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Short Notes on Microsatellite Marker Analysis

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Introduction

In genomics, a microsatellite is a short segment of DNA, usually one to six or more base pairs in length that is repeated multiple times in succession at a specific genomic location. These DNA sequences are almost always non-coding. Because the number of repeated segments within a microsatellite sequence varies between people, they can be used as polymorphic markers to study inheritance patterns in families or to create a DNA fingerprint from crime scene samples. Microsatellites, or tandem repeats of 1–6 bp, are common in higher organism genomes and typically exhibit high levels of polymorphism. The density of microsatellites varies between species, as does the frequency of various repeat motifs. Microsatellites are mostly found in non-coding DNA and are thought to be neutral markers. Mutations in simple repeats result in the insertion or deletion of one or more repeat units, which is broadly consistent with the stepwise mutation model [1-3].

About the Study

According to one model of microsatellite evolution, stationary length distributions result from a balance of length mutations, which promote repeat growth, and point mutations, which break long repeat arrays into smaller units. The primary mechanism of mutation is replication slippage, which occurs as a result of transient dissociation of the replicating DNA strands followed by misaligned re-association. The mismatch-repair system corrects the majority of primary mutations in microsatellites. Cells with a mismatch repair defect have a high rate of microsatellite mutation. The rate of microsatellite mutation generally increases with the number of repeats. Although the causes of this variation are not fully understood, there is significant variation in mutation rates among markers. Microsatellites, also known as simple sequence repeats (SSRs), are short tandem repeats (STRs) of DNA sequence motifs that are abundant in many genomes and have been widely used in genetic studies and molecular markers. Litt and Luty coined the term "microsatellites" in their work on the (TG) gene of cardiac actin. These repeats were created for the study of neurological diseases in humans, but their subsequent applications made them important in a variety of molecular fields.

Future Prospective

Repeat polymorphisms are typically caused by the addition or deletion of entire repeat units or motifs. As a result, different individuals exhibit variations in repeat numbers. In other words, polymorphisms in SSRs [4,5] are caused by differences in the number of repeats of the motif caused by polymerase strand slippage during DNA replication or by recombination errors. Strand-slippage replication is a type of DNA replication error that occurs when the template and nascent strands are mismatched. This means that the template strand has the potential to loop out, causing contraction. The emerging strand can also loop out, resulting in repeat expansion. SSR sequence contractions and expansions can also be caused by recombination events such as unequal crossing over and gene conversion. SSRs (simple sequence repeats), STRs (short tandem repeats), SSLPs (simple sequence length polymorphism), and VNTRs (variable number of tandem repeats) are a type of repetitive DNA sequence found in all living organisms.

Microsatellites are an excellent tool for a variety of approaches such as genotyping, mapping, and positional cloning of genes due to their presence in the genomes of all living organisms, high level of allelic variation, co-dominant mode of inheritance, and potential for automated analysis. SSR (simple sequence repeats), which are generated by amplifying in a PCR reaction with primers complementary to flanking regions; ISSR (inter-simple sequence repeats), which are based on the amplification of regions between inversely oriented closely spaced microsatellites; and SAMPL (selective amplification of microsatellite polymorphic loci), which uses AFLP (amplified fragment length polymorphism). The utility of the three above-mentioned markers for a variety of purposes in plants has been well documented.

Conflict of Interest

None.

Acknowledgement

None.

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