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Мухтарова Л.Р., Мухаметзянова А.А.

МЕТОДЫ АНАЛИЗА ДНК

Научный руководитель – ст.преподаватель Кинзягулова Л.Р.
Башкирский государственный медицинский университет, Уфа

В научной статье рассмотрены основные методы анализа ДНК, для каких целей они используются и где применяются.

Ключевые слова: ПЦР, секвенирование ДНК, титрование ДНК, полиморфизм длин рестрикционных фрагментов, генетический профилинг.

Mukhtarova L.R., Mukhametzyanova A.A.

TECHNIQUES OF DNA ANALYSIS

Scientific Advisor - Senior Teacher Kinzyagulova L.R.
Bashkir State Medical University, Ufa

The scientific article discusses the main methods of DNA analysis, for what purposes they are used and where they are used.

Key words: PCR, DNA sequencing, DNA titration, restriction fragment length polymorphism, genetic profiling.

DNA is the most important double-stranded macromolecule that provides storage, transmission from generation to generation and realization of genetic information. DNA diagnostics is a set of methods and technologies that allow you to read information encoded in DNA, identify damage in a particular gene that can cause various diseases or further lead to pathology. Materials such as blood, saliva, fetal material are more often used for DNA research, but sperm, cadaveric and exhumed material can also be used.

The study of DNA molecules helps to identify hereditary traits such as: a person's appearance and temperament, family ties, predisposition to various pathologies, reactions to various medications.

Also, genetic tests provide information about the presence of certain hereditary mutations or individual disorders in genes, which greatly facilitates the diagnosis of diseases and the selection of necessary preventive measures and treatment.

The main methods of DNA analysis :

1. Polymerase chain reactions
2. DNA sequencing
3. DNA titration
4. Restriction Fragment Length Polymorphism
5. Genetic profiling

1. Polymerase chain reactions

PCR method is widely used in the diagnosis of infectious diseases, the identification of genetic abnormalities, as well as in scientific research. It consists of 3 stages. In the first step, DNA molecules split into two chains when heated . The next step is annealing . As the temperature decreases, the primers attach to the ends of the entire DNA. This is followed by stretching, which has

a final sequence. The process of completing the second DNA chain occurs, Thus two strands of DNA are formed . There are more than 30 repetitions and each time the number doubles. Polymerase chain reactions are needed in microbiology, biology and especially medicine. This is especially important for scientific researchers, doctors and technical specialists. this means expanding or doubling DNA using different components. This method is useful for studying pathological processes and diseases. creating a new sequence takes about 5 minutes, not that much.

2. DNA sequencing

DNA sequencing is the process of determining the sequence of nucleotides in a DNA molecule. There is the Singer method, the Bayreuth sequencing method, the ion sequencing method, and the next generation sequencing method. DNA sequencing plays an important role in genetics, medicine, microbiology, chemistry, biology and other branches of science, helping scientists study, analyze and identify genetic changes associated with various diseases or phenotypes.

Determining the structure of the genome is not an easy task. It is responsible for DNA isolation, requires special processing (fragmentation, reformation, amplification) and obtaining information on a special organizing device. Genome sequencing can provide the most complete structural information about genetic materials and provide a detailed study of all individual genetic differences.

3. DNA titration

The DNA typing method consists in the fact that it is based on structural DNA variants of different people. This applies to hypervariable regions with structural polymorphism (they have several allelic forms). The main role in their formation belongs to short nucleotide sequences, called micro and macro satellite DNA contain 15-70 nucleotides and 2-5 base pairs. This sequence is represented in the form of blocks (loci) distributed in the genome and sleep structures (repetitive sequences). The number of tandem repetitions (hence the length of the locus) reaches 24 thousand. The presence of repeating elements in such homogeneous computing blocks looks like a manifestation of the structural polymorphism of these loci and, in particular, the duration of fractionation (FDR). [4].

4. Restriction fragment length polymorphism

Restriction fragment length polymorphism (RFLP) is a type of genetic polymorphism in which genomic DNA is studied. Endonuclease enzymes are involved in this process, which cut the DNA molecule in certain areas, resulting in impurities of different lengths due to the presence or absence of certain restriction sites, which can be found by amplification, cleavage using appropriate restrictive and electrophoretic separation of the obtained fragments.

RFPL is used in genetic and genomic studies to identify any changes in the genome, for example, to clarify the localization of point mutations, identify polymorphisms, various genetic

anomalies, and to diagnose heterozygous carriage. This method is also used to identify kinship relationships, in population genetics, and for plant and animal breeding.

5. Genetic profiling

DNA profiling is a DNA analysis technique used to identify or differentiate individuals based on the uniqueness of the genetic code. 99.1% of the genome is the same for all people and only 0.9% is individual for each person. With this method, we can study the genome and identify differences between people by 0.9% of the genome. Due to this, this method is used in forensic medicine, where it is necessary to identify a person by DNA, it is also used to establish paternity and solve problems related to inheritance.

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