33. Because the parents are heterozygous, both are A/a. Both twins could be albino or both twins could be normal (and = multiply, or = add). The probability of being normal ($A/-$) is $^3/_4$, and the probability of being albino (a/a) is $^1/_4$.

$$p(\text{both normal}) + p(\text{both albino})$$
$$p(\text{first normal}) \times p(\text{second normal}) + p(\text{first albino}) \times p(\text{second albino})$$
$$(^3/_4)(^3/_4) + (^1/_4)(^1/_4) = {}^9/_{16} + {}^1/_{16} = {}^5/_8$$

32. Charlie, his mate, or both, obviously were not pure-breeding, because his F_2 progeny were of two phenotypes. Let A = black and white, and a = red and white. If both parents were heterozygous, then red and white would have been expected in the F_1 generation. Red and white were not observed in the F_1 generation, so only one of the parents was heterozygous. The cross is:

P	$A/a \times A/A$
F_1	$1\ A/a : 1\ A/A$

Two F_1 heterozygotes (A/a) when crossed would give 1 A/A (black and white) : 2 A/a (black and white) : 1 a/a (red and white). If the red and white F_2 progeny were from more than one mate of Charlie's, then the farmer acted correctly. However, if the F_2 progeny came only from one mate, the farmer may have acted too quickly.

33. Because the parents are heterozygous, both are A/a. Both twins could be albino or both twins could be normal (and = multiply, or = add). The probability of being normal ($A/-$) is $^3/_4$, and the probability of being albino (a/a) is $^1/_4$.

$$p(\text{both normal}) + p(\text{both albino})$$
$$p(\text{first normal}) \times p(\text{second normal}) + p(\text{first albino}) \times p(\text{second albino})$$
$$(^3/_4)(^3/_4) + (^1/_4)(^1/_4) = {}^9/_{16} + {}^1/_{16} = {}^5/_8$$

34. The plants are approximately 3 blotched : 1 unblotched. This suggests that blotched is dominant to unblotched and that the original plant which was selfed was a heterozygote.

a. Let A = blotched, a = unblotched.

P	A/a (blotched) × A/a (blotched)
F_1	$1\ A/A : 2\ A/a : 1\ a/a$
	3 $A/-$ (blotched) : 1 a/a (unblotched)

b. All unblotched plants should be pure-breeding in a testcross with an unblotched plant (a/a), and one-third of the blotched plants should be pure-breeding.

35. In theory, it cannot be proved that an animal is not a carrier for a recessive allele. However, in an $A/-$ × a/a cross, the more dominant-phenotype progeny produced, the less likely it is that the parent is A/a. In such a cross, half the progeny would be a/a and half would be A/a. With n dominant phenotype progeny, the probability that the parent is A/a is $(^1/_2)^n$. (DNA sequencing can be used to prove heterozygosity, but without sequence level information, the level of certainty is limited by sample size.)

27. a. The data for both crosses suggest that both A and B mutant plants are homozygous for recessive alleles. Both F_2 crosses give 3:1 ratios of normal to mutant progeny. For example, let A = normal and a = mutant, then

P	$A/A \times a/a$	
F_1	A/a	
F_2	1 A/A	phenotype: normal
	2 A/a	phenotype: normal
	1 a/a	phenotype: mutant (no trichomes).

b. No. You do not know if the a and b mutations are in the same or different genes. If they are in the same gene then the F_1 will all be mutant. If they are in different genes, then the F_1 will all be wild type.

28. Each die has six sides, so the probability of any one side (number) is $^1/_6$. To get specific red, green, and blue numbers involves "and" statements that are independent. So each independent probability is multiplied together.

a. $(^1/_6)(^1/_6)(^1/_6) = (^1/_6)^3 = {}^1/_{216}$

b. $(^1/_6)(^1/_6)(^1/_6) = (^1/_6)^3 = {}^1/_{216}$

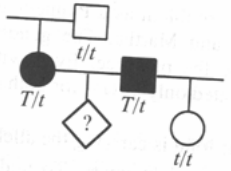
c. $(^1/_6)(^1/_6)(^1/_6) = (^1/_6)^3 = {}^1/_{216}$

d. To not roll any sixes is the same as getting anything but sixes:
$(1 - {}^1/_6)(1 - {}^1/_6)(1 - {}^1/_6) = (^5/_6)^3 = {}^{125}/_{216}$.

e. The easiest way to approach this problem is to consider each die separately. The first die thrown can be any number. Therefore, the probability for it

...more likely, given the rarity of the disease.

