# Silent mutations: The hidden changes in our DNA.

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## Introduction

Genetic mutations are often viewed as harmful changes in the DNA sequence that lead to diseases or alterations in physical traits. However, not all mutations have such noticeable effects. Some mutations, known as silent mutations, do not alter the protein that is produced, despite a change in the genetic code. These mutations are subtle and often go unnoticed, but they play an interesting role in the complex world of genetics. This article explores silent mutations, how they occur, their potential effects, and their significance in genetics [1].

A silent mutation is a change in the DNA sequence that does not result in a change to the amino acid sequence of the corresponding protein. This happens because of the redundancy in the genetic code. There are 64 possible codons (three-nucleotide sequences) that code for 20 amino acids, meaning that several different codons can code for the same amino acid. Silent mutations occur when a mutation changes a codon but still results in the same amino acid being added to the protein [2].

For example, the codons GAA and GAG both code for the amino acid glutamic acid. If a mutation changes a GAA codon to GAG, the protein produced will still contain glutamic acid in that position, and the mutation would be silent in terms of its functional impact on the protein [3].

Silent mutations generally occur due to substitutions in the DNA sequence, where one base is replaced by another. For example, a change from adenine (A) to guanine (G) can alter the codon, but if this change does not affect the resulting amino acid, it is considered silent. This is because the genetic code is degenerate, meaning that multiple codons can code for the same amino acid [4].

The genetic code's redundancy or "degeneracy" is crucial in allowing silent mutations to occur. This redundancy means that many amino acids are encoded by more than one codon. For example, the amino acid serine is encoded by six different codons, such as UCU, UCC, UCA, UCG, AGU, and AGC. If a silent mutation changes one of these codons but still results in the same amino acid being added to the protein, the mutation is considered silent [5].

Though silent mutations do not change the amino acid sequence of proteins, they can still have effects on cellular processes. One potential impact of silent mutations is on the efficiency of protein synthesis. The change in the DNA sequence could affect the mRNA (messenger RNA) molecule produced during transcription. This altered mRNA might be processed differently, influencing the rate at which the protein is synthesized [6].

Silent mutations can also affect gene expression and regulation. In some cases, the change in the DNA sequence could influence the way the gene is spliced or the way regulatory elements interact with the gene. Even if the final protein remains unchanged, the mutation could alter the timing or location of its production within the organism [7].

This can sometimes lead to subtle changes in phenotype, even though no obvious changes occur in the structure of the protein itself. Such effects might not be immediately apparent but could have long-term consequences, particularly if the mutation affects crucial biological pathways [8].

While silent mutations do not directly impact the function of a protein, they can play an important role in evolution. These mutations contribute to genetic variation, which is essential for natural selection and evolution. Because silent mutations do not affect an organism's fitness or survival, they can accumulate in the genome without causing harm [9].

Silent mutations are an important area of study in genetics and evolutionary biology. While they may seem inconsequential because they do not affect protein function, they can provide valuable information about the evolution of genomes and the mechanisms of DNA replication and repair. Furthermore, studying silent mutations can shed light on the complexity of gene regulation and how small changes in the genetic code can have broader effects on cellular processes [10].

### Conclusion

Silent mutations are often overlooked because they do not result in visible changes to an organism's phenotype or protein function. However, these hidden changes in the genetic code play a significant role in evolution, gene regulation, and the overall functioning of organisms. While they are typically harmless, silent mutations can contribute to genetic variation, provide insight into cellular processes, and have subtle but meaningful impacts on health and disease. Understanding the full extent of silent mutations helps researchers appreciate the complexity of genetics and the hidden factors that drive genetic diversity and evolution.

### References

 Khalifa A, Hamad S. Hiding secret Information in DNA sequences using silent mutations. Br J Math Comput Sci. 2015;11(5):1.

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- Mirkovic N, Marti-Renom MA, Weber BL, et al. Structurebased assessment of missense mutations in human BRCA1: Implications for breast and ovarian cancer predisposition. Can Res. 2004;64(11):3790-7.
- 3. Gibbs WW. The unseen genome: Gems among the junk. Sci Am. 2003;289(5):46-53.
- 4. Rafi SK, Fernández-Jaén A, Álvarez S, et al. High functioning autism with missense mutations in synaptotagmin-like protein 4 (SYTL4) and transmembrane protein 187 (TMEM187) genes: SYTL4-protein modeling, protein-protein interaction, expression profiling and microRNA studies. Int J Mol Sci. 2019;20(13):3358.
- Kikutake C, Suyama M. Possible involvement of silent mutations in cancer pathogenesis and evolution. Sci Rep. 2023;13(1):7593.
- 6. Thusberg J, Vihinen M. Pathogenic or not? And if so, then

how? Studying the effects of missense mutations using bioinformatics methods. Hum Mutat. 2009;30(5):703-14.

- Supek F, Miñana B, Valcárcel J, et al. Synonymous mutations frequently act as driver mutations in human cancers. Cell. 2014;156(6):1324-35.
- David A, Sternberg MJ. The contribution of missense mutations in core and rim residues of protein– protein interfaces to human disease. J Mol Biol. 2015;427(17):2886-98.
- 9. Clerx M, Heijman J, Collins P, et al. Predicting changes to I Na from missense mutations in human SCN5A. Sci Rep. 2018;8(1):12797.
- Thirumal Kumar D, George Priya Doss C. Role of E542 and E545 missense mutations of PIK3CA in breast cancer: A comparative computational approach. J Biomol Struct Dyn. 2017;35(12):2745-57.

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