1F08

BIOL 2500 FALL 2008

EXAMINATION 1

NAME [redacted]

PLEASE MAKE SURE THAT YOU WRITE YOUR NAME ON THE TOP OF EVERY PAGE
THIS PAGE IS RESERVED FOR GRADING.

THERE ARE 11 QUESTIONS AND 9 PAGES. YOU MAY USE THE REVERSE SIDE OF EACH PAGE AS SCRATCH PAPER.

Page 2 ____1____ (max 12)

Page 3 ____10____ (max 10)

Page 4 ____0____ (max 13)

} + 7.5 extra points

Page 5 ____3____ (max 16)

Page 6 ____15____ (max 15)

Page 7 ____9____ (max 11) + 1

Page 8 ____10____ (max 12) + 1

Page 9 ____6.5____ (max 11)

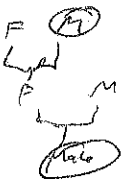
TOTAL: 54.5 + 12 ⇒ 66.5

Optional:

This test was _____ too short _____ too long _____ about right.

This test was _____ too easy _____ too hard _____ about right.

Name: [redacted] XXY?



1. A colorblind male child with one Barr body has a maternal grandfather who was color-blind. The boy's mother and father are phenotypically normal. Provide a genetic explanation for the origin of the color-blind and cytogenetic conditions in the child, including in which parent and at what stage the chromosomal event occurred that caused the abnormality. (3 points)

The color blind trait was on the X chromosome of the grandfather. There it was masked in the mother because she had another X chromosome. The boy with a genotype of XXY is colorblind as the normal X chromosome has form a Barr body, leaving only the abnormal chromosome. The nondisjunction that allowed this occured in meiosis (X) which could have occured in either parent [$XX^a + Y$ or $X^a + XY$].

2. Based on the following phage P1 transduction data, draw a map showing the order and relative distances between the genes *araA*, *cmlB*, and *pyrD* on the *E. coli* chromosome? (9 points)

NO.

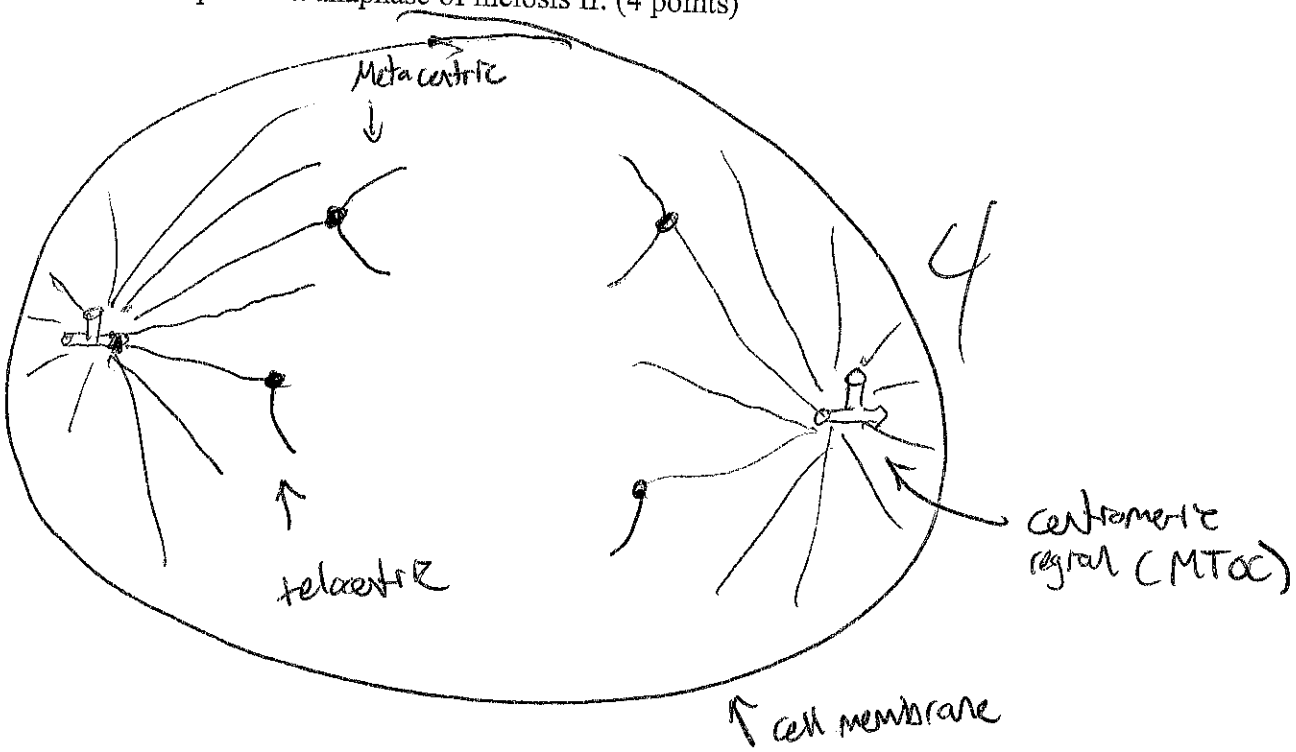
Donor	Recipient	Selected Marker	Unselected Marker*	Frequency
araA pyrD+	*araA+ pyrD*	*pyrD+*	*araA*	10/200
araA+ cmlB	*araA cmlB+*	*araA+*	*cmlB*	52/200
cmlB pyrD+	*cmlB+ pyrD*	*pyrD+*	*cmlB*	27/50

5/100
26/100
54/100

* 10/200 *pyrD+* colonies in the first transduction were also *araA*.

Name: [redacted] 10

3. A certain species has two pairs of chromosomes: a telocentric pair and a metacentric pair. Draw a cell of this species at anaphase of meiosis II. (4 points)



4. If a normal woman whose father has hemophilia (X-linked recessive) marries a man with Marfan syndrome (a rare autosomal dominant), what is the chance that) (1 point each):

X^hX

a. any son will have hemophilia? 50% X^hY or XY

Mm or MM?

