

ANSWERS TO Problem set questions from Exam 1 Unit – Basic Genetic Tests, Setting up and Analyzing Crosses, and Genetic Mapping

Basic genetic tests for complementation and/or dominance

1. You have isolated 20 new mutant yeast strains that are defective in synthesis of threonine, an amino acid.

(a)

strains of mating type α

strains of mating type **a**:

	wild-type	1	2	3	4	5	6	7	8	9	10
wild-type	+	+	+	+	+	+	+	+	+	-	+
11	+	+	-	+	+	-	+	+	+	-	+
12	+	-	+	+	+	+	-	-	+	-	+
13	+	-	+	+	+	+	-	-	+	-	+
14	-	-	-	-	-	-	-	-	-	-	-
15	+	+	-	+	+	-	+	+	+	-	+
16	+	+	+	-	+	+	+	+	+	-	-
17	+	+	+	+	-	+	+	+	-	-	+
18	+	-	+	+	+	+	-	-	+	-	+
19	+	+	+	+	-	+	+	+	-	-	+
20	+	+	-	+	+	-	+	+	+	-	+

(b) recessive: 1, 2, 3, 4, 5, 6, 7, 8, 10, 11, 12, 13, 15, 16, 17, 18, 19, 20

(c) dominant: 9, 14

(d) same gene: (1, 6, 7, 12, 13, 18), (2, 5, 11, 15, 20), (3, 10, 16), (4, 8, 17, 19)

(e) minimum: 3 (as the last two groups listed above could be in the same gene)

(f) maximum: 6

2. You have isolated a set of five yeast mutants that form dark red colonies instead of the usual white colonies of wild-type yeast.

- (a) that 4 is dominant and 1, 2, 3, 5 are recessive
- (b) two genes: (1, 3) and (2, 5)
- (c) the only ambiguity is if mutant 4 is in group (1,3) or group (2,5) or a different gene

3. You have isolated five new Arg⁻ mutants in yeast.

- (a) dom: 3, rec: 1, 2, 4, 5, three genes: (1, 5) and (2) and (4)
- (b) dom: 4, rec: 1, 2, 3, 5, three genes: (1, 2) and (3) and (5)

4. You have isolated twenty His⁻ yeast mutants.

(a)

		strains of mating type α										
		wild-type	1	2	3	4	5	6	7	8	9	10
strains of mating type a	11	+	-	-	+	+	-	-	+	?	+	+
	12	+	-	-	+	+	-	-	+	-	+	+
	13	+	?	-	?	?	?	?	-	?	-	?
	14	+	+	+	-	+	+	+	+	?	-	+
	15	+	-	-	+	+	-	-	+	?	+	+
	16	+	+	+	+	-	+	+	+	-	+	+
	17	+	+	+	+	+	+	+	+	?	+	+
	18	+	+	+	-	+	+	+	+	-	-	+
	19	+	+	+	+	-	+	+	+	?	+	+
	20	+	-	-	+	+	-	-	+	?	+	+

(b) cannot tell if 13 and 8 are dominant or in a different gene than the others

dom: perhaps 13 and 8

rec: perhaps 13 and 8, definitely: 1, 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 14, 15, 16, 17, 18, 19, 20

5 or 6 genes: 7 and 10 may in be one or two genes, and (1, 2, 5, 6, 11, 12, 15, 20) and (3, 9, 14, 18) and (4, 16, 19) and (17)

Human Pedigrees and Probability

1. The following pedigree shows the segregation of two different rare recessive traits.

(a) if unlinked autosomal = 12.5%

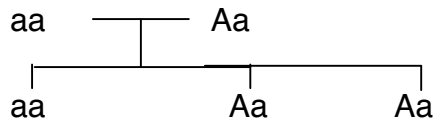
(b) if linked autosomal = 22.5%

(c) if male = 45%

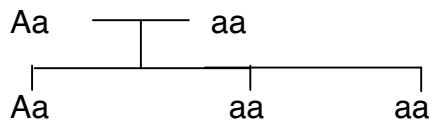
(d) if female = 0

2. Each of the families below exhibits a different very rare genetic disorder where individuals expressing the disorder are shown by solid symbols

