

## Exercises of Chap.3 page 72

### Exercise I p.72

- A.1. False, a silent mutation doesn't affect the phenotype
2. False, an insertion can occur in coding and non-coding regions
3. False, a wild type allele is an allele coding for the most common phenotype in a population.
4. True
5. False .....different DNA fragments
6. True
7. True
8. False, a genetic map shows the approximate location of a gene on a chromosome
9. False ....is nearly impossible
- B. 1.c
2. a,b,c
- 3.a,b,c,d
4. a,b
- 5.a,c
- 6.b
- 7.d
- 8.d
- 9.a
- 10.b

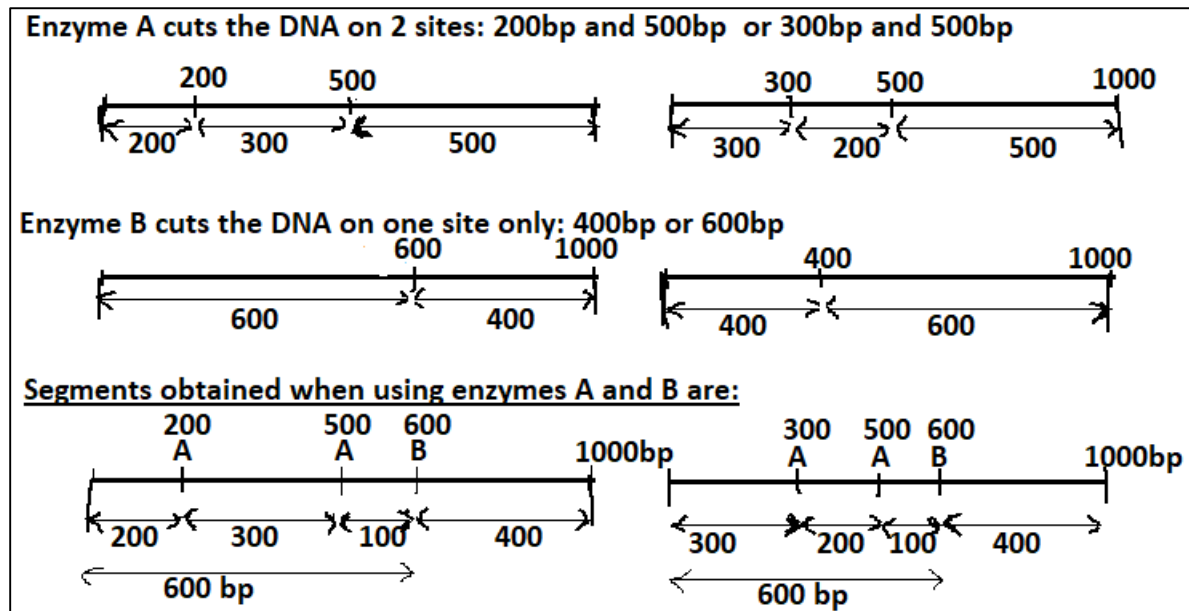
### Exercise II:

- a. TAC –TAA- CGG- ACA- TCA- ATT    Transcribed strand of DNA  
AUG- AUU-GCC-UGU-AGU-UAA    mRNA  
Met- Ile- Ala- Cys – Ser- Stop    Seq.of a.a
- b. TAC-TAC-GGA-CAT-CAA-TT    Transcribed strand of DNA  
AUG-AUG-CCU-GUA-GUU-AA    mRNA  
Met-Met-Pro-Val- Val    Seq.of a.a

### Exercise III

The size of DNA segment is:  $200+300+500=1000\text{bp}$ (enzyme A)

:  $400+600 = 1000\text{bp}$ (enzyme B)



#### Exercise IV

The DNA isolated from blood traces left at the scene of the crime and the DNA of the suspect are cut with the same restriction enzyme, electrophoresed and blotted onto a membrane. The membrane is hybridized with a DNA probe. The fingerprints are compared. If the 2 patterns are identical, then one can conclude that the blood traces at the scene of the crime are those of the suspect.

#### Exercise V

No, since the child's DNA fingerprint matches the DNA fingerprints of both the father and the mother.

#### Exercise VI

- Mutation by substitution, deletion, insertion
- TCT-AAA-TGG non-transcribed strand of DNA

UCU-AAA-UGG mRNA

Ser –Lys–Trp seq. of a.a

To obtain silent mutation, the 3<sup>rd</sup> nucleotide of base U of the 1<sup>st</sup> codon can be substituted by another nucleotide of base C, A or G; because each of the following codons UCU, UCC, UCA and UCG codes for the same amino acid Ser.

- Stop codons are UGA, UAG and UAA.

To obtain a stop codon, the 3<sup>rd</sup> nucleotide of base G in the 3<sup>rd</sup> codon can be substituted by another nucleotide of base A

#### Exercise VII

- When comparing the position of the 4 amino acids with the reference chromatogram, we deduce that the tetrapeptide contains : Asp+Ala+ Lys + Val

The molar mass is:  $133+89+146+117=485$

- b. The exact structure is difficult to specify because there are many possibilities:  
Asp-Ala-Lys-Val or Asp-Lys-Ala-Val or etc....since the change of one amino acid changes the sequence and hence the tetrapeptide.
- c. The chromatogram of individual Y shows only 3 amino acids: Asp,Ala and Lys. This means that the polypeptide has lost Val which is coded by 1 of the 4 codons:GUU,GUC,GUA,GUG. This can be explained by a mutation that occurred in the last codon leading to a stop codon UGA which leads to a tripeptide instead of tetrapeptide.

### **Exercise IX**

After cleavage with restriction enzyme, the restriction fragments are deposited in the well of a migration support(Agarose gel). At the beginning of the experiment, restriction fragments are separated by electrophoresis, after application of an electric field.Then they are incubated in the presence of a cDNA radioactive probe and hybridized. This results in 4 bands:a,b,c and d, with “a” the nearest and “d” the furthest from the well.

### **Exercise X**

- a. 3 types of  $\beta$ -globin are separated by electrophoresis. We can conclude that 3 different alleles of the gene coding for this polypeptide are present here.
- b. Each individual has 2 alleles.This is obvious for individuals 2,4,5 and 6(electrophoresis shows 2 bands for each of them)
- c. Individuals 1,3 and 7 have also 2 alleles of the same gene but they are identical(electrophoresis shows only one band for each one). One type of  $\beta$ -globin is thus produced.