b. any son will have Marfan syndrome? 50% mm or Mm

c. any son will have both traits? 25%

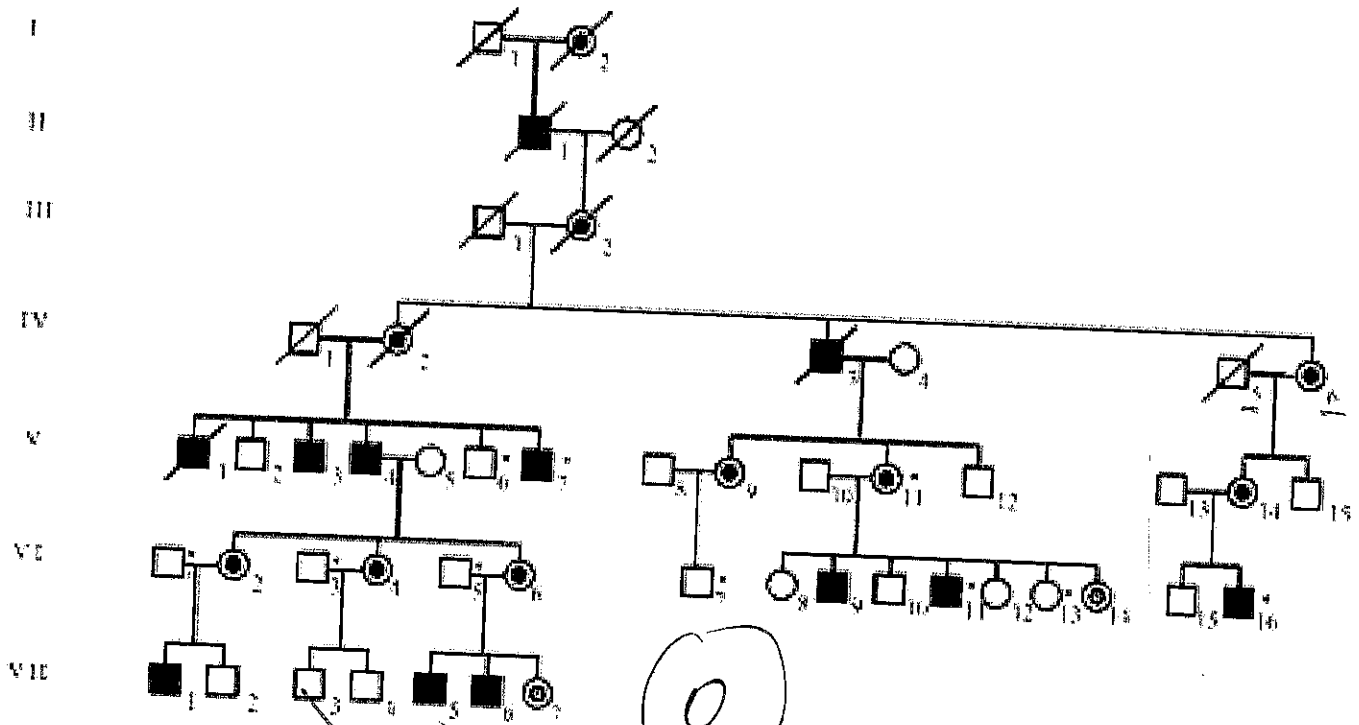
d. any daughter will have hemophilia? 0% either XX or X^hX

e. any daughter will have Marfan syndrome? 50% Mm or MM

f. any daughter will have both traits? 0%

Name: [redacted] 0

5. Below is a pedigree for a human hereditary disease, Åland Island eye disease (AIED). Give the inheritance pattern and most probable genotype(s) for individuals IV-5 and IV-6 and all of their descendents in generations V and VI. (10 points).



0

Autosomal ~~Dominant~~ Inheritance characteristics are shown here as every generation is affected. IV-6 likely has a genotype of Aa (A being the dominant Åland Island eye disease characteristic, a being the recessive wild type allele), IV-5 is likely aa as he is not affected. This means V-15 is also aa, and V-14 is Aa. VI-16 therefore is Aa, and VI-15 is aa, while their father, V-13 is aa.

6. Manx cats originated on the Isle of Man and are noted for having no tails, large hind legs, and a distinctive gait. When two Manx cats are mated, generally twice as many Manx kittens are produced as normal, long-tailed kittens. Propose a mechanism of inheritance for the Manx phenotype. (3 points)

Name: [redacted] RRgg rrGG RrGg $L^R L^R$ $L^C L^C$

RRGG RRGg RRgg RrGG RrGg RrGG rrGG rrGg rrgg

7. Two pure-breeding lines of plants are crossed. One line has red leaves and the other has green leaves. The F_1 all have green leaves with white flecks. The F_2 seedlings have the phenotypes in the table below. $L^C L^R$

Phenotype	Number of plants
Red leaves	63
Green leaves	44
Green leaves with white speckles	123

230

63/230 = 0.274 30% 5 4 3 3

44/230 = 0.191 20% 3 3

123/250 = 0.535 50% 8 9

9 3 3 1

3 ? 5

a. How many pairs of genes are responsible for producing the types of leaves. Give generalized genotypes for all the types of leaves mentioned. (4 points).
b. What are the genotypes of the P_1 and F_1? (6 points).
c. Use χ^2 analysis to support your hypothesis. (5 points)

a. Two pairs of genes are responsible for producing the types of leaves mentioned.

b.

c.

Ratio	Observed	Expected	O-E	O^2

[redacted]

Genetics Exam 1 Corrections

1. The color blind male child has a Barr body, meaning that he has one extra X chromosome in addition to his normal sex chromosomes that make him a human male. Therefore, this male child must have two X chromosomes and a Y chromosome (XXY), called Klinefelter Syndrome, a type of trisomy. However, since the male is colorblind both X chromosomes must have the recessive character, because if one was normal, he would not be colorblind, but a mosaic instead. Thus, his genotype is X^cX^cY where X^c is the X-linked recessive colorblind trait gene. The problem states that the parental grandfather was colorblind, i.e., he had the genotype X^cY. Thus, the boy's mother must have been X^cX, a mosaic for colorblindness, but phenotypically normal because of it, while his father was XY. Given this, since the boy is male, his Y chromosome came from his father, and both his X^c chromosomes came from his mother. This implicates his mother for the nondisjunction leading to the boy's Klinefelter Syndrome. The nondisjunction must have occurred during Meiosis II as in order for him to have two X^c chromosomes, the single X^c from his mother must have separated from the normal X in meiosis I, but come meiosis II, the sister chromatids of the X^c must have failed to segregate independently, ultimately leading to an X^cX^c gamete. good.

My previous answer was incorrect because I assumed that the nondisjunction occurred in meiosis I and that the Klinefelter Syndrome boy would be colorblind even though he would have been a mosaic. Because I assumed the disjunction happened during meiosis I, I also assumed that the disjunction could have occurred in either the mother or the father, because I thought the boys genotype would have been X^cXY.

+3 pts

[redacted]

Genetics Exam 1 Corrections

2. The frequency of transduction for the phage P1 is as follows:
   pyrD to araA: 10/200 x 100 = 5%
   pyrD to cmlB: 27/50 x 100 = 54%
   araA to cmlB: 52/200 x 100 = 26.[illegible]%

   +9 pts

   Clearly, because the transduction is more frequent with cmlB, cmlB is closer to pyrD than araA, making the order pyrD___cmlB_____araA. The relative distances between them can be determined looking at the percentages. Since pyrD to cmlB is slightly over twice the percentage of transduction of araA to cmlB we assume the distances to correlate with the percentages. Therefore, the map looks more like this: pyrD__ d ___cmlB_____ 2d _____araA where d is the distance between pyrD and cmlB and 2d is the distance between cmlB and araA.

