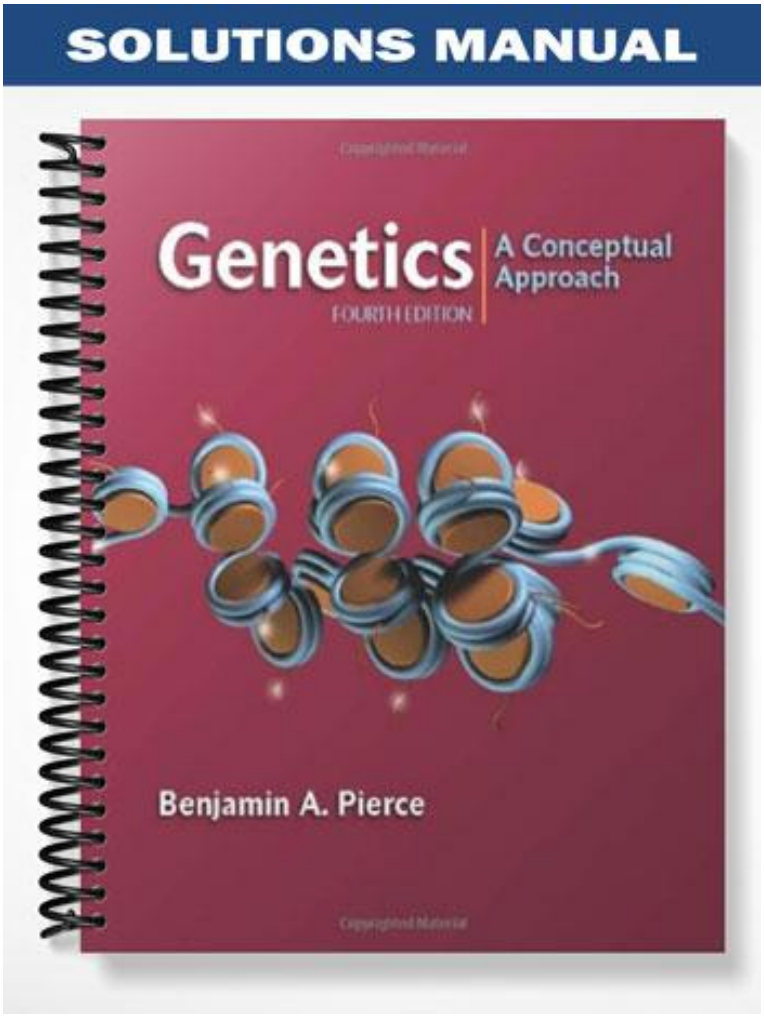
SOLUTIONS MANUAL



Chapter Three: Basic Principles of Heredity

COMPREHENSION QUESTIONS

Section 3.1

*****1. Why was Mendel's approach to the study of heredity so successful?
Mendel was successful for several reasons. He chose to work with a plant, Pisum sativum, *that was easy to cultivate, grew relatively rapidly, and produced many offspring whose phenotype was easy to determine, which allowed Mendel to detect mathematical ratios of progeny phenotypes. The seven characteristics he chose to study were also important because they exhibited only a few distinct phenotypes and did not show a range of variation. Finally, by looking at each trait separately and counting the numbers of the different phenotypes, Mendel adopted a reductionist experimental approach and applied the scientific method. From his observations, he proposed hypotheses that he was then able to test empirically.*

2. What is the difference between genotype and phenotype?
Genotype refers to the genes or the set of alleles found within an individual. Phenotype refers to the manifestation of a particular character or trait.

Section 3.2

*3. What is the principle of segregation? Why is it important?
The principle of segregation, or Mendel's first law, states that an organism possesses two alleles for any one particular trait and that these alleles separate during the formation of gametes. In other words, one allele goes into each gamete. The principle of segregation is important because it explains how the genotypic ratios in the haploid gametes are produced.

4. How are Mendel's principles different from the concept of blending inheritance discussed in Chapter 1?
Mendel's principles assert that the genetic factors or alleles are discrete units that remain separate in an individual organism with a trait encoded by the dominant allele being the only one observed if two different alleles are present. According to Mendel's principles, if an individual contains two different alleles, then the individual's gametes could contain either of these two alleles (but not both). Blending inheritance proposes that offspring are the result of blended genetic material from the parent and the genetic factors are not discrete units. Once blended, the combined genetic material could not be separated from each other in future generations.

5. What is the concept of dominance? How does dominance differ from incomplete dominance?
The concept of dominance states that when two different alleles are present in a genotype, only the dominant allele is expressed in the phenotype. Incomplete dominance occurs when different alleles are expressed in a heterozygous individual, and the resulting phenotype is intermediate to the phenotypes of the two homozygotes.

6. What are the addition and multiplication rules of probability and when should they be used?
The addition and multiplication rules are two rules of probability used by geneticists to predict the ratios of offspring in genetic crosses. The multiplication rule allows for predicting the probability of two or more independent events occurring together. According to the multiplication rule, the probability of two independent events occurring together is the product of their probabilities of occurring independently. The addition rule allows for predicting the likelihood of a single event that can happen in two or more ways. It states that the probability of a single mutually exclusive event can be determined by adding the probabilities of the two or more different ways in which this single event could take place. The multiplication rule allows us to predict how alleles from each parent can combine to produce offspring, while the addition rule is useful in predicting phenotypic ratios once the probability of each type of progeny can be determined.

7. Give the genotypic ratios that may appear among the progeny of simple crosses and the genotypes of the parents that may give rise to each ratio.

Genotypic ratio	*Parental genotype*
1:2:1	Aa × Aa
1:1	Aa × aa AA x Aa
Uniform progeny	AA × AA aa × aa AA × aa

*8. What is the chromosome theory of inheritance? Why was it important?
Walter Sutton developed the chromosome theory of inheritance. The theory states that genes are located on the chromosomes. The independent segregation of pairs of homologous chromosomes in meiosis provides the biological basis for Mendel's two rules of heredity.

Section 3.3

*9. What is the principle of independent assortment? How is it related to the principle of segregation?
According to the principle of independent assortment, genes for different characteristics that are at different loci segregate independently of one another. The principle of segregation indicates that the two alleles at a locus separate; the principle of independent assortment indicates that the separation of alleles at one locus is independent of the separation of alleles at other loci.

10. In which phases of mitosis and meiosis are the principles of segregation and independent assortment at work?
In anaphase I of meiosis, each pair of homologous chromosomes segregate independently of all other pairs of homologous chromosomes. The assortment is

dependent on how the homologs line up during metaphase I. This assortment of homologs explains how genes located on different pairs of chromosomes will separate independently of one another. Anaphase II results in the separation of sister chromatids and subsequent production of gametes carrying single alleles for each gene locus as predicted by Mendel's principle of segregation. Mendel's principles of independent assortment and segregation do not apply to mitosis, which produces cells genetically identical to each other and to the parent cell.

Section 3.4

11. How is the goodness-of-fit chi-square test used to analyze genetic crosses? What does the probability associated with a chi-square value indicate about the results of a cross?
The goodness-of-fit chi-square test is a statistical method used to evaluate the role of chance in causing deviations between the observed and the expected numbers of offspring produced in a genetic cross. The probability value obtained from the chi-square table refers to the probability that random chance produced the deviations of the observed numbers from the expected numbers.

APPLICATION QUESTIONS AND PROBLEMS

Chapter Opening Story

12. The inheritance of red hair was discussed in the opening story of this chapter. At times in the past, red hair in humans was thought to be a recessive trait and at other times, it was thought to be a dominant trait. What characteristics is red hair expected to exhibit as a recessive trait? What characteristics would it exhibit if it were a dominant trait?
Recessive Trait – Red hair would often appear in the children of parents who lacked red, when both parents would were heterozygous. In a mating between two red-haired parents, all of the offspring would be expected to have red hair.
Dominant Trait – Red hair would only appear in children if at least one of the parents had red hair because the child would have to inherit the red hair allele from a parent, who would therefore also have red hair. A mating between two red-haired parents might produce some children with non-red hair. A cross between two non-red parents would produce only non-red offspring.

Section 3.1

13. What characteristics of an organism would make it well suited for studies of the principles of inheritance? Can you name several organisms that have these characteristics?

