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Genetics and Molecular Biology (End-Sem Examination)

IIID

Instructions
1. No negative marks.
2. Each question carries ten marks.
3. Attempts any five questions (see three sections)
4. The maximum mark is 50.
5. Time 1 hr.
6. Date: 08-December-2024

Section 1: Attempt any TWO questions

Q1: How does the wobble hypothesis explain the degeneracy of the genetic code, and what are its implications for translational fidelity?

Q2: Analyze the consequences of a frameshift mutation near the start of a coding sequence versus one near the end. How do these differ in their impact on the resulting protein?

Q3: Evaluate the significance of the Hardy-Weinberg equilibrium in understanding population genetics. How might deviations from this equilibrium indicate evolutionary processes?

Q4: What role do epigenetic modifications, such as DNA methylation and histone acetylation, play in gene regulation, and how can they be influenced by environmental factors?

Section 2: Attempt any TWO questions

Q1: A bacterial population starts with 1,000 cells, and each cell divides every 20 minutes. Calculate the population size after 2 hours.

Q2: If a Mendelian trait is governed by a single gene with two alleles (A and a), and the allele frequencies are p=0.6 for A and q=0.4 for a, calculate the expected genotype frequencies under Hardy-Weinberg equilibrium.

Q3: In a dihybrid cross (AaBb x AaBb), if 800 offspring are produced, how many are expected to have the phenotype for both dominant traits (AB), assuming independent assortment?

Q4: If a population has a mutation rate of 10^{-6} per nucleotide per generation and a genome size of 3 million base pairs, calculate the expected number of new mutations per individual per generation.

Section 3: Mandatory Question

Illustrate the structure of a eukaryotic chromosome, including features such as telomeres, centromeres, and nucleosomes. Write an essay explaining the role of chromatin remodeling in gene expression and how it contributes to epigenetic regulation.