CHAPTER 2

Note: The answers to Comprehension questions are in Appendix B.

Concept check questions (in figure legends)

FIGURE 2.2
The male gamete is found within pollen grains.

FIGURE 2.3
The white-flowered plant is providing the sperm and the purple-flowered plant is providing the eggs.

FIGURE 2.4
A true-breeding strain maintains the same trait over the course of many generations.

FIGURE 2.6
Segregation means that the *T* and *t* alleles separate from each other so that a gamete receives one of them, but not both.

FIGURE 2.7
According to this hypothesis, two different genes are linked. The alleles of the same gene are not linked.

FIGURE 2.9
Independent assortment allows for new combinations of alleles among different genes to be found in future generations of offspring.

FIGURE 2.10
Such a parent could make two types of gametes, *Ty* and *ty*, in equal proportions.

FIGURE 2.12
Horizontal lines connect two individuals that have offspring together, and they connect all of the offspring that produced by the same two parents.

End-of-chapter Questions:

Conceptual Questions

C1. Mendel's work showed that genetic determinants are inherited in a dominant/recessive manner. This was readily apparent in many of his crosses. For example, when he crossed two true-breeding plants for a trait such as height (i.e., tall versus dwarf), all the F_1 plants were tall. This was not consistent with blending. Perhaps more striking was the result obtained in the F_2 generation: 3/4 of the offspring were tall and 1/4 were short. In other words, the F_2 generation displayed phenotypes that were like the parental generation. There did not appear to be a blending to create an intermediate phenotype. Instead, the genetic determinants did not seem to change from one generation to the next.

C2. In the case of plants, cross-fertilization occurs when the pollen and eggs come from different plants while in self-fertilization they come from the same plant.

C3. The genotype is the type of genes that an individual inherits while the phenotype is the individual's observable traits. Tall pea plants, red hair in humans, and vestigial wings in fruit flies are phenotypes. Homozygous, *TT*, in pea plants; a heterozygous carrier of the cystic fibrosis allele; and homozygotes for the cystic fibrosis allele are descriptions of genotypes. It is possible to have different genotypes and the same phenotype. For example, a pea plant that is *TT* or *Tt* would both have a tall phenotype.

C4. A true-breeding organism is a homozygote that has two copies of the same allele.

C5. Conduct a cross in which the unknown individual is bred to an individual that carries only recessive alleles for the gene in question.

C6. Diploid organisms contain two copies of each type of gene. When they make gametes, only one copy of each gene is found in a gamete. Two alleles cannot stay together within the same gamete.

C7. B. This statement is not correct because these are alleles of different genes.

C8. Genotypes: 1 *Tt* :1 *tt*
Phenotypes: 1 tall : 1 dwarf

C9. The recessive phenotype must be a homozygote. The dominant phenotype could be either homozygous or heterozygous.

C10. Here *c* is the recessive allele for constricted pods; *Y* is the dominant allele for yellow color. The cross is *ccYy* × *CcYy*. Follow the directions for setting up a Punnett square, as described in Chapter 2. The genotypic ratio is 2 *CcYY* : 4 *CcYy* : 2 *Ccyy* : 2 *ccYY* : 4 *ccYy* : 2 *ccyy*. This 2:4:2:2:4:2 ratio can be reduced to a 1:2:1:1:2:1 ratio.
The phenotypic ratio is 6 smooth pods, yellow seeds : 2 smooth pods, green seeds : 6 constricted pods, yellow seeds : 2 constricted pods, green seeds. This 6:2:6:2 ratio can be reduced to a 3:1:3:1 ratio.

C11. The genotypes are 1 *YY* : 2 *Yy* : 1 *yy*.
The phenotypes are 3 yellow : 1 green.

C12. Offspring with a recombinant (nonparental) phenotype are consistent with the idea of independent assortment. If two different traits were always transmitted together as unit, it would not be possible to get recombinant phenotypic combinations. For example, if a true-breeding parent had two dominant traits and was crossed to a true-breeding parent having the two recessive traits, the F_2 generation could not have offspring with one recessive and one dominant phenotype. However, because independent assortment can occur, it is possible for F_2 offspring to have one dominant and one recessive trait.