<u>Useful characteristics</u>
- *Are easy to grow and maintain*
- *Grow rapidly, producing many generations in a short period*

- *Produce large numbers of offspring*
- *Have distinctive phenotypes that are easy to recognize*

Examples of organisms that meet these criteria

- *Neurospora, a fungus*
- *Saccharomyces cerevisiae, a yeast*
- *Arabidopsis, a plant*
- *Caenorhabditis elegans, a nematode*
- Drosophila melanogaster, *a fruit fly*

Section 3.2

*14. In cucumbers, orange fruit color (*R*) is dominant over cream fruit color (*r*). A cucumber plant homozygous for orange fruits is crossed with a plant homozygous for cream fruits. The F_1 are intercrossed to produce the F_2.

a. Give the genotypes and phenotypes of the parents, the F_1, and the F_2.
The cross of a homozygous cucumber plant that produces orange fruit (RR) *with a homozygous cucumber plant that produces cream fruit* (rr) *will result in an* F_1 *generation heterozygous for the orange fruit phenotype.*

P RR × rr

↓

F_1 Rr *orange fruit*

Intercrossing the F_1 *will produce* F_2 *that are expected to show a 3:1 orange-to- cream-fruit phenotypic ratio.*

Rr × Rr

↓

1 RR *orange fruit*
2 Rr *orange fruit*
1 rr *cream fruit*

b. Give the genotypes and phenotypes of the offspring of a backcross between the F_1 and the orange parent.
The backcross of the F_1 *orange offspring* (Rr) *with homozygous orange parent* (RR) *will produce progeny that all have the orange fruit phenotype. However, one-half of the progeny will be expected to be homozygous for orange fruit and one-half of the progeny will be expected to be heterozygous for orange fruit.*

Rr *(F_1)* × RR *(orange parent)*

↓

½ RR *orange fruit*
½ Rr *orange fruit*

c. Give the genotypes and phenotypes of a backcross between the F_1 and the cream parent.
The backcross of the F_1 offspring (Rr) *with the cream parent* (rr) *is also a testcross. The product of this testcross should produce progeny, one-half of which are heterozygous for orange fruit and one-half of which are homozygous for cream fruit.*

Rr *(F_1)* × rr *(cream parent)*

↓

½ Rr *orange fruit*
½ rr *cream fruit*

15. J. W. McKay crossed a stock melon plant that produced tan seeds with a plant that produced red seeds and obtained the following results (J. W. McKay. 1936. *Journal of Heredity* 27:110–112).

Cross	**F_1**	**F_2**
tan ♀ × red ♂	13 tan seeds	93 tan, 24 red seeds

a. Explain the inheritance of tan and red seeds in this plant.
The F_1 generation contains all tan seed producing progeny and is the result of crossing a tan-seed-producing plant with a red-seed-producing plant. The F_1 result suggests that the tan phenotype is dominant to red. In the F_2 generation, the ratio of tan- to red-seed-producing plants is about 3.9 to 1, which is similar but not identical to a 3 to 1 ratio expected for monohybrid cross involving dominant and recessive alleles. The F_2 ratio suggests that the F_1 parents are heterozygous dominant for tan color.

b. Assign symbols for the alleles in this cross and give genotypes for all the individual plants.
We will define the tan allele as "R" and the recessive red allele as "r."
Tan-seed-producing ♀ parent: RR
Red-seed-producing ♂ parent: rr
F_1 tan-seed-producing offspring: Rr
F_2 tan-seed-producing offspring: RR *or* Rr
F_2 red-seed-producing offspring: rr

*16. White (*w*) coat color in guinea pigs is recessive to black (*W*). In 1909, W. E. Castle and J. C. Phillips transplanted an ovary from a black guinea pig into a white female whose ovaries had been removed. They then mated this white female with a white male. All the offspring from the mating were black in color (W. E. Castle and J. C. Phillips. 1909. *Science* 30:312–313).

a. Explain the results of this cross.
Although the white female gave birth to the offspring, her eggs were produced by the ovary from the black female guinea pig. The transplanted ovary produced only eggs containing the allele for black coat color. Like most mammals, guinea pig females produce primary oocytes early in development, and thus the transplanted ovary already contained primary oocytes produced by the black female guinea pig.

b. Give the genotype of the offspring of this cross.
*The white male guinea pig contributed a "*w*" allele, while the white female guinea pig contributed the "*W*" allele from the transplanted ovary. The offspring are thus* Ww.

c. What, if anything, does this experiment indicate about the validity of the pangenesis and the germ-plasm theories discussed in Chapter 1?
The transplant experiment supports the germ-plasm theory. According to the germ-plasm theory, only the genetic information in the germ-line tissue in the reproductive organs is passed to the offspring. The production of black guinea pig offspring suggests that the allele for black coat color was passed to the offspring from the transplanted ovary in agreement with the germ-plasm theory. According to the pangenesis theory, the genetic information passed to the offspring originates at various parts of the body and travels to the reproductive organs for transfer to the gametes. If pangenesis were correct, then the guinea pig offspring should have been white. The white coat alleles would have traveled to the transplanted ovary and then to into the white female's gametes. The absence of any white offspring indicates that pangenesis did not occur.

*17. In cats, blood type A results from an allele (I^A) that is dominant over an allele (i^B) that produces blood type B. There is no O blood type. The blood types of male and female cats that were mated and the blood types of their kittens follow. Give the most likely genotypes for the parents of each litter.

	Male parent	Female parent	Kittens
a.	blood type A	blood type B	4 kittens with blood type A, 3 with blood type B
b.	blood type B	blood type B	6 kittens with blood type B
c.	blood type B	blood type A	8 kittens with blood type A
d.	blood type A	blood type A	7 kittens with blood type A, 2 with blood type B
e.	blood type A	blood type A	10 kittens with blood type A
f.	blood type A	blood type B	4 kittens with blood type A, 1 with blood type B

a. Male with blood type A × Female with blood type B
Because the female parent has blood type B, she must have the genotype i^Bi^B. *The male parent could be either* I^AI^A *or* I^Ai^B. *However, as some of the offspring*

are kittens with blood type B, the male parent must have contributed an i^B *allele to these kittens. Therefore, the male must have the genotype of* I^Ai^B.

b. Male with blood type B × Female with blood type B
Because blood type B is caused by the recessive allele i^B*, both parents must be homozygous for the recessive allele or* i^Bi^B. *Each contributes only the* i^B *allele to the offspring.*

c. Male with blood type B × Female with blood type A
Again, the male with type B blood must be i^Bi^B. *A female with type A blood could have either the* I^AI^A *or* I^Ai^B *genotypes. Because all of her kittens have type A blood, this suggests that she is homozygous for the for* I^A *allele* (I^AI^A) *and contributes only the* I^A *allele to her offspring. It is possible that she is heterozygous for type A blood, but if so it is unlikely that chance alone would have produced eight kittens with blood type A.*

d. Male with blood type A × Female with blood type A
Because kittens with blood type A and blood type B are found in the offspring, both parents must be heterozygous for blood type A, or I^Ai^B. *With both parents being heterozygous, the offspring would be expected to occur in a 3:1 ratio of blood type A to blood type B, which is close to the observed ratio.*

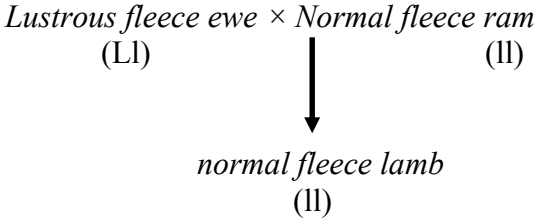
e. Male with blood type A × Female with blood type A
Only kittens with blood type A are produced, which suggests that each parent is homozygous for blood type A (I^AI^A), *or that one parent is homozygous for blood type A* (I^AI^A), *and the other parent is heterozygous for blood type A* (I^Ai^B). *The data from the offspring will not allow us to determine the precise genotype of either parent.*

f. Male with blood type A × Female with blood type B
On the basis of her phenotype, the female will be i^Bi^B. *In the offspring, one kitten with blood type B is produced. This kitten would require that both parents contribute an* i^B *to produce its genotype. Therefore, the male parent's genotype is* I^Ai^B. *From this cross, the number of kittens with blood type B would be expected to be similar to the number of kittens with blood type A. However, due to the small number of offspring produced, random chance could have resulted in more kittens with blood type A than kittens with blood type B.*

18. Joe has a white cat named Sam. When Joe crosses Sam with a black cat, he obtains one-half white kittens and one-half black kittens. When the black kittens are interbred, they produce all black kittens. On the basis of these results, would you conclude that white or black coat color in cats is a recessive trait? Explain your reasoning.
The black coat color is likely recessive. When Sam was crossed with a black cat, one-half the offspring were white and one-half were black. This ratio potentially indicates that one of the parental cats is heterozygous dominant while the other parental cat is homozygous recessive—a testcross. The interbreeding of the black kittens produced only black kittens, indicating that the black kittens are likely to be homozygous, and thus the black coat color is the recessive trait.

If the black allele was dominant, we would have expected the black kittens to be heterozygous, containing a black coat color allele and a white coat color allele. Under this condition, we would expect one-fourth of the progeny from the interbred black kittens to have white coats. Because this did not happen, we can conclude that the black coat color is recessive.

