

2005 7.03 Problem Set 1

Due before 5 PM on WEDNESDAY, September 21, 2005.

Turn answers in to the box outside of 68-120.

PLEASE WRITE YOUR ANSWERS ON THIS PRINTOUT.

1. Wild-type flies are brown in color. You have discovered two genes that control body color in flies -- gene A and gene B, which are on different autosomal chromosomes. You have three true-breeding mutant strains, all of which have black bodies.

Strain One (A^*/A^*) is homozygous for a dominant mutation in gene A.

Strain Two (A^-/A^-) is homozygous for a recessive mutation in gene A.

Strain Three (B^-/B^-) is homozygous for a recessive mutation in gene B.

Group Four are flies that result from mating Strain One to Strain Two.

Group Five are flies that result from mating Strain One to Strain Three.

Group Six are flies that result from mating Strain Two to Strain Three.

Group Seven are flies that result from mating Strain One to wild-type.

Group Eight are flies that result from mating Strain Two to wild-type.

Group Nine are flies that result from mating Strain Three to wild-type.

Predict the phenotypic ratio (the numerical ratio and the phenotype of each phenotypic class) of the offspring resulting from a cross between:

(a) Group Five and Group Nine

(b) Group Six and Group Eight

(c) Group Four and Group Seven

(d) Strain Three and Group Four

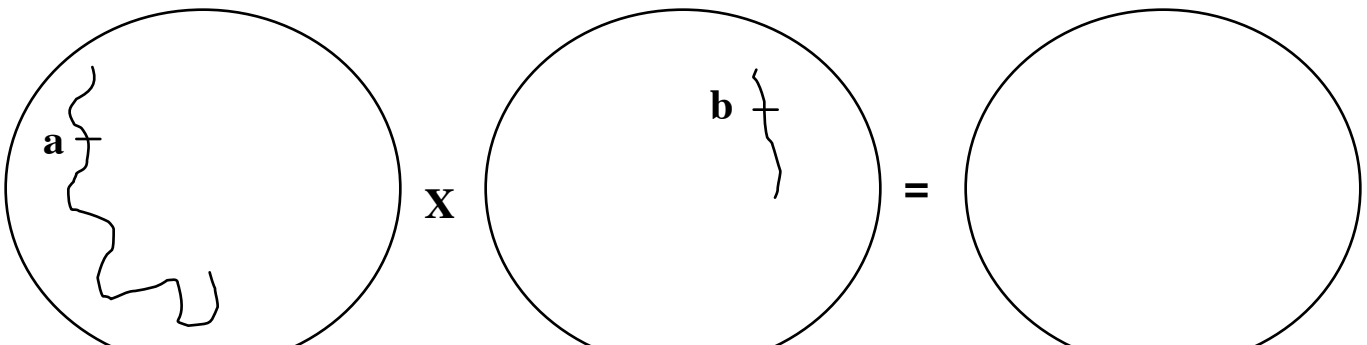
(e) Strain Two and Strain Three

(f) Strain One and Strain Two

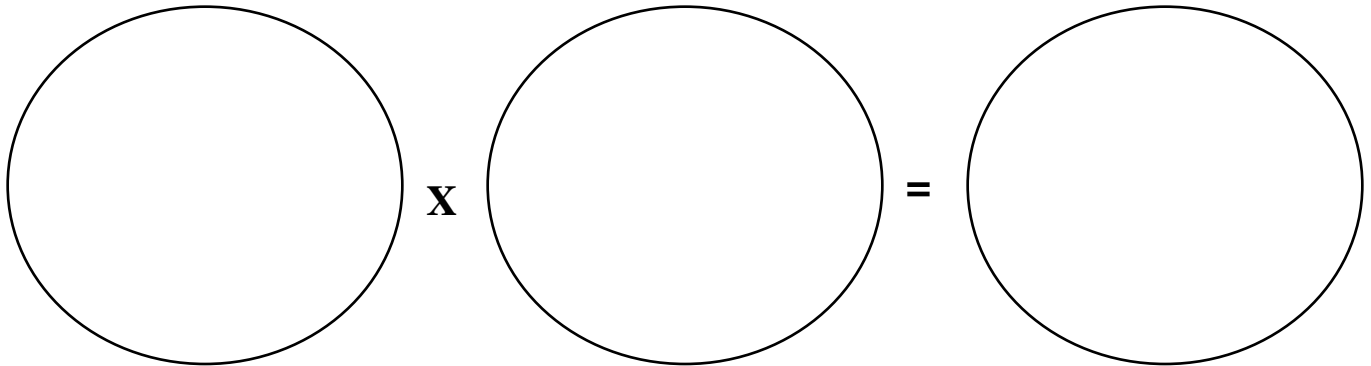
(g) List all of the above six crosses (parts (a) – (f)) that are proper complementation tests which clearly reveal whether two mutations are in the same gene or different genes.

