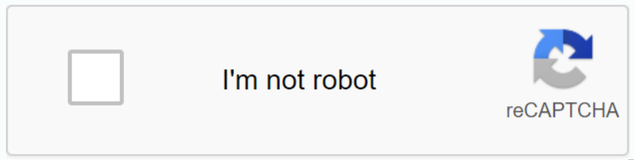

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Structure of dna double helix pdf

Describe the structure of DNA Dna structure is called a double spiral, which looks like a twisted staircase. Sugar and phosphate form the backbone, while nitrogen bases are located in the middle and hold two strands together. Nitrogen bases can only be paired in a certain way: pairing with T and C pairing with G. Due to the basic pairing, DNA strands complement each other, run in opposite directions, and are called antiparalel strands. DNA has the structure of a double spiral, with sugar and phosphate on the outside of the spiral, forming sugar-phosphate spine DNA. Nitrogen foundations are stacked indoors in pairs, as well as stairs stairs; couples are bound to each other by hydrogen bonds. These two strands of spiral run in opposite directions, so that the 5' carbon end of one strand faces the 3' carbon end of its corresponding strand. This antiparalic orientation is important for DNA replication and in many interactions with nucleic acid. DNA is a double helixnative DNA is an antiparallel double helix. The phosphate of the spine (marked curve lines) is on the outside, and the foundations are on the inside. Each base from one strand interacts through hydrogen bonding with the base from the enemy spring. Basic pairs Only certain types of basic pairing are allowed. For example, a certain purine can only be paired with a certain pyrimidine. That is, Aden's couple with Thymine, and Guanine pairs with Cytosine. This is known as the basic supplementary rule, because strands of DNA complement each other. If there is a sequence of one strand of AATTGGCC, the additional strand should sequence TTAACCGG. Antiparallel StrandsV double stranded DNA molecules, two strands run the antiparallel together so that one strand runs 5' to 3' and the other 3' to 5'. Phosphate of the spine is located on the outside, and the bases are in the middle. Adenine forms hydrogen bonds (or basic pairs) with thyme, and the guanine base is paired with cytosine. DNA replication During DNA replication, each strand is copied, resulting in a double dna spiral of the daughter containing one parent strand of DNA and a newly synthesized strand. At this time it is possible mutations can occur. Mutation is a change in the order of nitrogen bases. For example, in an AATTGGCC sequence, a mutation can cause the second T to change to G. Most of the time when it becomes DNA is able to repair itself and return the original base to the sequence. Sometimes, however, the repair is unsuccessful, which leads to the formation of various proteins. Many people believe that American biologist James Watson and English physicist Francis Crick discovered DNA in the 1950s. In fact, that is not the case. Earlier, DNA was first identified in the late 1860s by Swiss chemist Friedrich Miescher. Then, in the decades following Miescher's discovery, other scientists - not particularly Phoebus Levene and Erwin Chargaff - conducted a series of research efforts that further details of the DNA molecule, including its primary chemical components and the ways in which they have bonded together. Without the scientific basis provided by these pioneers, Watson and Crick may never have reached their breakthrough conclusion of 1953: that the DNA molecule exists in the form of a three-dimensional double spiral. First piece of the puzzle: Miescher discovers DNA Although few people realize it, 1869 was a landmark year in genetic research because it was the year in which Swiss physiological chemist Friedrich Miescher first identified what he called the nuclei inside the nuclei of human white blood cells. (The term nuclein was later changed to nucleic acid and finally to deoxyribonucleic acid or DNA.) Miescher's plan was to isolate and characterize not the nuclei (which no one was aware of at the time), but instead the protein components of leukocytes (white blood cells). Miescher thus made arrangements for the local surgical clinic to send him used, pus-coated bandages of patients; once he received the bandages, he planned to wash them, filter out the leukocytes and extract and identify various proteins in the white blood cells. But when he came across a substance from cell edibles that had chemical properties unlike any protein, including a much higher phosphorus content and resistance to proteolysis (protein digestion), Miescher realized he had discovered a new substance (Dahm, 2008). He feels the significance of his findings, Miescher wrote: It seems likely to me that an entire family of such slightly different substances containing phosphorus-containing appears, as a group of jade, the equivalent of protein (Wolf, 2003). More than 50 years passed before the significance of Miescher's discovery of nucleic acids was widely appreciated by the scientific community. For example, in a 1971 essay on the history of nucleic acid research, Erwin Chargaff noted that in the 1961 historical account of nineteenth-century science, Charles Darwin was mentioned 31 times, thomas huxley 14 times, but Miescher not once. This omission is all the more remarkable because, as Chargaff also noted, Miescher's discovery of nucleic acids was unique among the discoveries of four major cellular components (i.e. proteins, lipids, polysaccharides and nucleic acids) in that it could be dated accurately... One man, one place, one date. Laying the foundations: Levene explores the structure of DNA Meanwhile, although Miescher's name fell into the unknown of the twentieth century, other scientists