19. In sheep, lustrous fleece (*L*) results from an allele that is dominant over an allele for normal fleece (*l*). A ewe (adult female) with lustrous fleece is mated with a ram (adult male) with normal fleece. The ewe then gives birth to a single lamb with normal fleece. From this single offspring, is it possible to determine the genotypes of the two parents? If so, what are their genotypes? If not, why not?
Yes, it is possible to determine the genotype of each parent, assuming that the dominant lustrous allele (L) *exhibits complete penetrance. The ram and the single lamb must be homozygous for the normal allele* (l) *because both have the normal fleece phenotype. Because the lamb receives only a single allele* (l) *from the ram, the ewe must have contributed the other recessive* l *allele. Therefore, the ewe must be heterozygous for lustrous fleece.*
In summary:



*20. In humans, alkaptonuria is a metabolic disorder in which affected persons produce black urine Alkaptonuria results from an allele (*a*) that is recessive to the allele for normal metabolism (*A*). Sally has normal metabolism, but her brother has alkaptonuria. Sally's father has alkaptonuria, and her mother has normal metabolism.
a. Give the genotypes of Sally, her mother, her father, and her brother.
Sally's father, who has alkaptonuria, must be aa*. Her brother, who also has alkaptonuria, must be* aa *as well. Because both parents must have contributed one* a *allele to her brother, Sally's mother, who is phenotypically normal, must be heterozygous* (Aa). *Sally, who is normal, received the* A *allele from her mother but must have received an* a *allele from her father.*
The genotypes of the individuals are: Sally (Aa), *Sally's mother* (Aa), *Sally's father* (aa), *and Sally's brother* (aa).
b. If Sally's parents have another child, what is the probability that this child will have alkaptonuria?
Sally's father (aa) × *Sally's mother* (Aa)
Sally's mother has a ½ chance of contributing the a *allele to her offspring. Sally's father can contribute only the* a *allele. The probability of an offspring with genotype* aa *and alkaptonuria is therefore ½ × 1 = ½.*
c. If Sally marries a man with alkaptonuria, what is the probability that their first child will have alkaptonuria?

Since Sally is heterozygous (Aa)*, she has a ½ chance of contributing the* a *allele. Her husband with alkaptonuria* (aa) *can only contribute the* a *allele. The probability of their first child having alkaptonuria* (aa) *is ½ × 1 = ½.*

21. Suppose that you are raising Mongolian gerbils. You notice that some of your gerbils have white spots, whereas others have solid coats. What type of crosses could you carry out to determine whether white spots are due to a recessive or a dominant allele?
If white spots are recessive, then any gerbil with white spots must be homozygous for white spots (ww), *and a cross between two white-spotted gerbils* (ww × ww) *should produce offspring with only white spots. If white spots are dominant to solid, then a cross between a gerbil with white spots and a gerbil with a solid coat should produce either progeny all having solid coats* (WW × ww → Ww) *or progeny where one-half have solid coats and the other half have white spots* (Ww × ww → ½ Ww ½ ww).

*22. Hairlessness in American rat terriers is recessive to the presence of hair. Suppose that you have a rat terrier with hair. How can you determine whether this dog is homozygous or heterozygous for the hairy trait?
We will use h *for the hairless allele and* H *for the dominant. Because* H *is dominant to* h, *a rat terrier with hair could be either homozygous* (HH) *or heterozygous* (Hh). *To determine which genotype is present in the rat terrier with hair, cross this dog with a hairless rat terrier* (hh). *If the terrier with hair is homozygous* (HH)*, then no hairless offspring will be produced. However, if the terrier is heterozygous* (Hh) *then we would expect one-half of the offspring to be hairless.*

23. What is the probability of rolling one six-sided die and obtaining the following numbers?
a. 2
Because 2 is only found on one side of a six-sided die, then there is a 1/6 chance of rolling a two.
b. 1 or 2
The probability of rolling a 1 on a six-sided die is 1/6. Similarly, the probability of rolling a 2 on a six-sided die is 1/6. Because the question asks what is the probability of rolling a 1 or *a 2, and these are mutually exclusive events, we should use the additive rule of probability to determine the probability of rolling a 1 or a 2:*
*(*p *of rolling a 1) + (*p *of rolling a 2) =* p *of rolling either a 1 or a 2*
1/6 + 1/6 = 2/6 = 1/3 probability of rolling either a 1 or a 2
c. An even number
The probability of rolling an even number depends on the number of even numbers found on the die. A single die contains three even numbers (2, 4, 6). The probability of rolling any one of these three numbers on a six-sided die is 1/6. To determine the probability of rolling either a 2, a 4, or a 6, we apply the additive rule: 1/6 + 1/6 + 1/6 = 3/6 = ½.
d. Any number but a 6

The number 6 is found only on one side of a six-sided die. The probability of rolling a 6 is therefore 1/6. The probability of rolling any number but 6 is (1 – 1/6) = 5/6.

*24. What is the probability of rolling two six-sided dice and obtaining the following numbers?

a. 2 and 3

To calculate the probability of rolling two six-sided dice and obtaining a 2 and a 3, we will need to use the product and additive rules. There are two possible ways in which to obtain the 2 and the 3 on the dice.

There is a 1/6 chance of rolling a 2 on the first die and a 1/6 chance of rolling a 3 on the second die. The probability of this taking place is therefore 1/6 × 1/6 = 1/36.

There is also a 1/6 chance of rolling a 3 on the first die and a 1/6 chance of rolling a 2 of the second die. Again, the probability of this taking place is 1/6 × 1/6 = 1/36. So the probability of rolling a 2 and a 3 would be 1/36 + 1/36 = 2/36 or 1/18.

b. 6 and 6

There is only one way to roll two 6's on a pair of dice: the first die must be a 6 and the second die must be a 6. The probability is 1/6 × 1/6 = 1/36.

c. At least one 6

There are 3 ways in which to get at least one 6 in the roll of two dice. The first is to roll 6 on both dice, which we already determined has a probability of 1/36. The second way is to roll a 6 on the first die (1/6) and something other than a 6 on the second (5/6). When the multiplication rule is applied to this second possibility, we achieve an overall probability of 5/36. The third way would be to roll something other than a 6 in the first die (5/6) and a 6 on the second die (1/6) for an overall probability of 5/36. Using the addition rule to add the probabilities of these three different ways to achieve at least one 6, we arrive at the final answer of 11/36 chance.

d. Two of the same number (two 1's, or two 2's, or two 3's, etc.)

There are several ways to roll two of the same number. You could roll two 1's, two 2's, two 3's, two 4's, two 5's, or two 6's. Using the multiplication rule, the probability of rolling two 1s is 1/6 × 1/6 = 1/36. The same is true of two 2's, two 3's, two 4's, two 5's, and two 6's. Using the addition rule, the probability of rolling either two 1's, two 2's, two 3's, two 4's, two 5's, and two 6's is 1/36 + 1/36 +1/36 +1/36 +1/36 + 1/36 = 6/36 = 1/6.

e. An even number on both dice

Three out of the six sides of a die are even numbers, so there is a 3/6 probability of rolling an even number on each of the dice. The chance of having an even number on both dice is (3/6)(3/6) = 9/36, or ¼.

f. An even number on at least one die

Three out of the six sides of a die are even numbers, so the probability of rolling an even number on the one die is 3/6. The probability of not rolling an even number is 3/6. An even number on at least one die could be obtained by rolling (a) an even on the first but not on the second die (3/6 × 3/6 = 9/36), (b) an even

on the second die but not on the first (3/6 × 3/6 = 9/36), or (c) an even on both dice (3/6 × 3/6 = 9/36). Using the addition rule to obtain the probability of either a or b or c, we obtain 9/36 + 9/36 + 9/36 = 27/36 = ¾.

*25. In a family of seven children, what is the probability of obtaining the following numbers of boys and girls?

a. All boys
$(½)^7 = 1/128$

b. All children of the same sex
The children could be all boys or all girls:
$(½)^7$ chance of being all boys and $(½)^7$ chance of being all girls
1/128 + 1/128 = 2/128 or 1/64 chance of being either all boys or all girls

Parts c–e require the use of the binomial expansion. Let *a* equal the probability of being a girl and *b* equal the probability of being a boy. The probabilities of *a* and *b* are ½.

$(a + b)^7 = a^7 + 7a^6b + 21a^5b^2 + 35a^4b^3 + 35a^3b^4 + 21a^2b^5 + 7ab^6 + b^7$

c. Six girls and one boy
The probability for part (c) is provided for by the term $7a^6b$. Because the probabilities of a *and* b *are ½, then the overall probability is $7(½)^6(½) = 7/128$.*

d. Four boys and three girls
This probability is provided for by the term $35a^3b^4$. The overall probability is $35(½)^3(½)^4 = 35/128$.

e. Four girls and three boys
Using the term $35a^4b^3$, we see that the overall probability is $35(½)^4(½)^3 = 35/128$.

