

Name \_\_\_\_\_ Rec. Section \_\_\_\_\_ TA \_\_\_\_\_

**7.012 Fall 2018: Problem Set 2****Due: Wed 10/03/2018**

The solutions to these problems must be submitted electronically to your TA through the 7.012 Stellar site. All submissions must be received before 9:50 AM on October 3, 2018. Check your file to ensure it was successfully submitted. Only the material that is received prior to the deadline will be graded, no additional material will be accepted after the deadline.

**Question 1 (5 points)**

Congratulations! You have identified a new species of gourd in the wild and named it Gourdgeous. Gourds from Gourdgeous plants come in two general varieties: (i) those that have a waxy shell and are bitter, and (ii) those that have dry shells and are sweet. When you cross two true-breeding Gourdgeous plants from two varieties to each other, you get F1 generation plants that have waxy shells and are bitter in taste.

- a.) Write down dominant and recessive phenotypes for shell texture and taste in Gourdgeous plants.

Dominant phenotypes: \_\_\_\_\_

Recessive phenotypes: \_\_\_\_\_

- b.) Fill in the table below with all the potential genotypes for each phenotype provided.

*Indicate the alleles associated with dominant phenotypes by uppercase letters and alleles associated with recessive phenotypes by lowercase letters. Indicate the alleles for shell exterior as "A or a" and the alleles for taste as "B or b". Assume these traits lie on different autosomes.*

Phenotype	Possible genotype(s) for the phenotypes shown in wild plants	Possible genotype(s) for the phenotypes shown in true breeding plants
Waxy shell		
Dry shell		
Bitter taste		
Sweet taste		

- c.) You want to grow gourds for commercial purposes so you want to make sure that your two varieties (i) those that have a waxy shell and are bitter, and (ii) those that have dry shells and are sweet are really true breeding and not heterozygous for these traits. What genotype and phenotype gourd would you cross your two main strains to see if they are true breeding, if necessary? What are the expected results? Explain your reasoning

**Question 1, continued**

- d.) You cross two F1 plants to each other and obtain 1600 plants in the F2 generation. Fill in the Punnet square below with each genotype you expect. Indicate how many plants you expect from each phenotype.


- e.) Circle all waxy-shelled sweet plants in the Punnet square. What fraction of the waxy-shelled sweet plants are true-breeding?

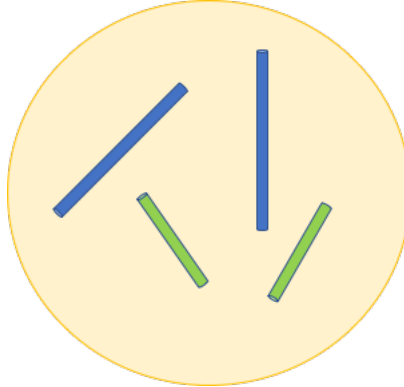
- f.) You study new gourd traits, shell color and seed texture. From the list and given info, indicate the trait(s) that is NOT Mendelian inheritance. The parental strains A and B are true breeding.

Strain	Phenotype
Strain A	Yellow shell and fuzzy seed
Strain B	Green shell and smooth seed
Strain A x Strain B Offspring	50% yellow shell, smooth seed 50% green shell, smooth seed

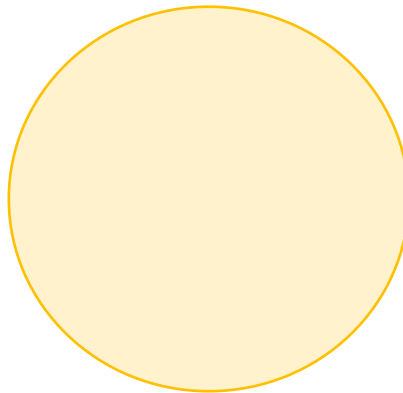
**Question 2 (5 points)**

A cross between two worms with genotypes AAbbDD and aaBBDD was performed. Shown below is the nucleus of a cell from the F1 generation from this cross, where the A/a and B/b genes are on the large chromosome and the D locus is on the small chromosome.