   I previously answered this question incorrectly as I did not answer it at all. I failed to interpret the meaning of the transduction data at the time of the test because I was confused by the formatting of the chart.

[redacted]

Genetics Exam 1 Corrections

X-linked recessive.

5. This pedigree demonstrates an X-linked dominant inheritance characteristic. This is apparent as approximately half of the sons and half of the daughters of affected females and normal males are affected whereas all of the daughters and none of the sons of an affected male and a normal female are affected. Given this IV-6 has the genotype X^AX where X is the normal chromosome and X^A has the X-linked dominant characteristic for AIED. This is apparent from the determination that it is X-linked dominant and her father is normal whereas her mother is affected, making her a heterozygote. IV-5 must be normal as he is not affected, which also holds true for V-13, V-15, and VI-15, their genotype being XY. Because they are male and have only one X chromosome, any aberration with this X chromosome shows up in the phenotype, thus we can conclude that unaffected males have a normal X. V-14 is XX^A like her mother because her father (IV-5) is normal, thus donating the X, while her mother (IV-6) donates the X^A. Finally, VI-16 is X^AY as he is affected, his Y coming from his father (V-13), his X^A from his mother (V-14).

My previous answer was incorrect because I believed the trait to have an autosomal dominant inheritance pattern. I did not consider the offspring of VI-3 and VI-4 which clearly are counter examples because VI-4 is affected while none of her children are, which would be impossible with an autosomal dominant inheritance pattern.

+ 0 pts

[redacted]

Genetics Exam 1 Corrections

6. The Manx characteristic could be linked to a single gene which encodes for a particular protein that could control mechanisms behind bone growth leading to a malformed spine (a short tail) as well as large hind legs that would lead to the distinctive gait. Given this fact, I propose a single gene responsible for these phenotypes. The trait would be a dominant characteristic, the wild type trait being recessive to it. The "M" mutant allele would somehow alter a necessary protein. Therefore, a normal cat would exhibit the genotype "mm". Given that twice as many Manx cats are produced than normal cats when two Manx cats are mated, I propose that the Manx cat phenotype is the result of a heterozygous condition "Mm". When two Manx cats are mated one would expect 1/4 normal cats "mm", 2/4 "Mm", and 1/4 "MM". If the mutant allele, when homozygous, led to inviable offspring that fail to develop, perhaps due to a complete lack of a particular protein, then the result would be 1/3 normal cats, to 2/3 Manx cats satisfying the phenotypic ratio condition as well as providing a plausible explanation for the method of inheritance. ✓

My previous answer was incorrect because I did not answer the question. In my mind, I thought there were separate alleles for a short tail and legs, but I could not fathom an inheritance pattern or a plausible explanation for that pattern.

+ 3 pts

[redacted]
Genetics Exam 1

7. Red Leaves – 63 / 230 *100 = 27.3 %
Green Leaves – 44 /230 *100 = 19.1%
Green with white speckles – 123 /230 *100 = 53.5 %
Total= 230
So, perhaps they are in a 4:3:9 ratio

   a. I suspect that there are two genes responsible for the phenotypes mentioned. The generalized genotypes for the phenotypes are as follows:

      Speckled: _ g _ r G-R-
      Red: _ _ RR [redacted] gg
      Green: GG _ r G-rr

   b. The genotypes of the P_1 and F_1 generations are as follows:

      P_1: GGRR x ggrr or GGrr x ggRR
      F_1: GgRr x GgRr

      This must be the case to give a ratio that fits the 4:3:9 proposed in conjunction with the genotypes of the F_2 generation. The F_1 must be two heterozygous for each gene, and to produce this, the P_1 must either be homozygous for both or just one of the genes (either GGRR and ggrr or GGrr and ggRR as shown above).

   c. Chi-Square Analysis:

Ratio	***Observed***	***Expected [230*Ratio]***	***Difference (O-E)***	D^2	D^2/E
9/16	123	129.375	-6.375	40.640625	0.31413
4/16	63	57.5	5.5	30.25	0.52609
3/16	44	43.125	0.875	0.765625	0.01775
				X^2=	0.85797
				P =	0.75

A p value of 0.75 means that we fail to reject the null hypothesis, which means that our hypothesis stands as a reasonable explanation for the phenotypic ratios observed.

[redacted]