26. Phenylketonuria (PKU) is a disease that results from a recessive gene. Two normal parents produce a child with PKU.

Because the two normal parents have a child with PKU, each parent must be heterozygous. We will define the recessive PKU allele as *p* and the dominant normal allele as *P*. Therefore, both parents have the genotype *Pp*.

a. What is the probability that a sperm from the father will contain the PKU allele?
The father has a ½ chance of donating a sperm with the PKU allele.

b. What is the probability that an egg from the mother will contain the PKU allele?
The mother's egg has a ½ chance of containing the PKU allele.

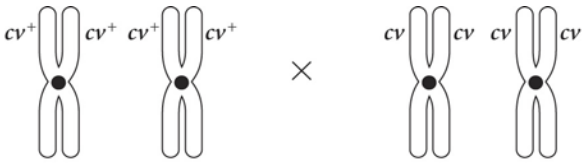
c. What is the probability that their next child will have PKU?
Each parent has a ½ chance of donating the p *allele to the child. So, the child has a ½ × ½ = ¼ chance of having PKU.*

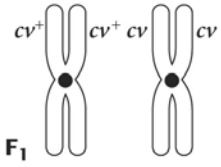
d. What is the probability that their next child will be heterozygous for the PKU gene?
Each parent has a ½ chance of donating the P *allele or a ½ chance of donating the* p *allele to the child. Therefore, the child has a (½ × ½) + (½ × ½) = ½ chance of being heterozygous.*

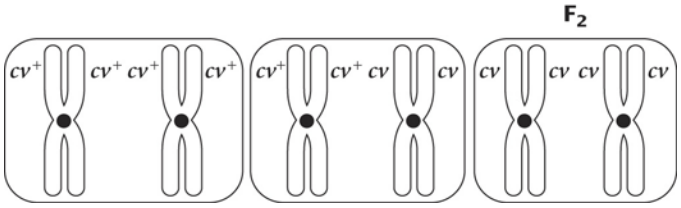
*27. In German cockroaches, curved wing (*cv*) is recessive to normal wing (*cv+*). A homozygous cockroach having normal wings is crossed with a homozygous cockroach having curved wings. The F_1 are intercrossed to produce the F_2. Assume

that the pair of chromosomes containing the locus for wing shape is metacentric. Draw this pair of chromosomes as it would appear in the parents, the F_1, and each class of F_2 progeny at metaphase I of meiosis. Assume that no crossing over takes place. At each stage, label a location for the alleles for wing shape (*cv* and *cv*+) on the chromosomes.

Parents:







*28. In guinea pigs, the allele for black fur (*B*) is dominant over the allele for brown (*b*) fur. A black guinea pig is crossed with a brown guinea pig, producing five F_1 black guinea pigs and six F_1 brown guinea pigs.

a. How many copies of the black allele (*B*) will be present in *each* cell from an F_1 black guinea pig at the following stages: G_1, G_2, metaphase of mitosis, metaphase I of meiosis, metaphase II of meiosis, and after the second cytokinesis following meiosis? Assume that no crossing over takes place.

The cross of a black guinea pig with a brown guinea pig produced black and brown guinea pigs in the offspring. Because the brown guinea pig is homozygous (bb), *the black guinea pig must be heterozygous* (Bb).

Black guinea pigs (Bb) × *Brown guinea pigs* (bb) → *F_1 five black guinea pigs* (Bb) *and six brown guinea pigs* (bb).

To determine the number of copies of the B *allele or the* b *allele at the different stages of the cell cycle, we need to remember that following the completion of S*

phase and prior to anaphase of mitosis and anaphase II of meiosis, each chromosome will consist of two sister chromatids.
In the F_1 black guinea pigs (Bb), *only one chromosome possesses the black allele, so we would expect in G_1 one black allele; G_2, two black alleles; metaphase of mitosis, two black alleles; metaphase I of meiosis, two black alleles; metaphase II of meiosis two black alleles but only in one-half of the cells (the remaining one-half will not contain the black allele); after cytokinesis of meiosis, one black allele but only in one-half of the cells produced by meiosis. (The remaining one-half will not contain the black allele.)*

b. How many copies of the brown allele (*b*) will be present in each cell from an F_1 brown guinea pig at the same stages? Assume that no crossing over takes place.
In the F_1 brown guinea pigs (bb), *both homologs possess the brown allele, so we would expect in G_1 two brown alleles; G_2, four brown alleles; metaphase of mitosis, four brown alleles; metaphase I of meiosis, four brown alleles; metaphase II, two brown alleles; and after cytokinesis of meiosis, one brown allele.*

Section 3.3

29. In watermelons, bitter fruit (*B*) is dominant over sweet fruit (*b*), and yellow spots (*S*) are dominant over no spots (*s*). The genes for these two characteristics assort independently. A homozygous plant that has bitter fruit and yellow spots is crossed with a homozygous plant that has sweet fruit and no spots. The F_1 are intercrossed to produce the F_2.

a. What will be the phenotypic ratios in the F_2?
P: homozygous bitter fruit, yellow spots (BB SS) × *homozygous sweet fruit and no spots* (bbss)
F_1: All progeny have bitter fruit and yellow spots (Bb Ss).
The F_1 are intercrossed to produce the F_2: Bb Ss × Bb Ss.
The F_2 phenotypic ratios are as follows:
9/16 bitter fruit and yellow spots
3/16 bitter fruit and no spots
3/16 sweet fruit and yellow spots
1/16 sweet fruit and no spots

b. If an F_1 plant is backcrossed with the bitter, yellow-spotted parent, what phenotypes and proportions are expected in the offspring?
The backcross of an F_1 plant (Bb Ss) *with the bitter, yellow-spotted parent* (BB SS) *will produce all bitter, yellow-spotted offspring.*

c. If an F_1 plant is backcrossed with the sweet, nonspotted parent, what phenotypes and proportions are expected in the offspring?
The backcross of a F_1 plant (Bb Ss) *with the sweet, nonspotted parent* (bb ss) *will produce the following phenotypic proportions in the offspring:*
¼ bitter fruit and yellow spots
¼ bitter fruit and no spots
¼ sweet fruit and yellow spots
¼ sweet fruit and no spots

30. In cats, curled ears (*Cu*) result from an allele that is dominant over an allele for normal ears (*cu*). Black color results from an independently assorting allele (*G*) that is dominant over an allele for gray (*g*). A gray cat homozygous for curled ears is mated with a homozygous black cat with normal ears. All the F_1 cats are black and have curled ears.
    a. If two of the F_1 cats mate, what phenotypes and proportions are expected in the F_2?
    If F_1 cats mated, GgCucu × GgCucu*, then the following proportions and phenotypes are expected in the F_2:*
        9/16 black with curly ears
        3/16 black with normal ears
        3/16 gray with curly ears
        1/16 gray with normal ears
    b. An F_1 cat mates with a stray cat that is gray and possesses normal ears. What phenotypes and proportions of progeny are expected from this cross?
    The mating of an F_1 cat (GgCucu) *with a gray cat with normal ears* (ggcucu) *is a testcross in which we would expect to produce equal numbers of all the different progeny classes:*
        ¼ black with curly ears
        ¼ black with normal ears
        ¼ gray with curly ears
        ¼ gray with normal ears

*31. The following two genotypes are crossed: *AaBbCcddEe* × *AabbCcDdEe*. What will the proportion of the following genotypes be among the progeny of this cross?
The simplest procedure for determining the proportion of a particular genotype in the offspring is to break the cross down into simple crosses and consider the proportion of the offspring for each cross.

AaBbCcddEe × AabbCcDdEe
Locus 1: Aa × Aa = *¼* AA, *½* Aa, *¼* aa
Locus 2: Bb × bb = *½* Bb, *½* bb
Locus 3: Cc × Cc = *¼* CC, *½* Cc, *¼* cc
Locus 4: dd × Dd = *½* Dd, *½* dd
Locus 5: Ee × Ee = *¼* EE, *½* Ee, *¼* ee

a. AaBbCcDdEe: *½* (Aa) × *½* (Bb) × *½* (Cc) × *½* (Dd) × *½* (Ee) = *1/32*
b. AabbCcddee: *½* (*Aa*) × *½* (*bb*) × *½* (*Cc*) × *½* (*dd*) × *¼* (*ee*) = *1/64*
c. aabbccddee: *¼* (*aa*) × *½* (*bb*) × *¼* (*cc*) × *½* (*dd*) × *¼* (*ee*) = *1/256*
d. AABBCCDDEE: *Will not occur. The* AaBbCcddEe *parent cannot contribute a* D *allele, and the* AabbCcDdEe *parent cannot contribute a* B *allele. Therefore, their offspring cannot be homozygous for the* BB *and* DD *gene loci.*

32. In mice, an allele for apricot eyes (*a*) is recessive to an allele for brown eyes (a^+). At an independently assorting locus, an allele for tan (*t*) coat color is recessive to an allele for black (t^+) coat color. A mouse that is homozygous for brown eyes and black coat color is crossed with a mouse having apricot eyes and a tan coat. The resulting

