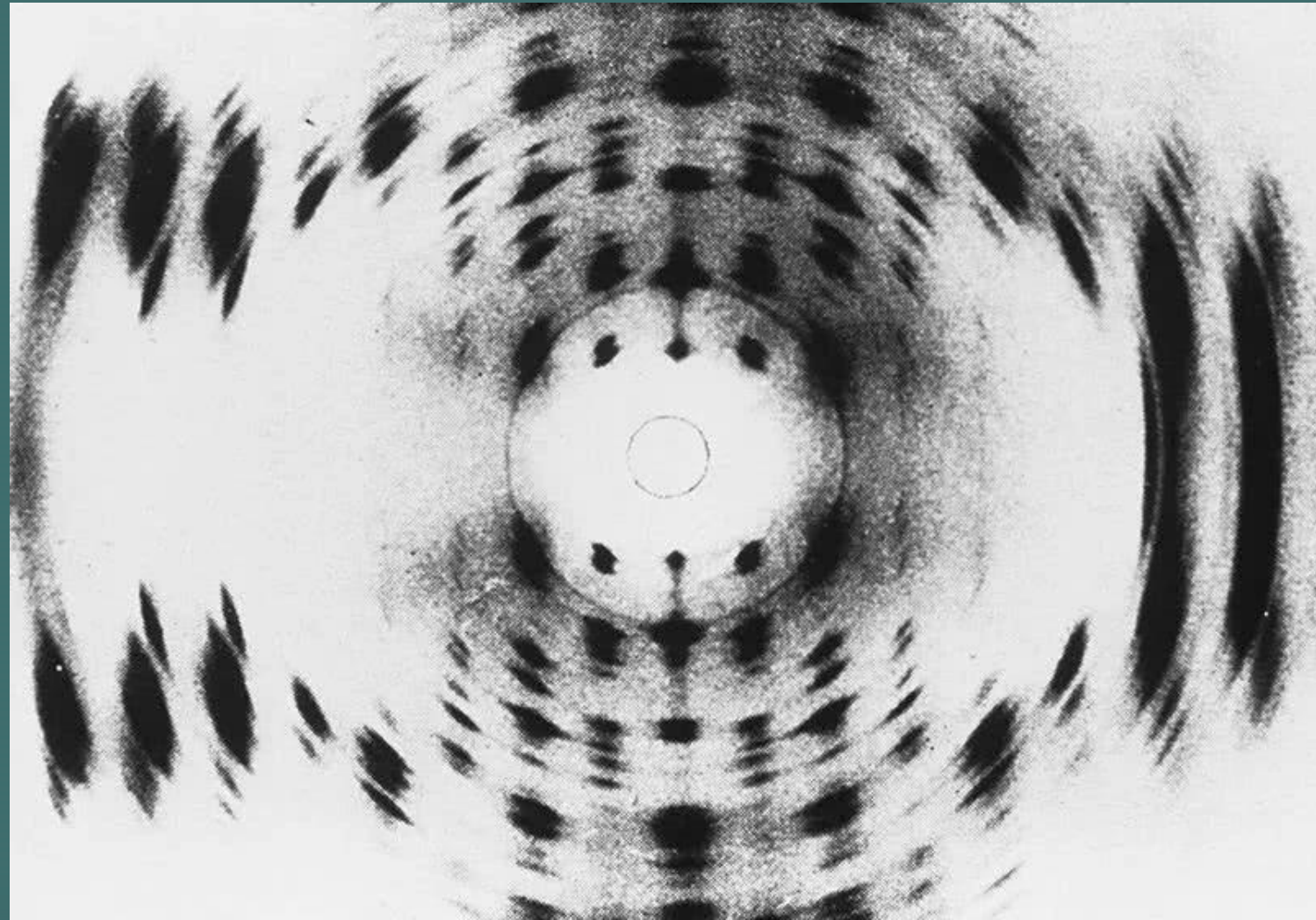
## 二、DNA双螺旋结构模型的构建

1951年春，在意大利举行的生物大分子结构会议上，展示了一张DNA的X射线的衍射幻灯片。

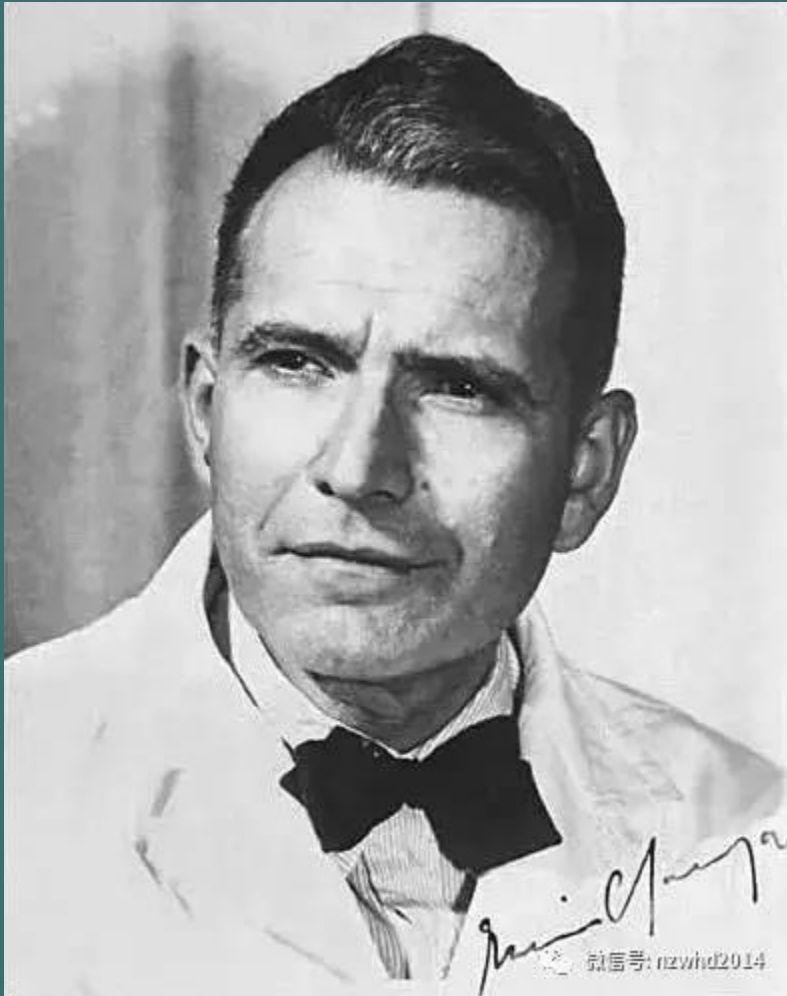


威尔金斯 ( M.Wilkins )

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埃尔文·查哥夫

DNA中的腺嘌呤与胸腺嘧啶数量几乎完全一样，鸟嘌呤与胞嘧啶的数量也是一样；  
即 $A=T$ ， $G=C$ ；

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No. 4356 April 25, 1953

NATURE  
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<sup>3</sup> Chargaff, E., for references see Zarnke, S., Braunman, G., and Chargaff, E., *Biochim. et Biophys. Acta*, 9, 402 (1952).

<sup>4</sup> Wyatt, G.R., *J. Gen. Physiol.*, 36, 201 (1952).

<sup>5</sup> Astbury, W.T., *Symp. Soc. Exp. Biol.*, 1, *Nucleic Acids*, 66 (Camb. Univ. Press, 1947).

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