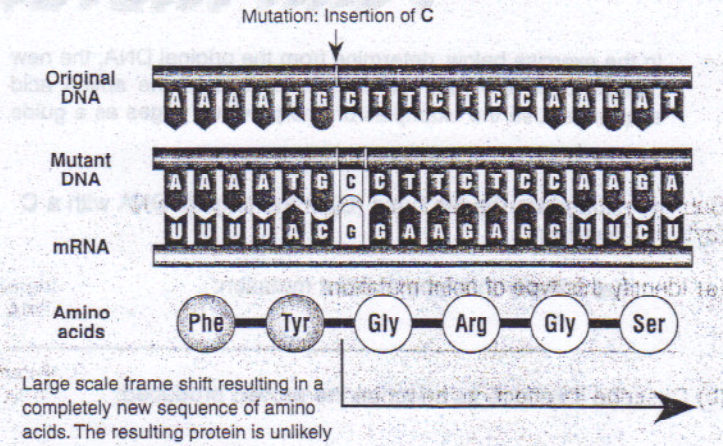
Reading frame shift by insertion

A major upset can occur when a single extra base is inserted into the DNA sequence. This has the effect of displacing all the other bases along one position and thereby creating a whole new sequence of codons. Such mutations are almost always likely to lead to a non-functional protein, but this does depend on the distance of the insertion or deletion from the START codon (i.e. the closer the insertion is to the START codon, the more the protein will be affected).

NOTE: could also lead to nonsense

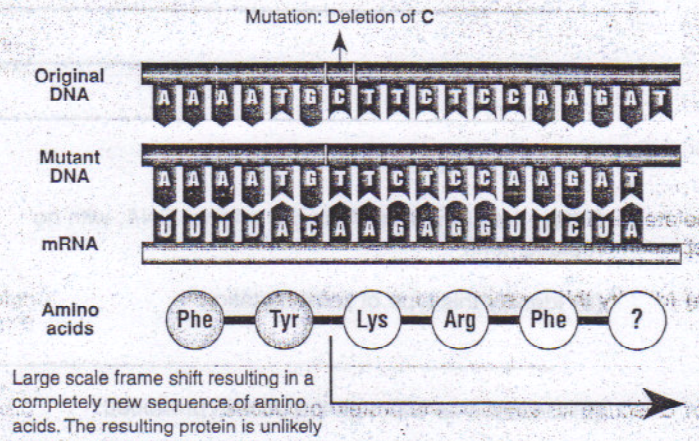


Large scale frame shift resulting in a completely new sequence of amino acids. The resulting protein is unlikely to have any biological activity.

Reading frame shift by deletion

In the same way that an insertion of an extra base into the DNA sequence has a large scale damaging effect, a deletion may also cause a frame shift. Again the result is usually a polypeptide chain of doubtful biological activity.

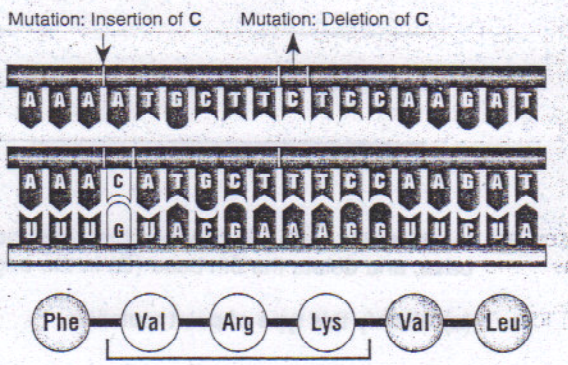
NOTE: could also lead to nonsense



Large scale frame shift resulting in a completely new sequence of amino acids. The resulting protein is unlikely to have any biological activity.

Partial reading frame shift

Both an insertion and a deletion of bases within a gene can cause a frame shift effect where each codon no longer has the correct triplet of three bases. In this example, three codons have been affected, along with the amino acids they code for. The error is limited to the codons including and between the insertion and deletion. There is no biological activity if the amino acids altered are important to the functioning of the resulting protein.



Altered chain which may or may not produce a protein with biological activity

Mutations involving change in only one nucleotide may have no observable effect on the phenotype of the organism; the subtle changes in the DNA sequence may still produce a chain of identical amino acids in the protein, or at least produce a protein that is unaffected by the change. Because of the degeneracy of the genetic code, many mutations of this type are unlikely to cause any change in the biological activity of the protein (there are exceptions, e.g. sickle cell disease).

1. Explain what is meant by a **reading frame shift**: _____

2. Not all gene mutations have the same effect on the organism, some are more disruptive than others.

   (a) Identify which type of gene mutations are the most damaging to an organism: _____

   (b) Explain why they are the most disruptive: _____

3. Explain why **biological activity** of a protein might be affected by a reading frame shift: _____