F_1 are intercrossed to produce the F_2. In a litter of eight F_2 mice, what is the probability that two will have apricot eyes and tan coats?
The F_1 will have brown eyes and tan coats, and the genotype $a^+a\ t^+t$.
The F_2 will be produced by intercrossing the F_1: $a^+a\ t^+t \times a^+a\ t^+t$. *By considering each locus individually with a simple cross, we can easily calculate the proportion of any offspring class in the F_2.*

Locus 1: $a^+a \times a^+a = ¼\ a^+a^+, ½\ a^+a, ¼\ aa$
Producing the phenotypic ratio: *¾ brown eyes* (a^+a^+ *or* a^+a)
¼ apricot eyes (aa)
Locus 2: $t^+t \times t^+t = ¼\ t^+t^+, ½\ t^+t, ¼\ tt$
Producing the phenotypic ratio: *¾ black coat* (t^+t^+, t^+t)
¼ tan coat (tt)

To determine the probability that, out of a litter of eight mice, two will have apricot eyes and a tan coat, we first need to determine the likelihood of an apricot mouse with a tan coat being produced from the mating of the F_1:
aa tt: *¼* (aa) × *¼* (tt) = *1/16.*

The probability of two mice with this phenotype can then be determined using the binomial expansion defining "a" as the probability that 1/16 of the mice will have apricot eyes and tan coats, while defining "b" as the probability that 15/16 will have another phenotype.

$$(a + b)^8 = a^8 + 8a^7b + 28a^6b^2 + 56a^5b^3 + 70a^4b^4 + 56a^3b^5 + 28a^2b^6 + 8ab^7 + b^8$$

The probability of having two apricot mice with tan coats is provided by the term $28a^2b^6$ in the binomial. The probability of "a" is 1/16, while the probability of "b" is 15/16. So the overall probability is $28(1/16)^2(15/16)^6 = 0.074$.

33. In cucumbers, dull fruit (*D*) is dominant over glossy fruit (*d*), orange fruit (*R*) is dominant over cream fruit (*r*), and bitter cotyledons (*B*) are dominant over nonbitter cotyledons (*b*). The three characters are encoded by genes located on different pairs of chromosomes. A plant homozygous for dull, orange fruit and bitter cotyledons is crossed with a plant that has glossy, cream fruit and nonbitter cotyledons. The F_1 are intercrossed to produce the F_2.
All of the F_1 plants have dull, orange fruit and bitter cotyledons (DdRrBb). *By intercrossing the F_1, the F_2 are produced. The expected phenotypic ratios in the F_2 can be calculated more easily by examining the phenotypic ratios produced by the individual crosses of each gene locus.*

F_1 are intercrossed: DdRrBb × DdRrBb

Locus 1: Dd × Dd = *¾ dull (*DD *and* Dd*); ¼ glossy (*dd*)*
Locus 2: Rr × Rr = *¾ orange (*RR *and* Rr*); ¼ cream (*rr*)*
Locus 3: Bb × Bb = *¾ bitter (*BB *and* Bb*); ¼ nonbitter (*bb*)*

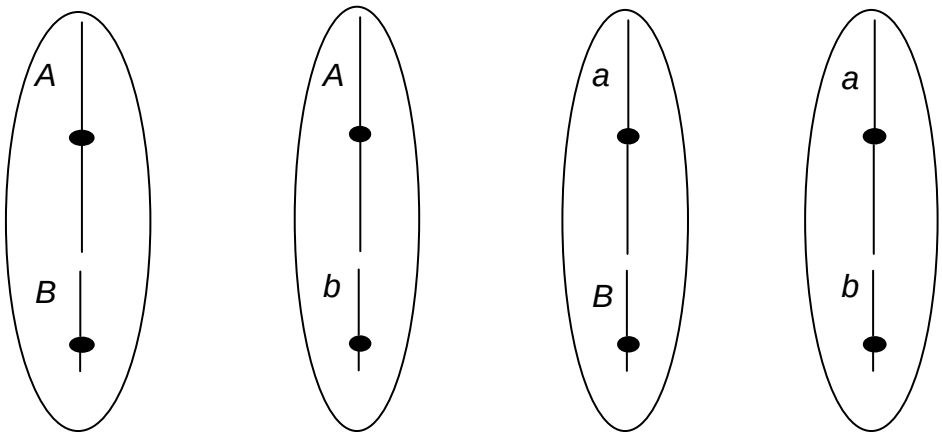
a. Give the phenotypes and their expected proportions in the F_2.
dull, orange, bitter: *¾ dull × ¾ orange × ¾ bitter = 27/64*
dull, orange, nonbitter: *¾ dull × ¾ orange × ¼ nonbitter = 9/64*
dull, cream, bitter: *¾ dull × ¼ cream × ¾ bitter = 9/64*
dull, cream, nonbitter: *¾ dull × ¼ cream × ¼ nonbitter = 3/64*
glossy, orange, bitter: *¼ glossy × ¾ orange × ¾ bitter = 9/64*
glossy, orange, nonbitter: *¼ glossy × ¾ orange × ¼ nonbitter = 3/64*
glossy, cream, bitter: *¼ glossy × ¼ cream × ¾ bitter = 3/64*
glossy, cream, nonbitter: *¼ glossy × ¼ cream × ¼ nonbitter = 1/64*

b. An F_1 plant is crossed with a plant that has glossy, cream fruit and nonbitter cotyledons. Give the phenotypes and expected proportions among the progeny of this cross.
Intercrossing the F_1 with a plant that has glossy, cream fruit and nonbitter cotyledons is an example of a testcross. All progeny classes will be expected in equal proportions because the phenotype of the offspring will be determined by the alleles contributed by the F_1 parent.
DdRrCc *(F_1)* × ddrrcc *(tester)*
*F_1 Locus 1 (*Dd*): ½* D *and ½* d
*F_1 Locus 2 (*Rr*): ½* R *and ½* r
*F_1 Locus 3 (*Cc*): ½* C *and ½* c
dull, orange, bitter: ½ dull × ½ orange × ½ bitter = 1/8
dull, orange, nonbitter: ½ dull × ½ orange × ½ nonbitter = 1/8
dull, cream, bitter: ½ dull × ½ cream × ½ bitter = 1/8
dull, cream, nonbitter: ½ dull × ½ cream × ½ nonbitter = 1/8
glossy, orange, bitter: ½ glossy × ½ orange × ½ bitter = 1/8
glossy, orange, nonbitter: ½ glossy × ½ orange × ½ nonbitter = 1/8
glossy, cream, bitter: ½ glossy × ½ cream × ½ bitter = 1/8
glossy, cream, nonbitter: ½ glossy × ½ cream × ½ nonbitter = 1/8

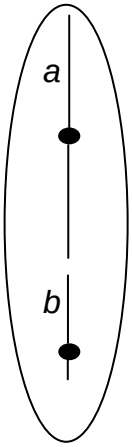
*34. *A* and *a* are alleles located on a pair of metacentric chromosomes. *B* and *b* are alleles located on a pair of acrocentric chromosomes. A cross is made between individuals having the following genotypes: *Aa Bb* × *aa bb*.

a. Draw the chromosomes as they would appear in each type of gamete produced by the individuals of this cross.

Gametes from *Aa Bb* individual:

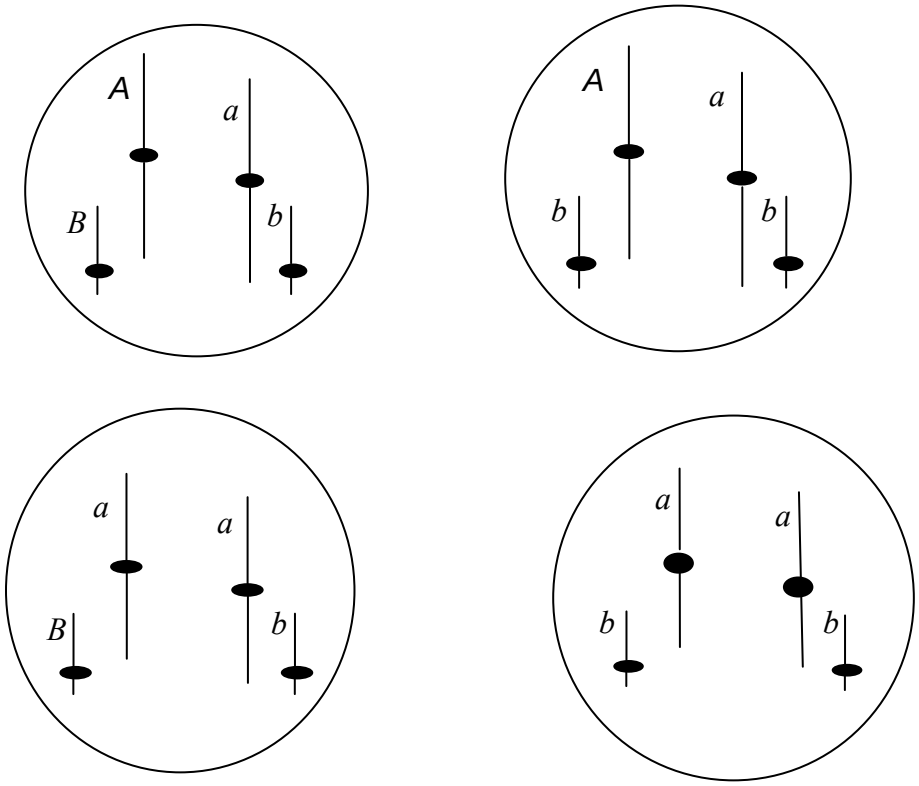


Gametes from *aa bb* individual:

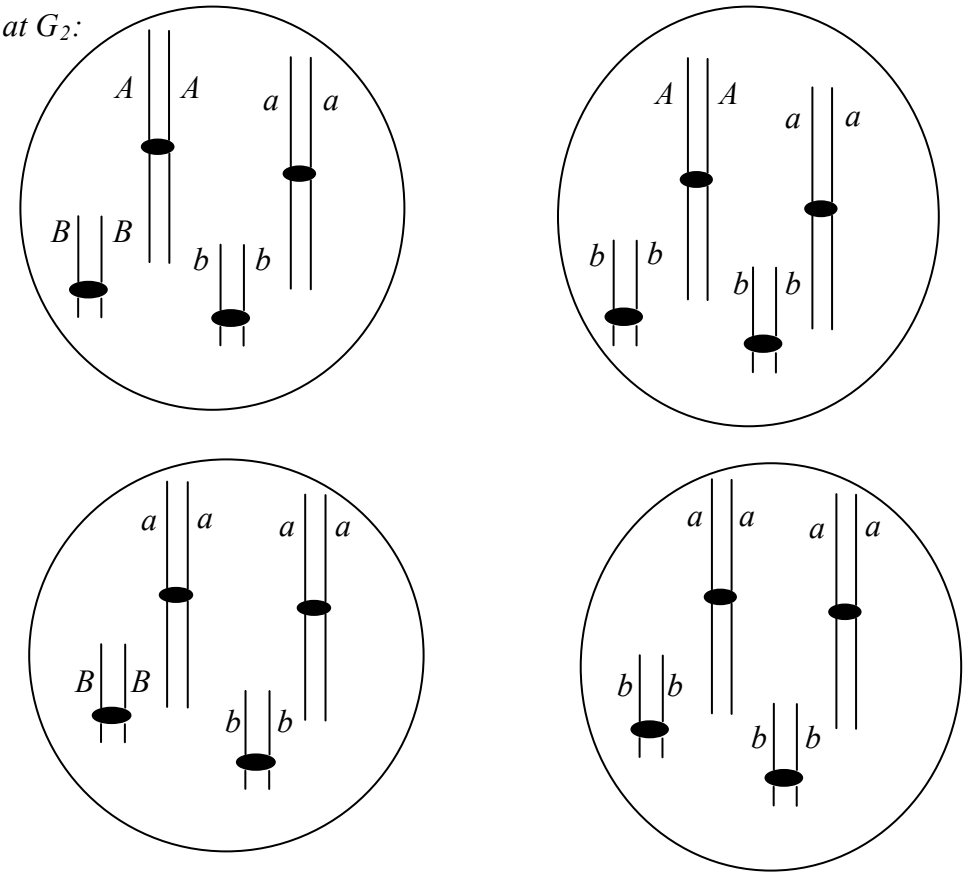


b. For each type of progeny resulting from this cross, draw the chromosomes as they would appear in a cell at G_1, G_2, and metaphase of mitosis.

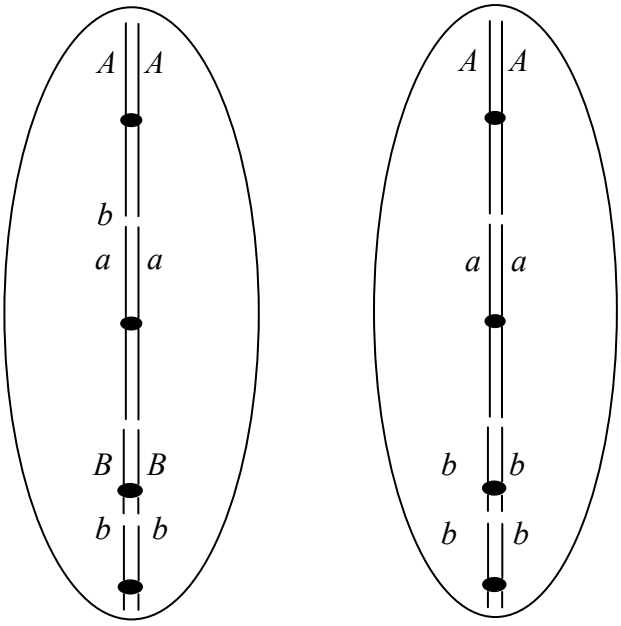
Progeny at G_1:

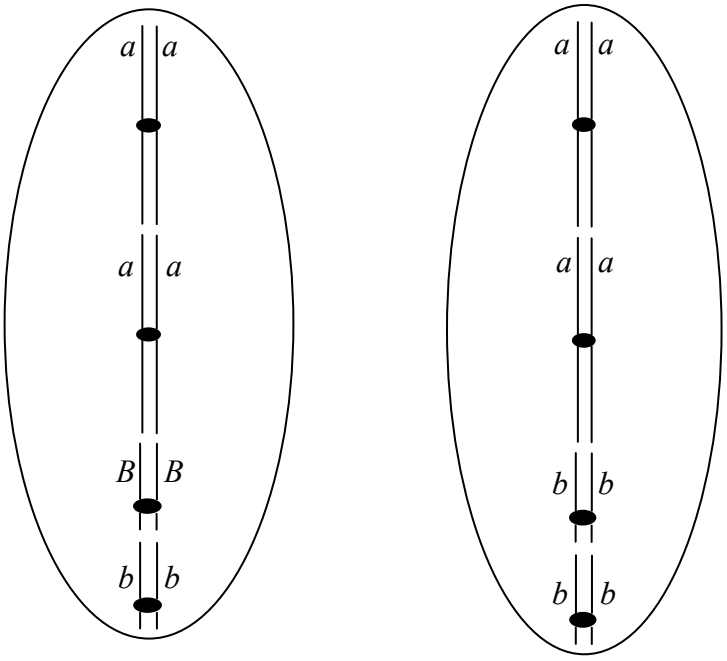


Progeny at G_2:



Progeny at metaphase of mitosis:





The order of chromosomes on metaphase plate can vary.

Section 3.4

*35. J. A. Moore investigated the inheritance of spotting patterns in leopard frogs (J. A. Moore. 1943. *Journal of Heredity* 34:3–7). The pipiens phenotype had the normal spots that give leopard frogs their name. In contrast, the burnsi phenotype lacked spots on its back. Moore carried out the following crosses, producing the progeny indicated.

Parent phenotypes	**Progeny phenotypes**
burnsi × burnsi	39 burnsi, 6 pipiens
burnsi × pipiens	23 burnsi, 33 pipiens
burnsi × pipiens	196 burnsi, 210 pipiens

a. On the basis of these results, what is the most likely mode of inheritance of the burnsi phenotype?
The cross of two burnsi individuals produced both burnsi and pipiens offspring. The result suggests that these individuals were heterozygous with each possessing a burnsi allele and a pipiens allele. The cross also suggests that the burnsi allele is dominant to the pipiens allele. The two crosses of burnsi and pipiens individuals suggest the crosses were between homozygous recessive individuals (pipiens) and heterozygous dominant individuals (burnsi).

b. Give the most likely genotypes of the parent in each cross.
We will define the burnsi allele as "B" *and the pipiens allele as* "B^+."
burnsi (BB^+) *× burnsi* (BB^+)

burnsi (BB^+) × *pipiens* ($B^+ B^+$)
burnsi (BB^+) × *pipiens* ($B^+ B^+$)

c. Use a chi-square test to evaluate the fit of the observed numbers of progeny to the number expected on the basis of your proposed genotypes.
In each of the crosses, we expect that the burnsi allele is dominant to the pipiens allele. By making that assumption, we can make predictions regarding the phenotypic ratios of the offspring and the genotypes of the parents.
For the cross of burnsi × burnsi ($BB^+ \times BB^+$)*, we would expect a phenotypic ratio of 3:1 in the offspring.*

Phenotype	*Observed (O)*	*Expected (E)*	*$(O–E)^2/E$ or (X^2)*
burnsi	*39*	*33.75*	*.81*
pipiens	*6*	*11.25*	*2.45*
Total	*45*	*45*	*3.26*

Degrees of freedom (df) = (number of phenotypic classes) – 1.
*Because there are two phenotypic classes, the degrees of freedom (df) are 1. From the chi-square table, we can see that the calculated chi-square value falls between 2.706 (*P *of .1) and 3.841 (*P *of .05). The probability is sufficient that differences between what we expected and what we observed could have been generated by chance and that our parents are as predicted,* ($BB^+ \times BB^+$).

