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 Define the following terms (5 points each):

**blastn** (be sure to distinguish blastn from other options, such as blastp)

**Basic Local Alignment Search Tool** – or some definition of what BLAST itself is (3 points)

**Nucleotide query** (1 point)

**Searching nucleotide database** (1 point)

**refseq**

**Unique accession numbers** (1 point) **curated/managed/selected** (3 points) by NCBI (1 point)– refseq is an NCBI creation

**semidominant alleles**

**Heterozygotes with two different semidominant alleles display an intermediate phenotype.**  
 You must mention heterozygotes for full credit. (5 points)

Heterozygotes display both phenotypes in codominance. (different concept!)

1. (5 points) At a given locus, two alleles, 1 and 2, are present in a population in Hardy-Weinberg equilibrium and no other alleles are present at appreciable frequencies. Homozygotes for allele 1 represent 36% of the population. What fraction is heterozygous?

$$\begin{aligned} \text{Allele 1} &= p^2 = 36\% & p &= 0.6 \\ 1 - p &= q = 0.4 \\ 2pq &= 2(0.24) = \mathbf{.48 \text{ or } 48\%} \text{ (5 points)} \end{aligned}$$

2. (5 points) Allele 2 confers an increased risk of early-onset Alzheimer's disease in a recessive manner. What fraction of the population shows this increased risk?

“...in a recessive manner.” – meaning homozygous for allele 2  
 $q = 0.4$        $q^2 = \mathbf{0.16 \text{ or } 16\%}$  (5 points)

You are studying a mutation in the yeast *Saccharomyces cerevisiae* that is temperature sensitive (no growth above 32 degrees). This mutation (which you name *mft2* for my favorite temperature sensitive 2) may be a new gene and you want to investigate.

First, you cross your haploid *mft2* strain to a haploid strain of the opposite mating type carrying *trp1* and *yfg4*, both recessive markers on chromosome IV. The phenotype of *trp1* is a requirement for tryptophan for growth and this gene is very tightly linked to the centromere. The phenotype of *yfg4* is temperature-sensitivity. However, in this case, there is no growth above 28 degrees. At 30 degrees, *yfg4* cells will not grow but *mft2* cells grow normally.

*YFG4* lies 11 map units to the right of *TRP1*, so the expected recombination frequency is 10%.

The resulting *mft2/MFT2; trp1 yfg4 / TRP1 YFG4* diploids are wild-type (they grow at 33 degrees without tryptophan) and sporulate normally.

You induce sporulation and examine the haploid spores.

3. Among the resulting haploid spores 50% are *trp1*. (5 points) What fraction of the *trp1* haploids are also *yfg4* (which you can test by growth at 30 degrees)?

Without recombination, you would expect to all spores to be *trp1 yfg4*. The recombination rate is 10%, therefore, **90% will be *trp1 yfg4*. (5 points)**

You identify 20 colonies that are *trp1YFG4*.

4. (5 points) If *MFT2* is unlinked (not on chromosome IV), what fraction of these 20 colonies do you expect to grow at 33 degrees?

**50% (5 points)** – equal chance of getting the unlinked *MFT2* chromosome with the wild-type or mutant allele

5. (6 points) In this case (*MFT2* is unlinked) could you determine whether it is near the centromere of the chromosome that it is on? Is so, how would you do that?

**Yes (2 points), You would carry out tetrad analysis and count tetratypes. (4 points)** The further *MFT2* is from the centromere, the greater proportion of tetratypes you would observe (up to 2/3). You must mention tetratypes for full credit, some explanation with discussion of recombination received partial credit.

6. (5 points) If *MFT2* is 2 cM. to the right of *YFG4*, what fraction of these 20 colonies do you expect to grow at 33 degrees?

*TRP1 YFG4 mft2* recombines between the *TRP1* and *YFG4* loci to yield *trp1 YFG4 mft2*  
*trp1 yfg4 MFT2*

Based on the crosses outlined above, barring recombination, your spores should have the genotype *trp1 YFG4 mft2*, which does not grow at 33 degrees. Only with recombination (at the rate of 2%) between *YFG4* and *MFT2* (the loci, not the alleles specifically) can there be growth at 33.

Rate of recombination = **2%** or **0.4 colonies** or **0 colonies** (0% requires explanation) **(5 points)**

7. (5 points) If *MFT2* lies precisely between *TRP1* and *YFG4*, what fraction of these 20 colonies do you expect to grow at 33 degrees?