30. a. By considering the pedigree (see below), you will discover that the cross in question is $T/t \times T/t$. Therefore, the probability of being a taster is $^3/_4$, and the probability of being a nontaster is $^1/_4$.



Also, the probability of having a boy equals the probability of having a girl equals $^1/_2$.

(1) p(nontaster girl) = p(nontaster) × p(girl) = $^1/_4 \times {}^1/_2 = {}^1/_8$
(2) p(taster girl) = p(taster) × p(girl) = $^3/_4 \times {}^1/_2 = {}^3/_8$
(3) p(taster boy) = p(taster) × p(boy) = $^3/_4 \times {}^1/_2 = {}^3/_8$

b. p(taster for first two children) = p(taster for first child) × p(taster for second child) = $^3/_4 \times {}^3/_4 = {}^9/_{16}$

The ratio of purple : blue : white would be 9:3:4.

The woman must be *A/O*, so the mating is *A/O* × *A/B*. Their children will be

Genotype	Phenotype
1/4 *A/A*	A
1/4 *A/B*	AB
1/4 *A/O*	A
1/4 *B/O*	B

2

Single Gene Inheritance

BASIC PROBLEMS

1. The human genome contains an estimated 20,000–25,000 genes located on 23 different chromosomes.

2. PFGE separates DNA molecules by size. When DNA is carefully isolated from *Neurospora* (which has seven different chromosomes) seven bands should be produced using this technique. Similarly, the pea has seven different chromosomes and will produce seven bands (homologous chromosomes will co-migrate as a single band).

3. There is a total of 4 m of DNA and nine chromosomes per haploid set. On average, each is $^4/_9$ m long. At metaphase, their average length is 13 μm, so the average packing ratio is 13×10^{-6} m : 4.4×10^{-1} m or roughly 1:34,000! This remarkable achievement is accomplished through the interaction of the DNA with proteins. At its most basic, eukaryotic DNA is associated with histones in units called nucleosomes and during mitosis, coils into a solenoid. As loops, it associates with and winds into a central core of nonhistone protein called the scaffold.

4. Because the DNA levels vary four-fold, the range covers cells that are haploid (gametes) to cells that are dividing (after DNA has replicated but prior to cell division). The following cells would fit the DNA measurements:

x	haploid cells
$2x$	diploid cells in G_1 or cells after meiosis I but prior to meiosis II
$4x$	diploid cells after S but prior to cell division

5. The key function of mitosis is to generate two daughter cells genetically identical to the original parent cell.

6. Two key functions of meiosis are to halve the DNA content and to reshuffle the genetic content of the organism to generate genetic diversity among the progeny.

7. Its pretty hard to beat several billions of years of evolution but it might be simpler if DNA did not replicate prior to meiosis. The same events responsible for halving the DNA and producing genetic diversity could be achieved in a single cell division if homologous chromosomes paired, recombined, randomly aligned during metaphase, and separated during anaphase, etc. However, you would lose the chance to check and repair DNA that replication allows.

8. In large part, this question is asking, why sex? Parthogenesis (the ability to reproduce without fertilization — in essence, cloning) is not common among multicellular organisms. Parthenogenesis occurs in a some species of lizards and fishes, and several kinds of insects but it is tbe only means of reproduction in only a few of these species. In plants, about 400 species can reproduce asexually by a process called apomixis. These plants produce seeds without fertilization. However, the majority of plants and animals reproduce sexually. Sexual reproduction produces a wide variety of different offspring by forming new combinations of traits inherited from both the father and the mother. Despite the numerical advantages of asexual reproduction, most multicellular species that have adopted it as their only method of reproducing have become extinct. However, there is no agreed upon explanation of why the loss of sexual reproduction usually leads to early extinction or conversely, why sexual reproduction is associated with evolutionary success.

