chapter 2

Mendel's Principles of Heredity

Synopsis

Chapter 2 covers the basic principles of inheritance that can be summarized as Mendel's Laws of Segregation (for one gene) and Independent Assortment (for more than one gene).

Key terms

genes and **alleles** of genes – A gene determines a trait; and there are different alleles or forms of a gene. The color gene in peas has two alleles: the yellow allele and the green allele.

genotype and **phenotype** – Genotype is the genetic makeup of an organism (written as alleles of specific genes), while phenotype is what the organism looks like.

homozygous and **heterozygous** – When both alleles of a gene are the same, the individual is homozygous for that gene (or *pure-breeding*). If the two alleles are different, the organism is heterozygous (also called a *hybrid*).

dominant and **recessive** – The dominant allele is the one that controls the phenotype in the heterozygous genotype; the recessive allele controls the phenotype only in a homozygote.

monohybrid or **dihybrid cross** – a cross between individuals who are both heterozygotes for one gene (monohybrid) or for two genes (dihybrid)

testcross – performed to determine whether or not an individual with the dominant trait is homozygous or heterozygous; an individual with the dominant phenotype but unknown genotype is crossed with an individual with the recessive phenotype

Key ratios

3:1 – Ratio of progeny phenotypes in a cross between monohybrids
[*Aa* × *Aa* → 3 *A*– (dominant phenotype) : 1 *aa* (recessive phenotype)]

1:2:1 – Ratio of progeny genotypes in a cross between monohybrids
(*Aa* × *Aa* → 1 *AA* : 2 *Aa* : 1*aa*)

1:1 – Ratio of progeny genotypes in a cross between a heterozygote and a recessive homozygote
(*Aa* × *aa* → 1 *Aa* : 1*aa* : 1*aa*)

1:0 – All progeny have the same phenotype. Can result from several cases:
[*AA* × – – → *A*– (all dominant phenotype)]
[*aa* × *aa* → *aa* (all recessive phenotype)]

9:3:3:1 – Ratio of progeny phenotypes in a dihybrid cross
(*Aa Bb* × *Aa Bb* → 9 *A*– *B*– : 3 *A*– *bb* : 3 *aa B*– : 1 *aa*)

Problem Solving

The essential component of solving most genetics problems is to DIAGRAM THE CROSS in a consistent manner. In most cases you will be given information about phenotypes, so the diagram would be:

Phenotype of one parent × phenotype of the other parent → phenotype(s) of progeny

The goal is to assign genotypes to the parents and then use these predicted genotypes to generate the genotypes, phenotypes, and ratios of progeny. If the predicted progeny match the observed data you were provided, then your genetic explanation is correct.

The points listed below will be particularly helpful in guiding your problem solving:

- Remember that **there are two alleles of each gene when describing the genotypes of individuals.** But if you are describing gametes, remember that **there is only one allele of each gene per gamete.**
- **You will need to determine whether a trait is dominant or recessive.** Two main clues will help you answer this question.
    - First, if the parents of a cross are true-breeding for the alternative forms of the trait, look at the phenotype of the F_1 progeny. Their genotype must be heterozygous, and their phenotype is thus controlled by the dominant allele of the gene.
    - Second, look at the F_2 progeny (that is, the progeny of the F_1 hybrids). The 3/4 portion of the 3:1 phenotypic ratio indicates the dominant phenotype.
- You should **recognize the need to set up a testcross** (to establish the genotype of an individual showing the dominant phenotype by crossing this individual to a recessive homozygote).
- You must **keep in mind the basic rules of probability:**
    - *Product rule:* If two outcomes must occur together as the result of independent events, the probability of one outcome AND the other outcome is the product of the two individual probabilities.
    - *Sum rule:* If there is more than one way in which an outcome can be produced, the probability of one OR the other occurring is the sum of the two mutually exclusive individual probabilities.
- Remember that **Punnett squares are not the only means of analyzing a cross**; **branched-line diagrams and calculations of probabilities according to the product and sum rules are more efficient ways of looking at complicated crosses** involving more than one or two genes.
- **You should be able to draw and interpret pedigrees**. When the trait is rare, look in particular for vertical patterns of inheritance characteristic of dominant traits, and horizontal patterns that typify recessive traits. Check your work by assigning genotypes to all individuals in the pedigree and verifying that these make sense.
- The vocabulary problem (the first problem in the set) is a useful gauge of how well you know the terms most critical for you understanding of the chapter.