C13. (a) It behaves like a recessive trait because unaffected parents sometimes produce affected offspring. In such cases, the unaffected parents are heterozygous carriers.
(b) It behaves like a dominant trait. An affected offspring always has an affected parent. However, recessive inheritance cannot be ruled out.

C14.

A. Barring a new mutation during gamete formation, the probability is 100% because the parents must be heterozygotes in order to produce a child with a recessive disorder.

B. Construct a Punnett square. There is a 50% chance of heterozygous children

C. Use the product rule. The chance of being phenotypically normal is 0.75 (i.e., 75%), so the answer is $0.75 \times 0.75 \times 0.75 = 0.422$, which is 42.2%.

D. Use the binomial expansion equation where $n = 3$, $x = 2$, $p = 0.75$, $q = 0.25$. The answer is 0.422, or 42.2%.

C15.

A. 100% because they are genetically identical.

B. Construct a Punnett square. We know the parents are heterozygotes because they produced a blue-eyed child. The fraternal twin is not genetically identical, but it has the same parents as its twin. The answer is 25%.

C. The probability that an offspring inherits the allele is 50% and the probability that this offspring will pass it on to his/her offspring is also 50%. We use the product rule: (0.5)(0.5) = 0.25, or 25%.

D. Barring a new mutation during gamete formation, the chance is 100% because they must be heterozygotes in order to produce a child with blue eyes.

C16. First construct a Punnett square. The chances are 75% of producing a solid pup and 25% of producing a spotted pup.

A. Use the binomial expansion equation where $n = 5$, $x = 4$, $p = 0.75$, $q = 0.25$. The answer is 0.396 = 39.6% of the time.

B. You can use the binomial expansion equation for each litter. For the first litter, $n = 6$, $x = 4$, $p = 0.75$, $q = 0.25$; for the second litter, $n = 5$, $x = 5$, $p = 0.75$, $q = 0.25$. Because the litters are in a specified order, we use the product rule and multiply the probability of the first litter times the probability of the second litter. The answer is 0.070, or 7.0%.

C. To calculate the probability of the first litter, we use the product rule and multiply the probability of the first pup (0.75) times the probability of the remaining four. We use the binomial expansion equation to calculate the probability of the remaining four, where $n = 4$, $x = 3$, $p = 0.75$, $q = 0.25$. The probability of the first litter is 0.316. To calculate the probability of the second litter, we use the product rule and multiply the probability of the first pup (0.25) times the probability of the second pup (0.25) times the probability of the remaining five. To calculate the probability of the remaining five, we use the binomial expansion equation, where $n = 5$, $x = 4$, $p = 0.75$, $q = 0.25$. The probability of the second litter is 0.025. To get the probability of these two litters occurring in this order, we use the product rule and multiply the probability of the first litter (0.316) times the probability of the second litter (0.025). The answer is 0.008, or 0.8%.

D. Because this is a specified order, we use the product rule and multiply the probability of the firstborn (0.75) times the probability of the second born (0.25) times the probability of the remaining four. We use the binomial expansion equation to calculate the probability of the remaining four pups, where $n = 4$, $x = 2$, $p = 0.75$, $q = 0.25$. The answer is 0.040, or 4.0%.

C17. If *B* is the black allele, and *b* is the white allele, the male is *bb*, the first female is probably *BB*, and the second female is *Bb*. We are uncertain of the genotype of the first female. She could be *Bb*, although it is unlikely because she didn't produce any white pups out of a litter of eight.

C18.

A. Use the product rule:

(1/4)(1/4)=1/16

B. Use the binomial expansion equation, where
$n = 4$, $p = ¼$, $q = ¾$, $x = 2$:
$P = 0.21$, or 21%

C. Use the product rule:
(1/4)(3/4)(3/4) = 0.14, or 14%

C19. The parents must be heterozygotes, so the probability is 1/4.

C20.