On the other hand, the immediate effects of such a scenario are obvious. All offspring will be genetically identical to their mothers, and males would be extinct within one generation.

9. As cells divide mitotically, each chromosome consists of identical sister chromatids that are separated to form genetically identical daughter cells. Although the second division of meiosis appears to be a similar process, the "sister" chromatids are likely to be different. Recombination during earlier meiotic stages has swapped regions of DNA between sister and nonsister chromosomes such that the two daughter cells of this division typically are not genetically identical.

10. The four stages of mitosis are: prophase, metaphase, anaphase, and telophase. The first letters, PMAT, can be remembered by a mnemonic such as: Playful Mice Analyze Twice.

The five stages of prophase I are: leptotene, zygotene, pachytene, diplotene, and diakinesis. The first letters, LZPDD, can be remembered by a mnemonic such as: Large Zoos Provide Dangerous Distractions.

F_1 phenotypes 0.6058 R S
0.1056 r s
0.1444 R s
0.1444 r S

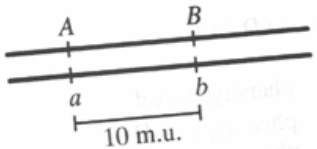
4. The cross is $E/e \cdot F/f \times e/e \cdot f/f$. If independent assortment exists, the progeny should be in a 1:1:1:1 ratio, which is not observed. Therefore, there is linkage. *E* *f* and *e* *F* are recombinants equaling one-third of the progeny. The two genes are 33.3 map units (m.u.) apart.

$$RF = 100\% \times 1/3 = 33.3\%$$

5. Because only parental types are recovered, the two genes must be tightly linked and recombination must be very rare. Knowing how many progeny were looked at would give an indication of how close the genes are.

6. The problem states that a female that is $A/a \cdot B/b$ is test crossed. If the genes are unlinked, they should assort independently and the four progeny classes should be present in roughly equal proportions. This is clearly not the case. The $A/a \cdot B/b$ and $a/a \cdot b/b$ classes (the parentals) are much more common than the $A/a \cdot b/b$ and $a/a \cdot B/b$ classes (the recombinants). The two genes are on the same chromosome and are 10 map units apart.

$$RF = 100\% \times (46 + 54)/1000 = 10\%$$



7. The cross is $A/A \cdot B/B \times a/a \cdot a/a$. The F_1 would be $A/a \cdot B/b$.

a. If the genes are unlinked, all four progeny classes from the test cross (including a/a ; b/b) would equal 25 percent.

b. With completely linked genes, the F_1 would produce only *A B* and *a b* gametes. Thus, there would be a 50 percent chance of having *a b*/*a b* progeny from a test cross of this F_1.

c. If the two genes are linked and 10 map units apart, 10 percent of the test cross progeny should be recombinants. Since the F_1 is *A B*/*a b*, *a b* is one of the parental classes (*A B* being the other) it should equal $1/2$ of the total parentals or 45 percent.

d. 38 percent (see part c).

1:1:1:1:1:1:1:1 ratio.

12. The four classes of data correspond to the parentals (largest), two groups of single crossovers (intermediate), and double crossovers (smallest).

13. By comparing the parentals with the double crossovers, gene order can be determined. The gene in the middle flips with respect to the two flanking genes in the double-crossover progeny. In this case, one parental is +++ and one double crossover is *p*++. This indicates that the gene for leaf color (*p*) is in the middle.

14. If only two of the three genes are linked, the data can still be grouped, but the grouping will differ from that mentioned in (12) above. In this situation, the unlinked gene will show independent assortment with the two linked genes. There will be one class composed of four phenotypes in approximately equal frequency, which combined will total more than half the progeny. A second class will be composed of four phenotypes in approximately equal frequency, and the combined total will be less than half the progeny. For example, if the cross were *a b*/+ + ; *c*/+ × *a b*/*a b* ; *c*/*c*, then the parental class (more frequent class) would have four components: *a b c*, *a b* +, + + *c*, and + + +. The recombinant class would be *a* + *c*, *a* + +, + *b c*, and + *b* +.