Genetics Exam 1 Corrections

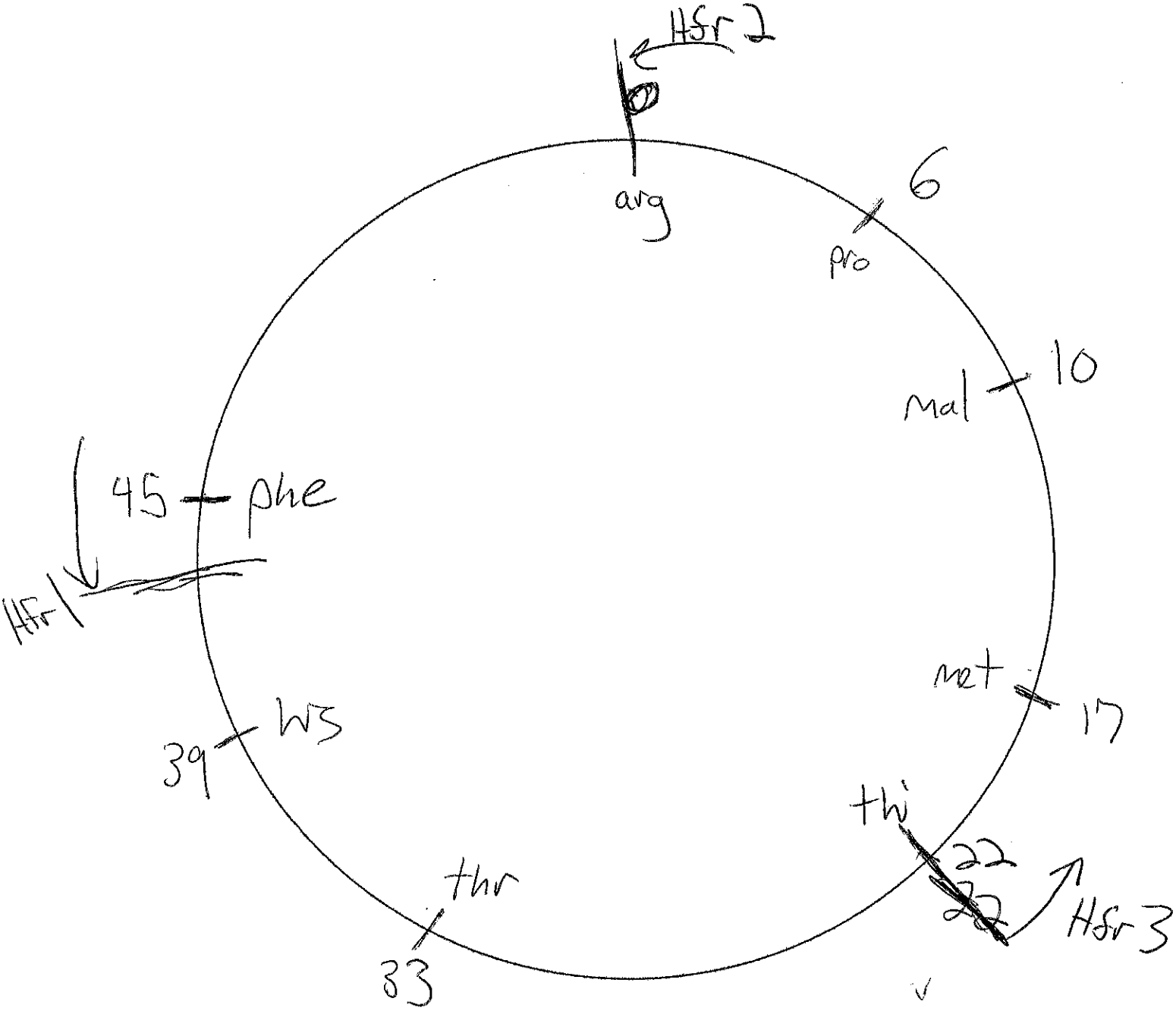
Question 7 continued

My previous answer was incorrect because I could not think of what the genotypes would be like and did not answer the question completely, leaving most of it blank.

[redacted]

Genetics Exam 1 Corrections

9. I previously answered this question incorrectly because I miscounted the distances between the genes in minutes, which ultimately changed all the other numbers for the other genes on my genetic map.



me: [redacted] Genetics C B A 6.5 D

11. Coat color in mice is controlled by four unlinked genes. The genotype *C_* permits pigment deposition in fur, whereas *cc* causes albinism. The genotype *B_* causes black pigmentation, whereas *bb* results in brown fur. The genotype *A_* causes deposition of a narrow band of yellow pigment near the tips of individual hairs, a condition called "black agouti" in black animals and "cinnamon" in brown animals. The genotype *dd* causes a dilution of fur color (it has no effect on albinism); genotype *D_* has no effect on coloration at all.

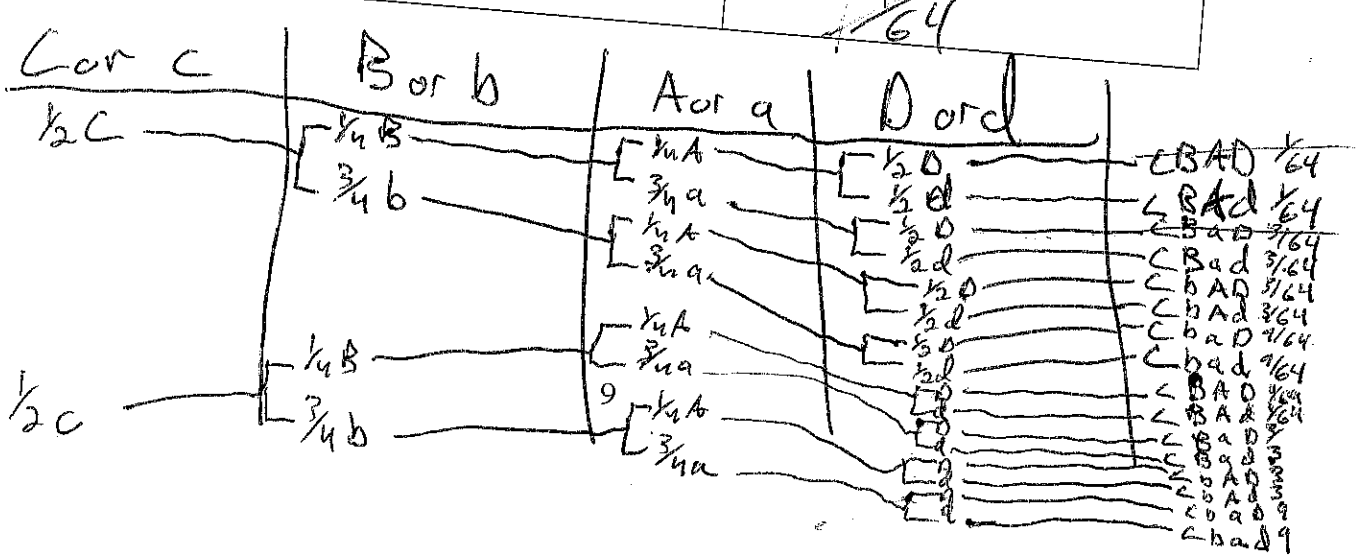
Mice of the genotypes given below were crossed:
Black Cinnamon
CcBbaaDd x *CcbbAaDd*

a. Give the phenotypes of these parental mice. (2 points)
Cc Bbaa Dd is black, Cc bb Aa Dd is cinnamon

b. Give the generalized genotypes and expected phenotypic ratios of the following types of offspring produced from the above mating: (9 points)

Phenotype	Generalized Genotype	Expected ratio of Phenotype
black	C_ B_ aa D_	15/64
black agouti	C_ B_ A_ D_	1/64
dilute black	C_ B_ aa dd	
dilute black agouti	C_ B_ A_ dd	
brown	C_ bb aa D_	
dilute brown	C_ bb aa dd	
cinnamon	C_ bb A_ D_	
dilute cinnamon	C_ bb A_ dd	
albino	cc - - - -	9/64

4.5



[redacted]

Genetics Exam 1 Corrections

10. Chart from linkage map for recessive gene characteristics:

Genes:	***A***	***B***	***C***	***D***	***E***
Organisms:	1	2	3	7	9
	5	6	4	11	
		8		12	
		10			

a. There are 5 different genes responsible for the coiled mutation (labeled a-e above).

b. Genotypes for these organisms are as follows. All of the genes have within them complementation groups that may have a character that produces the mutation. At these complementation groups, or cistrons, we would expect to find genetic differences. Therefore, here I use the nomenclature of uppercase letter with a + for a normal complete gene, and an uppercase letter with a number to indicate a mutated cistron.