Vocabulary

1.

a.	phenotype	4.	observable characteristic
b.	alleles	3.	alternate forms of a gene
c.	independent assortment	6.	alleles of one gene separate into gametes randomly with respect to alleles of other genes
d.	gametes	7.	reproductive cells containing only one copy of each gene
e.	gene	11.	the heritable entity that determines a characteristic
f.	segregation	13.	the separation of the two alleles of a gene into different gametes
g.	heterozygote	10.	an individual with two different alleles of a gene
h.	dominant	2.	the allele expressed in the phenotype of the heterozygote
i.	F_1	14.	offspring of the P generation
j.	testcross	9.	the cross of an individual of ambiguous genotype with a homozygous recessive individual
k.	genotype	12.	the alleles an individual has
l.	recessive	8.	the allele that does not contribute to the phenotype of the heterozygote
m.	dihybrid cross	5.	a cross between individuals both heterozygous for two genes
n.	homozygote	1.	having two identical alleles of a given gene

Section 2.1

2.

Prior to Mendel, **people held two basic misconceptions about inheritance.** First was the common idea of blended inheritance: that the parental traits become mixed in the offspring and forever changed. Second, many thought that one parent contributes the most to an offspring's inherited features. (For example, some people thought they saw a fully formed child in a human sperm.)

In addition, **people who studied inheritance did not approach the problem in an organized way.** They did not always control their crosses. They did not look at traits with clear-cut alternative phenotypes. They did not start with pure-breeding lines. They did not count the progeny types in their crosses. For these reasons, they could not develop the same insights as did Mendel.

3. **Several advantages exist to using peas for the study of inheritance:**

(1) Peas have a fairly rapid generation time (at least two generations per year if grown in the field, three or four generations per year if grown in greenhouses.
(2) Peas can either self-fertilize or be artificially crossed by an experimenter.
(3) Peas produce large numbers of offspring (hundreds per parent).
(4) Peas can be maintained as pure-breeding lines, simplifying the ability to perform subsequent crosses.
(5) Because peas have been maintained as inbred stocks, two easily distinguished and discrete forms of many traits are known.
(6) Peas are easy and inexpensive to grow.

In contrast, **studying genetics in humans has several disadvantages:**

(1) The generation time of humans is very long (roughly 20 years).
(2) There is no self-fertilization in humans, and it is not ethical to manipulate crosses.
(3) Humans produce only a small number of offspring per mating (usually only one) or per parent (almost always fewer than 20).
(4) Although people who are homozygous for a trait do exist (analogous to pure-breeding stocks), homozygosity cannot be maintained because mating with another individual is needed to produce the next generation.
(5) Because human populations are not inbred, most human traits show a continuum of phenotypes; only a few traits have two very distinct forms.
(6) People require a lot of expensive care to "grow".

There is nonetheless one major advantage to the study of genetics in humans: Because many inherited traits result in disease syndromes, and because the world's population now exceeds 6 billion people, a very large number of people with diverse, variant phenotypes can be recognized. These variations are the raw material of genetic analysis.

