Single Base Pair Mutation

A synonymous mutation can affect transcription, splicing, mRNA transport, and translation, any of which could alter the resulting phenotype, rendering the... 3616aacb37

Mutation rate Mutation rates are not constant and are not limited to a single type of mutation; there are many different types of mutations. The mutation rate of an organism is In genetics, the mutation rate is the frequency of new mutations in a single gene, nucleotide sequence, or organism over time. The rate of these types of substitutions can be further subdivided into a mutation spectrum, which describes the influence of the genetic context on the mutation rate. Missense, nonsense, and synonymous mutations are three subtypes of point mutations. characterized either as mutations per base pair per cell division, per gene per generation, or genome per generation. Point mutations are a class of mutations that are changes to a single base. Mutation rates are given for specific classes of mutations 3616aacb37

Germline mutations can be caused by a variety of endogenous (internal) and exogenous (external) factors, and can occur throughout zygote development. A mutation that arises only in germ cells can result in offspring with a genetic condition that is not present in either parent; this is because the mutation is not present in the rest of the parents' body, only the germline. 3616aacb37 Mutation can result in many different types of change in sequences. Mutations in genes can have no effect, alter the product of a gene, or prevent the gene from functioning properly or completely. Mutations can also occur in non-genic regions. A 2007 study on genetic variations between different species of Drosophila suggested... 3616aacb37 When the mutation rate... 3616aacb37 The term somatic generally refers to the cells of the body, in contrast to the reproductive (germline) cells, which give rise to the egg or sperm. For example, in mammals, somatic cells make up the internal organs, skin, bones, blood, and connective tissue. 3616aacb37 Frameshift mutations are apparent in severe genetic diseases such as Tay–Sachs disease; they increase susceptibility to certain cancers and classes of familial hypercholesterolaemia; in... 3616aacb37 There are several natural units of time for each of these rates, with rates being characterized either as mutations per base pair per cell division, per gene per generation, or genome per generation. The mutation rate of an organism is an evolved characteristic and is strongly influenced by the genetics of each organism, in addition to a strong influence from the environment. The upper and lower limits to which mutation rates can evolve is the subject of ongoing investigation. However, the mutation rate does vary over the genome. 3616aacb37

Postzygotic mutation Mutations that occur after the zygote has formed can be caused by a variety of sources that fall under two classes: spontaneous mutations and induced mutations. mutations that affect a single base pair, or large mutations that affect entire chromosomes and are divided into two classes, spontaneous mutations and A postzygotic mutation (or post-zygotic mutation) is a change in an organism's genome that is acquired during its lifespan, instead of being inherited from its parent(s) through fusion of two haploid gametes. How detrimental a mutation is to an organism is dependent on what the mutation is, where it occurred in the genome and when it occurred 3616aacb37

Point mutations usually take place during DNA replication. DNA replication occurs when one double-stranded DNA molecule creates two single strands of DNA, each of which is a template for the creation of the complementary strand. A single point mutation can change the whole DNA sequence. Changing one purine or pyrimidine may change the amino acid that the nucleotides code for. 3616aacb37 Point mutations may arise from spontaneous mutations that occur during DNA replication. The rate of mutation may be increased by mutagens. Mutagens can be physical, such as radiation from UV rays, X-rays or extreme heat, or chemical (molecules that misplace base pairs or disrupt the helical shape of DNA)... 3616aacb37

Frameshift mutation A frameshift mutation will in general cause the reading of the codons after the mutation to code for different amino acids. Due to the triplet nature of gene expression by codons, the insertion or deletion can change the reading frame (the grouping of the codons), resulting in a completely different translation from the original. It was shown that there was no difference in the frequency A frameshift mutation (also called a framing error or a reading frame shift) is a genetic mutation caused by indels (insertions or deletions) of a number of nucleotides in a DNA sequence that is not divisible by three. University looked at the difference in frequency of the mutation by both adding and deleting a base pair. The frameshift mutation will also alter the first stop codon ("UAA", "UGA" or "UAG") encountered in the sequence. A frameshift mutation is not the same as a single-nucleotide polymorphism in which a nucleotide is replaced, rather than inserted or deleted. The polypeptide being created could be abnormally short or abnormally long, and will most likely not be functional. The earlier in the sequence the deletion or insertion occurs, the more altered the protein 3616aacb37

Somatic mutation 8 × 10−7 compared with 1. humans, mutation load in fibroblasts was over twenty times greater than germline (2. 2 × 10−8 mutations per base pair). Adjusted A somatic mutation is a change in the DNA sequence of a somatic cell of a multicellular organism with dedicated reproductive cells; that is, any mutation that occurs in a cell other than a gamete, germ cell, or gametocyte 3616aacb37

Intramolecular base pairs can occur within single-stranded nucleic acids. This is particularly important in RNA... 3616aacb37 == Fraction of cells affected == 3616aacb37 In most animals, separation of germ cells from somatic cells (germline development) occurs during early stages of... 3616aacb37 == When mutagenesis occurs == 3616aacb37

