

## MIDTERM 1 ANSWER KEY

**Question 1. (5 points)**

You perform a cross between a black-eyed mouse and a red-eyed mouse of unknown genotypes, and all the progeny have black eyes (F1). You cross the F1 progeny with one another and you get 38 black-eyed mice and 14 red-eyed mice in the F2 generation.

cross 1: black-eyed mouse **X** red-eyed mouse (P)  
gives F1: all black-eyed

cross 2: black-eyed F1 **X** black-eyed F1  
gives F2:  
38 black-eyed  
14 red-eyed

- a) Using letters of your own choosing, state the most likely genotypes of the two parents (P) in cross 1, stating which phenotypes are dominant and using a capital letter for the dominant alleles.

**B = black (dominant), b = red (recessive)**

**Parents are BB x bb**

**½ pt.**

- b) Based on your answer to part (a), state the expected genotypes of the F1, and in what ratio they should occur

**All the F1 are Bb**

**½ pt.**

- c) Based on your answers to parts (a) and (b), state the expected genotypes of the F2 (progeny in cross 2), and in what ratio they should occur

**In cross 2, Bb x Bb → 1 BB : 2 Bb : 1 bb**

**½ pt.**

- d) State the phenotype of each genotype in the F2 and use this to predict the phenotypic ratios in the F2 generation:

**1 BB black**

**2 Bb black**

**1 bb red**

**→ 3 black : 1 red phenotypic ratio**

**1 pt.**

- e) Use a Chi Square test to determine whether the observed data are consistent with your model with a confidence of  $P < 0.05$ . Show your work and put a box around the  $\chi^2$  value, the P value, and your yes/no answer.

Class	Observed	Expected	(O-E) <sup>2</sup>	(O-E) <sup>2</sup> / E
B <sub>-</sub>	38	3/4 x 52 = 39	(38-39) <sup>2</sup> = 1	0.0256
bb	14	1/4 x 52 = 13	(14-13) <sup>2</sup> = 1	0.0769
				<b><math>\chi^2 = 0.10</math></b>

Degrees of freedom = number of classes - 1 = 1

<b><math>\chi^2 = 0.10</math></b>	<b>P &gt; 0.5</b>	<b>YES the data are consistent with the model</b>
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2.5 points for part (e) as follows: ½ pt for correct observed & expected numbers, ½ pt for calculation of  $\chi^2$ , ½ pt for DF value, ½ pt for P value, ½ pt for YES/NO answer. Note: if DF is not stated but P value is correct, you get credit for knowing the DF.

**Question 1. (5 points)**

You perform a cross between a red geranium and a white geranium of unknown genotypes, and all the progeny have red flowers (F1). You cross the F1 progeny with one another and you get 43 red-flowered geranium plants and 13 white-flowered geranium plants in the F2 generation.

cross 1: red geranium X white geranium (P)  
gives F1: all red

cross 2: red F1 X red F1  
gives F2:  
43 red  
13 white

- a) Using letters of your own choosing, state the most likely genotypes of the two parents (P) in cross 1, stating which phenotypes are dominant and using a capital letter for the dominant alleles.

R = red (dominant), r = white (recessive) ½ pt  
Parents in cross 1 are RR x rr

- b) Based on your answer to part (a), state the expected genotypes of the F1, and in what ratio they should occur

All the F1 are Rr ½ pt

- c) Based on your answers to parts (a) and (b), state the expected genotypes of the F2 (progeny in cross 2), and in what ratio they should occur

In cross 2, Rr x Rr → 1 RR : 2 Rr : 1 rr ½ pt

- d) State the phenotype of each genotype in the F2 and use this to predict the phenotypic ratios in the F2 generation 1 pt

1 RR red  
2 Rr red → 3 red : 1 white phenotypic ratio  
1 rr white

- e) Use a Chi Square test to determine whether the observed data are consistent with your model. Show your work and put a box around the  $\chi^2$  value, the P value, and your yes/no answer.