1: $A^1B^+C^+D^+E^+$
2: $A^+B^2C^+D^+E^+$
3: $A^+B^+C^3D^+E^+$
4: $A^+B^+C^4D^+E^+$
5: $A^5B^+C^+D^+E^+$
6: $A^+B^6C^+D^+E^+$
7: $A^+B^+C^+D^7E^+$
8: $A^+B^8C^+D^+E^+$
9: $A^+B^+C^+D^+E^9$
10: $A^+B^{10}C^+D^+E^+$
11: $A^+B^+C^+D^{11}E^+$
12: $A^+B^+C^+D^{12}E^+$

c. Mutants 1 and 2 had phenotypically normal offspring because the genes complemented one another. Mutant 1 has a mutant "A" gene and mutant 2 had a mutant "B" gene meaning that the normal "A^+" gene from mutant 2 could complement the abnormal "A" gene from mutant 1 in the offspring and the same for the normal "B^+" in mutant one, and the abnormal "B" in mutant 2. Mutants 1 and 5 do not give chromosomes that complement one another to their offspring. Because their mutations are on the same gene (gene A), meaning that A is expressed, the condition leads to the mutant phenotype.

[redacted]

Genetics Exam 1 Corrections

Question 10 continued:

I previously erred on this problem because I assumed that the mutation that occurred was an entire gene mutation rather than particular cistron mutations. Therefore, although the genotype made sense, it did not accurately represent the correct method of complementation that would occur.

[redacted]

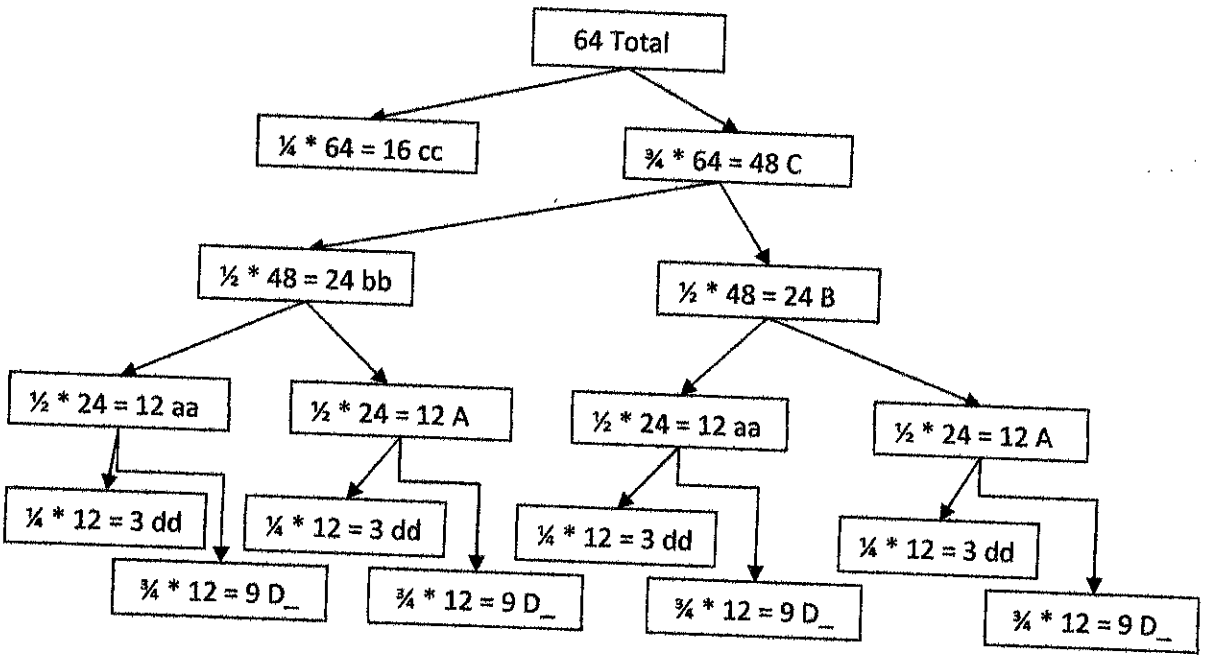
Genetics Exam 1 Corrections

11. Problem:

a. The CcBbaaDd mouse is black and the CcbbAaDd mouse is cinnamon based on the criteria that B_ is black pigmentation, bb is brown fur, A_ is agouti or cinnamon, aa is normal, cc is albino and C_ is normal, and D_ is normal, and dd is dilution.

b. Table:

Phenotype	Generalized Genotype	Expected Ratio of Phenotype
Black	C_B_aaD_	9/64
Black agouti	C_B_A_D_	9/64
Dilute black	C_B_aadd	3/64
Dilute black agouti	C_B_A_dd	3/64
Brown	C_bbaaD_	9/64
Dilute brown	C_bbaadd	3/64
Cinnamon	C_bbA_D_	9/64
Dilute cinnamon	C_bbA_dd	3/64
albino	cc_____	16/64



[redacted]
Genetics Exam 1 Corrections

Question 11 continued

I previously answered this question incorrectly because I improperly performed my phenotypic analysis leading me to improperly state the phenotypic ratios. I did not complete the problem either however because I ran out of time.

Biol 2500 Gen 1 F09

Grade Appeal for Question 9

I lost points on determining the F2 phenotypes for question 9. I had clearly written on top of the large green circle, that these ratios were for the F2 males. As, in 3/8 of all the males had red eyes and miniature wings.

I had also done a separate branch diagram for the F2 females on the bottom right of the paper, just above slash with the number "7".

The table at the very bottom was divided into male and female separately to show that x/8 of the males had a certain trait, and x/8 of all the females had a certain trait. For example, on my table it shows the ratio 3/8 followed by a male and female column, this is to show that 3/8 of all the males (only males, not females) had red eyes and miniature wings. For the female, it was to show that 3/8 of all the females (only females, not males) had red eyes and miniature wings.

Therefore I want the problem to be regraded.

6K- +3 pts

[redacted]
Test Corrections, Question 4
10/8/09

4) 341/162 is about 2 to 1, therefore out of all the progeny, about curlywinged is 2/3 and 1/3 is normal. The P1 generation were heterozygotes:

c = recessisive, normal
C=Dominant, curly

The expected genotypes are:
¼ cc
¼ CC ---- is too lethal, so flies with this genotype don't survive.
½ Cc

Recessive lethal. See textbook - +0pts

Since the ratio of phenotypes is 2:1, this suggests that this is a **lethal mutation**. Where being homozygous dominant is too lethal for the fly to survive, but in a heterozygote, the mutation acts as the dominant gene. recessive

My original answer was wrong because I made the mistake of thinking that the phenotypic ratio was 3:1 – which was wrong. The real phenotypic ratio is 2:1. Since I made that mistake, I followed up on the mistake by inaccurately interpreting the results of the punnette square.

[redacted]

Test Corrections, question 6
10/8/09

No.

