

Review Article

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A Review on Satellite DNA

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ABSTRACT

Satellite DNAs are hidden part of the genomes, initially just considered as junk DNA. Heterochromatic regions of the eukaryotic genome harbour DNA sequences that are repeated many times in tandem, collectively known as satellite DNAs. Different satellite sequences co-exist in the genome, thus forming a set called a satellite DNA library. Satellite DNA families accumulate in the in the heterochromatin in different parts of the eukaryotic chromosomes, mainly in pericentromeric and subtelomeric regions, there is currently an increasing appreciation of the functional significance of satellite DNA repeats and of their sequences. The study of insect satellite DNAs indicates the evolutionary conservation of certain features despite their sequence heterogeneity. Such features can include total length, monomer length, motifs, particular regions and/or secondary and tertiary structures.

Keywords: satellite DNA, minisatellite, microsatellite & centromere

ARTICLE INFO

CONTENTS

1.	Introduction.	95
2.	Minisatellite.	. 96
3.	Biological significance of satellite DNAs.	. 97
4.	Conclusion	97
5.	References	.97

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1. Introduction

Satellite DNA consists of very large arrays of tandemly repeating, non-coding DNA. Satellite DNA is the main component of functional centromere and form the main structural constituent of heterochromatin. Heterochromatic regions of the eukaryotic genome harbour DNA sequences that are repeated many times in tandem, collectively known as satellite DNAs. Its appearance as satellite bands that

A. Mounika et al, JPBR, 2016, 4(2): 95-98

separated from the "bulk" DNA upon density gradient centrifugation. Different satellite sequences co-exist in the genome, thus forming a set called a satellite DNA. (Ando S) (Blattes R)

The Structure of the Genome (5)

- Highly Repeated DNA Sequences represent about 1-10% of total DNA.
- Satellite DNAs short sequences that tend to evolve very rapidly.
- Minisatellite DNAs unstable and tend to be variable in the population; form the basis of DNA fingerprinting.
- Microsatellite DNAs shortest sequences and typically found in small clusters; implicated in genetic disorders.

Figure 1

Micro satellite –short tandem repeats:

A microsatellite is a tract of repetitive DNA in which certain DNA motifs are repeated, typically 5–50 times. Microsatellites occur at thousands of locations within an organism's genome; additionally, they have a higher mutation rate than other areas of DNA leading to high genetic diversity. (Doolittle WF)



2. Minisatellite

A minisatellite is a tract of repetitive DNA in which certain DNA motifs are typically repeated 5-50 times. Minisatellites are prominent in the centromeres and telomeres of chromosomes, the latter protecting the chromosomes from damage. The name "satellite" refers to the early observation that centrifugation of genomic DNA in a test tube separates a prominent layer of bulk DNA from accompanying "satellite" layers of repetitive DNA. (Gillespie D, Mazrimas JA)



Figure 3: Minisatellite DNA

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Tandem repeats & single nucleotide polymorphism:

Tandem repeats

- Tandem repeats occur in DNA when a pattern of two or more nucleotides is repeated and the repetitions are **adjacent** to each other
- Form different density band on density gradient centrifugation (from bulk DNA) -satellite

Example: A-T-T-C-G-A-T-T-C-G Tandem repeats: - Satellite DNA: - Microsatellite: - Minisatellite: - Minisatellite: - Minisatellite:





Figure 5

Satellite DNAs in Plant Sex Chromosomes:

Among flowering plants, the origin of dioecy appears to have independently occurred in about 6% of the genera. The most common case is the existence of XX/XY chromosomal complements and a Y-based sex-determining mechanism. However, there appear to be other alternatives, such as complex chromosomal systems (Yasmineh WG) (i.e. XX/XY_1Y_2 systems) and cases in which the sex spssecification is mediated by the balance between the number of X chromosomes and the number of autosomes (X/A balance). Though sex chromosomes have evolved independently in several different groups of organisms, they share common evolutionary pathways. (Mazrimas JA)

Identification and Quantification of Tandem Repeats:

A software package (k-Seek) that identifies and quantifies tandem repeats of 2 to 10mers from short read-based whole genome sequences .In short, each raw read is first broken into small fragments of equal lengths. complex sequences are expected to yield clusters with very few members, short repetitive fragments will form a large cluster. Once the kmer is identified, the number of repeats from the read is then tallied based on a word-search procedure. To capture tandem counts, only kmers that are either immediately preceded or followed by the same kmer are scored. Additionally, we exclude tandem repeats that span less than 50 bp to avoid microsatellites and to guard against ascertainment bias for small kmers (2–4mers), as they are easier to identify from short stretches of DNA than larger kmers. (Harrison PR)



tandem kmers

3. Biological significance of satellite DNAs

The biological importance of SSR, these are homopolymer tracts, for eg: can serve as protein binding signals, particularly as upstream promoter elements. Also, long homopolymer tracts are spaced non-randomly in the genome of *Dictyostelium discoideum*, suggesting a preferential linker DNA location in the repeating nucleosome structure of this AT-rich organism. (Abad JP)

DNA profiling: The DNA obtained is studied by mainly two mechanisms –by RFLP and by PCR analysis.

RFLP: These analyses are of two types

Multi locus polymorphism (MLP) and single locus polymorphism (SLP): The DNA digested and run on agarose is transferred to a membrane and probed with highly specified probe. Thus probe also hybridize with fragments of similar sequences. The hybridized probe is detected by autoradiography or in the case of alkaline phosphatase present in the probe by chemiluminescence. It is not possible to differentiate fragments differing by few repeats by this process.

PCR: This analysis is of two types

STR (short tandem repeats) and MVR (minisatellite variant repeat): Analyses. The most common type is to analyse STR. In this methods two probes complementary to the sequences flanking an STR is used to hybridize and each STR obtained is amplified by PCR. The resulting amplified product appears as distinct bands in agarose gel. Each STR has as many as 9 to 10 different alleles in human. Each individual has two loci for STR. Therefore it is necessary to analyse 9 in 10 repeats to attain a definite result. The information of the DNA obtained by such methods is used to interpret the results of the crime. (Ando S) (Blattes R)

Identification of criminals:

The main and most widely used application of DNA profiling is use of the technology to identify criminal.

Kinship analysis:

This method can be use to determine where two or more individual are members of the same family. It is also an important evidence for paternity testing in confirming the parents of a child.

Sex identification:

This can also be used for identification of sex by amplifying the sequence for Y chromosome.

4. Conclusion

The discovery and study of satellite DNA have done much to advance ideas about the molecular structure of chromosomes but so far little to explain the significance of this DNA itself. The involvement of satellite DNA is probably structural and changes in satellite sequences presumably bear witness to prolific alterations in constitutive heterochromatin in evolution. Such changes have stabilized within species such that each individual of a given species, as far as is known exhibits the same spectrum of satellite DNA is involved in mechanisms, resident in constitutive heterochromatin, which are essential to the balance of gene expression which we recognize as a species. Further studies of satellite DNA should reveal number of applications is having in various divisions.

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A. Mounika et al, JPBR, 2016, 4(2): 95–98

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