Class	Observed	Expected	(O-E) <sup>2</sup>	(O-E) <sup>2</sup> / E
R <sub>-</sub>	43	3/4 x 56 = 42	(43-42) <sup>2</sup> = 1	0.0238
rr	13	1/4 x 56 = 14	(13-14) <sup>2</sup> = 1	0.0714
				$\chi^2 = 0.10$

Degrees of freedom = number of classes - 1 = 1

$\chi^2 = 0.10$	P > 0.5	YES the data are consistent with the model
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2.5 points for part (e) as follows: ½ pt for correct observed & expected numbers, ½ pt for calculation of  $\chi^2$ , ½ pt for DF value, ½ pt for P value, ½ pt for YES/NO answer. Note: if DF is not stated but P value is correct, you get credit for knowing the DF.

**Question 2. (2 ½ points)**

You cross a pure-breeding blue sea-slug by a pure-breeding white sea-slug and all the F1 progeny are pale blue. You then cross the pale blue F1 slugs to one another and obtain 22 blue, 53 pale blue, and 25 white slugs in the F2 generation.

cross 1: blue slug **X** white slug (P)  
gives F1: all pale-blue

cross 2: pale-blue F1 **X** pale-blue F1  
gives F2:  
22 blue  
53 pale-blue  
25 white

- a) Using letters of your own choosing, state the most likely genotypes of the original two parents (P), stating which phenotypes are dominant and using a capital letter for the dominant alleles.  
**B = blue (dominant)**      ½ pt (also OK to say that white was dominant)  
**b = white (recessive)**      (also OK to say incomplete dominant)
- b) What is the genetic term used to explain the color of the F1?  
**Incomplete dominance**      1 pt
- c) Based on your answer in (a), state the expected genotypes of the F2, and in what ratio they should occur  
**1 BB : 2 Bb : 1 bb** ½ pt
- d) Based on your answers in (a) through (c), state the phenotype of each genotype in the F2 and use this to explain the phenotypic ratios in the F2 generation  
**Observed ratio is approx 1:2:1**      ½ pt
- 1 BB = blue**  
**2 Bb = pale blue → 1 blue : 2 pale : 1 white**  
**1 bb = white**

**Question 2. (2 ½ points)**

You discover that a laboratory strain of gerbils is deaf and you decide to use it as a model for hereditary deafness. You cross a purebred deaf gerbil to a purebred gerbil that can hear (“hearing” phenotype). All the F1 progeny have partial hearing loss (“hard-of-hearing” phenotype). You then cross the hard-of-hearing F1 gerbils to one another, and you obtain 27 deaf, 49 hard-of-hearing, and 24 hearing gerbils in the F2 generation.

cross 1: deaf gerbil **X** hearing gerbil  
gives F1: all hard-of-hearing

cross 2: hard-of-hearing F1 **X** hard-of-hearing F1  
gives F2:  
27 deaf  
49 hard-of-hearing  
24 hearing

- a) Using letters of your own choosing, state the most likely genotypes of the original two parents, stating which phenotypes are dominant and using a capital letter for the dominant alleles.

**H = hearing (dominant)**

**h = deaf (recessive)**

**Parents are HH x hh**

½ pt (also OK to say that deafness was dominant)  
(also OK to say incomplete dominant)

- b) What is the genetic term used to explain the phenotype of the F1?

**Incomplete dominance**

1 pt

- c) Based on your answer in (a), state the expected genotypes of the F2, and in what ratio they should occur

**1 HH : 2 Hh : 1 hh**

½ pt

- d) Based on your answers in (a) through (c), state the phenotype of each genotype in the F2 and use this to explain the phenotypic ratios in the F2 generation

**Observed ratio is approx 1:2:1**

½ pt

**1 HH = hearing**

**2 Hh = hard of hearing → 1 hearing : 2 hard-of-hearing : 1 deaf**

**1 hh = deaf**

**Question 3 (3 points)**

You have two purebred varieties of roses, one that has multiple flowers on each stem and red petals, and another that has one flower per stem and yellow petals. You are sure you could get rich if you could just get a multiple-flowered yellow-petalled rose bush. You cross your two purebred varieties and all the F1 progeny plants are identical, but your lab assistant forgets to write down the phenotype and then loses the plants. Nevertheless you still have a hundred F2 (progeny from self-crossing the F1 hybrids), and you find the F2 phenotypes as follows:

19	single-flowered red
18	multi-flowered yellow
8	single-flowered yellow
55	multi-flowered red

- a) Which phenotypes are dominant?