For the cross of burnsi × pipiens ($BB^+ \times B^+ B^+$)*, we would expect a phenotypic ratio of 1:1 in the offspring.*

Phenotype	*Observed (O)*	*Expected (E)*	*$(O–E)^2/E$ or (X^2)*
burnsi	*23*	*28*	*.89*
pipiens	*33*	*28*	*.89*
Total	*56*	*56*	*1.78*

*Because there are two phenotypic classes, the degrees of freedom (df) are 1. From the chi-square table, we can see that the calculated chi-square value falls between 0.455 (*P *of .5) and 2.706 (*P *of .1). The probability is sufficient that differences between what we expected and what we observed could have been generated by chance and that our parents are as predicted,* ($BB^+ \times B^+ B^+$).
For the second cross of burnsi × pipiens ($BB^+ \times B^+ B^+$)*, we would expect a phenotypic ratio of 1:1 in the offspring.*

Phenotype	*Observed (O)*	*Expected (E)*	*$(O–E)^2/E$ or (X^2)*
burnsi	*196*	*203*	*.24*
pipiens	*210*	*203*	*.24*
Total	*406*	*406*	*.48*

*Again because there are two phenotypic classes, the degrees of freedom (df) are 1. The calculated chi-square value falls between 0.455 (*P *of .5) and 2.706 (*P

of .1). The probability is sufficient that differences between what we expected and what we observed could have been generated by chance and that our parents are as predicted, (Pp × pp).

36. In the 1800s, a man with dwarfism who lived in Utah produced a large number of descendants: 22 children, 49 grandchildren, and 250 great-grandchildren (see the illustration of a family pedigree), many of whom were also dwarfs (F. F. Stephens. 1943. *Journal of Heredity* 34:229–235). The type of dwarfism found in this family is called Schmid-type metaphyseal chondrodysplasia, although it was originally thought to be achondroplastic dwarfism. Among the families of this kindred, dwarfism appeared only in members who had one parent with dwarfism. When one parent was a dwarf, the following numbers of children were produced.

Family in which one parent had dwarfism	**Children with normal stature**	**Children with dwarfism**
A	15	7
B	4	6
C	1	6
D	6	2
E	2	2
F	8	4
G	4	4
H	2	1
I	0	1
J	3	1
K	2	3
L	2	1
M	2	0
N	1	0
O	0	2
Total	52	40

a. With the assumption that Schmid-type metaphyseal chondrodysplasia is rare, is this type of dwarfism inherited as a dominant or recessive trait? Explain your reasoning?
The cumulative data from the above crosses suggest that the crosses are possibly the result of a homozygous individual mating with a heterozygous individual (potentially 1:1 ratio among the offspring). Assuming that the allele for Schmid-type metaphyseal chondrodysplasia is rare, we can also assume that it is unlikely that the normal individuals in each cross are all heterozygous for the allele. So it is likely that this type of dwarfism is inherited as a dominant trait with the individuals with the dwarf phenotype being heterozygous for that allele.

b. Based on your answer for part **a**., what is the expected ratio of dwarf and normal children in the families given in the table. Use a chi-square test to determine if the total number of children for these families (52 normal, 40 dwarfs) is significantly different from the number expected.

Assuming that the trait is dominant and that one parent is heterozygous for the dwarf allele and the other parent is homozygous for the normal allele, then we would expect a ratio of 1:1 for each cross.

Phenotype	*Observed (O)*	*Expected (E)*	*$(O–E)^2/E$ or (X^2)*
dwarf	*40*	*46*	*.78*
normal	*52*	*46*	*.78*
Total	*92*	*92*	*1.56*

*Because there are two phenotypic classes, the degrees of freedom (df) are 1. From the chi-square table, we can see that the calculated chi-square value falls between .455 (*P *of .5) and 2.706 (*P *of .1). The probability is relatively high that differences between what we expected and what we observed was generated by chance and that our parents are as predicted.*

c. Use chi-square tests to determine if the number of children in family C (1 normal, 6 dwarf) and the number in family D (6 normal, 2 dwarf) are significantly different from the numbers expected on the basis of your proposed type of inheritance. How would you explain these deviations from the overall ratio expected?

Phenotype	*Observed (O)*	*Expected (E)*	*$(O – E)^2/E$ or (X^2)*
dwarf	*6*	*3.5*	*1.79*
normal	*1*	*3.5*	*1.79*
Total	*7*	*7*	*3.58*

*The degrees of freedom (df) are 1. From the chi-square table, we can see that the calculated chi-square value falls between 2.706 (*P *of .1) and 3.841 (*P *of .05). Essentially, the phenotypic numbers of the offspring produced have a greater than 5% probability of occurring by chance. Although the percentage is low, it is above the 0.05 probability level, which is frequently used as the cutoff value for accepting that the variation is due to chance. So the probability is sufficient that differences between what we expected and what we observed could have been generated by chance.*

Phenotype	*Observed (O)*	*Expected (E)*	*$(O – E)^2/E$ or (X^2)*
dwarf	*2*	*4*	*1.0*
normal	*6*	*4*	*1.0*
Total	*8*	*8*	*2.0*

*The degrees of freedom (df) are 1. The calculated chi-square value falls between 0.455 (*P *of .5) and 2.706 (*P *of .1). Essentially, the results of the cross have between a 10% and 50% chance of occurring by chance. So, the probability is sufficient that differences between what we expected and what we observed could have been generated by chance.*

In both cases, the differences between the expected ratio and the observed ratio may be explained by the small number of offspring. With such a small sampling size, the variation may not be statistically relevant and due strictly to chance.

37. Pink-eye and albinism are two recessive traits found in the deer mouse *Peromyscus maniculatus.* In mice with pink-eye, the eye is devoid of color and appears pink from the blood vessels within it. Albino mice are completely lacking color both in their fur and in their eyes. F. H. Clark crossed pink-eyed mice with albino mice; the resulting F_1 had normal coloration in their fur and eyes. He then crossed these F_1 mice with mice that were pink-eyed and albino and obtained the following mice. It is very hard to distinguish between mice that are albino and mice that are both pink-eyed and albino, so he combined these two phenotypes together (F. H. Clark. 1936. *Journal of Heredity* 27:259–260).

Phenotype	**Number of progeny**
wild-type fur, wild-type eye color	12
wild-type fur, pink-eye	62
albino, albino, pink-eye	78
Total	152

a. Give the expected numbers of progeny with each phenotype if the genes for pink-eye and albinism assort independently.
We will define wild-type fur as "A" *and albino fur as* "a." *For wild-type eye color, we will use* "P" *and for red eye we will use* "p." *In the first cross, Clark crossed pink-eyed-mice with albino mice. It is likely that both the pink-eyed-mice and the albino mice were homozygous wild-type for the other allele:*

Pink- eye (AA pp) × *Albino* (aa PP) → *F_1 Normal eyes and fur* (Aa Pp)

He then crossed the F_1 mice with mice that were pink-eyed and albino (aa pp) which yielded wild-type, wild-type fur with pink eyes, and both albino fur with wild-type eyes and albino fur with pink eyes, which were difficult to distinguish between. If the two pairs of alleles are assorting independently, we would expect each phenotypic category to occur one-fourth of the time.

Wild-type (Aa Pp) × *Albino, pink-eye* (aa pp) →*¼ wild-type*
¼ wild-type fur and pink eyes
¼ albino fur and wild-type eyes
¼ albino fur and pink eyes

Because we cannot distinguish between albinos with wild-type eyes and albinos with pink eyes, we will combine those two phenotypic categories, and thus expect the combined ratio of albinos to be ½.

b. Use a chi-square test to determine if the observed numbers of progeny fit the number expected with independent assortment.

Phenotype	*Observed (O)*	*Expected (E)*	*$(O - E)^2 / E$ or (X^2)*
Wild-type	*12*	*38*	*17.7*
Wild-type, pink eyes	*62*	*38*	*15.2*
Albino, wild-type and albino, pink eyes	*78*	*76*	*.05*
Total	*152*	*19.5*	*32.95*

We have 3 phenotypic classes that we can observe, so the degrees of freedom = 3 – 1 = 3. The chi-square value is greater than 10.597 for a probability value less than .005, or 0.5% that random chance produced the observed ratio. The observed number of progeny do not fit the numbers expected due to independent assortment. It is likely that a phenomenon other than independent assortment accounts for the observed ratio.