continued to explore the chemical nature of a molecule formerly known as nuclei. One of the other scientists was the Russian biochemist Phoebus Levene. A doctor turned chemist, Levene was a prolific researcher, publishing more than 700 papers on the chemistry of biological molecules over the course of his career. Levene is credited with many firsts. For example, he was the first to find out the order of the three main components of one nucleotide (phosphate-sugar-base); first discover the carbohydrate component of RNA (ribose); first discover the carbohydrate component of DNA (deoxyribosis); and first correctly identify the way RNA and DNA molecules are put together. During the early years of Levene's career, levene and no other scientist at the time knew how the individual nucleotide components of DNA were arranged into space; The discovery of the spine of a DNA molecule containing sugar and phosphate was still years away. The large number of molecular groups made available for binding by each component of nucleotide meant that there were many alternative ways in which the components could be combined. Several scientists have put forward suggestions on how this might happen, but it was Levene's polynucleotide model that turned out to be the right one. Based on years of work using hydrolysis to break down and analyze yeast nucleic acids, Levene suggested that nucleic acids were composed of a series of nucleotides, and that each nucleotide was in turn composed of only one of four nitrogen-containing bases, a sugar molecule, and a phosphate group. Levene submitted his original proposal in 1919, which discredited other proposals that were put forward on the structure of nucleic acids. In Levene's own words, new facts and new evidence may cause it to change, but there is no doubt as to the polynucleotide structure of yeast nucleic acid (1919). In fact, many new facts and a lot of new evidence soon emerged, which caused changes to The Lion's proposal. One of the key discoveries during this period was the way nucleotides are ordered. Levene proposed a so-called tetranucleotide structure in which nucleotides were always combined in the same order (i.e. G-C-T-A-G-C-T-A, etc.). However, scientists eventually realised that Levene's proposed tetranucleotide structure was too simplistic and that the order of nucleotides along the DNA (or RNA) section was in fact highly variable. Despite this realization, Levene's proposed polynucleotide structure was exact in many ways. For example, we now know that DNA actually consists of a series of nucleotides and that each nucleotide has three components: the phosphate group; either ribose (in the case of RNA) or deoxyribosis (in the case of DNA) of sugar; and one base containing nitrogen. We also know that there are two basic categories of nitrogen bases: purines (adenine [A] and guanine [G]), each with two womb rings, and pyrimidines (cytosine [C], thymine [T], and uracil [U]), each with one ring. In addition, it is now widely accepted that RNA contains only A, G, C and U (without T), while DNA contains only A, G, C and T (without U) (Figure 1). Figure 1: Chemical structure of nucleotide. One nucleotide consists of three components: a base containing nitrogen, a five-carbon sugar and a phosphate group. The nitrogen base is either purine or Five-carbon sugar is either ribose (in RNA) or a molecule of deoxyribosis (in DNA). Strengthening the foundation: Chargaff formulates his rules Erwin Chargaff was one of a handful of scientists who expanded on Levene's work by revealing further details about the structure of DNA and thus further paving the way for Watson and Crick. Chargaff, an Austrian biochemist, read a famous 1944 paper by Oswald Avery and his colleagues at Rockefeller University that showed that hereditary units or genes consist of DNA. The paper had a profound impact on Chargaff, inspiring him to launch a research program that revolves around the chemistry of nucleic acids. From Avery's work Chargaff (1971) wrote this: This discovery, almost abruptly, seemed a harbinger of the chemistry of heredity and, moreover, made the probable nature of the nucleic acid gene... Avery gave us the first text of the new language, or rather showed us where to look for it. I decided to search for this text. As his first step in this search, Chargaff set out to see if there were any differences in DNA between the different species. After developing a new method of paper chromatography for separating and identifying small amounts of organic material, Chargaff came to two main conclusions (Chargaff, 1950). First, he noted that the nucleotide composition of DNA varies between species. In other words, the same nucleotides are not re-ranked in the same order as Levene suggests. Second, Chargaff concluded that almost all DNA -- no matter which organism or type of tissue it comes from--retains certain properties, even if its composition varies. In particular, the amount of adenine (A) is usually similar to the amount of thymine (T) and the amount of guanine (G) is usually close to the amount of cytosine (C). In other words, the total amount of purines (A + G) and the total amount of pyrimidines (C + T) are usually almost the same. (This second main conclusion is now known as the Chargaff Rule.) Chargaff's research was vital to the later work of Watson and Crick, but Chargaff himself could not imagine an explanation for these relationships - specifically, that tied to T and C bound to G in the molecular structure of DNA (Figure 2). Figure 2: What is chargaff's government? All DNA follows the Chargaff