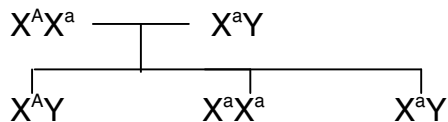
(a) either autosomal dominant



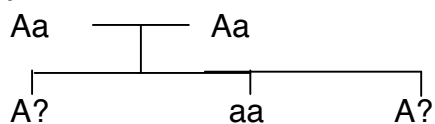
OR autosomal recessive



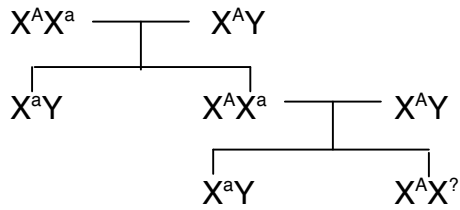
OR X-linked recessive



(b) only autosomal recessive



(c) only X-linked recessive



3. Each of the following pedigrees contains individuals carrying two different rare recessive traits indicated as follows:

- (a) only trait #1 = 40%
- (b) only trait #1 = 10%
- (c) only trait #1 = 10%

4. You have just been hired as a genetic counselor for a royal family that still engages in a significant amount of inbreeding.

- (a) first child = 8.3%
- (b) second child = 25%
- (c) if male = 12.5%
- (d) If female = 0%

5. The producers of a soap opera have hired you as a consultant.

- (a) Female 2 and Male 5 = 50%
- Female 6 and Male 4 = 25%
- Female 7 and Male 4 = 25%
- Female 3 and Male 8 = 100%

- (b) Female 2 and Male 5 = 50%
- Female 6 and Male 4 = 0%
- Female 7 and Male 4 = 0%
- Female 3 and Male 8 = 75%

- (c) Female 2 and Male 5: for son = 50% and for daughter = 50%
- Female 6 and Male 4: for son = 50% and for daughter = 0%
- Female 7 and Male 4: for son = 50% and for daughter = 0%
- Female 3 and Male 8: for son = 100% and for daughter = 100%

6. Each of the families below exhibits a different very rare genetic disorder where individuals expressing the disorder are shown by solid symbols

- (a) autosomal recessive 25% OR X-linked recessive son 50%, daughter 0%
- (b) autosomal dominant 50% OR autosomal recessive 50% OR X-linked recessive son 100%, daughter 0%
- (c) autosomal dominant 50% OR autosomal recessive 50%
- (d) only autosomal dominant 75%

Mendelian Genetics and calculating statistical significance using Chi Square

1. Consider a hypothetical insect species that has red eyes.

(a) Possibility #	F1	F2 (combining sons and daughters)
1)	All red	3/4 red, 1/4 white
2)	All red	3/4 red, 1/4 white
3)	All red	9/16 red, 7/16 white
4)	All red	9/16 red, 7/16 white
5)	All red	15/16 red, 1/16 white
6)	All red	15/16 red, 1/16 white

(b)

- 1) is consistent, chi-square value is 0.23
- 2) is consistent, chi-square value is 0.23
- 3) is not consistent, chi-square value is 5.12
- 4) is not consistent, chi-square value is 5.12
- 5) is not consistent, chi-square value is 8.70
- 6) is not consistent, chi-square value is 8.70

2. Consider the following mouse breeding experiment involving two different rare traits.

(a) they are both X-linked recessive

(b) you cannot reject the null hypothesis (that they are unlinked) because the chi-square value is 6.5

(c) 19 cM

3. In a cross between a male mouse from a true-breeding black strain and a female from a true-breeding tan strain, all of the F₁ progeny are gray.

(a) yes it is possible; if true, then the F₂ should be 1/4 black: 1/4 tan: 1/2 gray

(b) The parents are aaBB (black) and Aabb (tan). Thus the F₁ is AaBb (gray). Thus the F₂ is 9 A₋B₋ (gray): 3 A₋bb (tan): 3 aaB₋ (black): 1 aabb (dark brown).

(c) you cannot reject the null hypothesis (that the model in part **b** is correct) because the chi-square value is 0.77

(d) The parents are bb X^AY (tan) and BBX^aX^a (black). Thus the F₁ males are Bb X^AY (black) and the F₁ females are BbX^AX^a (gray). Thus the F₂ would consist of:

males – 3 B₋X^aY (black): 3 B₋X^AY (gray): 1 bbX^aY (brown): 1 bbX^AY (tan).

females -- 3 B₋X^aX^a (black): 3 B₋X^AX^a (gray): 1 bbX^aX^a (brown): 1 bbX^AX^a (tan).