Section 2.2

4. **a.** **Two phenotypes are seen in the second generation of this cross: normal and albino**. Thus, only one gene is required to control the phenotypes observed.

b. Note that the phenotype of the first generation progeny is normal color, and that in the second generation, there is a ratio of 3 normal : 1 albino. Both of these observations show that **the allele controlling the normal phenotype (*A*) is dominant to the allele controlling the albino phenotype (*a*).**

c. In a test cross, an individual showing the dominant phenotype but that has an unknown genotype is mated with an individual that shows the recessive phenotype and is therefore homozygous for the recessive allele. The male parent is albino, so **the male parent's genotype is *aa*.** The normally colored offspring must receive an *A* allele from the mother, so **the genotype of the normal offspring is *Aa*.** The albino offspring must receive an *a* allele from the mother, so **the genotype of the albino offspring is *aa*.** Thus, **the female parent must be heterozygous *Aa*.**

5. Because two different phenotypes result from the mating of two cats of the same phenotype, the short-haired parent cats must have been heterozygous. The phenotype expressed in the heterozygotes (the parent cats) is the dominant phenotype. Therefore, **short hair is dominant to long hair.**

6. **a.** Two affected individuals have an affected child and a normal child. This outcome is not possible if the affected individuals were homozygous for a recessive allele conferring piebald spotting, and if the trait is controlled by a single gene. Therefore, **the piebald trait must be the dominant phenotype.**

b. If the trait is dominant, the piebald parents could be either homozygous (*PP*) or heterozygous (*Pp*). However, because the two affected individuals have an unaffected child (*pp*), **they both must be heterozygous (*Pp*).** A diagram of the cross follows:

piebald	×	piebald	→	1 piebald	:	1 normal
Pp		*Pp*		*Pp*		*pp*

Note that although the apparent ratio is 1:1, this is not a testcross but is instead a cross between two monohybrids. The reason for this discrepancy is that only two progeny were obtained, so this number is insufficient to establish what the true ratio would be (it should be 3:1) if many progeny resulted from the mating.

7. **You would conduct a testcross between your normal-winged fly (*W*–) and a short-winged fly that must be homozygous recessive (*ww*).** The possible results are diagrammed here; the first genotype in each cross is that of the normal-winged fly whose genotype was originally unknown.

WW × *ww* → all *Ww* (normal wings)

Ww × *ww* → ½ *Ww* (normal wings) : ½ *ww* (short wings)

8. First diagram the crosses:

closed × open → F_1 all open → F_2 145 open : 59 closed

F_1 open × closed → 81 open : 77 closed

The results of the crosses fit the pattern of inheritance of a single gene, with the open trait being dominant and the closed trait recessive. The first cross is similar to those Mendel did with pure-breeding parents, although you were not provided with the information that the starting plants were true-breeding. **The phenotype of the F_1 plants is open, indicating that open is dominant. The closed parent must be homozygous for the recessive allele. Because only one phenotype is seen among the F_1 plants, the open parent must be homozygous for the dominant allele.** Thus, the parental cucumber plants were indeed true-breeding homozygotes.

The result of the self-fertilization of the F_1 plants shows a 3:1 ratio of the open : closed phenotypes among the F_2 progeny. **The 3:1 ratio in the F_2 shows that a single gene controls the phenotypes and that the F_1 plants are all hybrids (that is, they are heterozygotes).**

The final cross verifies the F_1 plants from the first cross are heterozygous hybrids because **this testcross yields a 1:1 ratio of open: closed progeny.** In summary, all the data are consistent with the trait being determined by one gene with two alleles, and open being the dominant trait.

9. **The dominant trait (short tail) is easier to eliminate from the population by selective breeding.** The reason is you can recognize every animal that has inherited the short tail allele, because only one such dominant allele is needed to see the phenotype. If you prevent all the short-tailed animals from mating, then the allele would become extinct.

On the other hand, the recessive dilute coat color allele can be passed unrecognized from generation to generation in heterozygous mice (who are *carriers*). The heterozygous mice do not express the phenotype, so they cannot be distinguished from homozygous dominant mice with normal coat color. You could prevent the homozygous recessive mice with the dilute phenotype from mating, but the allele for the dilute phenotype would remain among the carriers, which you could not recognize.

