Larbi Ben M'hidi University, Oum El Bouaghi   **Department: Sciences of Nature and Life**
1ˢᵗ year Master Biodiversity and Environment   **(2025/2026)**
Teacher: M. Mechri A.

The marking scheme of the exam (Genetic Basic of Biodiversity)

1. **Indicate whether each of the following statements is True (T) or False (F). (1.5 points)**

a. T	b. T	c. F	d. T	e. T	f. F

2. **Link the examples below to the corresponding selection types: (2 points)**

.3 اربط بين الأمثلة التالية و ما يتوافق مع نوع ....

a. Directional selection	b. Stabilizing Selection	c. Directional selection	d. Disruptive selection

3. **To which term ((1)gene flow, (2)genetic drift, (3)polyploidy, (4)metapopulation, (5)natural selection) do these different propositions correspond? (3.75 points)**

.3 إلى أي مصطلح ((1)....، (2)....، (3)....، (4)....، (5)....) تتوافق كل من المقترحات التالية؟

a. (3)	b. (2)	c. (2)	d. (1)	e. (5)

4. Greater ability to colonize new habitats than diploid ancestors.   Dosage effect of gene expression. Additive effect of the alleles increases the number of phenotypes.   Larger cells and nuclei compared to their respective diploid counterparts.   Reduced fertility. **(1 points)**

5. Quantitative genetics is the study of such characters in which many genes influence the trait. **(0.75 points)**

6. **Epistasis:** is the interaction between alleles at two loci, where the effect of one allele depends on the presence of alleles at a second locus.   **Synergistic epistasis**: The two loci produce together a greater effect than the sum of their individual effects. The alleles at these loci might work together to produce a higher fitness outcome. **Antagonistic epistasis**: This happens when the alleles at one locus reduce the beneficial effects of alleles at another locus, leading to a lower fitness outcome than if the effects of the loci were independent. **(2 points)**

7. Neo-Darwinian theory, is a key concept in modern evolutionary biology. Neo-Darwinism is an updated version of Charles Darwin's theory of evolution, incorporating Mendelian genetics and the understanding of how traits are inherited through genes. **(0.5 points)**

8. Single-nucleotide polymorphism (SNP), Polymorphic repetitive sequences (Short tandem repeats (STR), (Variable number of tandem repeats (VNTR)), insertion/deletion polymorphisms, transposable elements (TE), copy number variations (CNV) **(1.5 points)**

Exercise:

1. Using the underlined genotypic counts, calculate the allele frequencies in each population.(2 points)

.1 من أعداد ....، أحسب .... بالنسبة لكل ....

Population 1		Population 2	
Frequency of A	**Frequency of a**	**Frequency of A**	**Frequency of a**
Formula: $(2N_{AA} + N_{Aa})/2N$	Formula: $(2N_{aa} + N_{Aa})/2N$	Formula: $(2N_{AA} + N_{Aa})/2N$	Formula: $(2N_{aa} + N_{Aa})/2N$
Result: 0.66	Result: 0.34	Result: 0.41	Result: 0.59

2. Calculate the allele frequencies for the metapopulation (considering population 1 and population 2 as a single population).   .2 أحسب .... من أجل ....(.... و .... تعتبر .... واحدة) **(2 points)**

Frequency of A	**Frequency of a**
Formula: $(p_1+p_2)/2$	Formula: $(q_1+q_2)/2$
Result: 0.535	Result: 0.465

3. Calculate the expected heterozygosities (**He**) for the two populations.

.3 أحسب .... من أجل كل .... **(0.75 points)**

Population 1	**Population 2**
Formula: $1- (P^2+q^2)$	
Result: 0.4488	Result: 0.4838

4. Calculate the expected heterozygosity (**He**) for the metapopulation.

.4 أحسب ....من أجل .... **(0.5 points)**

Metapopulation
Formula: $1- (P^2+q^2)$
Result: 0.49755

5. Calculate F_{ST} .5 أحسب .... **(1 points)**

Formula: $Hs = (He_1+He_2)/2$ $F_{ST} = (H_T-H_S)/H_T$
Result: $Hs = 0.4663$, $F_{ST}= 0.062807$

6. There is 6.28% of genetic differentiation between the two poplations. **(0.75 points)**