(e) The parents are $BB X^aY$ (black) and $bb X^AX^A$ (tan). Thus the F1 males are $Bb X^AY$ (gray) and the F1 females are BbX^AX^a (gray). Thus the F2 would consist of:
 males – 3 B_X^aY (black): 3 B_X^AY (gray): 1 bbX^aY (brown): 1 bbX^AY (tan).
 females -- 3 $B_X^AX^?$ (gray): 1 $bbX^AX^?$ (tan).

Combining sons and daughters gives an overall ratio of 9 gray: 3 black: 3 tan: 1 brown.

4. Being a mouse geneticist, you maintain a large colony of mice.

(a) kinked-tail is dominant to wild-type

(b) 3/4 would have kinked tails

(c) The two gene model is that kinked-tail is dominant and caused by a single autosomal gene that is tightly linked to another autosomal gene that is responsible for the recessive phenotype of male sterility.

The parents are Ab/aB (kinked fertile male) and aB/aB (non-kinked fertile female). Thus the F1 mice are 1/2 Ab/aB (kinked fertile) and 1/2 aB/aB (non-kinked fertile). If you crossed an Ab/aB male to an Ab/aB female you get:

1/4 Ab/Ab (kinked and sterile if male), 1/2 Ab/aB (kinked fertile), 1/4 aB/aB (non-kinked fertile).

(d) Your colleague would not be able to maintain this strain because all of the males would be infertile, so one generation of the strain could never produce any offspring.

(e) Model One: The parents are $aaBBDD$ (non-kinked fertile short-tail) and $AaBBdd$ (kinked fertile long-tail). Thus the F1 would be 1/2 $AaBBDD$ (kinked fertile short-tail) and 1/2 $aaBBDD$ (non-kinked short-tail fertile).

Model Two: The parents are aaX^DX^D (non-kinked short-tail) and AaX^dY (kinked long-tail). Thus the F1 would be 1/4 AaX^DY (kinked short-tail male), 1/4 aaX^DY (non-kinked short-tail male), 1/4 AaX^DX^d (kinked short-tail female), and 1/4 aaX^DX^d (non-kinked short-tail female).

(f) Model One: The parents are $AaDd$ (kinked short-tail) and $AaDd$ (kinked short-tail). Thus the next generation would be 9 $A_D_$ (kinked short-tail): 3 $aaD_$ (non-kinked short-tail): 3 A_dd (kinked long-tail): 1 $aadd$ (non-kinked long-tail).

Model Two: The parents are AaX^DX^d (non-kinked short-tail) and AaX^DY (kinked long-tail). Thus the next generation would be:

females - 3/4 $A_X^DX^?$ (kinked short-tail), and 1/4 $aaX^DX^?$ (non-kinked short-tail).

males – 3/8 A_X^DY (kinked short-tail), 1/8 aaX^DY (non-kinked short-tail)

3/8 A_X^dY (kinked long-tail), 1/8 aaX^dY (non-kinked long-tail)

Mapping in flies by Two- and Three- factor crosses

1. Consider a portion of an autosome in *Drosophila*, which carries the following three mutations, each of which cause the corresponding recessive phenotype: b^- (black body), pr^- (purple eyes), and vg^- (vestigial wings).

(a) breed to a true-breeding purple eyed fly

(b) F1 would look like wild-type

(c) breed to true breeding homozygous recessive ($b^- pr^- vg^-$)

(d) two rarest classes: wild-type and the homozygous recessive (black body, purple eyes, vestigial wings)