*TRP1 mft2 YFG4* recombines to yield *trp1 mft2 YFG4* or *trp1 MFT2 YFG4* with equal frequency.  
*trp1 MFT2 yfg4*

**50% (5 points)** - there has to be a recombination even to get the *trp1 YFG4* genotype, therefore, if *MFT2* is in the middle, half of the recombination events will result in *trp1 MFT2 YFG4* and half *trp1 mft2 YFG4*.

8. (5 points) If *MFT2* lies 2 cM. to the left of *TRP1*, what fraction of these 20 colonies do you expect to grow at 33 degrees?

*mft2 TRP1 YFG4* recombines between the *TRP1* and *YFG4* loci to yield *MFT2 trp1 YFG4*  
*MFT2 trp1 yfg4*

Similar reasoning to 6, except reversed. Based on the crosses, the alleles *MFT2* and *trp1* will be together for the majority of the time, except for the 2% where recombination occurs resulting in *mft2 trp1*.

**98% or 19.6 colonies or 20 colonies** (100% only with explanation) **(5 points)**

9. (5 points) Here is the sequence of the template strand of a DNA fragment:

GTCGCCGTGCAATGATGTAGGCGACTATGGTTGA

Applying the standard **convention** for polarity (which end is 5' and which is 3'), which of the following would be the complementary, nontemplate, strand?

c) TCAACCATAGTCGCCTACATCATTGCACGGCGAC

Convention is that unlabeled nucleotide sequences read 5' (left) to 3' (right). **(5 points)**

(4 points each). In the following questions, one of the statements is true.

Circle either **a** or **b** (or **c**), next to the correct statement. Ambiguous marks (circling both, placing a mark between the two statements, etc.) will be considered wrong.

10. **b** In tetrad analysis, when two genes are **unlinked** the number of parental ditypes will be approximately equal to the number of nonparental ditypes.
11. **a** In tetrad analysis, when two genes are unlinked the relative number of tetratypes and nonparental ditypes **will depend on** their distance(s) from the centromere.
12. **a** The same mutant allele can be **dominant with respect to some traits and recessive with respect to others**.
13. **b** The kinetochore is a specialized structure in the **centromere** region of each chromatid that is specialized for conveyance.

14. (9 points) Label **each** of the following three statements as

**1**) true of DNA polymerase, **2**) true of RNA polymerase, **3**) true of both or **4**) true of neither.

  **1**   **a**. Requires a primer whose 3' end is base-paired to the template.

  **3**   **b**. Requires a template.

  **4**   **c**. Adds nucleotides to the 5' end of a polynucleotide chain in accordance with basepairing to a template strand.

15. (8 points) Label **each** of the following statements as **true** or **false**

**F** a. The probability of two or more **independent** events occurring together is the **sum** of the probabilities that each will occur by itself.

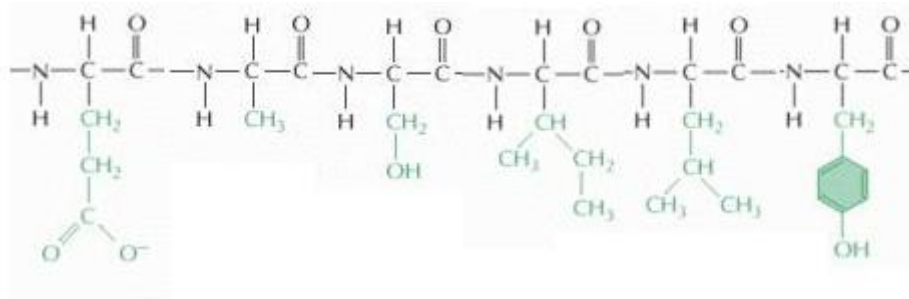
**T** b. The probability of two or more **independent** events occurring together is the **product** of the probabilities that each will occur by itself.

**F** c. The probability of two or more **mutually exclusive** events occurring together is the **sum** of the probabilities that each will occur by itself.

True was accepted for c) due to the question's wording

**F** d. The probability of two or more **mutually exclusive** events occurring together is the **product** of the probabilities that each will occur by itself.

16. (6 points). What is the sequence of this stretch of amino acids in single letter code?



**E            A            S            I            L            Y**

**Single letter code required for credit.**