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Advancements in Genetic Engineering

Opinion Article

Role of Whole Genome Sequencing in Determining the Genetic Code

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DESCRIPTION

Whole Genome Sequencing (WGS) analysis is phenotype driven and relies on targeting genes specific to the phenotype in the first instance. Whole genome sequencing test is intended to determine an individual's entire genetic makeup by sequencing their entire Deoxyribonucleic Acid (DNA). A genome is the complete genetic code of an individual. Whole Genome Sequencing (WGS) techniques have transformed outbreak investigations and disease detection because they can identify a disease-causing microorganism's entire DNA profile quickly and affordably. By mapping the genomes of bacteria, it is possible to determine their relationship as well as other factors such as virulence and antimicrobial resistance, and thus it is easy to understand how bacteria are related and have evolved over time. By monitoring highly resistant clones in the population and environment, WGS can also provide information on antimicrobial-resistant genes in bacteria.

Nucleotides are the fundamental building blocks of DNA. Nucleotides are classified into four types-A, G, T, and C. These are the four letters that make up the genetic code. Genome sequencing is a type of genetic test that allows doctors to sequence, or spell out, each of an individual's 3 billion letters. Certain changes, or variants, in this letter sequence can have an effect on health, so detecting these variations can help in disease diagnosis and treatment. As part of the normal genetic variation among humans, each of them will have variants in their genomes. Cells are the building blocks of our bodies and are specialized based on their location and function. A structure within each cell known as the nucleus contains information critical to the cell's growth, development, and function. This data is referred to as DNA or genetic code.

The interpretation of the variants discovered after the DNA letters are sequenced is a critical component of genome sequencing. A disease causing or pathogenic variant is a gene change that has an impact on health. A benign variant is one that does not appear to have any effect on the health of an individual. Benign variants may have no effect at all or may contribute to non-health related characteristics such as blond hair or brown eyes. The current state of knowledge as applied to these interpretations varies depending on the gene containing the variant and the type of variant involved. Because genome sequencing examines all of an individual's genes, variants in genes that are unrelated to the patient's primary set of symptoms but have an impact on health can be discovered. These genes include those linked to a higher risk of developing certain types of cancer or heart disease. If a family member is considering WGS, the potential "secondary findings" should be determined.

Furthermore, the results of genome sequencing, like many other genetic tests, may have an impact on the health risks of family members. As a result, the doctor should ideally interpret the results in the context of a thorough and accurate family history. There is no such thing as a perfect genetic test, and despite genome sequencing's granularity which cannot detect all types of genetic variation. A negative genome sequencing test result does not rule out the possibility of a genetic condition, and other genetic tests may be appropriate for the physician to consider.

CONCLUSION

Whole genome sequencing is a useful diagnostic tool in which a physician examines the patient's entire genetic code, looking for specific changes or variants in the code. Finding and interpreting specific disease-causing variants in a patient's genetic code can frequently lead to a more accurate and targeted diagnosis. Furthermore, Whole Genome Sequencing can reveal any genetic predispositions to diseases such as heart disease and certain types of cancer. This new approach to disease surveillance represents a paradigm shift in global disease prevention because it allows for faster and more accurate identification of the source of the outbreak, allowing for less disease spread and lower labour and production costs.

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