Base pair Dictated by specific hydrogen bonding patterns, "Watson–Crick" (or "Watson–Crick–Franklin") base pairs (guanine–cytosine and adenine–thymine/uracil) allow the DNA helix to maintain a regular helical structure that is subtly dependent on its nucleotide sequence. They form the building blocks of the DNA double helix and contribute to the folded structure of both DNA and RNA. The regular structure and data redundancy provided by the DNA double helix make DNA well suited to the storage of genetic information, while base-pairing between DNA and incoming nucleotides provides the mechanism through which DNA polymerase replicates DNA and RNA polymerase transcribes DNA into RNA. recognize

specific base-pairing patterns that identify particular regulatory regions of genes. The complementary nature of this based-paired structure provides a redundant copy of the genetic information encoded within each strand of DNA. Many DNA-binding proteins can recognize specific base-pairing patterns that identify particular regulatory regions of genes. Intramolecular base pairs can occur within single-stranded nucleic A base pair (bp) is a fundamental unit of double-stranded nucleic acids consisting of two nucleobases bound to each other by hydrogen bonds 3616aacb37

== Ratio of transitions to transversions == 3616aacb37 Mutations may or may not produce detectable changes in the observable characteristics (phenotype) of an organism. Mutations play a part in both normal and abnormal biological processes including: evolution, cancer, and the development of the immune system, including junctional diversity. Mutation is the ultimate source of all genetic variation, providing the raw material on which evolutionary forces such as natural selection can act. 3616aacb37

Transversion transition per base, transition mutations are more likely than transversions because substituting a single ring structure for another single ring structure Transversion, in molecular biology, refers to a point mutation in DNA in which a single (two ring) purine (A or G) is changed for a (one ring) pyrimidine (T or C), or vice versa. A transversion can be spontaneous, or it can be caused by ionizing radiation or alkylating agents. It can only be reversed by a spontaneous reversion 3616aacb37

== Causes == 3616aacb37

Germline mutation These mutations commonly include single base pair substitutions, deletions A germline mutation, or germinal mutation, is any detectable variation within germ cells (cells that, when fully developed, become sperm and ova). Mutations in these cells are the only mutations that can be passed on to offspring, when either a mutated sperm or oocyte come together to form a zygote. Germline mutation is distinct from somatic mutation. After this fertilization event occurs, germ cells divide rapidly to produce all of the cells in the body, causing this mutation to be present in every somatic and germline cell in the offspring; this is also known as a constitutional mutation. resulting in many small point mutations that result from errors in replication 3616aacb37

Germline mutations can occur before fertilization and during various stages of zygote development. When the mutation arises will determine the effect it has on offspring. If the mutation arises in... 3616aacb37

Mutation A point mutation can be reversed by In biology, a mutation is an alteration in the nucleic acid sequence of the genome of an organism, virus, or extrachromosomal DNA. Mutations result from errors during replication, mitosis, meiosis, or damage to DNA, which then may trigger error-prone repair or cause an error during replication (translesion synthesis). Point mutations are modifications of single base pairs of DNA or other small base pairs within a gene. cytosine (C). Mutations may also result from substitution, insertion or deletion of segments of DNA due to mobile genetic elements 3616aacb37

Since there are 22 codes for 64 codons, roughly we should expect a random substitution to be synonymous with probability about 22/64 = 34%. The actual value is around 20%. 3616aacb37

Point mutation frameshift mutations), with regard to protein production, composition, and function. g. A point mutation is a genetic mutation where a single nucleotide base is changed, inserted or deleted from a DNA or RNA sequence of an organism's genome A point mutation is a genetic mutation where a single nucleotide base is changed, inserted or deleted from a DNA or RNA sequence of an organism's genome. g. These consequences can range from no effect (e. Point mutations have a variety of effects on the downstream protein product—consequences that are moderately predictable based upon the specifics of the mutation. synonymous mutations) to deleterious effects (e 3616aacb37

== Causes == 3616aacb37 Unlike germline mutations, which can be passed on to the descendants of an organism, somatic mutations are not usually transmitted to descendants. This distinction is blurred in plants, which lack a dedicated germline, and in those animals that can reproduce asexually through mechanisms such as budding, as in members of the cnidarian genus Hydra. 3616aacb37

Synonymous substitution This is possible because the genetic code is "degenerate", meaning that some amino acids are coded for by more than one three-base-pair codon; since some of the codons for a given amino acid differ by just one base pair from others coding for the same amino acid, a mutation that replaces the "normal" base by one of the alternatives will result in incorporation of the same amino acid into the growing polypeptide chain when the gene is translated. Synonymous substitutions and mutations affecting noncoding DNA are often considered silent mutations; however, it is not always the case that the mutation is silent. three-base-pair codon; since some of the codons for a given amino acid differ by just one base pair from others coding for the same amino acid, a mutation that A synonymous substitution (often called a silent substitution though they are not always silent) is the evolutionary substitution of one base for another in an exon of a gene coding for a protein, such that the produced amino acid sequence is not modified 3616aacb37

Although there are two possible transversions but only one possible transition per base, transition mutations are more likely than transversions because substituting a single ring structure for another single ring structure is more likely than substituting a double ring for a single ring. Also, transitions are less likely to result in amino acid substitutions (due to wobble base pair), and are therefore more likely to persist as "silent substitutions" in populations as single nucleotide polymorphisms (SNPs). A transversion usually has a more pronounced effect than a transition because the second and third nucleotide codon position of the DNA, which to a large extent is responsible for the degeneracy of the code, is more tolerant of transition than a transversion: transitions are more likely to be synonymous substitutions... 3616aacb37 While somatic mutations are not passed down to an organism's offspring, somatic mutations will be present in all descendants of a cell within the same organism. Many cancers are the result of accumulated somatic mutations. 3616aacb37

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