- (a) Label the chromosomes with the appropriate alleles of the genes in the nucleus of the cell from the F1 generation.

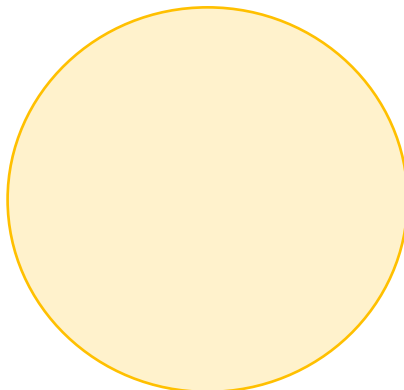


- (b) Now consider the nucleus drawn in part (a) during **mitosis**. Draw and align the chromosomes as they would appear in metaphase of **mitosis**. Label chromosomes with the appropriate alleles.



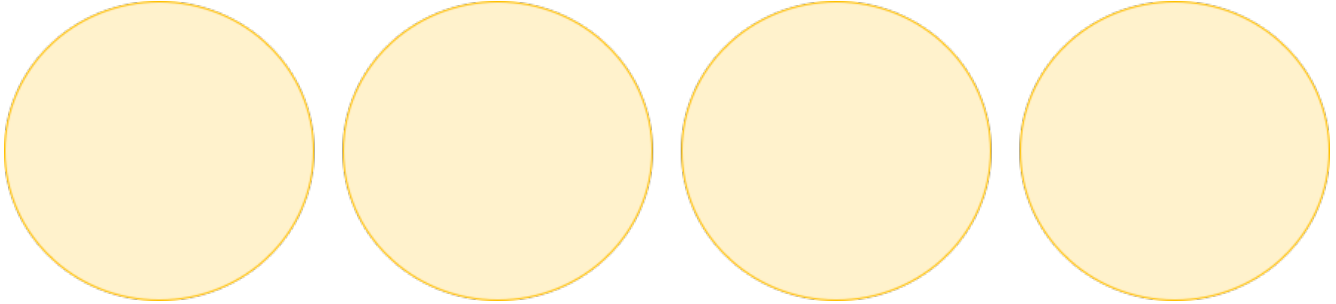
- (c) Now consider the diploid nucleus drawn in (a) during **meiosis**. Assume *no recombination*. Label chromosomes with appropriate alleles.

- i) On the diagram below, draw and align the chromosomes as they would appear in **metaphase I of meiosis I**.



**Question 2, continued**

- ii) Draw chromosomes as they will appear in the nuclei of the four gametes that will be produced at the end of meiosis you drew for part (i) after one recombination event between the A/a and B/b gene loci. Label the recombinant and parental alleles.

