Massachusetts Institute of Technology hhmi

StarGenetics

Name_____

Yeast Exercise 1

Goal

In this exercise, you will use StarGenetics, a software tool that simulates mating experiments, to analyze the nature and mode of inheritance of specific genetic traits.

Learning objectives

After completing this exercise, you will be able to:

1. Perform genetics experiments in the genetics cross simulator, StarGenetics.
2. Determine a yeast strain's mating type through the analysis of results from genetic crosses.
3. Determine whether a phenotype is dominant or recessive relative to another phenotype through the analysis of results from genetic crosses.
4. Determine whether mutations are in the same or different genes through the analysis of results from genetic crosses.

Getting started with StarGenetics

- To get to StarGenetics, please navigate to: **http://star.mit.edu/genetics/**.
- Click on the **Start** button to launch the application.
- Click **Trust** when a prompt appears asking if you trust the certificate.
- Click on **File → New** in the drop-down menu in the upper left hand corner.
- Click on the **Yeast Exercise 1** file.

You've just conducted a genetic screen for temperature-sensitive mutants in the yeast *Saccharomyces cerevisiae*. You have identified 20 haploid yeast mutants that can grow at 25°C, but not at 37°C. In addition to their temperature-sensitivity phenotype, all 20 mutants also carry a *ura3-* mutation, which means that they cannot grow unless the amino acid uracil is provided in their growth media.

You know that haploid yeast can be one of two possible mating types, either MAT**a** or MAT**alpha**. MAT**a** haploid yeast can mate with MAT**alpha** haploid yeast to produce a diploid. The mating types of the mutants that you identified in your genetic screen are unknown. To help you determine the mating type of each mutant, you also have two mating type tester strains. Since the mating type of each tester strain is known, you can use them to determine the unknown mating types of your mutants. The two tester strains carry a *lys9-* mutation, which means that they cannot grow unless the amino acid lysine is provided in their growth media. In all other respects, the tester strains are genetically wild type.

1 Determine the mating type of each of the 20 temperature-sensitive haploid mutants. Describe your method for determining this information. Specify the lawn, selection media and temperature that you used in your experiment.

- You can accomplish this task more efficiently by selecting the **Non-tetrad experiment** option within the **Choose experimental setup** window.
- All the 20 mutant strains and the two mating type tester strains can be found within the **Strains** box. To add ALL the strains within your **Strains** box to your experiment, click on the **Add all strains** button within the **Active Experiment** window.
- In addition to the strains box, all mutant strains and the mating type tester strains have been grown on individual plates in which colonies for a particular strain have grown and merged together resembling a mat or a lawn (see **Plate on a lawn of** window menu). Individual yeast colonies from one mating type can be replica plated onto lawns from strains of a different mating type to perform a mating experiment between two strains.

- Use crosses to the mating type tester strains (select strains to mate within the **Plate on a lawn of** window menu) and plate on appropriate media (select specific media to plate within the **And replica plate on** window menu). Click **Replica plate**.

Answer

2 Determine which of the temperature-sensitive mutant phenotypes are recessive and which are dominant relative to wild type. Describe your method for determining this information. Specify the lawn, selection media and temperature that you used in your experiment.

Answer

3 Although the 20 mutant strains share the inability to grow at 37°C, this does not indicate whether the observed temperature sensitivities are caused by mutations in the same gene or in different genes. To the extent possible, use crosses between the mutants to determine which have temperature-sensitive phenotypes caused by mutations in the same gene and which have phenotypes caused by mutations in different genes (i.e., perform a complementation test). If a particular mutant cannot be classified by this method, explain **WHY** this is the case.

Answer

4 During the complementation test, what observations did you make regarding Mutant 8? What explanation could account for these observations?

Answer

5 Based on the complementation test, what is the minimum and the maximum number of genes that you've identified in your genetic screen as having an effect on temperature-sensitivity? Explain your answer.

Answer