**Multi-flowered and Red**

$\frac{1}{2}$  pt (must state PHENOTYPES)

- b) Using letters of your own choosing, write out the likely genotypes of the two original purebred varieties, stating which phenotypes are dominant and using a capital letter for the dominant alleles.

1 pt (must state GENOTYPES)

**M=multi (dominant), m=single (recessive)**

**R=red (dominant), r=yellow (recessive)**

**Original purebred varieties were MMRR x mmrr**

- c) Infer the probable phenotype of the missing F1 plants

**MmRr = multi, red**

$\frac{1}{2}$  pt (must state PHENOTYPE)

- d) Demonstrate how you can explain the ratios of the F2 phenotypes on the basis of your model of the genotypes and the phenotypes associated with each genotype.

**A complete answer requires that you derive the ratios.**

$\frac{1}{2}$  pt for just *stating* that you get a 9:3:3:1 ratio

**Observed ratio is 8.8 : 3.0 : 2.9 : 1.3 or about 9:3:3:1**

9 M_R_	multi, red
3 M_rr	multi, yellow
3 mmR_	single, red
1 mmrr	single, yellow

$\frac{1}{2}$  pt for demonstrating **HOW** you get 9 M\_R\_, etc, in a dihybrid cross.

**Either a Punnet square, a tree, or multiplying probabilities would be fine here:**

	<b>MR</b>	<b>Mr</b>	<b>mR</b>	<b>mr</b>
<b>MR</b>	MMRR	MMRr	MmRR	MmRr
<b>Mr</b>	MMRr	MMrr	MmRr	Mmrr
<b>mR</b>	MmRR	MmRr	mmRR	mmRr
<b>mr</b>	MmRr	Mmrr	mmRr	mmrr

**Question 3 (3 points)**

There are two purebred varieties of horses, one that has a black coat with a red mane, and another that has a brown coat with a white mane. You are determined to get a horse with a black coat and a white mane. You arrange several crosses between the two purebred varieties, and all the F1 progeny are identical. Unfortunately all the F1 horses are stolen and you can't remember what they looked like. Fortunately, before the F1 horses were stolen, you had already obtained 100 F2 (progeny from mating the F1 hybrids with each other). The F2 phenotypes are as follows:

7	brown coat, white mane
24	black coat, white mane
50	black coat, red mane
19	brown coat, red mane

a) Which phenotypes are dominant?

**Black coat and red mane**      ½ pt (must state PHENOTYPES)

b) Using letters of your own choosing, write out the likely genotypes of the two parental varieties, stating which phenotypes are dominant and using a capital letter for the dominant alleles.

**B=black coat (dominant), b= brown coat (recessive)**

**R=red mane (dominant), r= white mane (recessive)**      1 pt

**Original purebred varieties were BBRR x bbr**      (must state GENOTYPES)

c) Infer the probable phenotype of the missing F1 horses so you can file a police report.

**BbRr = black coat, red mane**      ½ pt (must state PHENOTYPE)

d) Demonstrate how you can predict the ratios of the F2 phenotypes on the basis of your model of the genotypes and the phenotypes associated with each genotype.