(e) 1. $b^- pr^- vg^- / b^- pr^- vg^-$

2. $b^+ pr^+ vg^+ / b^- pr^- vg^-$

3. $b^- pr^+ vg^+ / b^- pr^- vg^-$

4. $b^+ pr^- vg^- / b^- pr^- vg^-$

5. $b^- pr^- vg^+ / b^- pr^- vg^-$

6. $b^+ pr^+ vg^- / b^- pr^- vg^-$

7. $b^- pr^+ vg^- / b^- pr^- vg^-$

8. $b^+ pr^- vg^+ / b^- pr^- vg^-$

(f) 1. four

2. four

3. sixty-one

4. sixty-one

5. twenty-six

6. twenty-six

7. four hundred nine

8. four hundred nine

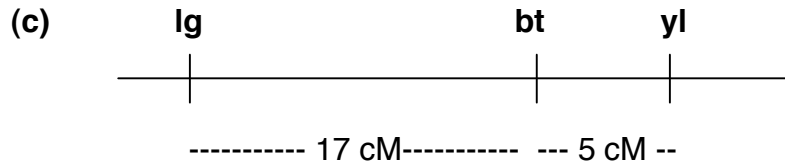
(g) 17.4 cM

(h) double crossovers aren't distinguished from parentals in a two-factor cross

2. Consider the three autosomal hypothetical recessive traits in *Drosophila*: bent wings (caused by the **bt** allele), yellow body (caused by the **yl** allele), and long bristles (caused by the **lg** allele).

(a) the P generation was bent-wings yellow-body (one parent) and long-bristled (other parent)

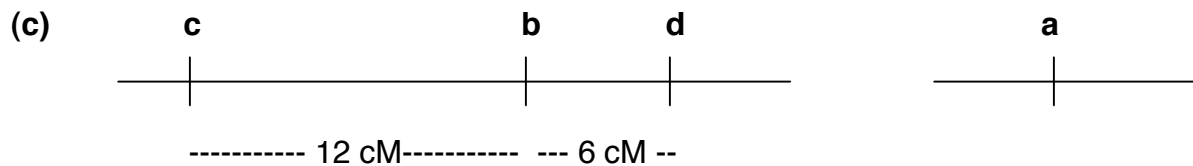
(b) 17 cM



3. Two different true-breeding *Drosophila* lines are crossed, and F₁ females from this cross are then crossed to males from a line that is homozygous for alleles that cause four different recessive traits.

(a) 15.6 cM

(b) don't know at the A/a locus, but one parent was b c d+ and the other was b+ c+ d



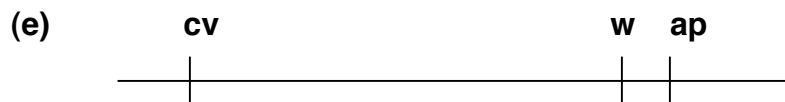
4. You have been studying eye color mutations in *Drosophila*, which normally have red eyes.

(a) are in same gene, because don't complement

(b) F1 males all have apricot eyes

(c) they are intra-genic recombinants

(d) 0.02 cM



5. The hypothetical *Drosophila* traits big-head, curly-wings, and weak-knees are autosomal recessive, and determined by the alleles **bh**, **cw**, and **wk** respectively. **(a)** most abundant:

1. big-headed straight-winged strong-kneed

2. small-headed curly-winged weak-kneed

intermediate:

3. small-headed straight-winged strong-kneed

4. big-headed curly -winged weak -kneed

5. big-headed straight-winged weak -kneed

6. small-headed curly -winged strong-kneed

least abundant:

7. big-headed curly -winged strong-kneed

8. small-headed straight-winged weak -kneed

(b) most abundant:

1. thirty

2. thirty

intermediate:

3. eight

4. eight

5. two

6. two

least abundant:

7. zero

8. zero

(c) because you didn't analyze enough offspring to see any double crossovers

Mapping in yeast by Tetrad analysis

1. You have isolated two different yeast mutants that will not grow on medium that lacks the amino acid arginine.

- (a) that 1 and 2 are both recessive and in different genes
- (b) Type 1 is TT, Type 2 is PD
- (c) yes, at 5 cM
- (d) 3 is dominant so you don't know its relationship to 1
- (e) Type 1 is TT, Type 2 is PD, Type 3 is NPD
- (f) no they are not linked
- (g) 1 and 3 must be in different genes
- (h) 2 and 3 must be in different genes, but the diploid would be unable to grow without supplemental arginine because 3 is dominant
- (i) 10 PD, 40 TT, 10 NPD
- (j) PD would have 4 Arg⁻ spores, NPD would have 2 Arg⁻ spores and 2 Arg⁺ spores, TT would have 3 Arg⁻ spores and 1 Arg⁺ spore