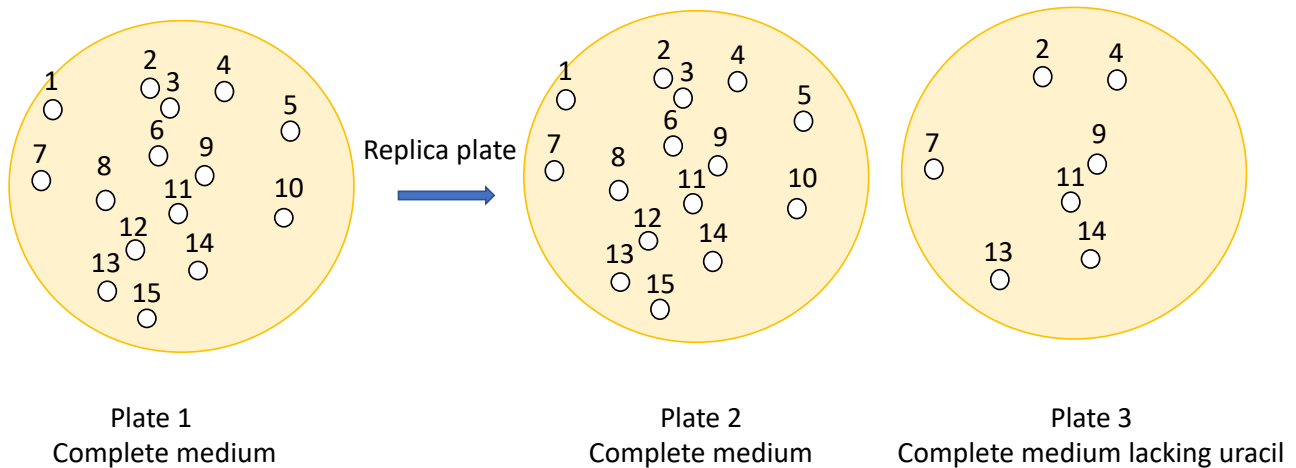


- iii) What would be the genotype of a worm you would cross the F1 generation worms to in order to find the map distance between genes A and B?
- iv) Assume that you performed that cross and obtained 200 offspring. You find that 60 had recombinant phenotypes and 140 had parental phenotypes. What is the map distance between A/a and B/b genes? Show your work.
- v) In accordance with part (iii), indicate for each gamete you drew above, roughly how many you would get from each type.
- vi) You study another gene C. After some crosses you find that gene C is 10 cM from gene A. Draw on a chromosome the possible arrangement(s) of genes A, B and C according to the information you have.

**Question 3 (6 points)**

You want to identify  $\text{Ura}^-$  mutants which are defective in the production of the essential nucleotide uracil and would not survive if the medium lacks uracil. You have in the lab haploid wild-type yeast that have been mutagenized with UV light. You allow the mutagenized yeast to grow into isolated colonies. Assume each colony is composed of yeast harboring a single mutation.

Below is your selection strategy to identify yeast that defective in uracil production. Colonies from the plate 1 with mutagenized yeast colonies have been transferred onto plates 2 and 3 by replica plating.



- A.) What is the purpose of replica plating onto plate 2?
- B.) Give an explanation for the growth behavior of colonies that grow on plate 3.
- C.) List the numbers for colonies that are  $\text{Ura}^-$  (i.e. colonies that fail to synthesize uracil) and the plate from you will pick them.
- D.) You want to put mutants into complementation groups. What does it mean in words when two mutants are in the same complementation group? Choose correct statement(s) from the list below:
- ☐ The mutations are in genes that may encode for the same protein
  - ☐ The mutations are in genes that are related by sequence but function in different pathways.
  - ☐ The mutations are in genes that may encode for different proteins in the same pathway
  - ☐ The mutations are in genes that may encode for different proteins in parallel pathways that each can independently make the same essential compound
  - ☐ The mutations that cause dominant phenotypes are always in the same complementation group.

**Question 3, continued**

You repeat this experiment multiple times and isolate 4 new mutants (m1-m4) that are deficient in uracil production. Now you want to perform a complementation test to put mutants into complementation groups. You set up matings as shown in the table below. The growth behavior of diploids are also shown. A (+) indicates growth on plates containing complete medium lacking uracil; a (-) indicates lack of growth on plates containing complete medium lacking uracil.

Plate	Matings	Growth on plates lacking uracil
1	m1 x WT	+
2	m2 x WT	+
3	m3 x WT	-
4	m4 x WT	+
5	m1 x m2	+
6	m3 x m4	-
7	m1 x m4	+
8	m2 x m4	-
9	m2 x m3	
10	m1 x m1	

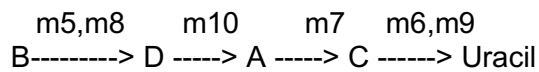
E.) Your postdoc says you did not need to set up the four plates (1-4) shown on the rows above. Explain to your postdoc why you need results of these matings.

F.) Indicate the complementation groups for all of the mutated genes in the mutants 1-4. If you cannot do so, explain.

G.) Fill in the expected results for matings 9 and 10. If you cannot, explain.

