

Overview of DNA Sequencing method

Martin S*

Department of Molecular biology, Mount Sinai School of Medicine, New York, USA

SUMMARY

DNA sequencing is the way toward deciding the grouping of nucleotides inside a DNA particle. Each organic entity's DNA comprises of a remarkable grouping of nucleotides. Deciding the grouping can help researchers analyze DNA between organic entities, which can help show how the creatures are connected. This implies that by sequencing a stretch of DNA, it will be feasible to know the request in which the four nucleotide bases – adenine, guanine, cytosine, and thymine – happen inside that nucleic corrosive particle.

The need of DNA sequencing was first made clear by Francis Crick's hypothesis that the succession of nucleotides inside a DNA atom straightforwardly affected the amino corrosive groupings of proteins. At that point, the conviction was that a totally sequenced genome would prompt a quantum jump in understanding the natural chemistry of cells and organic entities. Present day DNA sequencing comprises of high-throughput strategies which permit whole DNA arrangements to be found very quickly.

This innovation has permitted numerous organizations to begin offering at-home DNA testing. Large numbers of the "results" found by these tests are just connections found between a hereditary variation and a specific condition.

Notwithstanding, innovation has additionally permitted researchers to test the DNA of numerous organic entities to more readily comprehend developmental connections. An article titled "Nitrogen Base Sequence Analysis and Characterization of Mutations in Gene Coding Region That Can Lead to High Levels of Resistance in Tuberculosis Patients in Jayapura, Papua Province-Indonesia" which was written by Prof. Yohanis Ngili which discusses that The disease of tuberculosis in Papua Province, Indonesia. The manuscript reveals the aspects of mutations in rpoB512 gene results in causing of high resistance of *M. tuberculosis*. Most of the mutations occurring in the β -subunit RNA polymerase are found in region I (the position of amino acid residues 505 to 537) and region II (the position of amino acids 562 to 572).

These results of analysis suggest that Amino acid changes in this residue caused the greatest effect on the *M. tuberculosis* phenotype on the Mtb isolate in Papua Province of Indonesia. Another article by same Prof. Yohanis Ngili entitled Genetic Mutations in the Papuan Human Mitochondrial Genome: Studies in Gene Control Regions and Gene Coding Using REPLI-g. This manuscript is all about the Study Analysis and DNA mutations in Papuan humans with comparison of several world ethnicities both in coding region and gene control region.

This manuscript reveals that mutation analysis shows that there were several mutations in mtG region fragments and most of the mutations outside the D-loop regions are in the ATP6 region and the results of analysis of gene coding region provides that there are enough variability of mutations between tribes in Papua which are quite high and this study is quite interesting to examine more deeply on bioethnoanthropological studies.

USES OF DNA SEQUENCING

Conventional, chain-end innovation and HTS techniques are utilized for various applications today. Sanger sequencing is presently utilized generally for once more beginning sequencing of a DNA atom to acquire the essential grouping information for a living being or quality.

The generally short 'peruses' falling off a HTS response (30-400 base sets contrasted with the almost 1,000 make the whole genome of a creature from HTS techniques alone. Every so often, Sanger sequencing is likewise expected to approve the consequences of HTS.

Correspondence to: Sier Martin, Department of Infectious Diseases, Mount Sinai School of Medicine, New York, USA; E-mail: Siermartinler@mssm.edu

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