rule, which states that the total number of purines in the DNA molecule is equal to the total number of pyrimidines. Putting the evidence together: Watson and Crick suggest Double Helix Chargaff realize that A=T and C=G, combined with some very important X-ray crystallography work by English researchers Rosalind Franklin and Maurice Wilkins, contributed to Watson and Crick deriving a three-dimensional, double-helical model for DNA structure. Watson and Crick's discovery was also a possible recent advance in the building model, or the installation of possible three-dimensional structures based on known molecular distances and angles of binding, advanced American biochemist Linus Pauling. In fact, Watson and Crick feared they would scoop up Pauling, who designed another model for the three-dimensional structure of DNA just months before they did. In the end, however, Pauling's prediction was incorrect. Using cardboard cutouts representing the individual chemical components of four bases and other nucleotide subuds, Watson and Crick moved molecules around on their desktop computers as if putting puzzles together. They were introduced for a while with a flawed understanding of how various elements of thyme and guanine (namely carbon, nitrogen, hydrogen and oxygen rings) were configured. It wasn't until the suggestion of American scientist Jerry Donohue that Watson decided to create new cardboard cutouts from two bases to see if another atomic configuration could make a difference. It happened. Not only did the complementary bases now fit perfectly together (i.e. A with T and C with G), with each pair holding hydrogen bonds together, but the structure also reflected the Chargaff government (Figure 3). Figure 3: Double helic structure of DNA. 3-dimensional double spiral structure of DNA, correctly serviced by James Watson and Francis Crick. Complementary bases are held together as a pair of hydrogen bonds. Although scientists have made some minor changes to the Watson and Crick model, or have worked it out since its inception in 1953, the model's four main features remain the same today. These properties are as follows: DNA is a double spiral, with two strands connected by hydrogen bonds. Bases are always paired with Ts, and Cs are always paired with Gs, which is consistent with and accounts for Chargaff's rule. Most double helices of DNA are right-handed; this means that if you were to hold your right hand out, with your thumb pointing up and your fingers curled around your thumb, your thumb would represent an os spiral and your fingers would represent the sugar-phosphate spine. Only one type of DNA, called Z-DNA, is left-handed. The double DNA spiral is parallel to the parallel, which means that the 5' end of one strand is paired with the 3' end of its complementary strand (and vice versa). As shown in Figure 4, nucleotides are interconnected by groups of phosphates which bind the 3' end of one sugar to the 5' end of another sugar. Not only are the underlying DNA pairs connected by hydrogen bonding, but the outer edges of the nitrogen-containing base are exposed and also available for potential hydrogen bonding. These hydrogen bonds provide easy access to DNA for other molecules, including proteins, which play an important role in DNA re-application and expression (Figure 4). Figure 4: Basic pairing in DNA. Two hydrogen bonds link T to A; three hydrogen bonds connect G to C. One of the that scientists have developed on the Watson and Crick model is through the identification of three different conformations of the double DNA spiral. In other words, the exact geometry and dimensions of the double spiral may vary. The most common fleshiness in most living cells (which is the one shown in most double-spiral diagrams, and the one designed by Watson and Crick) is known as B-DNA. There are also two other conformations: A-DNA, a shorter and wider form that has been detected in dehydrated DNA samples and rarely under normal physiological circumstances; and Z-DNA, left-handed conformation. Z-DNA is a transient form of DNA that exists only occasionally in response to certain types of biological activity (Figure 5). Z-DNA was first discovered in 1979, but its existence was until recently largely ignored. Scientists have since discovered that some proteins bind very strongly to Z-DNA, suggesting that Z-DNA plays an important biological role in protecting against viral disease (Rich & Zhang, 2003). Figure 5: Three different conformations of a double DNA spiral. (A) A-DNA is a short, wide, right hand spiral. (B) B-DNA, a structure designed by Watson and Crick, is the most common conformation in most living cells. (C) Z-DNA, unlike A- and B-DNA, is left-handed. Summaries of Watson and Crick were not discoverers of DNA, but rather the first scientists to articulate an accurate description of this molecule's complex, double-helical structure. In addition, Watson and Crick's work was directly dependent on the research of many scientists before them, including Friedrich Miescher, Phoebus Levene, and Erwin Chargaff. Thanks to such researchers, we now know a great deal about genetic structure and continue to make great stri progress in understanding the human genome and the importance of DNA for life and health. Chargaff, E. Chemical specificity of nucleic acids and mechanism of their enzymatic degradation. Experientia 6, 201-209 (1950) ---. Foreword to grammar biology. Science 171, 637–642 (1971) Dahm, R. DNA Discovery: Friedrich Miescher and the first years of nucleic acid research. 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