A. 1/4

B. 1, or 100%

C. (3/4)(3/4)(3/4) = 27/64 = 0.42, or 42%

D. Use the binomial expansion equation, where
$n = 7$, $p = 3/4$, $q = 1/4$, $x = 3$:
$P = 0.058$, or 5.8%

E. The probability that the first plant is tall is 3/4. To calculate the probability that among the next four, any two will be tall, use the binomial expansion equation, where $n = 4$, $p = 3/4$, $q = 1/4$, and $x = 2$:
$P = 0.21$
Then calculate the overall probability of these two events:
(3/4)(0.21) = 0.16, or 16%

C21.

A. *T Y R, T y R, T Y r, T y r*

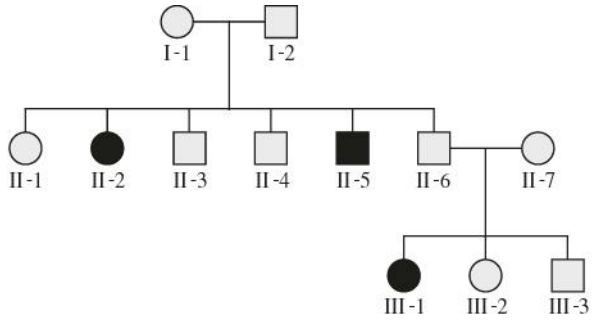
B. *T Y r, t Y r*

C. *T Y R, T Y r, T y R, T y r, t Y R, t Y r, t y R, t y r*

D. *t Y r, t y r*

C22. It violates the law of segregation because two copies of one gene are in the gamete. The two alleles for the *A* gene did not segregate from each other.

C23. It is recessive inheritance. The pedigree is shown here. Affected individuals are shown with filled symbols.



The mode of inheritance appears to be recessive. Unaffected parents (who must be heterozygous) produce affected children.

C24. Based on this pedigree, the disease is likely to be a dominant trait because an affected child always has an affected parent. In fact, it is a dominant disorder.

C25.

A. 3/16

B. (9/16)(9/16)(9/16) = 729/4096 = 0.18

C. (9/16)(9/16)(3/16)(1/16)(1/16) = 243/1,048,576 = 0.00023, or 0.023%

D. Another way of looking at this is that the probability it will have round, yellow seeds is 9/16. Therefore, the probability that it will not is 1 – 9/16 = 7/16.

C26. It is impossible for the F_1 individuals to be true-breeding because they are all heterozygotes.

C27. This problem is a bit unwieldy, but we can solve it using the multiplication method.

For height, the ratio is 3 tall : 1 dwarf.
For seed texture, the ratio is 1 round : 1 wrinkled.
For seed color, they are all yellow.
For flower location, the ratio is 3 axial : 1 terminal.
Thus, the product is
(3 tall + 1 dwarf)(1 round + 1 wrinkled)(1 yellow)(3 axial + 1 terminal)
Multiplying this out, the answer is
9 tall, round, yellow, axial
9 tall, wrinkled, yellow, axial
3 tall, round, yellow, terminal
3 tall, wrinkled, yellow, terminal
3 dwarf, round, yellow, axial
3 dwarf, wrinkled, yellow, axial
1 dwarf, round, yellow, terminal
1 dwarf, wrinkled, yellow, terminal

C28. 2 *TY*, *tY*, 2 *Ty*, *ty*, *TTY*, *TTy*, 2 *TtY*, 2 *Tty*

It may be tricky to think about, but you get 2 *TY* and 2 *Ty* because either of the two *T* alleles could combine with *Y* or *y*. Also, you get 2 *TtY* and 2 *Tty* because either of the two *T* alleles could combine with *t* and then combine with *Y* or *y*.