**Question 3, continued**

You determine that the pathway for uracil biosynthesis involves four precursor compounds, A-D. Here is the pathway for uracil biosynthesis. The intermediates A-E and the steps that enzymes encoded by genes from mutants m5-m10 are involved in are also shown.



H.) Fill in the table below where a (+) indicates growth on minimal media supplemented with the indicated precursor, a (-) indicates lack of growth. For example, all mutants grow on minimal media supplemented with uracil.

Mutant	Minimal media supplemented with compounds				
	A	B	C	D	Uracil
<b>m5</b>					+
<b>m6</b>					+
<b>m7</b>					+
<b>m8</b>					+
<b>m9</b>					+
<b>m10</b>					+

I.) Which intermediate will accumulate in mutants shown below?

m9: \_\_\_\_\_

m5: \_\_\_\_\_

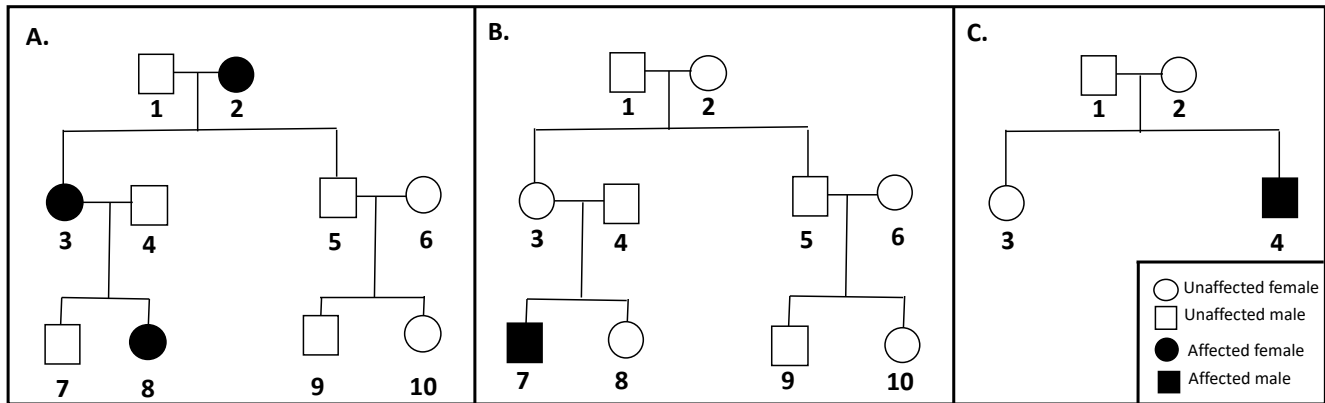
J.) Which intermediate will accumulate in a haploid yeast cell that contains the following double mutations?

m5 and m7: \_\_\_\_\_

m9 and m10: \_\_\_\_\_

**Question 4 (4 points)**

Geneticists studying humans rely upon the analysis of pedigrees to determine the genetic basis of certain traits such as heritable diseases. In the following pedigrees, shaded symbols represent affected individuals.



A.) Indicate with a checkmark in the table below what mode(s) of inheritance is consistent with these pedigrees. Assume complete penetrance. Assume individuals marrying into the families do not carry any disease-related genes.

Mode of inheritance	A	B	C
autosomal recessive			
X-linked recessive			
autosomal dominant			
X-linked dominant			

B.) List **all** possible genotypes of the following individuals for all possible modes of inheritance from part (a). Use the symbols  $A$ ,  $a$ ,  $X^A$ ,  $X^a$ .

Mode of inheritance	Individual 2 from pedigree A	Individual 1 from pedigree B	Individual 2 from pedigree C
autosomal recessive			
X-linked recessive			
autosomal dominant			
X-linked dominant			

C.) If the following individuals from the indicated pedigrees marry healthy individuals with no disease-related genes and have children, what is the probability that their children will have the disease? Calculate this probability for all possible modes of inheritance from part (a). Indicate if the probability is different depending on the sex of the child.

Individual 8 from Pedigree A:

Individual 8 from Pedigree B:

Individual 4 from Pedigree C: