2005 7.03 Problem Set 1 ANSWER KEY

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. **A*A* B^+B^+ black**
Strain Two (A^-/A^-) is homozygous for a recessive mutation in gene A. **A^-A^- B^+B^+ black**
Strain Three (B^-/B^-) is homozygous for a recessive mutation in gene B. **A^+A^+ B^-B^- black**

Group Four are flies that result from mating Strain One to Strain Two. **A*A^- B^+B^+ black**
Group Five are flies that result from mating Strain One to Strain Three. **A*A^+ B^-B^+ black**
Group Six are flies that result from mating Strain Two to Strain Three. **A^-A^+ B^-B^+ brown**
Group Seven are flies that result from mating Strain One to wild-type. **A*A^+ B^+B^+ black**
Group Eight are flies that result from mating Strain Two to wild-type. **A^-A^+ B^+B^+ brown**
Group Nine are flies that result from mating Strain Three to wild-type. **A^+A^+ B^-B^+ brown**

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

---------- 5 BLACK----------: ------- 3 BROWN----------
1 A*$A^+$$B^-B^-$: 1 A*$A^+$$B^+B^+$: 2 A*$A^+$$B^-B^+$: 1 $A^+A^+$$B^-B^-$: 2 $A^+A^+$$B^+B^-$: 1 $A^+A^+$$B^+B^+$

(b) Group Six and Group Eight
------- 2 BLACK---------- : ---------- 6 BROWN ----------
1 $A^-A^-$$B^+B^-$: 1 $A^-A^-$$B^+B^+$: 2 $A^+A^-$$B^+B^-$: 2 $A^+A^-$$B^+B^+$: 1 $A^+A^+$$B^+B^-$: 1 $A^+A^+$$B^+B^+$

(c) Group Four and Group Seven
1 A*A*B^+B^+ : 1 A*$A^-$$B^+B^+$: 1 A^+A*B^+B^+ : 1 $A^+A^-$$B^+B^+$
---------- 3 BLACK---------- : 1 BROWN

(d) Strain Three and Group Four
1 $A^*A^+B^+B^-$: 1 $A^+A^-B^+B^-$
1 BLACK : 1 BROWN

(e) Strain Two and Strain Three
all $A^+A^-B^+B^-$
all BROWN

(f) Strain One and Strain Two
all $A^*A^-B^+B^+$
all BLACK

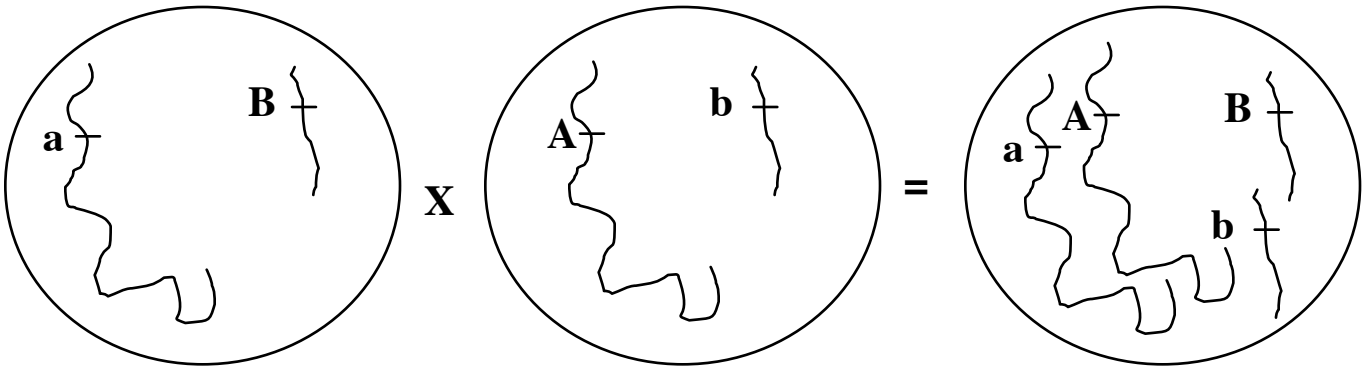
(g) List all of the above six crosses (parts **(a)** – **(f)**) that are proper complementation tests which clearly reveal whether two mutations are in the same gene or different genes.

Part e) is a proper complementation test that clearly shows that wild-type alleles of A and B will rescue the mutant phenotype if the mutations are on different genes but not if they are on the same gene.

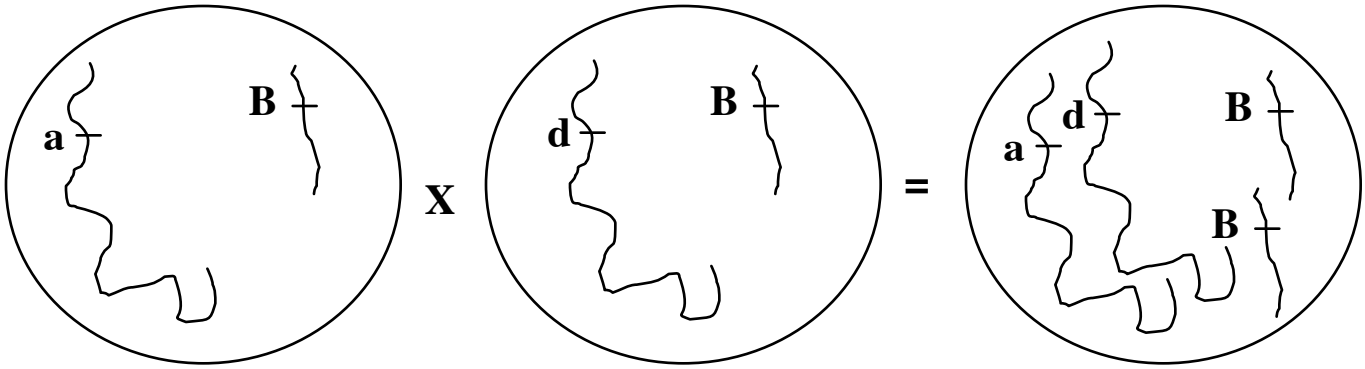
Other crosses are not complementation tests because, either, mutations giving dominant phenotypes were used (and these cannot be used in complementation tests), or strains that were not true-breeding were used.
Using strains that are not true-breeding is not the proper way to do a complementation test, because then multiple genotypes and phenotypes are produced instead of just one, which allows room for error in reading results (and a reliance on getting the expected ratios, rather than simply seeing all mutant organisms or all wild-type organisms).

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.

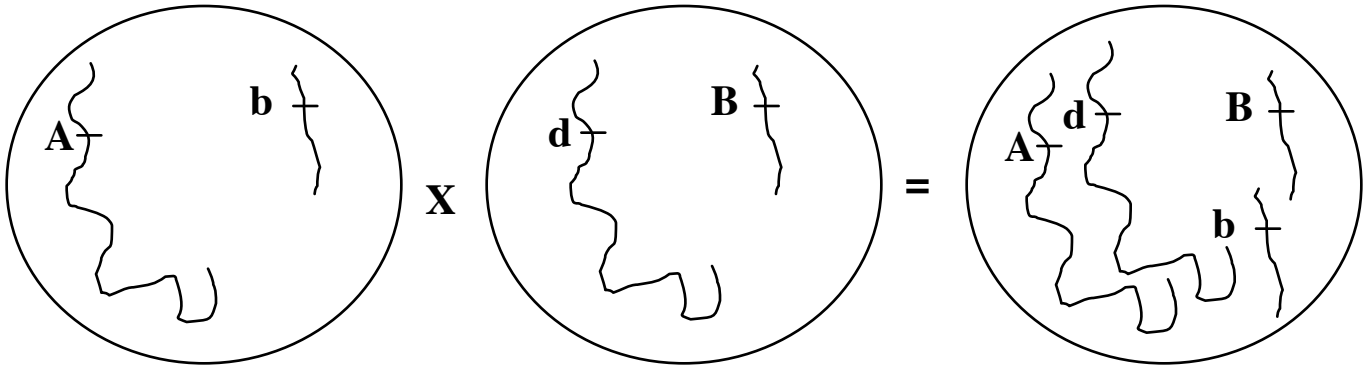
First cross: You mate haploid yeast of genotype “a” to haploid yeast of genotype “b.”



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.

We see three phenotypes from one gene so we can guess that we have incomplete dominance, giving us the 3rd phenotype as a blending between the other two.
GG= dark green
Gg= medium green
gg= pale green

P: GG x gg = all Gg (F1)
F1: Gg x Gg = 1 GG : 2 Gg : 1 gg
(13: 23: 14 is roughly equal to 1:2:1)

(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.

GgBB, or **ggBB,** or **GGBB,** or **GgBb,** or **ggBb,** or **GGBb = blue**
ggbb = pale green
Ggbb = medium green
GGbb = dark green

P: GGbb x ggBB = GgBb (F1) (since all of these birds are blue, we assume that the presence of blue overpowers the ability to be green – these two genes must be acting together to determine color. The B locus determines whether the bird is blue or not. If the bird is not blue, then the G locus is allowed to determine which shade of green the bird is.)

F1: GgBb x GgBb =
12 [GgBB, or **ggBB,** or **GGBB,** or **GgBb,** or **ggBb,** or **GGBb]: 1 GGbb : 2 Ggbb : 1 ggbb**
(since we see our green birds return, we assume that a bird can not express any blue without a B allele)

(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.

p 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

Don't reject hypothesis **can reject hypothesis**

Observed = 37 blue, 7 medium green, 4 dark green, 2 pale green
Expected = 37.5 blue, 6.25 medium green, 3.125 dark green, 3.125 pale green

Chi squared value = $\frac{(0.5)^2}{37.5} + \frac{(0.75)^2}{6.25} + \frac{(0.875)^2}{3.125} + \frac{(1.125)^2}{3.125} = 0.747$

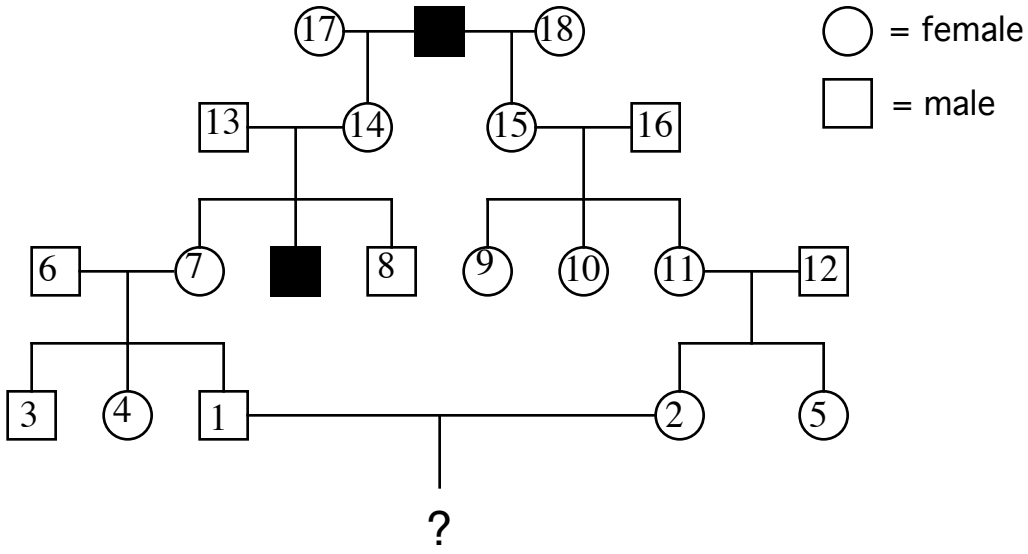
Degrees of freedom= # of classes(which is 4) – 1 = 3
p = 0.747
We can not reject our hypothesis, which is outlined in (b)

(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.