BASIC PROBLEMS

1. You perform the following cross and are told that the two genes are 10 m.u. apart.

$$A\ B/a\ b \times a\ b/a\ b$$

Among their progeny, 10 percent should be recombinant (*A b/a b* and *a B/a b*) and 90 percent should be parental (*A B/a b* and *a b/a b*). Therefore, *A B/a b* should represent $^1/_2$ of the parentals or 45 percent.

2.

P	*A d / A d* × *a D / a D*	
F_1	*A d / a D*	
F_2	1 *A d / A d*	phenotype: A d
	2 *A d / a D*	phenotype: A D
	1 *a D / a D*	phenotype: a D

3. P *R S/r s* × *R S/r s*

gametes

$^1/_2$ (1 – 0.35)	*R S*
$^1/_2$ (1 – 0.35)	*r s*
$^1/_2$ (0.35)	*R s*
$^1/_2$ (0.35)	*r S*

F_1 genotypes

0.1056 *R S/R S*	0.1138 *r s/r S*
0.1056 *r s/r s*	0.1138 *r s/R s*
0.2113 *R S/r s*	0.0306 *R s/R s*
0.1138 *R S/r S*	0.0306 *r S/r S*
0.1138 *R S/R s*	0.0613 *R s/r S*

24. **a.** You do not expect the mutation to be recessive. This would be an example of a haploinsufficient gene since one copy of the wild-type allele does produce enough protein product for normal function.

b. An important assumption would be that having five of eight units of protein product would result in an observable phenotype. It also assumes that the regulation of the single wild-type allele is not affected. Finally, if the mutant allele was leaky rather than null, there might be sufficient protein function when heterozygous with a wild-type allele.

45. The cross is $C/c \times c/c$ so there is a $^1/_2$ chance that a progeny would be black (C/c). Because each progeny's genotype is independent of the others, the chance that all 10 progeny are black is $(^1/_2)^{10}$.

46. P $s^+/s^+ \times s/Y$

$\downarrow$

F_1	$^1/_2\ s^+/s$	normal female
	$^1/_2\ s^+/Y$	normal male

$s^+/s \times s^+/Y$

$\downarrow$

F_2	$^1/_4\ s^+/s^+$	normal female
	$^1/_4\ s^+/s$	normal female
	$^1/_4\ s^+/Y$	normal male
	$^1/_4\ s/Y$	small male

P $s^+/s \times s/Y$

$\downarrow$

Progeny	$^1/_4\ s^+/s$	normal female
	$^1/_4\ s/s$	small female
	$^1/_4\ s^+/Y$	normal male
	$^1/_4\ s/Y$	small male

9. The cross is female X^dX^d ; p/p × male X^DY ; P/P where P = dominant allele for pink and d = recessive allele for dwarf.

F_1 $\quad$ $^1/_2$ X^DX^d : P/p (pink female)
$\quad\quad\quad$ $^1/_2$ X^dY ; P/p (dwarf, pink male)

F_2 $\quad$ $^1/_{16}$ X^DX^d : P/P (pink female)
$\quad\quad\quad$ $^1/_8$ X^DX^d : P/p (pink female)
$\quad\quad\quad$ $^1/_{16}$ X^DX^d : p/p (wild type female)
$\quad\quad\quad$ $^1/_{16}$ X^dX^d : P/P (dwarf, pink female)
$\quad\quad\quad$ $^1/_8$ X^dX^d : P/p (dwarf, pink female)
$\quad\quad\quad$ $^1/_{16}$ X^dX^d : p/p (dwarf female)
$\quad\quad\quad$ $^1/_{16}$ X^DY ; P/P (pink male)
$\quad\quad\quad$ $^1/_8$ X^DY ; P/p (pink male)
$\quad\quad\quad$ $^1/_{16}$ X^DY ; p/p (wild type male)
$\quad\quad\quad$ $^1/_{16}$ X^dY ; P/P (dwarf, pink male)
$\quad\quad\quad$ $^1/_8$ X^dY ; P/p (dwarf, pink male)
$\quad\quad\quad$ $^1/_{16}$ X^dY ; p/p (dwarf male)

15. Assuming independent assortment and simple dominant/recessive relationships of all genes, the number of genotypic classes expected from selfing a plant heterozygous for n gene pairs is 3^n and the number of phenotypic classes expected in 2^n.