**A complete answer requires that you derive the ratios.**

½ pt for just *stating* that you get a 9:3:3:1 ratio

**Observed ratio is 8.0 : 3.8 : 3.0 : 1.1 or about 9:3:3:1**

9 B_R_	black coat, red mane
3 B_rr	black coat, white mane
3 bbRR	brown coat, red mane
1 bbr	brown coat, white mane

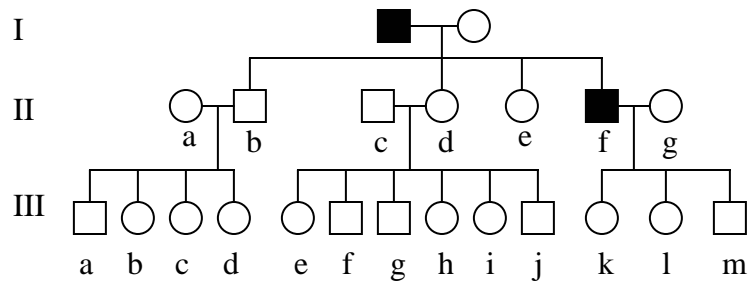
½ pt for demonstrating **HOW** you get 9 M\_R\_, etc, in a dihybrid cross.

**Either a Punnet square, a tree, or multiplying probabilities would be fine here**

	<b>BR</b>	<b>Br</b>	<b>bR</b>	<b>br</b>
<b>BR</b>	BBRR	BBRr	BbRR	BbRr
<b>Br</b>	BBRr	BBrr	BbRr	Bbrr
<b>bR</b>	BbRR	BbRr	bbRR	bbRr
<b>br</b>	BbRr	Bbrr	bbRr	bbrr

**Question 4 (3 points)**

The following pedigree is for a family with a history of a rare, late-onset disease caused by a single, dominant mutation. Those individuals who are already suffering from the disease are shaded black. However, some additional individuals in generations II and III also have the mutant allele and will develop the disease but have not yet shown symptoms. Assume that individuals marrying into the family have no history of the disease (that is, they are homozygous recessive for the gene). Also assume that the diseased male in generation I is heterozygous for the disease gene.



a) Is this disease X-linked or autosomal?

Must be autosomal because fathers cannot pass X-linked diseases to sons 1 pt

b) If individuals IIIg and IIa had a child together, what is the probability that the child would develop the disease later in life?

II-a is presumed hh because marrying into family ½ pt

P( II-d is Hh) = ½ because parents are Hh x hh ½ pt

P(III-g is Hh) = P( II-d is Hh) x ½ = ½ x ½ = ¼ ½ pt

P(child is Hh) = P(III-g is Hh) x ½ = ¼ x ½ = 1/8 ½ pt

Answer 1/8

Total 2 pts for part (b)

Question does not say to show work, so the following answers also got full credit:

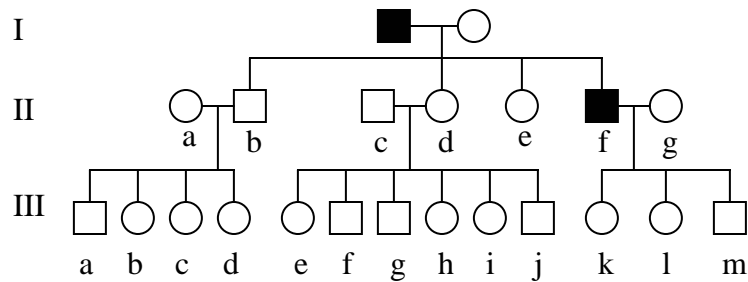
$$\frac{1}{2} \times \frac{1}{2} \times \frac{1}{2} = \frac{1}{8}$$

or simply

$$\frac{1}{8}$$

**Question 4 (3 points)**

The following pedigree is for a family with a history of a rare, late-onset disease caused by a single, dominant mutation. Those individuals who are already suffering from the disease are shaded black. However, some additional individuals in generations II and III also have the mutant allele and will develop the disease but have not yet shown symptoms. Assume that individuals marrying into the family have no history of the disease (that is, they are homozygous recessive for the gene). Also assume that the diseased male in generation I is heterozygous for the disease gene.



a) Is this disease X-linked or autosomal?

