

## 7.03 Problem Set 1

Due before 3 PM on Wednesday, February 16

Hand in answers in recitation section or in the box outside of 68-120

**1.** In the StarGenetics problem PS1-1 (download “StarGenetics PS1-1.sgz” from the Problem Set menu of the 7.03 web site and open it in the StarGenetics java application) you are given 20 temperature sensitive haploid yeast mutants, which can grow at 25°C, but can’t grow at 37°C. Strains 1 – 10 are *ura3<sup>-</sup>* (i.e. they can’t grow unless uracil is provided in the growth medium), and strains 11 – 20 are *leu2<sup>-</sup>* (i.e. they can’t grow unless leucine is provided in the growth medium). You are also given two mating type tester strains: these are strains of known mating type (labeled MATa and MATalpha) and carry *lys9<sup>-</sup>* mutations (i.e. they can’t grow unless lysine is provided in the growth medium) but are wild type in all other respects. (Unless otherwise specified, all plating media are at 25°C)

- a) First use crosses to the mating type tester strains and plating on the appropriate media to determine the mating type of each mutant strain.
- b) Determine which of the mutants are recessive and which are dominant.
- c) To the extent that it is possible, use crosses among the temperature sensitive mutants to organize the mutants into complementation groups (genes). [Hint: some of the strains are double mutants – meaning that they have temperature sensitive mutations in two different genes.]
- d) Based on this complementation data, what is the minimum number of genes that are represented by your collection of temperature sensitive mutants? What is the maximum number of genes?

**2.** In the StarGenetics problem PS1-2 (StarGenetics PS1-2.sgz) you will be investigating yeast mutants that are resistant to a toxic compound known as FOA. You are given 12 mutants that were isolated as FOA resistant (FOA<sup>r</sup>) by their ability to grow on medium with FOA added (+FOA). Mutants 1 – 6 are mating type a (MATa) and carry a *leu2<sup>-</sup>* mutation, whereas mutants 7 – 12 are mating type alpha (MATalpha) and carry a *ura3<sup>-</sup>* mutation (i.e. they can’t grow unless uracil is provided in the growth medium). You are also provided with the same *lys9<sup>-</sup>* mating type tester strains as in Problem 1.

- a) First use crosses to the mating type tester strains and plating on the appropriate media to determine which of the mutants are recessive and which are dominant for the FOA<sup>r</sup> trait.
- b) Use crosses among the FOA<sup>r</sup> mutants to organize them into complementation groups.
- c) Based on this complementation data, what is the minimum number of genes that are represented by your collection of FOA<sup>r</sup> mutants? What is the maximum number of genes?

**3.** In the StarGenetics problem PS1-3.sgz you are provided with four mutant male flies that are wingless as well as wild-type male and female flies with normal wings.

By performing the appropriate crosses classify each of the mutants in terms of the basic mode of inheritance of the wingless trait (autosomal recessive, autosomal dominant, X-linked recessive, or X-linked dominant). For your answer report the results of key crosses explaining your reasoning. Finally,

give the genotype for each of the four mutant male flies, being careful to define your designation for the wild type and mutant alleles. Finally indicate which of these mutants could have come from a true-breeding line.

**4.** Consider the following four genetic mechanisms to produce a wingless fly that involve unlinked autosomal genes:

- a)** Recessive allele of a single gene: wild type = A/A; wingless = a/a
- b)** Recessive alleles of one *and* another gene: wild type = A/A, B/B; wingless = a/a, b/b
- c)** Recessive alleles of one *or* another gene: wild type = A/A, B/B; wingless = a/a, b/b; or a/a, B/- ; or A/-, b/b
- d)** Recessive allele of one gene *and* dominant allele ( $B^D$ ) of another gene: wild type = A/A, B/B; wingless = a/a,  $B^D/-$

For each mechanism a true breeding wingless fly crossed to wild type will produce F1 progeny with normal wings, but when the F1 flies are crossed among themselves different phenotypic ratios in the F2 generation will be produced for each mechanism. Determine the expected F2 phenotypic ratios for each of the mechanisms **a – d**.

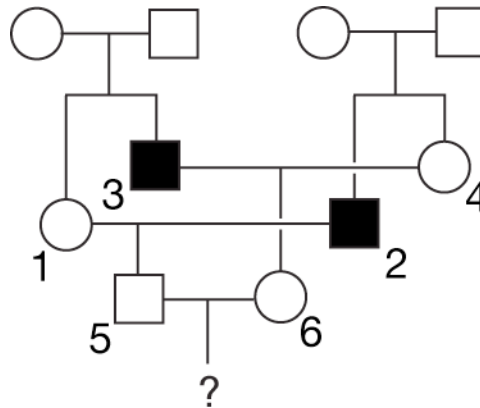
In the StarGenetics problem PS1-4.sgz you are provided with four mutant male flies each from a different true breeding strain representing one of the four mechanisms outlined above. By carrying out the appropriate crosses and statistical tests assign one of strain to each mechanism. For your answer you should produce a “lab notebook” showing the crosses you performed the results in terms of the number of progeny of different types and the statistical tests you applied to the data to arrive at your conclusions.

The table below gives chi square values for 1, 2 and 3 degrees of freedom. Use the convention that for  $p < 0.05$  there is a statistically significant difference between the observed results and the results expected for a given model.

<i>p</i> value:	.995	.975	0.9	0.5	0.1	0.05	0.025	0.01	0.005
df = 1	.000	.000	.016	.46	2.7	3.8	5.0	6.6	7.9
df = 2	.01	.05	.21	1.4	4.6	6.0	7.4	9.2	10.6
df = 3	.07	.22	.58	2.4	6.3	7.8	9.3	11.3	12.8

(Note that you may need to take some care in producing enough progeny for a significant result – the flies are set to produce 50 progeny per cross and each individual fly can only mate 10 times.)

**4.** The pedigree below shows inheritance of a rare trait – the filled squares represent males with the trait. To analyze this pedigree assume the trait in males 2 and 3 are caused by alleles of the same gene. Also assume complete penetrance of the trait and that no new mutations arise in the individuals shown.



For parts **a – e**, assume the trait is autosomal.

- a)** Is the trait dominant or recessive? Explain your reasoning.
- b)** Given that individuals 1 and 2 have an unaffected child (individual 5), use Bayes' Theorem to calculate the probability that individual 1 is a carrier.
- c)** If individuals 1 and 2 had a second child, what is the probability that this child would have the trait?
- d)** If individuals 5 and 6 had a child, what is the probability this child would have the trait?
- e)** If individuals 5 and 6 had an unaffected child, what is the probability that their next child would have the trait?

For parts **f – j**, assume the trait is X-linked.

- f)** Given that individuals 1 and 2 have an unaffected son (individual 5), what is the probability that individual 1 is a carrier?
- g)** Given that individuals 3 and 4 have an unaffected daughter (individual 6), what is the probability that individual 4 is a carrier?
- h)** What is the probability that individual 6 is a carrier?
- i)** If individuals 3 and 4 had a second daughter, what is the probability that she would have the trait?
- j)** If individuals 5 and 6 have a son, what is the probability that he would have the trait?
- k)** If individuals 5 and 6 had an unaffected son, what is the probability that if their next child were a son that he would have the trait?