2. You are studying a type of yeast that has two different chromosomes in its genome. You have isolated three mutations, “a,” “b” and “d,” each of which causes the same phenotype. When you mate a strain containing any one of these three mutations to wild-type, the resulting diploid exhibits the wild-type phenotype. You are in the process of doing complementation tests with these mutants. You discover that “a” and “b” do complement each other, but “a” and “d” do not. The corresponding wild-type alleles are “A,” “B” and “D.” Draw in the correct alleles that exist at each of these loci (A, B, and D) in each of the nine yeast cells drawn below. Make sure to put the alleles in their correct locations, as determined by those already drawn in for you. Also make sure to draw in the chromosomes to any cell whose chromosome(s) is/are missing.

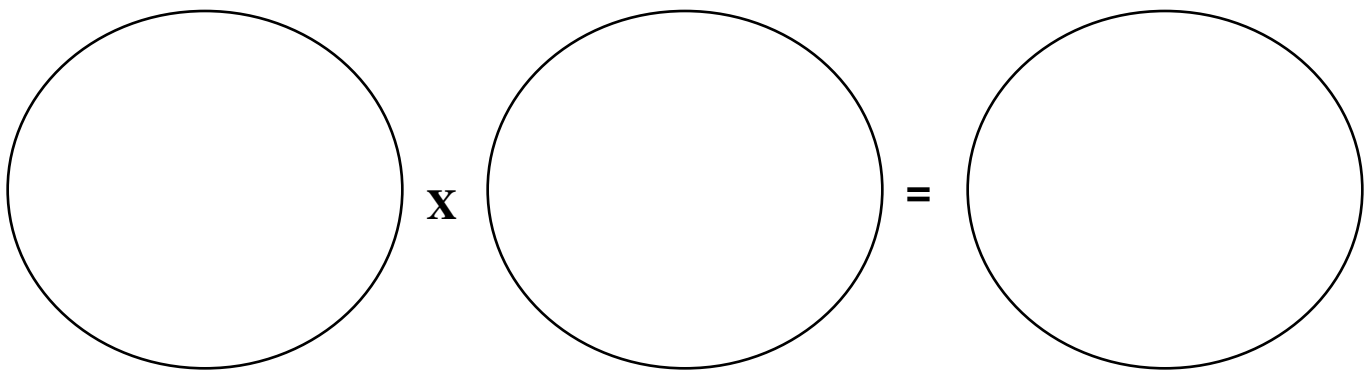
First cross: You mate haploid yeast of genotype “a” to haploid yeast of genotype “b.”



Second cross: You mate haploid yeast of genotype “a” to haploid yeast of genotype “d.”



Third cross: You mate haploid yeast of genotype “b” to haploid yeast of genotype “d.”



3. You are studying the inheritance of feather color in a new species of bird. You cross a true-breeding dark green bird to a true-breeding pale green bird. All of the resulting F1 birds are medium green. You then cross two medium green F1 birds, and analyze the resulting F2 generation. You obtain 50 birds: 13 are dark green, 23 are medium green, and 14 are pale green. We have not covered linkage and sex-linkage yet, so do not take those considerations into account during this problem.