16. a. The data for both crosses suggest that both A and B mutant plants are homozygous for a recessive allele. Both F_2 crosses give 3:1 normal to mutant ratios of progeny. For example, let A = normal and a = mutant, then

P	$A/A \times a/a$	
F_1	A/a	
F_2	1 A/A	phenotype: normal
	2 A/a	phenotype: normal
	1 a/a	phenotype: mutant (no trichomes).

b. The cross is $A/A\ ;\ b/b \times a/a\ ;\ B/B$ to give the F_1 of $A/a\ ;\ B/b$. This is then test crossed (crossed to $a/a\ ;\ b/b$) to give

$\frac{1}{4}$ $A/a\ ;\ B/b$ (normal)
$\frac{1}{4}$ $A/a\ ;\ b/b$ (no trichomes)
$\frac{1}{4}$ $a/a\ ;\ B/b$ (no trichomes)
$\frac{1}{4}$ $a/a\ ;\ b/b$ (no trichomes)

or 1 normal : 3 no trichomes.

17. a. $C/c\ ;\ S/s \times C/c\ ;\ S/s$ There are 3 short:1 long, and 3 dark:1 albino. Therefore, each gene is heterozygous in the parents.

b. $C/C\ ;\ S/s \times C/-\ ;\ s/s$ There are no albino, and there are 1 long:1 short indicating a testcross for this trait.

c. $C/c\ ;\ S/S \times c/c\ ;\ S/-$ There are no long, and there are 1 dark:1 albino.

d. $c/c\ ;\ S/s \times c/c\ ;\ S/s$ All are albino, and there are 3 short:1 long.

e. $C/c\ ;\ s/s \times C/c\ ;\ s/s$ All are long, and there are 3 dark:1 albino.

f. $C/C\ ;\ S/s \times C/-\ ;\ S/s$ There are no albino, and there are 3 short: 1 long.

g. $C/c\ ;\ S/s \times C/c\ ;\ s/s$ There are 3 dark:1 albino, and 1 short:1 long.

18. a. and b. Cross 2 indicates that purple (G) is dominant to green (g), and cross 1 indicates cut (P) is dominant to potato (p).

Cross 1: $G/g\ ;\ P/p \times g/g\ ;\ P/p$ There are 3 cut : 1 potato, and 1 purple : 1 green.

Cross 2: $G/g\ ;\ P/p \times G/g\ ;\ p/p$ There are 3 purple : 1 green, and 1 cut : 1 potato.

Cross 3: $G/G\ ;\ P/p \times g/g\ ;\ P/p$ There are no green, and there are 3 cut:1 potato.

Cross 4: $G/g\ ;\ P/P \times g/g\ ;\ p/p$ There are no potato, and there are 1 purple:1 green.

Cross 5: $G/g\ ;\ p/p \times g/g\ ;\ P/p$ There are 1 cut:1 potato, and there are 1 purple:1 green.

19. a. From cross 6, Bent (B) is dominant to normal (b). Both parents are "bent," yet some progeny are "normal."

b. From cross 1, it is X-linked. The trait is inherited in a sex-specific manner — all sons have the mother's phenotype.

c. In the following table, the Y chromosome is stated; the X is implied.

	Parents		Progeny	
Cross	Female	Male	Female	Male
1	*b*/*b*	*B*/Y	*B*/*b*	*b*/Y
2	*B*/*b*	*b*/Y	*B*/*b*, *b*/*b*	*B*/Y, *b*/Y
3	*B*/*B*	*b*/Y	*B*/*b*	*B*/Y
4	*b*/*b*	*b*/Y	*b*/*b*	*b*/Y
5	*B*/*B*	*B*/Y	*B*/*B*	*B*/Y
6	*B*/*b*	*B*/Y	*B*/*B*, *B*/*b*	*B*/Y, *b*/Y

20. ***Unpacking the Problem***

1. *Normal* is used to mean wild type, or red eye color and long wings.
2. Both *line* and *strain* are used to denote pure-breeding fly stocks, and the words are interchangeable.
3. Your choice.
4. Three characters are being followed: eye color, wing length, and sex.
5. For eye color, there are two phenotypes: red and brown. For wing length, there are two phenotypes: long and short. For sex, there are two phenotypes: male and female.
6. The F_1 females designated normal have red eyes and long wings.
7. The F_1 males that are called short-winged have red eyes and short wings.
8. The F_2 ratio is

$\frac{3}{8}$ red eyes, long wings

14. Because the "half" inherited is very random, the chances of receiving exactly the same half is vanishingly small. Ignoring recombination and focusing just on which chromosomes are inherited from one parent (for example, the one they inherited from their father or the one from their mother?), there are 2^{23} = 8,388,608 possible combinations!