**Must be autosomal because fathers cannot pass X-linked diseases to sons 1 pt**

b) If individuals III<sub>m</sub> and II<sub>a</sub> had a child together, what is the probability that the child would develop Huntington disease? ~~Show your work, circle your answer.~~ the disease later in life? **[Correction, as announced during the exam]**

**II-a is presumed hh ½ pt**

**P(II-f is Hh) = 1 because of disease ½ pt**

**P(III-m is Hh) = ½ because his parents are Hh x hh ½ pt**

**P(child would be Hh) = P(III-m is Hh) x ½ = ½ x ½ = ¼ ½ pt**

**Answer ¼**

Total 2 pts for part (b)

Question does not say to show work, so the following answers also got full credit:

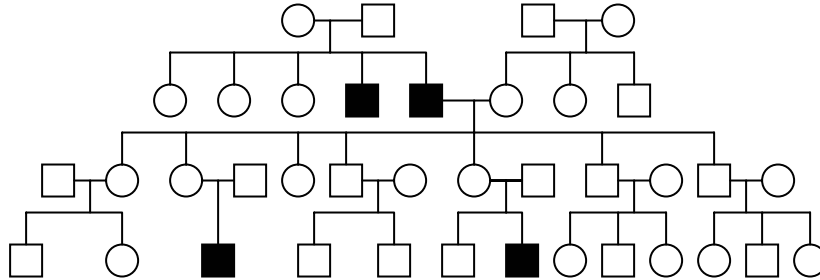
$$\frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$$

or simply

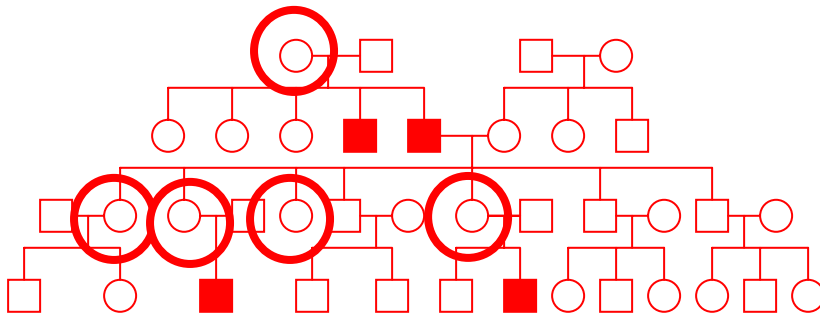
$$\frac{1}{4}$$

**Question 5 (4 points)**

A family with a rare disorder presents the following family tree:



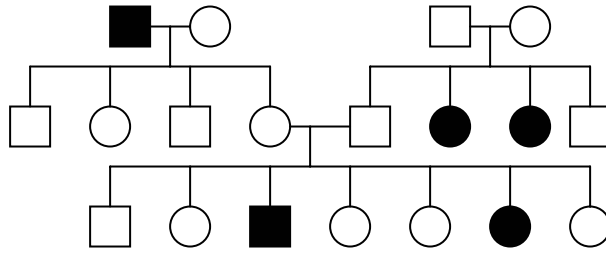
- a) What is the most likely mode of inheritance?  
X linked recessive    1 pt (½ pt for X linked, ½ pt for recessive)
  
- b) Cite the 2 facts about the pedigree that give the most support for your conclusion.  
 1 pt: (½ pt for each fact up to 2 acceptable facts). For example:  
Skips generations therefore recessive  
Inherited by sons through unaffected mothers  
All the sons of carrier mothers are affected, and none of the daughters  
None of the children of affected males are affected  
Disease is only expressed in males, therefore suspect sex linkage  
Deduct ½ pt for every “fact” that is false
  
- c) Circle all individuals that MUST be heterozygous  
 Total 2 pts: ½ pt off for each missed or extra individual.



If you made a *STATED* assumption that is fully consistent with the question, answer will be graded for that model.

