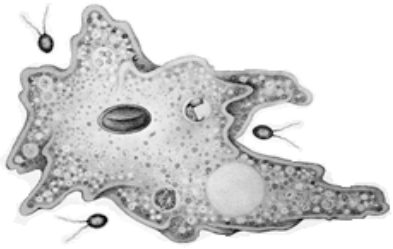
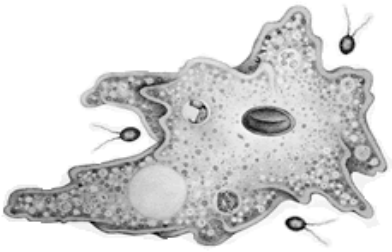
MCDB 2222 coreBIO: Practice exam for midterm 2 - Spring 2018



Carefully read each question to determine what the question wants you to do.



Q1: An organism requires the amino acid lysine in its food. You transfer a population of organisms to a diet in which lysine is missing. Mutations that enable the organism to grow in the absence of lysine are possible. Predict (and explain) what will happen to the rate at which such mutations appear when the organism is transferred to an lysine free diet.

Q1A: When the organism is stressed, errors during DNA synthesis increase and DNA repair becomes less efficient (why?). Compare the rate of lysine+ mutations to the overall mutation rate under these conditions and explain your thinking. How might the absence of lysine influence mutation rate?

Q1B: The organism is capable of catalyzing the synthesis of a wide range of small molecules, including many amino acids. What type of mutation would lead to the ability to grow in the absence of lysine.

Q1C: In the Luria-Delbruck experiment, the number of phage resistance mutations differed greatly between cultures (populations), some had few or none, others had many - why was that and what did they conclude from that observation?

Q2: You use DNA damaging radiation or mutagenic chemicals to generate mutations in population of organisms, such as the fruitfly *Drosophila*. You mate the mutagenized organisms, and discover a dominant cinnamon-colored eye phenotype. Outline how you would establish that the phenotype was due to an allele at a single genetic locus?

Q2A: What would limit your ability to conclude that the effect was associated with a single gene?

Q2B: What would force you to conclude that the phenotype was due to the synergistic effects of alleles at two different genetic loci (genes)?

Q2C: Why would this mutagenesis approach not work so well in humans (or the mouse)?

Q3: When considering a potentially mutagenic chemical in the environment, what factors will determine whether it is mutagenic in a particular organism?

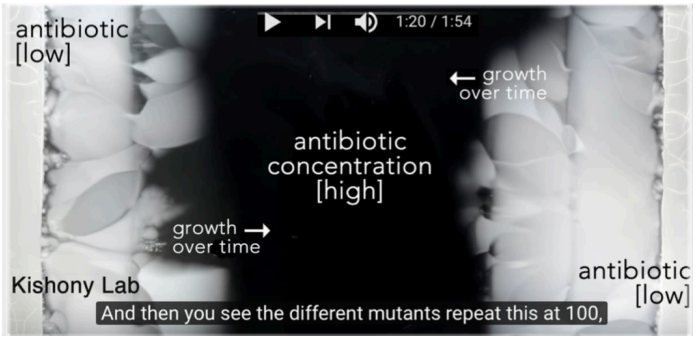
REPEAT QUESTION: Provide a molecular mechanism for how an amorphic mutation could produce a dominant allele.

Q4: In a particular environment, an organism achieves an optimal phenotype. Assuming that it were physicochemically possible, why would the absence of mutation (0% error rate + perfect error repair) be selected against, evolutionarily?

Q4A: Assume that you have two organisms, a host and a viral pathogen. Which would be expected to benefit from a higher mutation rate (and why)?

Q4B: In a sexual organism, describe the factors (including population size) that influence the rate at which a new mutation becomes an allele.

Q4C: In the megaplate evolution of antibiotic resistance experiment, the size of the steps in antibiotic concentration cannot be too big - why? How does antibiotic resistance arise in the wild?



Q4D: Explain what is happening when the growth of bacteria pauses at the boundaries between antibiotic concentrations?

Q4E: Why do doctors insist that you take all of the antibiotic they prescribe for you?

Q5: You are studying a particular phenotype (say, brain development). If you were asked to design a screen of a genome to identify all of the genes involved in brain development using the CRISPR CAS9 system, how would you begin? What factors would complicate your analysis?

Q5A: Why would not every mutation produce a phenotype?

Q5B: How might you use CRISPR CAS9 mutagenesis to delete a specific gene?

Q6: To carry out a Mendelian analysis, what is necessary in the organisms used?

Q6A: How did Mendel control mating in peas?

Q7: How would you recognize whether genes are linked?

Q7A: Assume that two alleles produce a similar, but not identical phenotype - how would you determine whether they are alleles of the same gene?

Q7B: Explain why a single genetic cross (producing only a few offspring) cannot be used to determine if two genes are linked.

Q7C: How does the number of offspring analyzed influence the certainty of a Chi square analysis?

Q7D: You are asked to analyze the results of a dihybrid cross: what would signal that the genes are linked?

Q7E: How would you used dihybrid crosses to map genes along a chromosome?.

Q8: How would you determine if alleles of the same gene interact?

Q8A: How would you determine if alleles of two different genes interact?

Q8B: If, over time and in a large population, the percentage of alleles of a particular gene is observed to change in ways not predicted by Mendelian rules - what is happening?

Q9: You are looking at a Genomicus map - how would you expect the extent of synteny around a particular gene to change as a function of evolutionary distance (what is evolutionary distance)?

Q9A: How would loss of synteny influence the ability of two organisms to produce viable offspring?

Q10: How might a hypermorphic or hypomorphic allele in one gene complement an allele in another gene?

Q10A: Draw out a biosynthetic pathway and describe how alleles in gene encoding various steps could interact genetically.