Dumpy	Black	bristles	Classification
+	+	+	SCO
+	b	+	SCO
+	b	hk	NCO
dp	+	hk	SCO
+	+	hk	DCO
dp	b	hk	SCO
dp	b	+	DCO
dp	+	+	NCO

a) These genes are linked because the expressed phenotypic ratios are not matching expected phenotypic ratios for a trihybrid cross (three genes), therefore we can tell that these genes are linked (a form of epistasis). The expected phenotypic ratios for a trihybrid cross are 27:9:9:9:3:3:3:1. This says that there should be just one phenotype that should be predominantly expressed, however we can see that there are two phenotypes that are predominantly expressed. Not a trihybrid cross - it's a testcross.

b) ** Had to handwrite some items for clarity*** [redacted]
Since the b gene is switched, therefore the b gene is in the middle

$\frac{b\ +\ hK}{+\ dp\ +}$ $\frac{+\ +\ hK}{b\ dp\ +}$

c) P1 flies:

$\frac{dp\ +\ +}{dp\ +\ +} \cdot \frac{+\ b\ hK}{+\ b\ hK}$

F1 flies:

$\frac{dp\ +\ +}{+\ b\ hK} \cdot \frac{dp\ b\ hK}{dp\ b\ hK}$

d) b gene is in the middle, therefore…

$\frac{+\ b\ hK}{dp\ +\ +}$ $\frac{dp\ +\ +}{+\ +\ +}$

Since dumpy gene switches, therefore the distance is between dp and b

Distance b/w dp & b: (172+169+8+6)/1000 x 100 = 35.5 cM
Distance b/w b & hk: (21 + 19+8+6)/1000 x 100 = 5.4 cM

Genetic Map: dp__35.5cM_____b____5.4cM___hk

e) coefficient of coincidence: observed DCOs/Expected DCOs = (8+6)/(.355 x .054 x1000) = **.73**
f) interference: 1- coefficient of coincidence = 1 - .73 = **.27**

My original answer to part a was wrong, because my answer does not address phenotypes, it says "genes appear in some form of recombinants" which doesn't make sense because it should have said more along the lines of "the expressed genes (ie phenotypes) were ~~lower than~~ not as expected for a trihybrid cross". My original answer to part c for the female F1 fly is wrong because I wrote the genotype in the wrong order because neither the P1 female nor male were wild type for all the genes, therefore it would be impossible to have an F1 with a chromosome with all wild and another one with all mutants, there's actually a mix, as shown in my answer.

1 F09

BIOL 2500 FALL 2009

EXAMINATION 1

NAME [redacted]

PLEASE MAKE SURE THAT YOU WRITE YOUR NAME ON THE TOP OF EVERY PAGE
THIS PAGE IS RESERVED FOR GRADING.

THERE ARE 9 QUESTIONS AND 8 PAGES. YOU MAY USE THE REVERSE SIDE OF EACH PAGE AS SCRATCH PAPER.

Page 2 10 (max 10) 10

Page 3 ~~14~~ 15 (max ~~15~~) —

Page 4 12 (max 12)

Page 5 15 (max 18)

Page 6 12 (max ~~12~~) —

Page 7 20 (max 20) 20

Page 8 7 (max 10) +3

TOTAL: 91 (max 100) (94)

Name: [redacted]

1. Based on the following phage P1 transduction data where the recipient was *a-*, *b-*, *c-*, draw a map showing the order and relative distances between genes *a*, *b*, and *c* on the *E. coli* chromosome. (6 points)

Selected Marker	Number	Unselected Marker*	Number
a+	200	*b+*	60
		b-	140
		c+	20
		c-	180
c+	*250*	*a+*	25
		a-	225
		b+	5
		b-	245

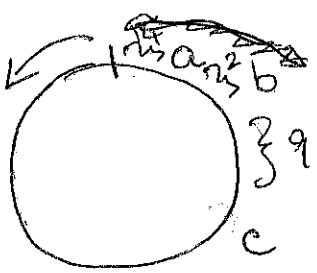
→ 60/200 = .3
→ 140/200 = .7
→ 20/200 = .1
→ 180/200 = .9
→ 25/250 = .1
→ 5/250 = .02

Therefore, a & b are closest, a & c are next closest & b & c are the farthest apart (looking at their frequencies). The closer they are, the higher the frequency.

c ——— a ——— b

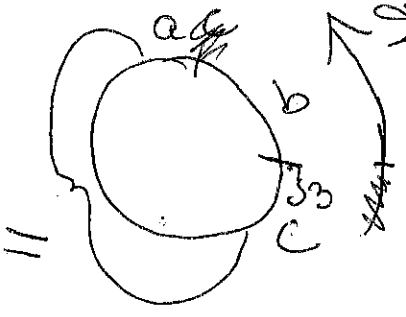
2. Two Hfr strains were compared in matings with an F- strain having multiple mutations in genes *a*, *b*, *c*, *d*, etc.) . With HfrA, the markers *a+*, *b+*, and *c+* were transmitted at 14, 16, and 25 minutes, respectively. With HfrB, markers *a+* and *c+* were transmitted at 14 and 3 minutes, respectively. What time of entry would you expect for marker *b+* in the HfrB strain? (4 points)

Hfr A
a⁺ - 14 minutes
b⁺ - 16 minutes
c⁺ - 25 minutes



Hfr B
a⁺ - 14 minutes
c⁺ - 3 minutes
b⁺ - ?

C can't be first



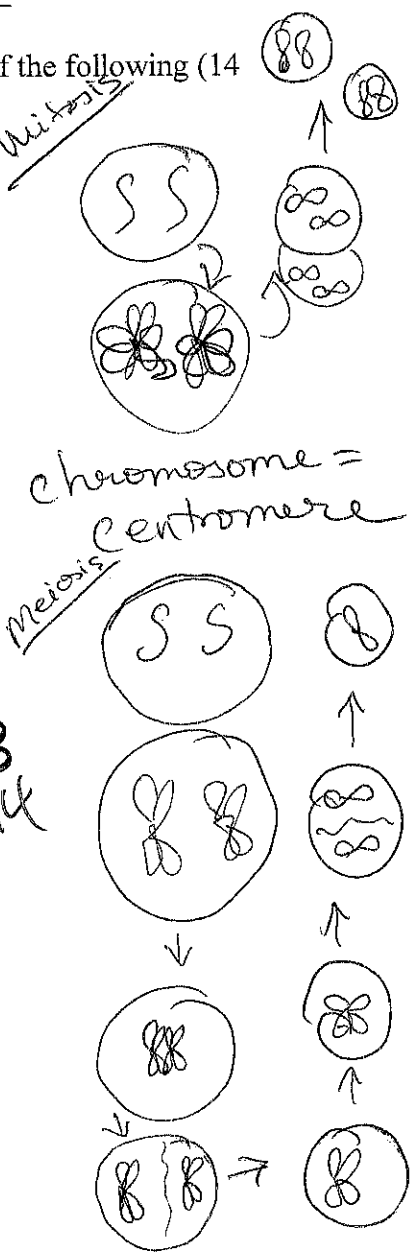
the time of entry of marker b⁺ should be 12 minutes