10. The problem already states that only one gene is involved in this trait, and that the dominant allele is dimple (*D*) while the recessive allele is nondimple (*d*).

a. Diagram the cross described in this part of the problem:

nondimple ♂ × dimpled ♀ → proportion of F_1 with dimple?

Note that the dimpled woman in this cross had a *dd* (nondimpled) mother, so the dimpled woman MUST be heterozygous. We can thus rediagram this cross with genotypes:

dd (nondimple) ♂ × *Dd* (dimple) ♀ → ½ *Dd* (dimpled) : ½ *dd* (nondimpled)

One half of the children produced by this couple would be dimpled.

b. Diagram the cross:

dimple (*D?*) ♂ × nondimpled (*dd*) ♀ → nondimple F_1 (*dd*)

Because they have a nondimple child (*dd*), the husband must have a *d* allele to contribute to the offspring. **The husband is thus of genotype *Dd*.**

c. Diagram the cross:

dimple (*D?*) ♂ × nondimpled (*dd*) ♀ → eight F_1, all dimpled (*D*–)

The *D* allele in the children must come from their father. The father could be either *DD* or *Dd*, but **it is most probable that the father's genotype is *DD*.** We cannot rule out completely that the father is a *Dd* heterozygote. However, if this was the case, the probability that all 8 children would inherit the *D* allele from a *Dd* parent is only $(1/2)^8 = 1/256$.

11. **a.** The only unambiguous cross is:

homozygous recessive × homozygous recessive → all homozygous recessive

The only cross that fits this criteria is: dry × dry → all dry. Therefore, **dry is the recessive phenotype (*ss*) and sticky is the dominant phenotype (*S*–).**

b. A 1:1 ratio comes from a testcross of heterozygous sticky (*Ss*) × dry (*ss*). However, **the sticky x dry matings here include both the *Ss* × *ss* AND the homozygous sticky (*SS*) × dry (*ss*).**

A 3:1 ratio comes from crosses between two heterozygotes, *Ss* × *Ss*, but the sticky individuals are not only *Ss* heterozygotes but also *SS* homozygotes. Thus the sticky x sticky matings in this human population are a mix of matings between two heterozygotes (*Ss* × *Ss*), between two homozygotes (*SS* × *SS*) and between a homozygote and heterozygote (*SS* × *Ss*). **The 3:1 ratio of the heterozygote cross is therefore obscured by being combined with results of the two other crosses.**

12. Diagram the cross:

black × red → 1 black : 1 red

No, you cannot tell how coat color is inherited from the results of this one mating. In effect, this was a test cross – a cross between animals of different phenotypes resulting in offspring of two phenotypes. This does not indicate whether red or black is the dominant phenotype. To determine which phenotype is dominant, remember that an animal with a recessive phenotype must be homozygous. Thus, **if you mate several red horses to each other and also mate several black horses to each other, the crosses that always yield only offspring with the parental phenotype must have been between homozygous recessives.** For example, if all the black × black matings result in only black offspring, black is recessive. Some of the red × red crosses (that is, crosses between heterozygotes) would then result in both red and black offspring in a ratio of 3:1. To establish this point, you might have to do several red × red crosses, because some of these crosses could be between red horses homozygous for the dominant allele. You could of course ensure that you were sampling heterozygotes by using the progeny of black × red crosses (such as that described in the problem) for subsequent black × black or red × red crosses.

13. a. **1/6** because a die has 6 different sides.

b. There are three possible even numbers (2, 4, and 6). The probability of obtaining any one of these is 1/6. Because the 3 events are mutually exclusive, use the sum rule: 1/6 + 1/6 + 1/6 = 3/6 = **1/2.**

c. You must roll either a 3 or a 6, so 1/6 + 1/6 = 2/6 = **1/3.**

d. Each die is independent of the other, thus the product rule is used: 1/6 × 1/6 = **1/36.**

e. The probability of getting an even number on one die is 3/6 = 1/2 (see part [b]). This is also the probability of getting an odd number on the second die. This result could happen either of 2 ways – you could get the odd number first and the even number second, or *vice versa*. Thus the probability of both occurring is 1/2 × 1/2 × 2 = **1/2.**

