

The Applications of DNA Technology

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ABOUT THE STUDY

DNA molecule (DNA) is a polymer made up of two polynucleotide chains that form a double helix around one another. Genetic material included in all recognized creatures, including many viruses, is essential to their growth, development, function, and reproduction. DNA and Ribonucleic Acid (RNA) are examples of nucleic acids. Along with proteins, lipids, and complex carbohydrates, nucleic acids are one of the four major groups of macromolecules that are essential for all recognized forms of life. The two DNA strands are known as polynucleotides because they are constructed from simpler monomeric units called nucleotides. Each nucleotide is made up of a phosphate group, a deoxyribose sugar, and one of the four nitrogen-containing nucleobases. An alternating sugar-phosphate backbone is created when the nucleotides are linked together in a chain by covalent bonds between the sugar of one nucleotide and the phosphate of the next. According to the base pairing principles, hydrogen bonds are formed between the nitrogenous bases of the two different polynucleotide strands to form double-stranded DNA. The two groups of complementary nitrogenous bases are pyrimidines and purines. Adenine and guanine are the purines in DNA, while thymine and cytosine are the pyrimidines.

Uses in technology

Genetic engineering: There are procedures for extracting DNA from living things, such as phenol-chloroform extraction, and manipulating it in a lab, including restriction digests and polymerase chain reactions. These methods are heavily utilized in recombinant DNA technology in modern biology and biochemistry. Recombinant DNA is a synthetic DNA sequence created by humans and put together from different DNA sequences. By utilizing a viral vector, they can be converted into organisms in the form of plasmids or in the suitable format. The resulting genetically altered organisms can be grown in agriculture, utilized in medical research, or used to create goods like recombinant proteins.

DNA profiling: In order to identify a matching DNA of an individual, such as a culprit, forensic experts can use DNA obtained

in blood, semen, skin, saliva, or hair recovered at a crime scene. DNA profiling, often known as DNA fingerprinting, is the official name for this procedure. The lengths of variable repetitive DNA segments, such as short tandem repeats and minisatellites, are compared between individuals during DNA profiling. When it comes to finding a matching DNA, this methodology is typically incredibly reliable. Numerous cases have been re-examined as a result of the advancement of forensic science and the capacity to now achieve genetic matching on minute amounts of blood, skin, saliva, or hair. At the time of the initial investigation, evidence could not have been found due to scientific limitations. This, along with the repeal of the double jeopardy legislation in some jurisdictions, may allow for the reopening of cases if the evidence presented at the initial trial was insufficient to persuade the jury. Serious criminal suspects might be asked to submit a DNA sample for matching reasons. The most straightforward argument against forensically obtained DNA matches is to assert that there has been evidence contamination. As a result, new cases of serious crime are handled in a methodical, stringent manner.

DNA enzymes or catalytic DNA: Deoxyribozymes were initially identified in 1994. They are also known as DNAzymes or catalytic DNA. *In vitro* selection, also known as systematic evolution of ligands by exponential enrichment, is a combinatorial method used to choose single stranded DNA sequences from a vast pool of randomly generated DNA sequences (SELEX). DNAzymes catalyze a wide range of chemical processes, such as the cleavage and ligation of RNA and DNA, the phosphorylation and dephosphorylation of amino acids, the creation of carbon-carbon bonds, etc.

Bioinformatics: The study of bioinformatics entails the creation of methods for storing, data-mining, searching, and manipulating biological data, including information on DNA nucleic acid sequences. These have produced significant advancements in computer science, particularly in the fields of database theory, machine learning, and string searching algorithms. To look for certain nucleotide sequences, string searching or matching algorithms-which locate instances of a sequence of letters inside a larger sequence of letters-were devised. To find similar sequences

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and the specific mutations that distinguish them, the DNA sequence can be matched with other DNA sequences. These methods are used to investigate evolutionary relationships and protein function, particularly multiple sequence alignment.

DNA nanotechnology: The self-assembling branched DNA complexes with beneficial features produced by DNA nanotechnology take advantage of the special molecular recognition capabilities of DNA and other nucleic acids. Thus, DNA serves as a structural component rather than a biological information carrier. Due to this, two-dimensional periodic lattices and three-dimensional structures resembling polyhedra have been produced. These DNA structures have been utilized as templates for the arrangement of other molecules, such as gold nanoparticles and streptavidin proteins, in nanomechanical devices and algorithmic self-assembly.

History and anthropology: Geneticists can deduce the evolutionary history of species, or their phylogeny, by comparing DNA sequences because DNA accumulates mutations over time that are then passed down through the generations.

This branch of evolutionary biology known as phylogenetics is a potent instrument. Population geneticists can determine a population's history by comparing DNA sequences within the same species. This can be employed in research spanning from anthropology to ecological genetics.

Information storage: Since DNA has a far higher storage density than electronic devices, it has a great deal of potential as a data storage medium. Its actual application, however, has been hampered by expensive costs, sluggish read and write times, and poor dependability.