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Commentary

Characteristics of DNA Hybridization Technique and Its Role in Molecular Biology

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DESCRIPTION

Hybridization is the technique where in complementary single-stranded DNA and/or RNA molecules bond together to form a double-stranded molecule. DNA hybridization is a very powerful tool in molecular biology. The bonding is depending on the ideal base-pairing across the 2 single-stranded molecules. In 1965, scientist, depict a method of hybridization that combined several modifications to become the standard. Since the 1970s, it has become an essential tool in biology and biotechnology, and a core component of molecular technologies such as DNA microarrays.

DNA-DNA hybridization is a molecular biology technique that measures the degree of genetic similarity between pools of DNA sequences. It is commonly used to determine the genetic distance between two organisms and is widely used in phylogeny and taxonomy. DNA-DNA hybridization methods are widely used for identifying genomic species using the nitrocellulose filter method, the S1 endonuclease method, the hydroxyapatite method, and the quantitative bacterial point filter method. All of these methods are time consuming, tedious, and can only be used in special circumstances. The organism's DNA is labeled and mixed with unlabeled DNA for comparison. The mixture is incubated to dissociate the DNA strands and then cooled to form new hybrid double-stranded DNA. Hybridized sequences with a high degree of similarity are tightly bonded with each other and also more energy is required to separate them, we can say that they separate when heated to a higher temperature than dissimilar sequences. This process is known as "DNA melting". Hybridization enables identification and cloning of specific genes, analysis of mRNA levels within cells, analysis of copy number of sequences within the genome. One of the most eminent examples of the application of hybridization is the discovery of the evolutionary relationships between humans and other primates. DNA hybridization techniques have shown that modern humans are more closely related to chimpanzees than to other primates such as gorillas, orangutans and monkeys.

Using DNA hybridization techniques, similar analyzes was performed on other organisms in the animal and plantkingdoms, thereby constructing family trees. DNA is the genetic material of all living organisms and also involved in the transmission of genetic information from generation to generation. Evolution is associated with genetic changes in populations, and such changes are reflected in the nitrogen base pair composition of DNA. The degree of species relatedness between organisms can be determined by examining similarities in DNA base pair composition. Species with similar base pairs are considered genetically closed species, whereas species with more dissimilar base pairs are considered genetically distant species. Such analyses are performed using DNA hybridization techniques and supported by other additional techniques such as DNA sequencing, fossil finds and anatomical data. The basic principle of DNA hybridization technology is based on the Chargaff rule of complementary base pairing in DNA. Therefore, both DNA strands interact with each other through hydrogen bonding between complementary base pairs. A purine-pyrimidine base pair holds both strands together. Adenine is always paired with thymine on the opposite strand *via* two hydrogen bonds and vice versa. Similarly, hydrogen bonding is possible between guanine and cytosine on opposite strands. Guanine and cytosine interact through three hydrogen bonds. Cluster analysis of the hybridization profiles revealed taxonomic relationships among the tested bacterial strains at the species level resolution. Hybridization is associated with, increased intraspecific genetic diversity of the populations involved, creation of new species, and extinction of species by genetic assimilation, and reduction of highly invasive genotypes. The main environmental factor that affects hybridization is temperature, if the temperature is too high, the strands will melt and if it is too low they need to be forced together. Another important factor is pH, too much alkaline will separate the strands and if they are too acidic, they will clump together. This suggests that this approach is useful for both identifying bacteria and determining genetic distances between bacteria. The main limitation is that the generation of DIG-labeled probes and standards requires high-quality DNA and careful assessment of probe specificity. Overall, the CKB analysis provides a meaningful ecological fingerprint of the highly bio diverse micro biota based on the major cultural bacteria. DNA hybridization is a technique implemented in medical diagnostic testing and genetic screening.

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