There are four different results, depending on the genotype of the randomly selected blue bird. The randomly selected light green bird will always be ggbb. The four possible outcomes are: all blue, OR half blue and half medium green, OR half blue and half light green, OR half blue and one-quarter medium green and one-quarter light green.

ggBB	**x**	**ggbb**	**=**	**all ggBb (all blue)**
GgBB	**x**	**ggbb**	**=**	**1 GgBb: 1ggBb (all blue)**
GGBB	**x**	**ggbb**	**=**	**all GgBb (all blue)**
ggBb	**x**	**ggbb**	**=**	**1 ggBb: 1ggbb (1blue: 1light green)**
GgBb	**x**	**ggbb**	**=**	**1 GgBb: 1Ggbb: 1ggBb: 1ggbb (2blue: 1 med. gr: 1 lt. gr)**
GGBb	**x**	**ggbb**	**=**	**1 GgBb: 1 Ggbb (1blue: 1 med Green)**

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.)

X-linked recessive

The two affected males are X^aY

Individuals #13, 16, 6, 8, 12, 3, and 1 are X^AY

Individuals #14 and 15 are $X^A X^a$

Individuals #17 and 18 are assumed to be $X^A X^A$ (because the trait is very rare)

Individuals #7, 9, 10, 11, 4, 2, and 5 are either $X^A X^a$ or $X^A X^A$

The disease can not be dominant because we have affected children with unaffected parents. The disease is also assumed to NOT be autosomal recessive because the affected man in the third generation would have gotten an "a" allele from Individual #13. However the statement is made that the trait is very rare. With very rare traits, you should assume that people marrying into a pedigree are not carrying the rare allele.

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

… an affected son?

p(Ind #2 is carrier) = p(Ind. #11 is carrier) * p(egg contains "a" allele) = 1/2*1/2 = 1/4

p(affected son) = p(Ind. #2 is carrier) * p(egg contains "a" allele) * p(sperm contains Y)
= (1/4) * (1/2) * (1/2) = 1/16

… an affected daughter?

0%
The father must have an "A" allele since he is unaffected so this couple will never have an affected daughter.

… an unaffected son?

p(unaffected son)
= [p(Ind #2 not carrier) * p(egg contains wt allele) * (sperm contains Y)]
+ [p(Ind #2 carrier) * p(egg contains wt allele) * p(sperm contains Y)]
= [3/4 * 1 * 1/2] + [1/4 * 1/2 * 1/2] = 7/16

… an unaffected daughter?

p(unaffected daughter) = 1 – p(affected son) – p (unaffected son) – p(affected daugter)
= 1 – (1/16) – (7/16) – (0)
= 0.5

(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.

X = Individual Two is a carrier
notX = Individual Two is not carrier and is therefore $X^A X^A$
Y = the two sons that Individual Two has had are both healthy

P(X) = 1/4 (this is because Individual #11 has a 1/2 chance of being a carrier)
P(notX) = 3/4
P(Y|X) = p(1st egg contains "A" allele) * p(2nd egg contains "A" allele) = 1/2*1/2 = 1/4
P(Y|notX) = p(1st egg contains "A" allele) * p(2nd egg contains "A" allele) = 1*1 = 1

$$P(X/Y) = \frac{p(Y/X) * p(X)}{[p(Y/X) * p(X)] + [p(Y/notX) * p(notX)]}$$

P(X|Y) = 1/13
p(next child is an affected child)
= p(mother is carrier) * p(egg contains "a" allele) * p(sperm contains Y)
= 1/13 * 1/2 * 1/2
= 1/52