**Question 5 (4 points)**

A family with a rare disorder presents the following family tree:



a) What is the most likely mode of inheritance?

Autosomal recessive 1 pt (½ pt for autosomal, ½ pt for recessive)

b) Cite the 2 facts about the pedigree that give the most support for your conclusion.

1 pt: (½ pt for each fact up to 2 acceptable facts). For example:

Affected individuals have unaffected parents, so must be recessive

Skips generations (in left side of family) as expected for recessive

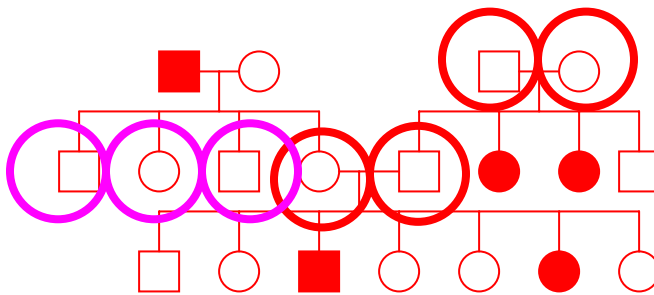
Same parents can have both affected sons and affected daughters, so not sex linked

Affected individuals are both male and female, so not sex linked

Deduct ½ pt for every “fact” that is false

c) Circle all individuals that MUST be heterozygous

Total 2 pts: ½ pt off for each missed or extra individual. The three individuals in pink are grouped together: just ½ pt if you missed any of them.



If you made a STATED assumption that is fully consistent with the question, answer will be graded for that model.

**Question 6 (2 ½ points)**

The two parents of a cross have the genotypes:

Parent 1      Aa BB cc Dd EE ff

Parent 2      AA Bb Cc DD ee Ff

- a) How many different kinds of gametes can Parent 1 form? How many different kinds of gametes can Parent 2 form? How many squares would you need in a Punnett square to diagram this cross?

Parent 1 can produce  $2 \times 1 \times 1 \times 2 \times 1 \times 1 = 4$  kinds of gametes ½ pt

Parent 2 can produce  $1 \times 2 \times 2 \times 1 \times 1 \times 2 = 8$  kinds of gametes ½ pt

This would represent  $8 \times 4 = 32$  entries in a Punnett square ½ pt

- b) What fraction of the progeny will have the same phenotype as Parent 1?

Assuming capital letters are dominant alleles, complete dominance, then:

Parent 1 phenotype requires A\_B\_ccD\_E\_F\_

$1 \times 1 \times \frac{1}{2} \times 1 \times 1 \times \frac{1}{2} = \frac{1}{4}$  will have phenotype of Parent 1 ½ pt

- c) What fraction of the progeny will be pure breeding for all the traits?

None can be pure breeding (homozygous for every trait) because all the progeny will be heterozygous for E. ½ pt

**Question 6 (2 ½ points)**

The two parents of a cross have the genotypes:

Parent 1      Aa BB cc Dd EE ff

Parent 2      AA Bb Cc DD ee Ff

- a) How many different genotypes can the progeny of this cross have? How many different phenotypes?

There can be  $2 \times 2 \times 2 \times 2 \times 1 \times 2 = 32$  (or  $2^6$ ) different genotypes 1 pt

(Assuming capital letters are dominant and assuming complete dominance)

There can be  $1 \times 1 \times 2 \times 1 \times 1 \times 2 = 4$  different phenotypes ½ pt

- b) What fraction of the progeny will have the same phenotype as Parent 2?

None

[Because the 2<sup>nd</sup> parent is homozygous for the recessive allele of e, and all of the progeny will be Ee, none of the progeny will be phenotypically identical to Parent 2]

½ pt

- c) In the progeny of this cross, how many different genotypes could produce the phenotype A\_B\_ccD\_E\_ff?

$2 \times 2 \times 1 \times 2 \times 1 \times 1 = 8$  different genotypes could arise in this cross that would be consistent with this phenotype

½ pt

**Question 7 (5 points)**

You mate pure-breeding white mice with another pure-breeding strain of brown mice, and all the F1 are black. When the black F1 are crossed with one another, you obtain 90 black, 30 brown, and 40 white offspring (F2).

