

Biol/ MBios 301 (General Genetics) Spring 2003
Second Midterm Examination A (100 points possible) Key
April 1, 2003

10 Multiple Choice Questions-4 pts. each (Choose the best answer)

1. Transcription involves:
 - a. mapping genes in bacteria using a viral carrier
 - b. reading an mRNA to yield an amino acid sequence in a protein
 - c. taking up DNA into a cell and changing its genetic makeup
 - d. reading a DNA strand and making a complementary messenger RNA**

2. Which of the following are differences between the RNAs as they are initially transcribed in prokaryotes and eukaryotes?
 - a. The RNAs grow in the 5' to 3' direction in prokaryotes but not eukaryotes.
 - b. An AUG codon which will be used to signal the start of translation is present in those RNAs which will code for proteins in eukaryotes but not in prokaryotes.
 - c. Four ribonucleotides, (A, G, C and U) are present in eukaryotes but not prokaryotes
 - d. Polycistronic messenger RNAs are often present in prokaryotes but not in eukaryotes.**
 - e. UAA, UAG and UGA are present in the transcript to signal where translation should stop in prokaryotes but not in eukaryotes.

3. Which of the following is NOT characteristic of DNA replication in eukaryotes?
 - a. Replication is bidirectional from each origin of replication.
 - b. There is a single origin of replication on each chromosome.**
 - c. Replication proceeds in the 5' to 3' direction on the new strand.
 - d. Small fragments are synthesized and joined on one of the two growing strands.
 - e. Replication is semi-conservative; each newly synthesized double helix has one old and one new strand.

4. Which of the following is NOT a property of the genetic code:
 - a. Codons are normally read in an overlapping manner.**
 - b. Codons are redundant, with more than one codon for most amino acids.
 - c. Codons are almost universal in their relation to amino acids.
 - d. There are three stop codons in virtually all systems
 - e. Codons are triplet (three ribonucleotides in length)

5. The normal function of an aminoacyl tRNA synthetase enzyme is to:
- Transcribe a tRNA off of the DNA template
 - Transcribe an mRNA off of the DNA template
 - Join a specific amino acid to a specific transfer RNA**
 - Serve as a binding site for RNA polymerase
 - Catalyze a peptide bond between adjacent amino acids in a protein.
6. Which of the following are NOT among the significant sources of the “extra” DNA present in eukaryotic genomes:
- Introns
 - Microsatellites
 - Transposable elements
 - Satellite DNA
 - Genes coding for the histones present in the nucleosome structure of the chromosomes.**
7. A consensus sequence observed when comparing regions adjacent (“upstream”) to genes of diverse origins may indicate:
- that replication of those genes is dispersive in nature
 - that the sequence has an important common function such as RNA polymerase binding**
 - that those genes do not fold as normal during chromosome packing
 - that the genes were of eukaryotic origin
 - that the genes were of prokaryotic origin
8. Choose the correct statements about the most common structure of DNA.
- The two strands are paired by hydrogen bonds between the bases, with A pairing with T, and G pairing with C.
 - The two strands run in opposite orientations (one 5'-3', one 3'-5') with respect to each other.
 - Backbone consists of alternating sugars and phosphate groups.
- 1,2,3**
 - 1,2
 - 1,3
 - 2,3
 - 1

9. A frameshift mutation refers to:
- a mutation which changes a single amino acid in a protein.
 - a small insertion or deletion mutation which changes the amino acids inserted in a protein from that point on.**
 - a mutation which results in termination of protein synthesis.
 - a mutation which does not cause a change in the amino acids present in a protein.
 - a mutation in a promoter region.
10. What is the main advantage of the Ames test for mutation detection?
- Chemicals that could damage DNA or cause cancer in humans can be detected quickly and inexpensively.**
 - Even a small amount of DNA can be amplified.
 - DNA can be sequenced more rapidly.
 - Chemicals can be synthesized in bacteria.
 - Chromosome rearrangements can be mapped and ordered in relation to human chromosomes.
- 10 Short Identification- 2 Pts. each
11. lytic infection- *infection of a host cell by a virus in which the virus replicates and the host cell (e.g., bacterium in the case of a phage) lyses (bursts).*
12. xeroderma pigmentosum- *a genetic disease in which affected individuals are unable to repair DNA damage caused by UV light and as a result have a high incidence of skin cancer.*
13. primase- *enzyme which synthesizes the short RNA primer which is used to initiate DNA replication.*
14. intron- *extra genetic material present within eukaryotic genes which does not code for proteins and which is spliced out during RNA processing.*
15. polytene chromosome- *chromosome found in the salivary glands of Drosophila which has replicated many times without dividing. Detailed band pattern present along the chromosome allows rearrangements such as inversions, deletions or duplications to be identified and described in detail.*
16. topoisomerase- *enzyme which nicks DNA, allowing unwinding during the replication process.*

17. generalized transduction- *transfer of DNA from one bacterium to another by a virus in which any bacterial gene can potentially be transferred. This process can be used for detailed mapping of bacterial genes on the chromosome.*
18. duplication- *production of an extra copy of a region of a chromosome. This can be an important process in evolution by providing extra copies of genes which may then evolve new functions.*
19. transposable element- *genetic material which can move from one site to another on a chromosome.*
20. minimal medium- *the simplest medium on which bacteria can grow. Mutants unable to grow on minimal medium are one important type of mutant which has been studied in bacterial genetics.*

8 Problems (40 Points total)

21. (6 Pts.) What are two advantages of polymerase chain reaction/ microsatellite analysis as compared with Southern blot/ RFLP analysis for genetic typing of humans?