*38. In the California poppy, an allele for yellow flowers (*C*) is dominant over an allele for white flowers (*c*). At an independently assorting locus, an allele for entire petals (*F*) is dominant over an allele for fringed petals (*f*). A plant that is homozygous for yellow and entire petals is crossed with a plant that is white and fringed. A resulting F_1 plant is then crossed with a plant that is white and fringed, and the following progeny are produced: 54 yellow and entire; 58 yellow and fringed, 53 white and entire, and 10 white and fringed.

a. Use a chi-square test to compare the observed numbers with those expected for the cross.
Parents: yellow, entire petals (CC FF) × *white, fringed petals* (cc ff) → *F_1* (Cc Ff)
For the cross of a heterozygous F_1 individual (Cc Ff) with a homozygous recessive individual (cc ff) we would expect a phenotypic ratio of 1:1:1:1 for the different phenotypic classes.

Phenotype	*Observed (O)*	*Expected (E)*	*$(O - E)^2 / E$ or (X^2)*
Yellow, entire	*54*	*43.75*	*2.40*
Yellow, fringed	*58*	*43.75*	*4.64*
White, entire	*53*	*43.75*	*1.96*
White, fringed	*10*	*43.75*	*26.0*
Total	*175*	*175*	*35*

Degrees of freedom = 4 – 1 = 3. The chi-square value is greater than 12.838 for a probability value less than .005, or 0.5% that random chance produced the observed ratio of California poppies.

b. What conclusion can you make from the results of the chi-square test?
From the chi-square value, we can see that it is unlikely that random variations produced the observed ratio. Some other phenomena must be acting.

c. Suggest an explanation for the results.
The number of plants with the cc ff *genotype is much less than expected. Possibly, the* cc ff *genotype may be sublethal. In other words, California poppies with the homozygous recessive genotypes may be less viable than the other possible genotypes.*

CHALLENGE QUESTIONS

Section 3.2

39. Dwarfism is a recessive trait in Hereford cattle. A rancher in western Texas discovers that several of the calves in his herd are dwarfs, and he wants to eliminate this undesirable trait from the herd as rapidly as possible. Suppose that the rancher hires you as a genetic consultant to advise him on how to breed the dwarfism trait out of the herd. What crosses would you advise the rancher to conduct to ensure that the allele causing dwarfism is eliminated from the herd?
To eliminate the recessive dwarfism allele from the herd, you will need to rid the herd of any heterozygous individuals—assuming that heterozygous individuals have a phenotype similar to the homozygous normal individuals. In essence, the farmer wants to create a homozygous normal cattle population. The first step is to advise the farmer to cull from the herd any bulls and cows that when mated produced a dwarf calf. Because the dwarf calf must be homozygous for the dwarf allele, each parent had to contribute the dwarf allele to the calf; thus, each parent is heterozygous. Next, a possible way to determine if any of the remaining cows are heterozygous is to perform a series of testcrosses using a dwarf bull. In the progeny produced by such a cross, ½ are expected to be normal and ½ are expected to be dwarfs if the cow was heterozygous. Any cows that produce dwarf calves should be eliminated from the herd. If the cow is homozygous, no dwarf calves will be produced. Unfortunately, due to the limited number of offspring (typically one) produced by each cow for each mating, several matings for each cow would be necessary to determine if she is heterozygous.

The farmer may not think it practical to purchase a dwarf bull, or even that the dwarf bull would be able to mate with the cows. A second method would be to cross the cows with a bull that is known to be heterozygous normal. For a cross between this bull and a heterozygous cow, we would expect ¾ normal offspring and ¼ dwarfs. A homozygous cow mated with a heterozygous bull would not produce any dwarf offspring. Again, several matings would be necessary to determine if the cow is heterozygous. The farmer will not want to keep the progeny of these crosses because,

if the cow is heterozygous, the chance that her normal offspring are carriers of the dwarf allele is 50%.
In either scenario, the process for building a pure-breeding herd will take several years and careful monitoring of the offspring.

*40. A geneticist discovers an obese mouse in his laboratory colony. He breeds this obese mouse with a normal mouse. All the F_1 mice from this cross are normal in size. When he interbreeds two F_1 mice, eight of the F_2 mice are normal in size and two are obese. The geneticist then intercrosses two of his obese mice, and he finds that all of the progeny from this cross are obese. These results lead the geneticist to conclude that obesity in mice results from a recessive allele.

A second geneticist at a different university also discovers an obese mouse in her laboratory colony. She carries out the same crosses as the first geneticist and obtains the same results. She also concludes that obesity in mice results from a recessive allele. One day, the two geneticists meet at a genetics conference, learn of each other's experiments, and decide to exchange mice. They both find that, when they cross two obese mice from the different laboratories, all the offspring are normal. However, when they cross two obese mice from the same laboratory, all the offspring are obese. Explain their results.
The first geneticist has identified an obese allele that he believes to be recessive. We will define his allele as o_1 *and the normal allele as* O_1. *The obese allele appears to be recessive based on the series of crosses he performed.*

Cross 1 with possible genotype:
Obese (o_1o_1) × *Normal* (O_1O_1) → *F_1 All normal* (O_1o_1)

Cross 2 with possible genotypes:
F_1 normal (Oo_1) × *F_1 normal* (O_1o_1) → *F_2 8 normal* (O_1O_1 and O_1o_1)
2 obese (o_1o_1)

Cross 3 with possible genotypes:
Obese (o_1o_1) × *Obese* (o_1o_1) → *All Obese* (o_1o_1)

A second geneticist also finds an obese mouse in her colony and performs the same types of crosses, which indicate to her that the obese allele is recessive. We will define her obese allele as o_2 *and the normal allele as* O_2.

The cross of obese mice between the two different laboratories produced only normal mice. These different alleles are both recessive. However, they are located at different gene loci. Essentially, the obese mice from the different labs have separate obesity genes that are independent of one another.
The likely genotypes of the obese mice are as follows:

Obese mouse 1 ($o_1o_1\,O_2O_2$) × *Obese mouse 2* ($O_1O_1\,o_2o_2$)
→ *F_1 All normal* ($O_1o_1\,O_2o_2$)

41. Albinism is a recessive trait in humans. A geneticist studies a series of families in which both parents are normal and at least one child has albinism. The geneticist

reasons that both parents in these families must be heterozygotes and that albinism should appear in one-fourth of the children of these families. To his surprise, the geneticist finds that the frequency of albinism among the children of these families is considerably greater than ¼. Can you think of an explanation for the higher-than-expected frequency of albinism among these families?
The geneticist has indeed identified parents who are heterozygous for the albinism allele. However, by looking only at parents who have albino children, he is missing parents who are heterozygous and have no albino children. Since most parents are likely to have only a few children, the result is that the frequency of albino children produced by parents with an albino child will be higher than what would be predicted. If he were to consider the offspring of normal heterozygous parents with no albino children, along with the parents who have albino children, the expected frequency of albino offspring would most likely approach ¼.

42. Two distinct phenotypes are found in the salamander *Plethodon cinereus*: a red form and a black form. Some biologists have speculated that the red phenotype is due to an autosomal allele that is dominant over an allele for black. Unfortunately, these salamanders will not mate in captivity; so the hypothesis that red is dominant over black has never been tested.

    One day a genetics student is hiking through the forest and finds 30 female salamanders, some red and some black, laying eggs. The student places each female and her eggs (about 20 – 30 eggs per female) in separate plastic bags and takes them back to the lab. There, the student successfully raises the eggs until they hatch. After the eggs have hatched, the student records the phenotypes of the juvenile salamanders, along with the phenotypes of their mothers. Thus, the student has the phenotypes for 30 females and their progeny, but no information is available about the phenotypes of the fathers.

    Explain how the student can determine whether red is dominant over black with this information on the phenotypes of the females and their offspring.
    To determine whether red is dominant over black the student will need to examine the colors and phenotypic ratios of the colors found in the offspring of each salamander. Certain trial assumptions will have to be made.

    If black is recessive, the following assumptions about the phenotypic ratios in the offspring of the black females can be made:

    Black female × black male → all black offspring
    Black female × red male (heterozygous) → ½ black offspring; ½ red offspring
    Black female × red male (homozygous) → all red offspring

    If red is dominant, then the following assumptions about the phenotypic ratios in the offspring of the red females can be made:

    Red female (homozygous) × black male → all red offspring
    Red female (heterozygous) × black male → ½ red offspring; ½ black offspring
    Red female (homozygous or heterozygous) × red male (homozygous) → all red
    Red female (homozygous) × red male (homozygous or heterozygous) → all red

Red female (heterozygous) × red male (heterozygous) → ¾ red offspring; ¼ black offspring

The key ratio will be any female salamander that produces offspring with a 3:1 phenotypic ratio. If in the offspring of a red salamander, a ratio of 3:1 red is produced, then the red allele is dominant over the black. If, however, in the offspring of a black salamander, a 3:1 phenotypic ratio of black to red is observed, then black is the dominant allele.