C29. The drone is *sB* and the queen is *SsBb*. According to the laws of segregation and independent assortment, the male can make only *sB* gametes, while the queen can make *SB*, *Sb*, *sB*, and *sb*, in equal proportions. Therefore, male offspring will be *SB*, *Sb*, *sB*, and *sb*, and female offspring will be *SsBB*, *SsBb*, *ssBB*, and *ssBb*. The phenotypic ratios, assuming an equal number of males and females, will be:

Males	*Females*
1 normal wings/black eyes	2 normal wings, black eyes
1 normal wings/white eyes	2 short wings, black eyes
1 short wings/black eyes	
1 short wings/white eyes	

C30. The genotype of the F_1 plants is *Tt Yy Rr*. According to the laws of segregation and independent assortment, the alleles of each gene will segregate from each other, and the alleles of different genes will

randomly assort into gametes. A *Tt Yy Rr* individual could make eight types of gametes: *TYR, TyR, Tyr, TYr, tYR, tyR, tYr,* and *tyr,* in equal proportions (i.e., 1/8 of each type of gamete). To determine genotypes and phenotypes, you could make a large Punnett square that would contain 64 boxes. You would need to line up the eight possible gametes across the top and along the side, and then fill in the 64 boxes. Alternatively, you could either the multiplication method or forked-line method described in Figure 2.11. The genotypes and phenotypes are as follows:
1 *TT YY RR*
2 *TT Yy RR*
2 *TT YY Rr*
2 *Tt YY RR*
4 *TT Yy Rr*
4 *Tt Yy RR*
4 *Tt YY Rr*
8 *Tt Yy Rr* = 27 tall, yellow, round
1 *TT yy RR*
2 *Tt yy RR*
2 *TT yy Rr*
4 *Tt yy Rr* = 9 tall, green, round
1 *TT YY rr*
2 *TT Yy rr*
2 *Tt YY rr*
4 *Tt Yy rr* = 9 tall, yellow, wrinkled
1 *tt YY RR*
2 *tt Yy RR*
2 *tt YY Rr*
4 *tt Yy Rr* = 9 dwarf, yellow, round
1 *TT yy rr*
2 *Tt yy rr* = 3 tall, green, wrinkled
1 *tt yy RR*
2 *tt yy Rr* = 3 dwarf, green, round
1 *tt YY rr*
2 *tt Yy rr* = 3 dwarf, yellow, wrinkled
1 *tt yy rr* = 1 dwarf, green, wrinkled

C31. Construct a Punnett square to determine the probability of these three phenotypes. The probabilities are 9/16 for round, yellow; 3/16 for round, green; and 1/16 for wrinkled, green. Use the multinomial expansion equation described question 4 in More Genetic TIPS, where $n = 5$, $a = 2$, $b = 1$, $c = 2$, $p = 9/16$, $q = 3/16$, $r = 1/16$. The answer is 0.007, or 0.7%.

C32. The wooly haired male is a heterozygote, because he has the trait and his mother did not. (He must have inherited the normal allele from his mother.) Therefore, he has a 50% chance of passing the wooly allele to his offspring; his offspring have a 50% of passing the allele to their offspring; and these grandchildren have a 50% chance of passing the allele to their offspring (the wooly haired man's great-grandchildren). Because this is an ordered sequence of independent events, we use the product rule: $0.5 \times 0.5 \times 0.5 = 0.125$, or 12.5%. Because no other Scandinavians are on the island, the chance is 87.5% for the offspring being normal (because they could not inherit the wooly hair allele from anyone else). We use the binomial

expansion equation to determine the likelihood that one out of eight great-grandchildren will have wooly hair, where $n = 8$, $x = 1$, $p = 0.125$, $q = 0.875$. The answer is 0.393, or 39.3%.

C33.

A. Construct a Punnett square. Because it is a rare disease, we would assume that the mother is a heterozygote and the father is normal. The chances are 50% that the man in his thirties will have the allele.

B. Use the product rule: 0.5 (chance that the man has the allele) times 0.5 (chance that he will pass it to his offspring), which equals 0.25, or 25%.

C. We use the binomial expansion equation. From part B, we calculated that the probability of an affected child is 0.25. Therefore the probability of an unaffected child is 0.75. For the binomial expansion equation, $n = 3$, $x = 1$, $p = 0.25$, $q = 0.75$. The answer is 0.422 or 42.2%.