f. The probability of any specific number on a die = 1/6. The probability of the same number on the other die =1/6. The probability of both occurring at same time is 1/6 x 1/6 = 1/36. The same probability is true for the other 5 possible numbers on

the dice. Thus the probability of any of these mutually exclusive situations occurring is 1/36 + 1/36 + 1/36 + 1/36 + 1/36 + 1/36 = 6/36 = **1/6.**

g. The probability of getting two numbers both over four is the probability of getting a 5 or 6 on one die (1/6 + 1/6 = 1/3) and 5 or 6 on the other die (1/3). The results for the two dice are independent events, so 1/3 × 1/3 = **1/9.**

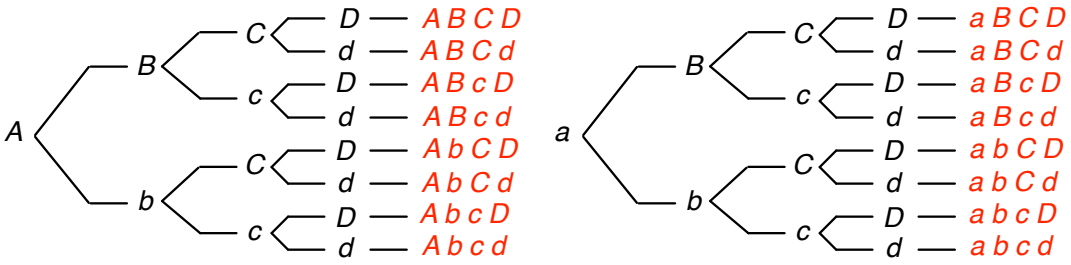
14. **The probability of drawing a face card = 0.231** (= 12 face cards / 52 cards). **The probability of drawing a red card = 0.5** (= 26 red cards / 52 cards**). The probability of drawing a red face card = probability of a red card × probability of a face card = 0.231 × 0.5 = 0.116.**

15. **a.** The *Aa bb CC DD* woman can produce 2 genetically different eggs that vary in their allele of the first gene (*A* or *a*). She is homozygous for the other 3 genes and can only make eggs with the *b C D* alleles for these genes. Thus, using the product rule (because the inheritance of each gene is independent), she can make 2 × 1 × 1 × 1 = **2 different types of gametes:** (*A b C D* and *a b C D*).

b. Using the same logic, an *AA Bb Cc dd* woman can produce 1 × 2 × 2 × 1 = **4 different types of gametes:** *A* (*B* or *b*) (*C* or *c*) *d*.

c. A woman of genotype *Aa Bb cc Dd* can make 2 × 2 × 1 × 2 = **8 different types of gametes:** (*A* or *a*) (*B* or *b*) *c* (*D* or *d*).

d. A woman who is a quadruple heterozygote can make 2 × 2 × 2 × 2 = **16 different types of gametes:** (*A* or *a*) (*B* or *b*) (C or *c*) (*D* or *d*). This problem (like those in parts (a-c) above) can also be visualized with a branched-line diagram.



16. **a.** The probability of any phenotype in this cross depends only on the gamete from the heterozygous parent. The probability that a child will resemble the quadruply heterozygous parent is thus 1/2*A* × 1/2*B* × 1/2*C* × 1/2*D* = 1/16. The probability that a child will resemble the quadruply homozygous recessive parent is 1/2*a* × 1/2*b* × 1/2*c* × 1/2*d* = 1/16. **The probability that a child will resemble either parent is then 1/16 + 1/16 = 1/8.** This cross will produce 2 different phenotypes for each gene or 2 × 2 × 2×2 = **16 potential phenotypes.**

b. The probability of a child resembling the recessive parent is 0; the probability of a child resembling the dominant parent is 1 × 1 × 1 × 1 = 1. **The probability that a child will resemble one of the two parents is 0 + 1 = 1. Only 1 phenotype is possible in the progeny (dominant for all 4 genes),** as $(1)^4 = 1$.

