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A Brief Note on Genetic Biomarker

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DESCRIPTION

A genetic marker is indeed a genotype or DNA sequence that has a specific location on a chromosome and can be used to identify individuals or species. It can be defined as an observable variation which may occur as a result of a mutation or modification in the genomic loci [1]. A genetic marker can be either a short DNA sequence, including that enclosing a single location change (single nucleotide polymorphism, SNP), or a long one, such as minisatellites. For many years, gene mapping was restricted to trying to identify organisms rooted in traditional phenotype markers. It included genes that encrypted easily observable traits like blood types or seed forms. The insufficient number of these types of characteristics in several microbes hampered mapping attempts [2]. This stimulated the improvement of gene markers, which could recognize genetic traits in organisms which are not immediately evident (such as protein variation) [3,4]. In this there are two different types of biomarkers. a) Biochemical markers that detect variation at the gene encoding level, such as adjustments in bioactive peptides; and b) molecular markers that detect variation at the DNA level, including such nucleic acid changes, such as deletion, duplication, inversion, and/or insertion [5]. Indicators can be inherited in two ways: Dominant/recessive or co-dominant. When the biological pattern of homo-zygotes differs from those of hetero-zygotes, a marker is said to be co-dominant. Co-dominant markers are usually more insightful than dominant markers. The use of genetic markers can be used to examine the connection between an inherited disease as well as its genetic cause (for example, a particular mutation of a gene that results in a defective protein) [6,7]. It is well known that DNA fragments that really are close with each other on a chromosome tend to be inherited together. This property allows for the use of a marker, which can then be used to determine the exact pattern of inheritance of a genotype which has yet to be precisely localized. In genealogical DNA testing for genetic genealogy, genetic markers are used to ascertain genetic divergence among individuals or populations [8]. Uniparental markers (on mitochondrial or Y chromosomal DNA) are now being researched to determine maternal or paternal lineages. For all ancestries, autosomal markers are being used. Because homozygotes provide little information, genetic variants must be easily identifiable, associated with a particular locus, and strongly polymorphic. The marker could be detected directly utilizing RNA sequencing or indirectly using allozymes, RFLP, AFLP, RAPD, and SSR are among the ways of studying the genome or phylogenetic. They could be used to create genetic maps of any organism under study. There was some disagreement about the transmissible agent of CTVT (Canine Transmissible Venereal Tumor). Many researchers theorize that virus like particles were responsible for the cell's transformation, whereas others believed that the cell itself might cause disease other canines as an allograft. Scientists were able to do is provide solid proof that the malignant tumor cell evolved into a transmittable parasite using specific genes [9,10]. Furthermore, single molecule genetic markers were used to resolve the problems of organic transmitting, breed of origin (phylogenetic), and canine tumour age.

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Conflict of Interest

The author's declared that they have no conflict of interest.

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