Many possible answers, e.g.,

Less DNA needed

DNA can be of lower quality (e.g., may be older)

Faster

Less expensive

It is not clear that it is necessarily more accurate

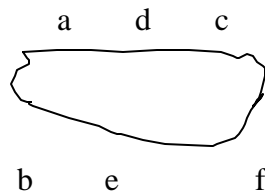
22. (6 pts.) Draw a genetic map for the genes A, B, C, D, E and F based on the following data set from interrupted mating experiments conducted with three different Hfr strains of E. coli.

Strain 1, order of transfer (first to last) A, D, C, F

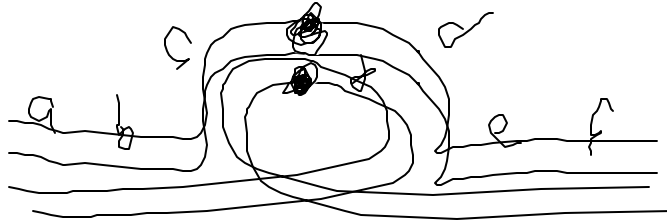
Strain 2, order of transfer (first to last) B, E, F, C

Strain 3, order of transfer (first to last) D, A, B, E

This is a circular map with the order: A D C F E B (BACK TO A)



23. (4 pts.) Diagram a single crossover within a pericentric inversion in an individual heterozygous for the inversion, and the products (gametes produced) from such an event, indicating the nature of any abnormalities transmitted. (The gene order on the normal chromosome is abcdef, the inversion chromosome has an order abdcef, and the crossover and the centromere are located between c and d.)



Products: Noncrossover: abcdef abdcef Crossover: abcdba fedcef
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24. (8 pts.) Associate each of the following eight structures or processes with one of the following: transcription, RNA processing or translation

Promoter	<u>transcription</u>
5' cap addition	<u>RNA processing</u>
Splicing of introns	<u>RNA processing</u>
Stop codon	<u>Translation</u>
RNA polymerase	<u>Transcription</u>
Ribosome	<u>Translation</u>
Transfer RNA	<u>Translation</u>
Addition of poly A tail	<u>RNA processing</u>

25. (4 pts). You digest human genomic DNA with the restriction enzyme EcoRI and use a specific 30-base sequence from a transposable element as a probe in Southern blots. There are no EcoRI cut sites in the 30-base probe. The gel you are running can detect bands from 100 to 10,000 kb in size. In 50 different people, each person had between 5 and 50 bands that hybridized with the 30-base probe. What does this tell you about the numbers of copies of the transposable element present in humans?

Basically, the results indicate that the number of copies of the element vary among individuals, and that the band number of 5 to 50 provides a minimal estimate of the number of copies of the element. It is a minimal estimate because (a) not all of the sites where the element are present will result in a band within the size range indicated, and (b) some individuals will be homozygous at the locus of interest (resulting in a single band) while others will be heterozygous (resulting in two bands) and we cannot immediately determine the proportions of each. If man are homozygous this could lead us to underestimate the number of sites with the element.

This question would have been more technically accurate if we said that the gel can detect bands from 100 to 10,000 bp (not kb) in size.

26. (4 pts.) A new breed of cattle, derived from the black angus (all black) breed, is identified which has a light colored body but dark tips on the ears and other cool parts of the body. Propose a possible explanation for the origin of this new breed and a way to test your hypothesis.

Possible explanation: A temperature-sensitive mutation in a gene coding for an enzyme involved in pigmentation (similar to the situation in Siamese cats). This could be tested biochemically (e.g., by seeing if a particular enzyme is temperature sensitive in laboratory studies) or by putting a cold pack on the animal and seeing if pigment appears in the area which has been artificially cooled.

27. (4 pts.) A small deletion on chromosome 16 is found to be inherited in a very large family in Spain over several generations. There is no noticeable phenotype associated with this change except that about 15% of the people with the deletion develop cancer of the esophagus. Propose an explanation for these results.

This might be the result of deletion of a tumor suppressor gene in the region on chromosome 16. Individuals heterozygous for the deletion have an increased chance of developing cancer because they only need to have a mutation in one copy (rather than two) of the gene.

28. (4 pts.) There are fewer transfer RNAs than the 61 codons which code for amino acids in the genetic code. What model explained how this might be possible? Briefly describe the model.

The “wobble” hypothesis proposed by Crick explained how you could have fewer tRNAs than codons. Under this model, the anticodon region of some tRNAs could pair with more than one codon, resulting in the same amino acid being inserted for more than one codon.