C34. Use the product rule. If the woman is heterozygous, there is a 50% chance of having an affected offspring: $(0.5)^7 = 0.0078$, or 0.78%, of the time. This is a pretty small probability. If the woman has an eighth child who is unaffected, however, she has to be a heterozygote, because it is a dominant trait. She would have to pass a normal allele to an unaffected offspring. The answer is 100%.

Experimental Questions

E1. Pea plants are relatively small and hardy. They produce both pollen and eggs within the same flower. Because a keel covers the flower, self-fertilization is quite easy. In addition, cross-fertilization is possible by the simple manipulation of removing the anthers in an immature flower and later placing pollen from another plant. Finally, peas exist in several variants.

E2. The experimental difference depends on where the pollen comes from. In self-fertilization, the pollen and eggs come from the same plant. In cross-fertilization, they come from different plants.

E3. Two generations would take two growing seasons. About 1 and 1/2 years.

E4. According to Mendel's law of segregation, the genotypic ratio should be 1 homozygote dominant : 2 heterozygotes : 1 homozygote recessive. The data table considers only the plants with a dominant phenotype. The genotypic ratio should be 1 homozygote dominant : 2 heterozygotes. The homozygote dominants would be true-breeding while the heterozygotes would not be true-breeding. This 1:2 ratio is very close to what Mendel observed.

E5. In a single-factor cross, the experimenter is only concerned with the outcome of a single trait. In a two-factor cross, the experimenter follows the pattern of inheritance for two different traits.

E6. All three offspring had black fur. The ovaries from the albino female could only produce eggs with the dominant black allele (because they were obtained from a true-breeding black female). The actual phenotype of the albino mother does not matter. Therefore, all offspring would be heterozygotes (*Bb*) and have black fur.

E7. The data are consistent with two genes (let's call them gene 22 and gene 24) that exist in two alleles each, a susceptible allele and a resistant allele. The observed data approximate a 9:3:3:1 ratio. This is the expected ratio if two genes are involved, and if resistance is dominant to susceptibility.

E8. If we construct a Punnett square according to Mendel's laws, we expect a 9:3:3:1 ratio. Because a total of 556 offspring were observed, the expected numbers of offspring with different phenotypes are
556 × 9/16 = 313 round, yellow
556 × 3/16 = 104 wrinkled, yellow
556 × 3/16 = 104 round, green
556 × 1/16 = 35 wrinkled, green
If we plug the observed and expected values into the chi square equation, we get a value of 0.51. With four categories, our degrees of freedom equal $n - 1$, or 3. If we look up the value of 0.51 in the chi square table (see Table 2.1), we see that it falls between the P values of 0.80 and 0.95. This means that the probability is between 80% and 95% that any deviation between observed results and expected results was caused by random sampling error. Therefore, we accept the hypothesis. In other words, the results are consistent with the law of independent assortment.

E9. No, the law of independent assortment applies to transmission patterns of two or more genes. In a single-factor cross, you are monitoring only the transmission pattern of a single gene.

E10.

A. If we let c^+ represent normal wings and c represent curved wings, and e^+ represent gray body and e represent ebony body:
Parental Cross: $cce^+e^+ \times c^+c^+ee$.
F_1 generation is heterozygous: c^+ce^+e
An F_1 offspring crossed to a fly with curved wings and ebony body is represented as:
$c^+ce^+e \times ccee$
The F_2 offspring have this 1:1:1:1 ratio:
$c^+ce^+e : c^+cee : cc\ e^+e : ccee$

B. The phenotypic ratio of the F_2 flies would be 1:1:1:1:
normal wings, gray body : normal wings, ebony bodies : curved wings, gray bodies : curved wings, ebony bodies

C. From part B, we expect 1/4 of each category. There are a total of 444 offspring. The expected number of each category is 1/4 × 444, which equals 111.

$$\chi^2 = \frac{(114 - 111)^2}{111} + \frac{(105 - 111)^2}{111} + \frac{(111 - 111)^2}{111} + \frac{(114 - 111)^2}{111}$$

$$\chi^2 = 0.49$$

With 3 degrees of freedom, a value of 0.49 or greater is likely to occur between 80% and 95% of the time. Therefore, we accept our hypothesis.