2. You want to construct a haploid yeast strain with two different mutations in the Leu2 gene.

- (a) the two loci are tightly linked, so you don't see NPDs
- (b) 2a and 2b are both in the same gene, so the two single mutant spores and the double mutant spore would all pass and fail the same complementation tests
- (c) Cross each of the three spores (two single mutants and one double mutant) to a wild-type. Induce sporulation of the resulting diploid and analyze ~100 tetrads. If you ever see a 3 Leu⁻ : 1 Leu⁺ tetrad, then it was the double mutant. If you always see 2 Leu⁻ : 2 Leu⁺ tetrads, then it was one of the two single mutants.
- (d) the two loci are linked at 25 cM

3. You have isolated three new His⁻ yeast mutants in mating type α .

- (a) there is a single mutation in the mutant strain
- (b) Type 4 is TT, Type 3 is PD, Type 5 is NPD
- (c) There are two mutations, and each one gives a His⁻ phenotype alone, and the loci are linked at 14 cM
- (d) Type 2 is TT, Type 3 is PD
- (e) There are two mutations, and a strain needs both mutations to have a His⁻ phenotype, and the loci are linked at 5 cM

4. You are studying biosynthesis of the amino acid serine in yeast and you know that three different genes that are required (Ser1, Ser2, and Ser3).

(a) 1 and X are unlinked

(b) the upper limit is 2 cM. 2 and X are likely to be in the same gene

(c) X and 3 are linked at 10 cM

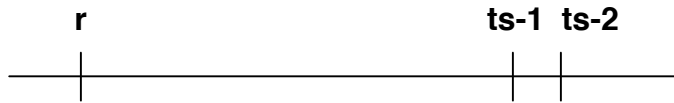
Mapping in phage

1. You have isolated two temperature-sensitive mutations in an essential gene of phage λ .

(a) 0.6 mu

(b) one half would be rough

(c)



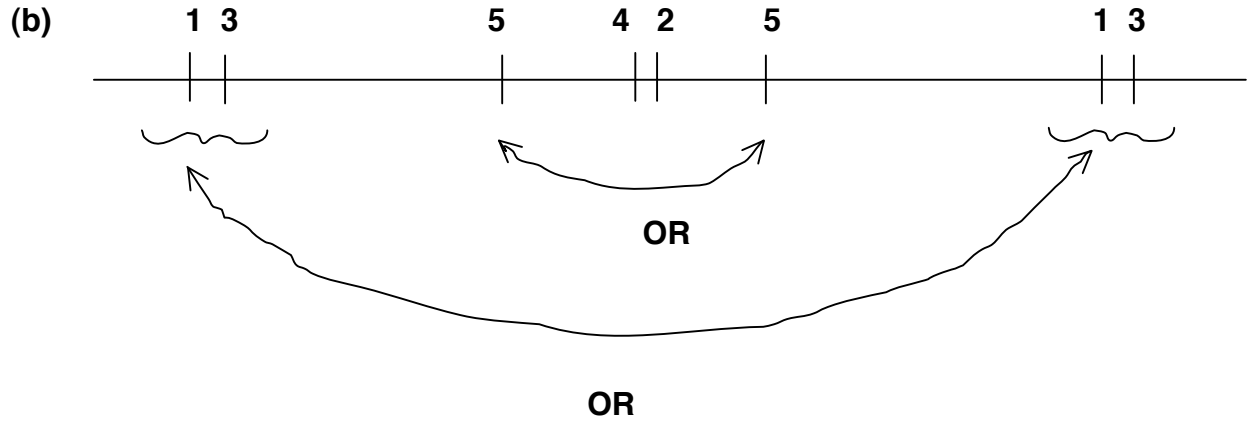
2. In a phage cross that you perform, bacteria are simultaneously infected with wild-type phage and a phage that is mutant at three different loci: **a**, **b**, and **c**.

What are the eight possible genotypes that would result from this cross and what fraction of the total progeny would each represent?

a+	b+	c+	44.5%
a	b	c	44.5%
a+	b	c	0.5%
a	b+	c+	0.5%
a+	b+	c	5%
a	b	c+	5%
a+	b	c+	0.05%
a	b+	c	0.05%

3. Wild type phage λ produces turbid plaques because about 10% of the infected cells become lysogens (that is, the bacterial host chromosomes harbor a dormant copy of the phage genome) and are therefore immune to further infection and lysis by other phage.