(a) Propose a one-gene genetic model that explains the inheritance of feather color in this bird that is consistent with these results. By “propose a genetic model,” we mean define all possible genotypes and their associated phenotypes. Then give the genotypes of the birds in each generation of each cross described.

(b) You cross a true-breeding dark green bird to a true-breeding blue bird. All of the resulting F1 birds are blue. You then cross two blue F1 birds, and analyze the resulting F2 generation. You obtain 50 birds: 37 are blue, 4 are dark green, 7 are medium green, and 2 are pale green.

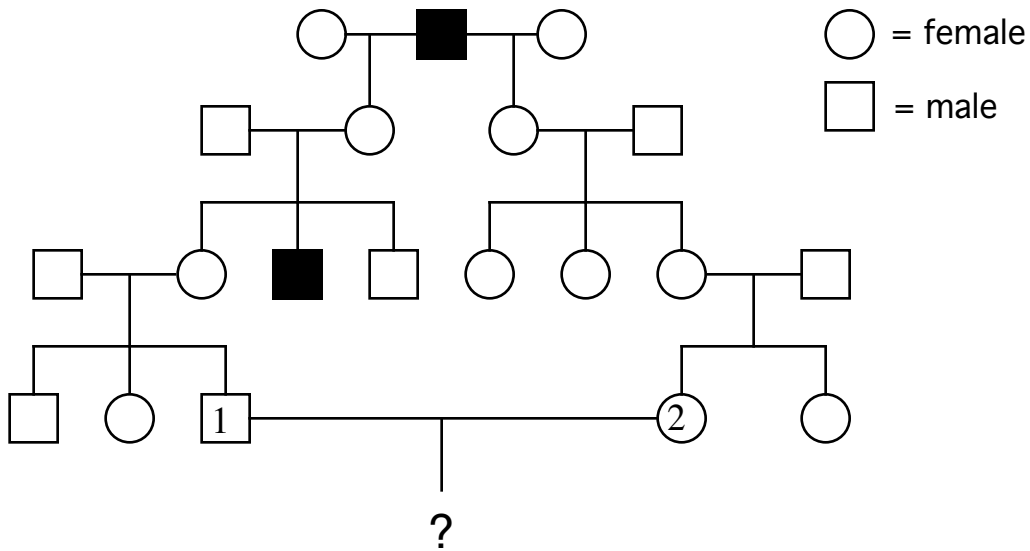
Propose a two-gene genetic model that explains the inheritance of color in this bird that is consistent with all of the data in this problem.

(c) Use chi-square analysis to test whether the numbers of F2 progeny you saw in part **(b)** correlate with the expected numbers based on your genetic model. For the chi square test you do, give the numbers of observed and expected organisms in each phenotypic class, the degrees of freedom, and your calculated value for χ^2 . Also state what your conclusion is based on the results of this chi-square test.

<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

(d) Based on your model, how many different results might you expect to get if you crossed one randomly selected light green bird from the F2 to one randomly selected blue bird from the F2? For each possible result, state the phenotypic ratio present in the progeny obtained.

4. This problem deals with the following pedigree, which shows the inheritance of a very rare trait.



(a) Assume that the inherited disorder is expressed with complete penetrance and that there are no new mutations. What mode(s) of inheritance is/are consistent with this pedigree? (Your choices are: X-linked dominant, X-linked recessive, autosomal recessive, autosomal dominant.)

(b) For **each** consistent mode of inheritance, what are the probabilities that Individuals 1 and 2 will have:

... an affected son?

... an affected daughter?

... an unaffected son?

... an unaffected daughter?

(c) Use Bayes' theorem to calculate the probability that the next child of Individuals 1 and 2 will be affected with the disorder, given the new knowledge that the couple already has two healthy sons. Do this calculation for each mode of inheritance consistent with the pedigree.