

Dna techniques may be used to correct a point mutation essay sample

[Science](#), [Genetics](#)



Point mutation is an error at a particular point on the DNA molecule. Since the changes occur in DNA, in order to fix the mutation, scientists have to find out where something went wrong in the DNA structure and how to fix it.

Technology improved and in recent years, we got new skills and we are able to change natural changes of DNA for our profit. It is still being worked on, but scientists can do a lot of impressing things with DNA structure now.

Point mutations might initiate very dangerous changes in human bodies. One of the most dangerous affects is cancer. Cancers arise from the buildup of multiple mutations in genes regulating cellular growth and differentiation. Identification of such mutations in numerous genes represents a significant challenge in genetic analysis, particularly when the majority of DNA in a tumor sample is from wild-type stroma. Due to their subtle nature, the point mutations are the most difficult to detect of all the genetic alterations.

Mutations are detected and localized by the presence and size of the RNA fragments generated by cleavage at the mismatches.

The single strand conformation polymorphism is another method. It consist of detection of polymorphisms of human DNA by gel electrophoresis as single-strand conformation polymorphisms. It is based on the differences in the secondary structure of single-strand DNA molecules differing in a single nucleotide, which also is frequently reflected in an alteration of their electrophoretic mobility in nondenaturing gel electrophoresis.

In denaturing gradient gel electrophoresis, the double stranded DNA is subjected to electrophoresis in gel that has an increasing concentration of

denaturant along the length of the gel. It works by separation of random fragments of DNA according to properties of their sequences. The fragment melts while traveling through the gel. The melting proceeds in segments, called melting domains, because of the cooperative nature of the denaturation of the double-stranded DNA because DNA fragments differ by single base pair substitutions separated in denaturing gradient gels which corresponds with melting theory.

When a domain melts, the fragment assumes a branched structure that causes significant retardation of movement. Thus, the position of the fragment in the gel after a certain time of electrophoresis is determined by the history of melting of the fragment that is altered if the sequence is different. The principle of separation in DGGE is such that sequence changes in the melting domain of highest stability cannot be detected, because the fragment no longer has a branched structure when the last domain melts. If, however, a stretch of sequence that serves as an extremely stable domain is attached to one side of the fragment, then mutations at any sites within certain types of sequence context can be detected by DGGE. The fact is that nearly all single base substitutions in DNA fragments joined to a GC-clamp can be detected by denaturing gradient gel electrophoresis. This extra sequence of extremely high stability can be conveniently attached to the target sequence of PCR by using one primer that has 40 nucleotides of an artificial GC-rich sequence (GC-clamp) extending at its 5'-end. With the use of this clamp, DGGE may be able to detect nearly all possible mutations in any given sequences.

Hybridization with radioactively labeled allelic specific oligonucleotides also has been applied to the detection of specific point mutations. The method is based on the differences in the melting temperature of short DNA fragments differing by a single nucleotide. Single point mutations have been also detected by the creation or destruction of restriction fragment length polymorphisms.

These methods of trying to fight point mutation really work, but they are not perfected yet. Scientists are still trying to find new ways that are more effective and that work for sure in any cases. Right now, it is done in labs and it is hard work because scientists have to think a lot on it and figure out where something went wrong in the DNA structure, but hopefully, in near future, computers will be able to do all the work and many lives will be saved.