(a) 2 groups: (1, 3) and (2, 4, 5)

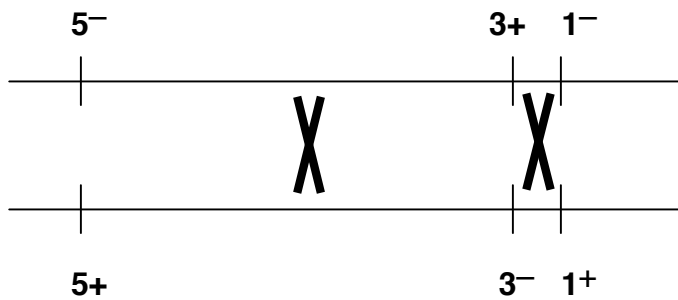


1 and 3 can be in either order, and are 2 mu away from 5, 4, and 2.
 5 can be on either side of 4 and 2, and is 0.2 mu away from that pair.

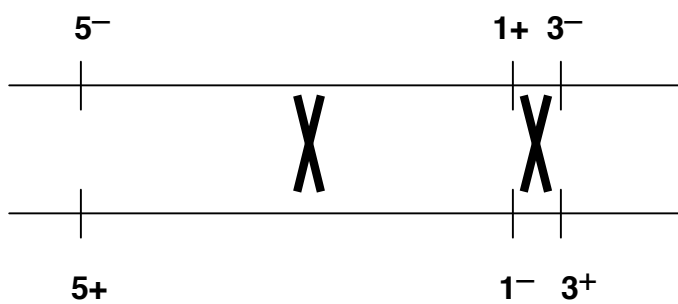


OR

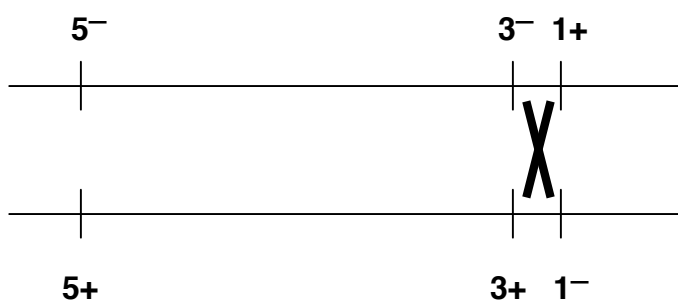




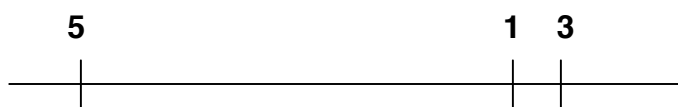
(e)



OR



(f)

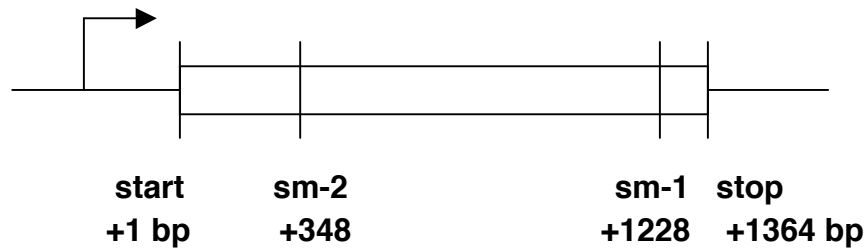


4. Imagine that you are studying a new type of phage.

(a) 2.2 mu

(b) sm-1: nonsense or frameshift, sm-2: missense

(c)



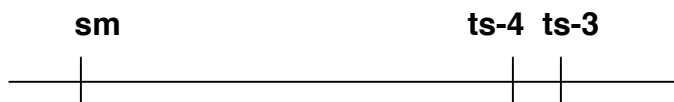
(d) closer to the sm-2 locus

5. You have isolated two temperature-sensitive mutations in phage λ that lie in the same essential gene.

(a) 1.6 mu

(b) 800 bp

(c)



6. You have two useful strains of phage λ with mutations in the **cl** gene.

(a) 0.8 mu

(b) 0.9 kb

(c) 17.6 kDa

(d) CAA (gln), CAG (gln), UGG (trp), CGA (arg)