c. The probability that a child would show the dominant phenotype for any one gene is 3/4 in this sort of cross (remember the 3/4 : 1/4 monohybrid ratio of

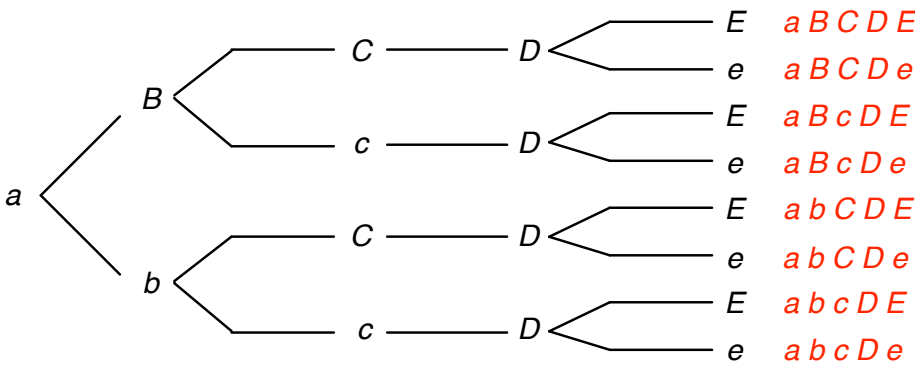
phenotypes), so **the probability of resembling the parent for all four genes is $(3/4)^4 = 81/256$.** There are 2 phenotypes possible for each gene, so $(2)^4 = 16$ **different kinds of progeny.**

d. **All progeny will resemble their parents** because all of the alleles from both parents are identical, **so the probability = 1.** There is only 1 phenotype possible for each gene in this cross; because $(1)^4 = 1$, the child can have only **one possible phenotype** when considering all four genes.

17. a. The combination of alleles in the egg and sperm allows only one genotype for the zygote: ***aa Bb Cc DD Ee*.**

b. Because the inheritance of each gene is independent, you can use the product rule to determine the number of different types of gametes that are possible: 1 x 2 x 2 x 1 x 2 = **8 types of gametes.** To figure out the types of gametes, consider the possibilities for each gene separately and then the possible combinations of genes in a consistent order. For each gene the possibilities are: *a*, (*B* : *b*), (*C* : *c*), *D*, and (*E* : *e*). The possibilities can be determined using the product rule. Thus for the first 2 genes [*a*] × [*B* : *b*] gives [*a B* : *a b*] × [*C* : *c*] gives [*a B C* : *a B c* : *a b C* : *a b c*] × [*D*] gives [*a B C D* : *a B c D* : *a b C D* : *a b c D*] × [*E* : *e*] gives [***a B C D E* : *a B C D e* : *a B c D E* : *a B c D e* : *a b C D E* : *a b C D e* : *a b c D E* : *a b c D e***].

This problem can also be visualized with a branched-line diagram:



18. The first two parts of this problem involve the probability of occurrence of two independent traits: the sex of a child and galactosemia. The parents are heterozygous for galactosemia, so there is a 1/4 chance that a child will be affected (that is, homozygous recessive). The probability that a child is a girl is 1/2. The probability of an affected girl is therefore $1/2 \times 1/4 = 1/8$.

a. Fraternal (non-identical) twins result from two independent fertilization events and therefore the probability that both will be girls with galactosemia is the product of their individual probabilities (see above); $1/8 \times 1/8 =$ **1/64**.

b. For identical twins, one fertilization event gave rise to two individuals. The probability that both are girls with galactosemia is **1/8**.

