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Microsatellite Marker Analysis: A Brief Note

Marcella Faria*

Genetics Laboratory, Department of Biotechnology, Agricultural University of Athens, Greece

About the Study

A microsatellite is a brief DNA segment that is repeated several times in succession at a particular genomic site. It typically ranges in length from one to six base pairs or more. Almost always, these DNA sequences are non-coding. Microsatellites can be used as polymorphic markers to examine inheritance patterns in families or to construct a DNA fingerprint from crime scene evidence because the number of repeated segments within a microsatellite sequence differs between individuals. Higher organism genomes frequently contain microsatellites, or tandem repetitions of 1-6 bp, which frequently show significant levels of variability. Both the density of microsatellites and the frequency of different repeat motifs differ between species. Microsatellites are assumed to be neutral indicators because they are primarily found in non-coding DNA. The stepwise mutation concept is often supported by the observation that mutations in simple repeats cause the insertion or deletion of one or more repeat units [1-3].

One theory of the evolution of microsatellites proposes that stationary length distributions are the consequence of a balance between length mutations, which encourage repeat growth, and point mutations, which fragment lengthy repeat arrays into smaller units. Replication slippage, which results from a brief dissociation of the replicating DNA strands followed by a misaligned reassociation, is the main mechanism of mutation. The bulk of initial mutations in microsatellites are corrected by the mismatch-repair system. A high incidence of microsatellite mutation is present in cells with a deficiency in mismatch repair. The amount of repeats tends to enhance the rate of microsatellite mutation. There is a sizable difference in mutation rates among markers, while the reasons for this heterogeneity are not entirely understood. Simple sequence repeats (SSRs), commonly referred to as microsatellites, are short tandem repeats (STRs) of DNA sequence motifs that are prevalent in many genomes and are frequently employed as molecular markers and in genetic research. In their research on the (TG) gene of cardiac actin, Litt and Luty first used the term "microsatellites." These repetitions were developed to investigate human neurological disorders, but their subsequent uses rendered them crucial in a number of scientific disciplines.

Future Perspective

The addition or deletion of whole repeat units or motifs is the most common reason for repeat polymorphisms. As a result, repeat counts vary depending on the individual. In other words, polymorphisms in SSRs [4,5] are brought on by variations in the number of repeats of the motif brought on by DNA replication mistakes or polymerase strand slippage. Strand-slippage replication is a type of DNA replication error that occurs when the template and nascent strands are mismatched. This indicates that the template strand may loop out and result in contraction. Additionally, the developing strand may loop, leading to recurrent expansion. Recombination events like uneven crossing over and gene conversion can also result in SSR sequence reductions and expansions. There are several types of repeated DNA sequences that are present in all living things, including SSRs (simple sequence repeats), STRs (short tandem repeats), SSLPs (simple sequence length polymorphism), and VNTRs (varying number of tandem repeats).

Due to their inclusion in the genomes of all living organisms, their high level of allelic variation, their co-dominant mode of inheritance, and the potential for automated analysis, microsatellites are an excellent tool for a variety of approaches such as genotyping, mapping, and positional cloning of genes. Inter-simple sequence repeats (ISSR) are based on the amplification of regions between inversely oriented closely spaced microsatellites, SSR (simple sequence repeats), which are produced by amplifying in a PCR reaction with primers complementary to flanking regions, and SAMPL (selective amplification of microsatellite polymorphic loci), which uses AFLP (amplified fragment length polymorphism). It is commonly known that plants can use the three aforementioned markers for a number of functions.

Conflict of Interest

None.

Acknowledgement

None.

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***Address for Correspondence:** Marcella Faria, Genetics Laboratory, Department of Biotechnology, Agricultural University of Athens, Greece, E-mail: Fmarcella@gmail.com*

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