= 0.134, $p > 0.50$, nonsignificant; hypothesis cannot be rejected

14. a. This is simply a matter of counting genotypes; there are nine genotypes in the Punnett square. Alternatively, you know there are three genotypes possible per gene, for example *R*/*R*, *R*/*r*, and *r*/*r*, and since both genes assort independently, there are $3 \times 3 = 9$ total genotypes.

b. Again, simply count. The genotypes are

1 *R*/*R* ; *Y*/*Y*	1 *r*/*r* ; *Y*/*Y*	1 *R*/*R* ; *y*/*y*	1 *r*/*r* ; *y*/*y*
2 *R*/*r* ; *Y*/*Y*	2 *r*/*r* ; *Y*/*y*	2 *R*/*r* ; *y*/*y*	
2 *R*/*R* ; *Y*/*y*			
4 *R*/*r* ; *Y*/*y*			

c. To find a formula for the number of genotypes, first consider the following:

Number of genes	Number of genotypes	Number of phenotypes
1	$3 = 3^1$	$2 = 2^1$
2	$9 = 3^2$	$4 = 2^2$
3	$27 = 3^3$	$8 = 2^3$

Note that the number of genotypes is 3 raised to some power in each case. In other words, a general formula for the number of genotypes is 3^n, where n equals the number of genes.

For allelic relationships that show complete dominance, the number of phenotypes is 2 raised to some power. The general formula for the number of phenotypes observed is 2^n, where n equals the number of genes.

d. The round, yellow phenotype is *R*/– ; *Y*/–. Two ways to determine the exact genotype of a specific plant are through selfing or conducting a testcross.

With selfing, complete heterozygosity will yield a 9:3:3:1 phenotypic ratio. Homozygosity at one locus will yield a 3:1 phenotypic ratio, while homozygosity at both loci will yield only one phenotypic class.

With a testcross, complete heterozygosity will yield a 1:1:1:1 phenotypic ratio. Homozygosity at one locus will yield a 1:1 phenotypic ratio, while homozygosity at both loci will yield only one phenotypic class.

Independent Assortment of Genes

BASIC PROBLEMS

1. a. The expected phenotypic ratio from the self cross of *A*/*a* ; *B*/*b* is

9	*A*/— ; *B*/—
3	*A*/— ; *b*/*b*
3	*a*/*a* ; *B*/—
1	*a*/*a* ; *b*/*b*

b. The expected genotypic ratio from the self cross of *A*/*a* ; *B*/*b* is

1	*A*/*A* ; *B*/*B*
2	*A*/*A* ; *B*/*b*
1	*A*/*A* ; *b*/*b*
2	*A*/*a* ; *B*/*B*
4	*A*/*a* ; *B*/*b*
2	*A*/*a* ; *b*/*b*
1	*a*/*a* ; *B*/*B*
2	*a*/*a* ; *B*/*b*
1	*a*/*a* ; *b*/*b*

c. and d. The expected phenotypic and genotypic ratios from the test cross of *A*/*a* ; *B*/*b* is

1	*A*/*a* ; *B*/*b*
1	*A*/*a* ; *b*/*b*
1	*a*/*a* ; *B*/*b*
1	*a*/*a* ; *b*/*b*

2. The resulting cells will have the identical genotype as the original cell: *A*/*a* ; *B*/*b*.

36. The results suggest that winged (*A*/–) is dominant to wingless (*a*/*a*) (cross 2 gives a 3 : 1 ratio). If that is correct, the crosses become

Pollination	Genotypes	Number of progeny plants: Winged	Wingless
winged (selfed)	*A*/*A* × *A*/*A*	91	1*
winged (selfed)	*A*/*a* × *A*/*a*	90	30
wingless (selfed)	*a*/*a* × *a*/*a*	4*	80
winged × wingless	*A*/*A* × *a*/*a*	161	0
winged × wingless	*A*/*a* × *a*/*a*	29	31
winged × wingless	*A*/*A* × *a*/*a*	46	0
winged × winged	*A*/*A* × *A*/–	44	0
winged × winged	*A*/*A* × *A*/–	24	0

The five unusual plants are most likely due either to human error in classification or to contamination. Alternatively, they could result from environmental effects on development. For example, too little water may have prevented the seed pods from becoming winged even though they are genetically winged.