E11. You would expect a ratio of 3 normal : 1 long neck. In other words, there should be 1/3 as many long-necked mice as normal mice. If you multiply 522 times 1/3, the expected value is 174. However, only 62 were observed. Therefore, it appears that 174 – 62, or 112, mice died during early embryonic development; 112 divided by 174 gives us the percentage that died, which equals 0.644, or 64.4%.

E12. Follow the same basic chi square analysis used before. We expect a 3:1 ratio, or 3/4 of the dominant phenotype and 1/4 of the recessive phenotype.
The observed and expected values are as follows (rounded to the nearest whole number):

Observed*	Expected	$\frac{(O-E)^2}{E}$
5,474	5,493	0.066
1,850	1,831	0.197
6,022	6,017	0.004
2,001	2,006	0.012
705	697	0.092
224	232	0.276
882	886	0.018
299	295	0.054
428	435	0.113
152	145	0.338
651	644	0.076
207	215	0.298
787	798	0.152
277	266	0.455
		$\chi^2 = 2.15$

*Due to rounding, the observed and expected values may not add up to precisely the same number. Because $n = 14$, there are 13 degrees of freedom. If we look up this value in the chi square table, we have to look between 10 and 15 degrees of freedom. In either case, we would expect the value of 2.15 or greater to occur more than 99% of the time. Therefore, we accept the hypothesis.

E13. This means that a deviation value of 1.005 or greater (between the observed and expected data) would occur 80% of the time. In other words, it is fairly likely to obtain this value due to random sampling error. Therefore, we accept our hypothesis.

E14. The dwarf parent with terminal flowers must be homozygous for both genes, because it is expressing these two recessive traits: *ttaa,* where *t* is the recessive dwarf allele, and *a* is the recessive allele for terminal flowers. The phenotype of the other parent is dominant for both traits. However, because this parent was able to produce dwarf offspring with axial flowers, it must have been heterozygous for both genes: *TtAa.*

E15. The hypothesis is that disease sensitivity and herbicide resistance are dominant traits and they are governed by two genes that assort independently. According to this hypothesis, the F_2 generation should yield a ratio of 9 disease sensitive, herbicide resistant : 3 disease sensitive, herbicide sensitive : 3 disease resistant, herbicide resistant : 1 disease resistant, herbicide sensitive. Because there are a total of 288 offspring produced, the expected numbers would be

$9/16 \times 288 = 162$ disease sensitive, herbicide resistant
$3/16 \times 288 = 54$ disease sensitive, herbicide sensitive
$3/16 \times 288 = 54$ disease resistant, herbicide resistant
$1/16 \times 288 = 18$ disease resistant, herbicide sensitive

$$\chi^2 = \frac{(157-162)^2}{162} + \frac{(57-54)^2}{54} + \frac{(54-54)^2}{54} + \frac{(20-18)^2}{18}$$

$$\chi^2 = 0.54$$

If you look up this value in the chi square table under 3 degrees of freedom, the value lies between the 0.95 and 0.80 probability values. Therefore, you expect a value equal to or greater than 0.54, at least 80% of the time, due to random sampling error. Therefore, you would accept the hypothesis.

Questions for Student Discussion/Collaboration

1. The methods for making a Punnett square and using the multiplication method are described in the chapter. Presumably, the multiplication method (or the forked-line method) will work a lot faster.

2. If we construct a Punnett square, the following probabilities will be obtained:
   tall with axial flowers 3/8
   dwarf with terminal flowers 1/8
   The probability of being tall with axial flowers or dwarf with terminal flowers is then:
   3/8 + 1/8 = 4/8 = 1/2
   We use the product rule to calculate the probability of the ordered events of the first three offspring being tall and axial or dwarf and terminal, and fourth offspring being tall and axial:
   (1/2)(1/2)(1/2)(3/8) = 3/64 = 0.047 = 4.7%

3. Ignore the other genes. The cross is *Rr* × *RR*. All of the offspring will have round seeds. The probability is 100%