- a) Suggest a likely genetic model for the inheritance of coat color in this cross. Use letters of your own choosing, define the phenotypes of each allele, using capital letters for dominant alleles. State the genotypes of the 2 purebreeding parental strains, the genotypes of the F1, and the genotypes of the F2. Show that the phenotypic ratio in the F2 follows from the genotypes according to your model.

The most consistent ratio is 9:3:4 which suggests **RECESSIVE EPISTASIS**

**B dominant (black), b recessive (brown)**

**C dominant (normal), c recessive (white, epistatic to the B gene)**

Parental cross	<b>BB cc (white) x bbCC (brown)</b>
F1	<b>BbCc (black)</b>
F2	<b>9 B_C_ (black) 3 bbC_ (brown) → 9 black: 4 white : 3 brown 3 B_cc (white) 1 bbcc (white)</b>

1 pt for model. *IF YOU PROPOSED incomplete dominance for your model, lose 1/2 point because the predicted ratio does not fit the data as well; the rest of your answer graded according to the other version of the question.*

1 pt for allele definitions and genotypes of P, F1 and F2

1 pt for showing that phenotypic ratio in F2 follows from the model

- b) Propose a test cross that would test your model of the genotype of white mice in the F2, and predict the outcome.

For example: Cross white F2 to true-breeding brown mice (bbCC)

Model predicts:

1/4 of white mice bbcc → all progeny in test cross bbCc (brown)

1/4 of white mice BBcc → all progeny in test cross BbCc (black)

1/2 of white mice Bbcc → half the progeny BbCc (black) and half bbCc (brown)

1 pt for specifying an informative test cross, 1 pt for correctly predicting outcomes

*A test cross must involve an individual in the F2 identified only by PHENOTYPE, crossed by a test strain of known homozygous genotype in order to reveal the genotype of the F2 individual being tested. It is not valid to select an F2 GENOTYPE, this is what you don't know yet!*

*white F2 x bbCC is the best test (distinguishes all classes of white F2s as shown above)*

*white F2 x BBcc is uninformative, cc does not segregate and B cannot be scored*

*white F2x bbcc uninformative, cc does not segregate and B cannot be scored*

*white F2 x BBCC is uninformative (phenotypes will be B regardless of F2 genotype)*

A few of you provided both models (incomplete dominant and recessive epistasis) and suggested a test cross that could distinguish between them. If you did that, you're a pro!

**Question 7 (5 points)**

You mate pure-breeding white mice with another pure-breeding strain of brown mice, and all the F1 are black. When the black F1 are crossed with one another, you obtain 80 black, 40 brown, and 40 white offspring (F2).

- a) Suggest a likely genetic model for the inheritance of coat color in this cross. Use letters of your own choosing, define the phenotypes of each allele, using capital letters for dominant alleles. State the genotypes of the 2 purebreeding parental strains, the genotypes of the F1, and the genotypes of the F2. Show that the phenotypic ratio in the F2 follows from the genotypes according to your model.

The most consistent ratio is 1:2:1 which suggests INCOMPLETE DOMINANCE.

B dominant (brown), b recessive (white), "intermediate" phenotype Bb = black.

Parental cross	bb (white) x BB (brown)
F1	Bb (black)
F2	1 BB (brown) 2 Bb (black) 1 bb (white)

1 pt for model. *IF YOU PROPOSED recessive epistasis for your model, lose 1/2 point because the predicted ratio does not fit the data as well. The rest of your answer graded according to the other version of the question. If you wrote that you rejected incomplete dominance because black is an unlikely intermediate phenotype between brown and white, we gave you the full point anyway.*

1 pt for allele definitions and genotypes of P, F1 and F2

1 pt for showing that phenotypic ratio in F2 follows from the model

- b) Propose a test cross that would test your model of the genotype of white mice in the F2, and predict the outcome.