37. a. The disorder appears to be dominant because all affected individuals have an affected parent. If the trait was recessive, then I-1, II-2, III-1, and III-8 would all have to be carriers (heterozygous for the rare allele).

b. Assuming dominance, the genotypes are
I : *d*/*d*, *D*/*d*
II : *D*/*d*, *d*/*d*, *D*/*d*, *d*/*d*
III : *d*/*d*, *D*/*d*, *d*/*d*, *D*/*d*, *d*/*d*, *d*/*d*, *D*/*d*, *d*/*d*
IV : *D*/*d*, *d*/*d*, *D*/*d*, *d*/*d*, *d*/*d*, *d*/*d*, *d*/*d*, *D*/*d*, *d*/*d*

c. The mating is *D*/*d* × *d*/*d*. The probability of an affected child (*D*/*d*) equals $^1/_2$, and the probability of an unaffected child (*d*/*d*) equals $^1/_2$. Therefore, the chance of having four unaffected children (since each is an independent event) is: $^1/_2 \times {}^1/_2 \times {}^1/_2 \times {}^1/_2 = {}^1/_{16}$.

38. a. *Pedigree 1*: The best answer is recessive, because two unaffected individuals had affected progeny. Also, the disorder skips generations and appears in a mating between two related individuals.

Pedigree 2: The best answer is dominant, because two affected parents have an unaffected child. Also, it appears in each generation, roughly half the progeny are affected, and all affected individuals have an affected parent.

Pedigree 3: The best answer is dominant, for many of the reasons stated for pedigree 2. Inbreeding, while present in the pedigree, does not allow an

explanation of recessive because it cannot account for individuals in the second or third generations.

Pedigree 4: The best answer is recessive. Two unaffected individuals had affected progeny.

b. Genotypes of pedigree 1:
Generation I: *A*/–, *a*/*a*
Generation II: *A*/*a*, *A*/*a*, *A*/*a*, *A*/–, *A*/–, *A*/*a*
Generation III: *A*/*a*, *A*/*a*
Generation IV: *a*/*a*

Genotypes of pedigree 2:
Generation I: *A*/*a*, *a*/*a*, *A*/*a*, *a*/*a*
Generation II: *a*/*a*, *a*/*a*, *A*/*a*, *A*/*a*, *a*/*a*, *a*/*a*, *A*/*a*, *A*/*a*, *a*/*a*
Generation III: *a*/*a*, *a*/*a*, *a*/*a*, *a*/*a*, *a*/*a*, *A*/–, *A*/–, *A*/–, *A*/*a*, *a*/*a*
Generation IV. *a*/*a*, *a*/*a*, *a*/*a*

Genotypes of pedigree 3:
Generation I: *A*/–, *a*/*a*
Generation II: *A*/*a*, *a*/*a*, *a*/*a*, *A*/*a*
Generation III: *a*/*a*, *A*/*a*, *a*/*a*, *a*/*a*, *A*/*a*, *a*/*a*
Generation IV. *a*/*a*, *A*/*a*, *A*/*a*, *A*/*a*, *a*/*a*, *a*/*a*

Genotypes of pedigree 4:
Generation I: *a*/*a*, *A*/–, *A*/*a*, *A*/*a*
Generation II: *A*/*a*, *A*/*a*, *A*/*a*, *a*/*a*, *A*/–, *a*/*a*, *A*/–, *A*/–, *A*/–, *A*/–, *A*/–
Generation III: *A*/*a*, *a*/*a*, *A*/*a*, *A*/*a*, *a*/*a*, *A*/*a*

39. a. The pedigree is