OPEN ACCESS Freely available online

Journal of Clinical Chemistry and Laboratory Medicine

Perspective

Overview on Different Methods to Identify DNA Sequence

Robert Schloss*

Department of Genome Sciences, Harvard Medical School, Boston, Massachusetts, USA

DESCRIPTION

The order of nucleotides in deoxyribonucleic acid is called as deoxyribonucleic acid sequencing. Any technique or technology for identifying the order of the four bases: purine, guanine, cytosine, and thymine. The Sanger method or di-deoxy method was created by English biochemist Frederick Sanger, which was among the first generation sequencing technologies to emerge at that time. DNA chains were manufactured on a template strand in the Sanger method, which became the more widely used of the two procedures, although chain growth was stopped when one of the template strands was damaged. The incorporation of four potential dideoxy nucleotides that lack a 3' hydroxyl group prevented the inclusion of another nucleotide.Each of different locations of that particular nucleotide in the template DNA was represented by the population of nested, truncated DNA molecules. The most extensive method for examining the genome is whole genome sequencing. The ability to get valuable information about the complete genetic code and rapidly falling sequencing costs make this approach a viable research tool. Both genome wide analysis and very focused techniques can give researchers with insightint DNA methylation patterns at a single nucleotide level in methy lation sequencing, harnessing the potential of NGS. Targeted res equencing isolates and sequences a selection of genes or portions of the genome, allowing scientists to focus time, resources, and analysis on specific areas of interest. ChIP sequencing (ChIPSeq) is a technique that combines chromatin immunoprecipitation (ChIP) tests and sequencing is an effective tool for identifying tran scription factor and other protein DNA binding sites across the whole genome. Biomedical research involving disease classification, diagnosis, an d treatment today requires DNA sequencing, genome annotatio n, and gene expression analysis as a minimum. To understand the accurate annotation and functionof genetic data, researchers are excitingly attempting to perceive knowledge. DNA sequencing and synthesis are two critical instruments for reading and writing DNA and as processes, they are rapidly improving and becoming less expens-ive and sophisticated as time passes. Operators can examine DNA sequences over time using their existing operational routines and also using no downhole tools. DNA next-generation sequencing is scalable processing and storage, and software.developments for handling DNA are all based on three essential technological advances. Cross-linked polyacrylamide slab gels were frequently used to separate DNA sequencing fragments at high resolution.

The sequence of DNA can reveal a wealth of genetic information , including genes that code for proteins, regulatory instructions that can turn genes on or off, and disease causing mutations. High throughput DNA sequencing is another term for NGS methods.

Their development was aided by the Human Genome Project,and they are generally quick, simple, and inexpensive DNA sequencing procedure.These innovative, high through output technologies include nanopore and microfluidic sequencing. Many distinct factors can produce changes or mutations in DNA sequences. The Maxam Gilbert method discovered by American molecular scientists Alla n M.Maxam and Walter Gilbert.

There are various forms of gene mutations, and they can affect anything from a single cell to an entire organism. A big stretch of DNA that contains several different genes is called a base pair. H ereditary (germline) or acquired mutations are both possible (so matic).

Because hereditary mutations are passed down from one generat ion to the next, they are present from the moment of conception and can be found in every cell of the offspring's body. Acquired mutations occur at some point during a person's life and are thus present in only some cells, rather than all of the body's cells. Environmental factors such as UV radiation or a mistake in DNA replication during cell reproduction are common causes of acqui red mutations. Unless the mutation occurs in a person's gametes , these mutations cannot be transmitted down to the next generation. After the DNA has been sequenced, the Ensembl BLAST/BLATtools may be used to match it to a gene, locate its placement in a published reference genome, and identify changes. Using a database of known SNPs, such as dbSNPs, they can then be checked for mutations. SIFT and PolyPhen are two programmes that can be used to anticipate the effect of a mutation on a protein and determine whether it is disease-causing. The process of determining the nucleotide sequence. (As, Ts, Cs, and Gs) in a fragment of DNA is known as DNA sequencing.

Correspondence to: Robert Schloss, Department of Genome Sciences, Harvard Medical School, Boston, Massachusetts, USA, E-mail: roberts25@gmail.com

Received: 11- Jan-2022, Manuscript No. JCCLM-22-16125; **Editor assigned:** 13-Jan-2022, PreQC No. JCCLM-22-16125 (PQ); **Reviewed:** 28-Jan-2022, QC No. JCCLM-22-16125; **Revised:** 31-Jan-2022, Manuscript No. JCCLM-22-16125 (R); **Published:** 7- Feb-2022, DOI: 10.35248/JCCLM.22.05.204.

Citation: Schloss R (2022) Overview on Different Methods to Identify DNA Sequence. J Clin Chem Lab Med. 5:204.

The target DNA is duplicated several times in Sanger sequencing, resulting in pieces of various lengths. In a tube, primer, DNA polymerase, and DNA nucleotides are mixed with the DNA sample to be sequenced (dATP, dTTP, dG TP, and dCTP).The for dye-labeled, chain terminating, di-deoxy nucleotides are also introduced in lesser quantities then the regular nucleotides. Sanger sequencing is expensive and inefficient for larger-scale projects, such as the sequencing of an entire genome or metagenome (the collective genome of a microbial community).For large-scale operations, such as the sequencing of a whole genome or metagenome (a microbial community's). Sanger sequencing is expensive and inefficient. The job of sequencing a full genome (all of organism's DNA) is still difficult.It entails slicing the genome's DNA into many smaller p ieces, sequencing them, and putting the sequences together into a single lengthy "consensus."