

# 7.03 Exam 3

**Name:** \_\_\_\_\_

**TA:** Alex Bagley      Alice Chi      Dave Harris      Max Juchheim  
Doug Mills      Rishi Puram      Bethany Redding      Nate Young

**Section time:** \_\_\_\_\_

**Exam starts at 11:05 and ends at 11:55**

**There are nine pages including this cover page  
Please write your name on each page.**

Please...

- Look over the entire exam so you don't spend too much time on hard questions leaving easy questions unanswered.
- Check your answers to make sure that they make sense.
- To help us give partial credit, show your work and state any assumptions that you make.

<b>Question 1</b>	<b>34 points</b>
<b>Question 2</b>	<b>36 points</b>
<b>Question 3</b>	<b>30 points</b>

Name: \_\_\_\_\_

**1.** You are studying how yeast cells grow on sucrose and you find that both sucrose and glucose regulate expression of the *SUC1* gene, which encodes an enzyme for sucrose breakdown. *SUC1* is not expressed in cells grown without sucrose, but is induced when sucrose is added to the growth medium. In cells grown in medium that contains both sucrose and glucose, *SUC1* is not expressed. You have isolated mutations in three different genes that alter *SUC1* regulation, called **A<sup>-</sup>**, **B<sup>-</sup>** and **C<sup>-</sup>**. All three mutations are recessive and none of the mutations are linked to one another or to *SUC1*. *SUC1* expression in wild type yeast and each of the three mutants are shown below.

	<u><i>SUC1</i> expression</u>		
	- sucrose	+ sucrose	+ sucrose & glucose
Wild type	-	+	-
<b>A<sup>-</sup></b>	+	+	-
<b>B<sup>-</sup></b>	-	-	-
<b>C<sup>-</sup></b>	-	+	+

(a 6 pts.) For each of the three genes, state whether it affects regulation by sucrose or glucose and whether it is a positive activator or a negative regulator.

Gene **A**

Gene **B**

Gene **C**

Name: \_\_\_\_\_

You cross an **A<sup>-</sup>** mutant to a **B<sup>-</sup>** mutant. After tetrads are dissected and evaluated for *SUC1* expression in either the presence or absence of sucrose, (no glucose is present in this experiment) the following tetrad types are observed.

<u>Type 1</u>	<u>Type 2</u>	<u>Type3</u>
constitutive	constitutive	constitutive
constitutive	constitutive	constitutive
regulated	regulated	uninducible
uninducible	regulated	uninducible

(b 8 pts.) What is the phenotype of the **A<sup>-</sup> B<sup>-</sup>** double mutant? Explain how you arrived at your answer.

(c 10 pts.) Draw a model showing the interactions between the different regulatory factors encoded by **A** and **B**. Be sure to include the *SUC1* gene and to indicate where and how sucrose acts.

Name: \_\_\_\_\_

Next, you construct a set of deletions within the promoter region of the *SUC1* gene (+1 indicates the first transcribed nucleotide). The ability of each of these deletions to express *SUC1* in cells grown on different sugars is shown below.

	-300	-250	-200	-150	-100	-50	+1	- sucrose	+ sucrose	+ sucrose & glucose
1)	_____	_____	_____	_____	_____	_____	_____	-	+	-
2)	_____	_____	_____	_____	_____	_____	_____	-	+	+
3)	_____	_____	_____	_____	_____	_____	_____	-	-	-
4)	_____	_____	_____	_____	_____	_____	_____	-	+	-
5)	_____	_____	_____	_____	_____	_____	_____	-	+	-
6)	_____	_____	_____	_____	_____	_____	_____	-	-	-

(d 5 pts.) The DNA sequence of gene **C** reveals that this gene is likely to encode a DNA-binding protein. Assuming that the product of gene **C** binds to the promoter region of the *SUC1* gene, where is it most likely to bind? Explain your reasoning.

(e 5 pts.) In general, upstream activation sequences function normally regardless of their distance from the start of transcription. Which of the deletion mutants shown above show this to be true for the upstream activation sequence that responds to sucrose activation?

Name: \_\_\_\_\_

**2. (a 12 pts.)** Recently your lab has become interested in the function of a mouse gene called *myb*. To determine when and where *myb* is expressed during development you decide to construct a reporter for *myb* expression that can be examined in developing mice. Describe the basic procedure that you would use to produce a useful reporter for *myb* expression. For your answer include such specifics as cell type(s), a diagram of the DNA construct, the site of integration, and any additional breeding steps needed to obtain mice useful for your study.

**(b 8 pts.)** From the procedure above you obtain two different lines of mice carrying integrated *myb* reporter constructs. You cross heterozygous mice from Line 1 to one another and score how many of the resulting progeny carry the reporter construct and how many don't. You repeat the procedure for Line 2. The results of these two crosses are shown below.

	Contain Reporter	Do not contain Reporter
Progeny from Line 1 heterozygotes:	74	24
Progeny from Line 2 heterozygotes:	41	23

Provide an explanation for this data, keeping in mind that you did the same number of crosses for each line, but obtained fewer progeny overall from the Line 2 crosses.

Name: \_\_\_\_\_

(c 10 pts.) With Line 1, you design a screen looking for regulators of *myb* expression, after mutagenesis with a chemical mutagen. You find a mutant mouse (M) that has increased expression of your construct. The regulatory mutant M is genetically recessive and after extensive mapping experiments, you narrow down the location of the regulatory mutation to a region that contains two genes, TF1 and Db. Describe how you would construct a useful mouse model to test the idea that Db is a regulator of *myb* expression. For your answer include the cell type(s) you would target, a diagram of the DNA construct, the site of integration, and any additional breeding steps needed to get mice useful for your study.

Name: \_\_\_\_\_

(d 8 pts.) Using any mice generated in parts **a-c**, describe how you would carry out breeding experiments to test whether the mutation M is an allele of the Db gene. For your answer, include possible results and how you would interpret them.

**3. (a 6 pts.)** Consider a blood antigen called D. The allele for this antigen is dominant (i.e. individuals who are either D/d or D/D will express the antigen). If 84% of a population in Hardy-Weinberg equilibrium expresses the D antigen, what percent of the population are heterozygous for the D allele?

(b 6 pts.) The population in part (a) mixes in equal numbers with a population in which all of the individuals express the blood antigen. After one generation of random interbreeding between the two populations what percent of the population will express the antigen?

Name: \_\_\_\_\_

(c 9 pts.) You find an isolated population in which an unusual allele for the blood antigen (called  $d^*$ ) is quite prevalent. By analyzing the DNA from this population you find that 18% of the population has genotype  $D/d^*$ , but none of the thousands of individuals examined has genotype  $d^*/d^*$ . Explain this result by assuming that  $d^*$  is a balanced polymorphism. For your answer calculate parameters  $h$  (the heterozygous advantage for  $d^*$ ) and  $S$  (the selective disadvantage of  $d^*/d^*$ ).

(d 9 pts.) Consider a population in which 1% of matings are between second cousins, but all other matings are between unrelated individuals (second cousins have great grandparents in common). If half of the individuals with a recessive trait have parents that are second cousins, what is the (approximate) allele frequency for the trait.

---

**Question 1** 34 points:\_\_\_\_\_

**Question 2** 36 points:\_\_\_\_\_

**Question 3** 30 points:\_\_\_\_\_

**Total** :\_\_\_\_\_