For example: Cross to true-breeding brown mice (BB) x F2 white mice

Model predicts F2 white mice bb → all progeny in test cross Bb (black)

1 pt for specifying an informative test cross, 1 pt for correctly predicting outcomes

*A test cross must involve an individual in the F2 identified only by PHENOTYPE, crossed by a test strain of known homozygous genotype in order to reveal the genotype of the F2 individual being tested. It is not valid to select an F2 GENOTYPE, this is what you don't know yet! But if your answer in part (a) stated that all the white F2 were bb, you got credit for stating that you test crossed a bb mouse by the test strain.*

*white F1 x BB is the best test of incomplete dominance (recovers the intermediate pheno)  
white F1 x bb does at least verify that your white F1 are homozygous, so we accepted it*

A few of you provided both models (incomplete dominant and recessive epistasis) and suggested a test cross that could distinguish between them. If you did that, you're a pro!

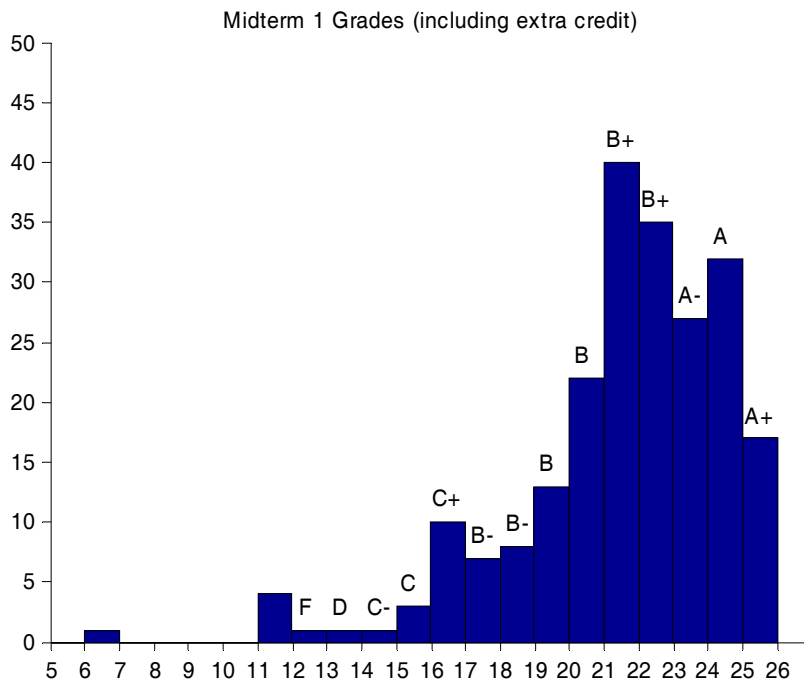
**EXTRA CREDIT (1 point): Do you know how much you know?**

**Estimate your score on questions 1-7: \_\_\_\_\_.**

**The maximum score is 25 points. The smallest unit of credit is ½ a point.**

20% of students guessed their raw score within ½ point and earned +1 point extra credit  
20% additional students guessed within 1 point and earned ½ point extra credit.

Extra credit was marked on the papers incorrectly (1pt given only for exact guess and ½ point given only for a guess within ½ a point) but the correction has already been made on the master grade sheet. You do NOT need to turn in your paper for a re-grade for this.

**Notes on grading:**

The mean and std score on the two versions of the test were identical.

As explained on the syllabus, there is no curve, which worked in your favor this exam, because a lot of you did very well. The cutoff for each grade is the lower boundary of the bar (for example: a score of exactly 21 gets B+).

The letter grades shown here are just for your information, we will not round off your score to a letter grade for each exam. We will add up all your points on both midterms and the final and THEN apply thresholds for final letter grades. There are 75 points still to go in the class (plus 2 extra credit points), so in theory you can still get a 4.0 (A or A+) for the class if your score was 19 or higher, which is almost all of you.