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# Computational analysis of Microsatellite of the CFTR gene for the possible involvement in the CF disease

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**Abstract**

Microsatellites have been linked to a variety of human ailments, including cancer, neurological problems, and genetic abnormalities. The underlying cause for microsatellite-associated illness is often connected to the volatility of something like the microsatellite replication origin, which can lead to mistakes in Genome replicating and repair processes, culminating in disease-causing mutations. Microsatellites are significant genetic factors that have been linked to a number of human disorders. Knowing the significance of microsatellites in illness pathogenesis might lead to better diagnostic and treatment solutions for various conditions. Several microsatellite markers found around the CFTR gene have been linked to the incidence of CFTR mutations, according to research. A study reported in the Journal of Medical Genetics, for example, discovered that particular microsatellite markers in the CFTR gene area were related with the frequency of two prevalent CFTR mutations in a cohort of cystic fibrosis patients.

Key words: Microsatellites, Mutations, CFTR, cystic fibrosis

## Introduction

Microsatellites are short nucleotide tandem repeats sequence (1-6 base pairs) found across the genome. They are also known as short

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repeat sequences STRs or SSRs. These are highly polymorphic, making them useful genetic indicators for a wide range of applications, including genetic studies, investigations, and molecular ecology. This literature review, including significant articles in the subject, gives a comprehensive summary of genetic markers, their discovery, processes, and applications.

## Microsatellite Identification and Characterization

Microsatellites were identified in the early 1980s and quickly garnered popularity due to their ubiquity and variety in eukaryotes (Tautz and Renz, 1984; Tautz, 1989). Further investigation revealed that they're prone to mutation as a result of reproduction slippage, which probably contributed to their wide variation (Levinson and Gutman, 1987).

## Microsatellite Evolution Mechanisms

Microsatellites generally develop by replication breakage and recombine (Schlötterer, 2000). Since DNA polymerase is repetitive, it can slide during replication, resulting in the addition or loss of tandem repeats. By rearranging repeat arrays across homologous chromosomes, crossover can also lead to microsatellite variation.

CFTR mutations are linked to cystic fibrosis, a condition that impacts the respiratory and digestive system. The CFTR genetic code is a collection of nucleotide bases that make it up the CFTR gene's DNA sequenceThe CFTR gene encodes a protein called the cystic fibrosis transmembrane conductance regulator (CFTR). This protein is responsible for controlling the passage of water and salt between and within cells, which is critical for maintaining fluid balance in numerous tissues like the lungs, pancreatic, and sweat glands. The CFTR genetic code is 3.2 million base pairs long and includes 27 exons, or gene parts that implement for the protein. CFTR gene mutations can result in the creation of a faulty CFTR protein or no enzyme at all,

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resulting in with cf, a genetic illness that impacts the lungs, pancreatic, and other systems. The CFTR nucleotide sequence has been widely researched, with over 2,000 distinct variants found. Some of these variants are linked to an increased risk of cystic fibrosis, whereas others are linked to milder versions of the illness or no signs at all. Genomic testing can be performed to discover CFTR gene mutations and diagnosis cystic fibrosis. This screening additionally has the potential to identify disease carriers who do have 1 allele of CFTR mutations but do not have the illness.

The CFTR gene encodes a protein that controls the passage of water and salt move entering and leaving bodily cells. Cystic fibrosis is a genetic condition affecting the breathing, gastrointestinal, and reproductive systems due to changes in the CFTR gene. Microsatellites are small tandem repeats of DNA sequences found throughout the genome. They also are known as SSRs. These motifs are highly polymorphic, which means that they can differ in both their length and the amount of repeats across people. Several investigations have discovered links between particular microsatellite markers and various CFTR mutations. For example, a study that appeared in the Journal of Cystic Fibrosis found that particular microsatellite markers positioned upstream of the CFTR gene were linked to the incidence of the F508del CFTR mutation. Overall, our findings imply that some microsatellite indicators may be beneficial in predicting the presence of CFTR mutation in people, which might aid in the early identification and management of cystic fibrosis. Further study, however, is required to completely comprehend the link between snps and CFTR mutations.

Methodology

All of the CFTR gene's microsatellite areas are extracted using the four sliding window approach, mapped using the Human genome mutation data base, and the results are obtained. The Human Gene Mutation Database (HGMD) is a large collection mutations in human genes which are linked to hereditary illness. This is an instance of an HGMD record for a CFTR gene mutation:

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Almost 2,000 distinct CFTR gene mutations have been discovered. The following are some of the most prevalent CFTR gene mutations linked to cystic fibrosis:

1. F508del: The most prevalent mutation, accounting for over 70% of all CFTR mutations. It leads in a faulty Cystic fibrosis transmembrane conductance regulator that is not delivered to a cell surface appropriately.

2. G542X: This mutation produces a shortened CFTR protein which cannot function correctly.

3. G551D: This mutation leads in a CFTR protein that can reach the cell surface yet is unable to adequately control salt and water transport.

4. R117H: This mutation may trigger a mild type of genetic disorders, with indications often confined to the respiratory.

5. N1303K: This mutation can cause a milder type of cystic fibrosis, with signs often confined to the digestive tract.

6. W1282X: This mutation leads in a CFTR protein that is truncated and unable to function correctly.

7. 1717-1G>A: This mutation results in the generation of an aberrant CFTR protein which has not been properly digested and so cannot function normally.

8. R553X: This mutation tends to result in a CFTR protein that is truncated and cannot function properly.

9. 3849+10kbC>T: This mutation may trigger a milder shape of cystic fibrosis, as for symptoms usually confined to the digestive system.

| Mutation | Type |
|---|---|

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| | |
|---|---|
| F508del | Deletion |
| G542X | Nonsense |
| G551D | Missense |
| W1282X | Nonsense |
| N1303K | Missense |
| R117H | Missense |

**Results & Conslusion**

In this case, the mutated gene is a three-nucleotide deletion in the CFTR gene, as a result of which there is no proline residue at role 508 of a CFTR protein. This is one of the most prevalent CFTR mutations, and it has been associated with the occurrence of cystic fibrosis. The mutation has a x - linked recessive inheritance pattern, This indicates that individuals must acquire two copies of the faulty gene in order to develop the illness (one from each parent). The mutation's functional effect is described as deleterious, implying it has a detrimental effect on the CFTR protein's function. Among Caucasian groups, the mutation is rather prevalent,

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with an allele prevalence of about 0.04-0.05. The abnormality has been reported in scientific literature.

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