10

Name: _____

3. Salamanders have 2n = 24 chromosomes. Determine the per cell number of the following (14 points): n = 12

a. Chromatids at metaphase of mitosis 48
b. Chromosomes at metaphase of mitosis 24
c. Centromeres at metaphase of mitosis 24
d. Chromatids at anaphase of mitosis 0
e. Chromosomes at anaphase of mitosis 48
f. Centromeres at anaphase of mitosis 48
g. Tetrads at metaphase I of meiosis 12
h. Chromosomes at metaphase I of meiosis 24
i. Chromatids at metaphase I of meiosis 48
j. Chromosomes at anaphase I of meiosis 24 +1 = 13 14
k. Chromatids at anaphase I of meiosis 48
l. Tetrads at metaphase II of meiosis 0
m. Chromosomes at metaphase II of meiosis 12
n. Chromosomes at anaphase II of meiosis 24



chromosome = centromere

4. Two curly-winged *Drosophila* are mated and produce an F_1 that consists of 341 curly-winged and 162 normal flies. Explain this inheritance pattern. (4 points)

c = recessive, normal
C = Dominant, curly ✓

Parents were heterozygotes

	C	c
C	CC	Cc
c	Cc	cc

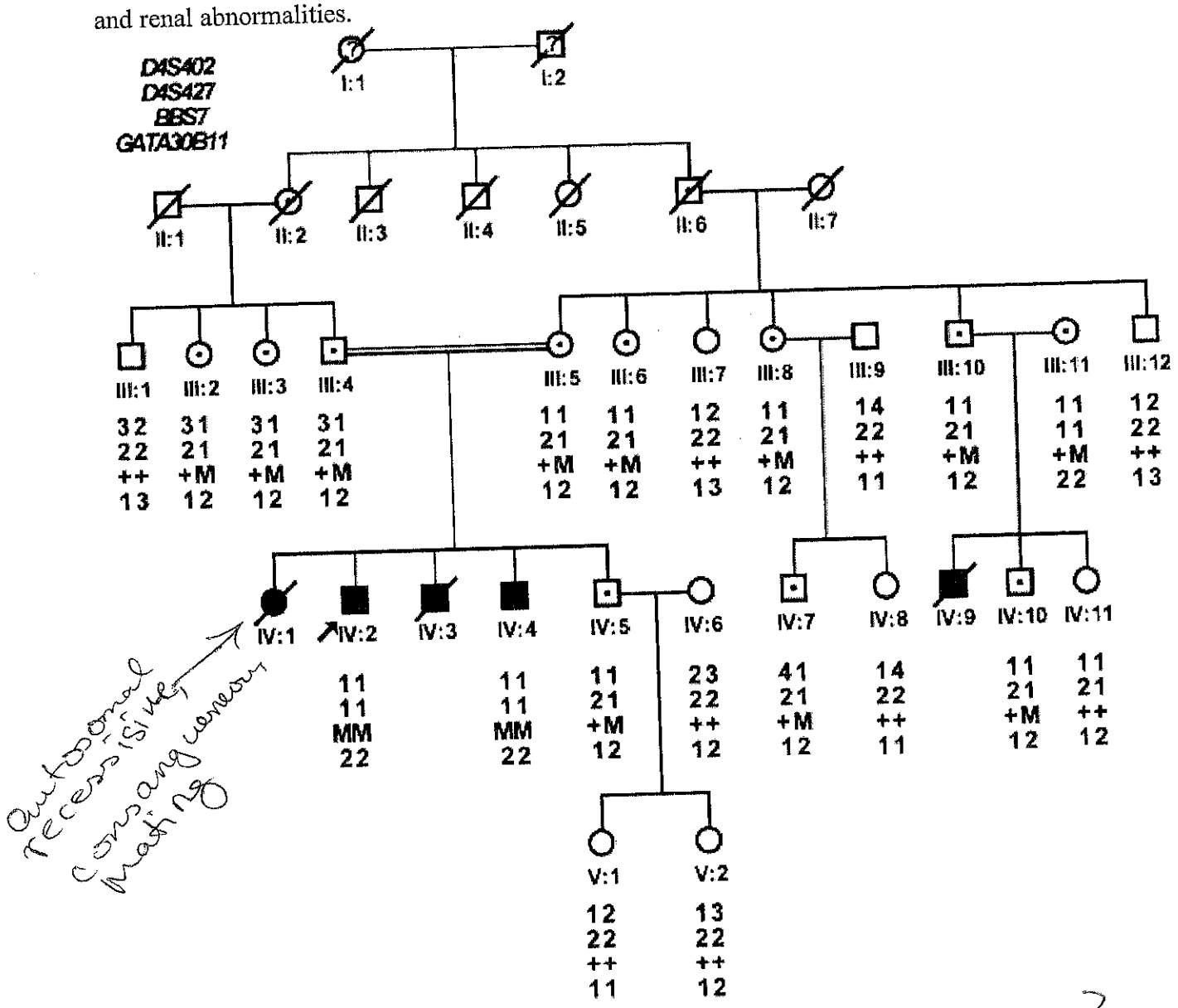
3 : 1 ratio
3 times as many curly-winged as normal ✓

Curly-wings are autosomal dominant & parents were heterozygotes for curly wings

1

Name: _____ 12

5. Below is a pedigree for a rare human hereditary disease, Bardet-Biedl syndrome. This disorder is characterized by pleiotropic defects including obesity, retinal dystrophy, polydactyly, and renal abnormalities.



a. What is mechanism of inheritance for Bardet-Biedl syndrome in this family? (3 points) → 3 autosomal recessive

b. Give the most probable genotype(s) for individuals III-4 and III-5 and all of their descendents in generation IV. (7 points).

c. What does the arrow pointing to individual IV-2 indicate? (2 points) That the study started because of this person (proband) 2

A = dominant
a = recessive

III-4 = Aa

III-5 = Aa

IV-1, 2, 3, 4 – aa

IV-5 = Aa 4 ?

Name: _____ 15

6. Three of the many mutations in *Drosophila melanogaster* that affect body color, wing shape, or bristle morphology are black (*b*) body versus gray in the wild type; dumpy (*dp*) wings that are obliquely truncated, versus long wings in the wild type; and hooked (*hk*) bristles at the tip versus normal bristles in the wild type. From the cross of a dumpy female with a black, hooked male, all the F_1 were wild type for all three characters. The testcross of an F_1 female with a dumpy, black, hooked male gave the following results:

→ wild type is dominant

Phenotype	Number of progeny		black	dumpy	bristles
wild type	169		+	+	+
black	19		b	+	+
black, hooked	301	NCO	b	+	hK
dumpy, hooked	21		+	dp	hK
hooked	8	DCO	+	dp	hK
hooked, dumpy, black	172		b	dp	+
dumpy, black	6	DCO	b	dp	+
dumpy	304	NCO	+	dp	+
	Total 1000				

$\frac{+\ b\ +}{+\ +\ hK} \cdot \frac{+\ b\ hK}{dp\ dp\ +}$

a. How can you tell that these genes are linked? (2 points)
b. Which gene is in the middle? (2 points)
c. Give the genotypes of the P_1 and F_1 flies that were crossed. (4 points)
d. Construct a genetic map for these three genes. (5 points)
e. What is the coefficient of coincidence? (3 points)
f. What is the interference? (2 points).

a- They are linked because all the genes appear in some form of recombinants, there are flies w/ just one mutation, flies w/ all three, flies w/ two × flies w/ no mutati → therefor they didn't assoc independ

b- $\frac{b\ +\ hK}{+\ dp\ +} \cdot \frac{+\ +\ hK}{b\ dp\ +}$ 2

in DCO, b has switched, therefore b is in the middle

the b gene

c- P_1 flies:

$\frac{dp\ +\ +}{dp\ +\ +} \cdot \frac{+\ b\ hK}{}$ doesn't say X-linked but O.K.

F_1 flies:

$\frac{dp\ b\ hK}{+\ +\ +} \cdot \frac{dp\ b\ hK}{}$ 3

Name: [redacted]

7. In a screen for zebrafish mutants that are defective in cardiovascular development, ten mutations were isolated that resulted in cardiac arrhythmias in the mutant fish. Female and male mutants were intercrossed and the ability of the F_1s' hearts to beat normally (+) or not (-) was assessed. The results are shown below.

	m116	*m139*	*m158*	*m276*	*tb218*	*tc318d*	*te381b*	*tj201*	*tm117c*	*tx218*
m116	-	-	-	-	+	-	-	+	+	+
m139		-	-	-	+	-	-	+	+	+
m158			-	-	+	-	-	+	+	+
m276				-	+	-	-	+	+	+
tb218					-	+	+	+	+	+
tc318d						-	-	+	+	+
te381b							-	+	+	+
tj201								-	+	+
tm117c									-	+
tx218										-

a. How many different genes were identified in this screen? (3 points)
b. Assign genotypes to all of the mutants. (5 points)
c. Explain why the F_1 hybrids between mutants *m116* and *tb218* had a different phenotype than the hybrids between mutant *m116* and *tc318d*. (4 points)

a. m116, m139, m158, m276, tc318d, te381b
~~m139~~, ~~m158~~, ~~m276~~, ~~tc318d~~, ~~te381b~~
~~m158~~, ~~m276~~, ~~tc318d~~, ~~te381b~~
~~m276~~, ~~tc318d~~, ~~te381b~~
2 tb218
~~tc318d~~, ~~te381b~~
3 tj201
4 tm117c
5 tx218

5 genes were identified ✓ 3

b.

Mutation	Genotype
m116	a_1a_1BBCCDDEE
m139	a_2a_2BBCCDDEE
m158	a_3a_3BBCCDDEE
m276	a_4a_4BBCCDDEE
~~tb~~ 218	AAbbCCDD
tc 318d	aaBBCCDD
te 381b	aaBBCCDD
tj 201	AABBeeDD
tm 117c	AABBCCdd
tx 218	AABBCCDD

e: smaller c

c. They had different phenotypes, because m116 & tb218 complemented each other → they are mutations on different genes. While m116 & tc318d are mutations on the same gene, therefore they did not complement each other.

Name: _____

8. You were given a packet of 200 tomato seeds, all produced from matings involving the same parents. These seeds produced 12 plants with yellow fruits and hairless stems, 16 with yellow fruits and very hairy stems, 28 with yellow fruits and scattered short hairs on the stems, 32 with red fruit and very hairy stems, 38 with red fruit and hairless stems, and 74 with red fruits and scattered short hairs on the stems.

a. Explain the inheritance of fruit color and stem hairs and give the genotypes and phenotypes of the parents and the expected phenotypic ratios of their 200 offspring. (12 points)
b. Use chi-square analysis to determine if your hypothesis is consistent with the data. (8 points)

12 yellow, hairless
16 yellow, v. hairy
28 yellow, short
32 red, v. hairy
38 red, hairless
74 red, short

Ratio of fruit color

yellow – 56
red – 144

fruit color is autosomal dominant → w/ red being dominant

Ratio of stem hairs

50 – hairless
102 – short
48 – v. hairy

about 1:2:1 ratio, incomplete dominance for stem hairs w/ short hairs being a "blend" of v. hairy & hairless

Genotypes of parents: $Yy\ H^{V}H^{N} \times Yy\ H^{V}H^{N}$

phenotypes of parents: They were red/fuzzy short hairs on their stems

Y = red
y = yellow
$H^{N}H^{N}$ = short hair
$H^{V}H^{V}$ = very hairy
$H^{N}H^{N}$ = no hair

$H^{S}\ H^{N}$

$H^{S}H^{S}\ H^{N}H^{S}$

$H^{N}H^{S}\ H^{N}H^{N}$

20

Name: _____

9. Miniature wings in Drosophila result from an X-linked gene (X^m) that is recessive to an allele for long wings (X^{m+}). Sepia eyes are produced by an autosomal gene (s) that is recessive to an allele for red eyes (S) A female fly with miniature wings and sepia eyes is crossed to a male that has normal wings and is homozygous for red eyes. The F_1 are intercrossed to produce the F_2. Give the phenotypic ratios expected in the F_1 and F_2. (10 points)

P_1 : $\frac{X^m s}{X^m s} \cdot \frac{X^{m+} S}{Y S}$

X^{m+}	X^m	X^m	
X^{m+}	$X^m X^{m+}$	$X^m X^m$	males have miniature wings
Y	$X^m Y$	$X^m Y$	

F_1: ① all females have long wings and red eyes

② all males have miniature wings & red eyes

	S	S
S	S_s	S_s
S	S_s	S_s

everyone has red eyes — hooray!

F2 Females

	X^m	X^{m+}
X^m	$X^m X^m$	$X^{m+} X^m$
Y	$X^m Y$	$X^{m+} Y$

3/4 S_ : 1/2 $X^m Y$ = 3/8 red eyes, miniature wings; 1/2 $X^{m+} Y$ = 3/8 red eyes, normal wings

1/4 ss : 1/2 $X^m Y$ = 1/8 sepia, miniature wings; 1/2 $X^{m+} Y$ = 1/8 sepia, long wings

	S	s
S	SS	Ss
s	Ss	ss

3:1 red eyes – 3, sepia – 1

For F2 females

3/4 S_ : 1/2 $X^m X^m$ = 3/8 ; 1/2 $X^m X^{m+}$ = 3/8

1/4 ss : 1/2 $X^m X^m$ = ; 1/2 $X^m X^{m+}$ =

F2 ratio	Male	Female
3/8	red eyes, miniature wings	red, miniature wings
3/8	red eyes, normal wings	red, normal wings
1/8	sepia, miniature wings	sepia, miniature wings
1/8	sepia, normal wings	sepia, normal wings

Name: [redacted]