For parts c-g, remember that each child is an independent genetic event. The sex of the children is not at issue in these parts of the problem.

c. Both parents are carriers (heterozygous), so the probability of having an unaffected child is 3/4. The probability of 4 unaffected children is 3/4 x 3/4 x 3/4 x 3/4 = **81/256**.

d. The probability that at least one child is affected is all outcomes except the one mentioned in part (c). Thus, the probability is 1 - 81/256 = **175/256**. Note that this general strategy for solving problems, where you first calculate the probability of all events except the one of interest, and then subtract that number from 1, is often useful for problems where direct calculations of the probability of interest appear to be very difficult.

e. The probability of an affected child is 1/4 while the probability of an unaffected child is 3/4. Therefore 1/4 ×1/4 × 3/4 × 3/4 = **9/256**.

f. The probability of 2 affected and 1 unaffected in any one particular birth order is 1/4 × 1/4 × 3/4 = 3/64. There are 3 mutually exclusive birth orders that could produce 2 affecteds and 1 unaffected – unaffected child first born, unaffected child second born, and unaffected child third born. Thus, there is a 3/64 + 3/64 + 3/64 = **9/64** chance that 2 out of 3 children will be affected.

g. The phenotype of any particular child is independent of all others, so the probability of an affected child is **1/4**.

19. Diagram the cross, where *P* is the normal pigmentation allele and *p* is the albino allele:

normal (*P?*) × normal (*P?*) → albino (*pp*)

An albino must be homozygous recessive *pp*. The parents are normal in pigmentation and therefore could be *PP* or *Pp*. Because they have an albino child, **both parents must be carriers (*Pp*). The probability that their next child will have the *pp* genotype is 1/4**.

20. Diagram the cross:

yellow round × yellow round → 156 yellow round : 54 yellow wrinkled

The monohybrid ratio for seed shape is 156 round : 54 wrinkled = 3 round : 1 wrinkled. The parents must therefore have been heterozygous (*Rr*) for the pea shape gene. All the offspring are yellow and therefore have the *Yy* or *YY* genotype. **The parent plants were *Y– Rr* × *YY Rr*** (that is, you know at least one of the parents must have been *YY*).

21. Diagram the cross:

smooth black ♂ × rough white ♀ → F_1 rough black

→ F_2 8 smooth white : 25 smooth black : 23 rough white : 69 rough black

a. Since only one phenotype was seen in the first generation of the cross, we can assume that the parents were true breeding, and that the F_1 generation consists of heterozygous animals. **The phenotype of the F_1 progeny indicates that rough and black are the dominant phenotypes. Four phenotypes are seen in the F_2 generation so there are two genes controlling the phenotypes in this cross. Therefore, *R* = rough, *r* = smooth; *B* = black, *b* = white.** In the F_2 generation, consider each gene separately. For the coat texture, there were 8 + 25 = 33 smooth

: 23 + 69 = 92 round, or a ratio of ~1 smooth : ~3 round. For the coat color, there were 8 + 23 = 31 white : 25 + 69 = 94 black, or about ~1 white : ~3 black, so the F_2 progeny support the conclusion that the F_1 animals were heterozygous for both genes.

b. An F_1 male is heterozygous for both genes, or *Rr Bb*. The smooth white female must be homozygous recessive; that is, *rr bb*. Thus, *Rr Bb* × *rr bb* → 1/2 *Rr* (rough) : 1/2 *rr* (smooth) and 1/2 *Bb* (black) : 1/2 *bb* (white). The inheritance of these genes is independent, so apply the product rule to find the expected phenotypic ratios among the progeny, or **1/4 rough black : 1/4 rough white : 1/4 smooth black : 1/4 smooth white**.

22. Diagram the cross:

YY rr × *yy RR* → all *Yy Rr* → 9/16 *Y*– *R*– (yellow round) : 3/16 *Y*– *rr* (yellow wrinkled) : 3/16 *yy R*– (green round) : 1/16 *yy rr* (green wrinkled).

Each F_2 pea results from a separate fertilization event. The probability of 7 yellow round F_2 peas is $(9/16)^7$ = 4,782,969/268,435,456 = **0.018**.

23. **a.** First diagram the cross, and then figure out the monohybrid ratios for each gene:

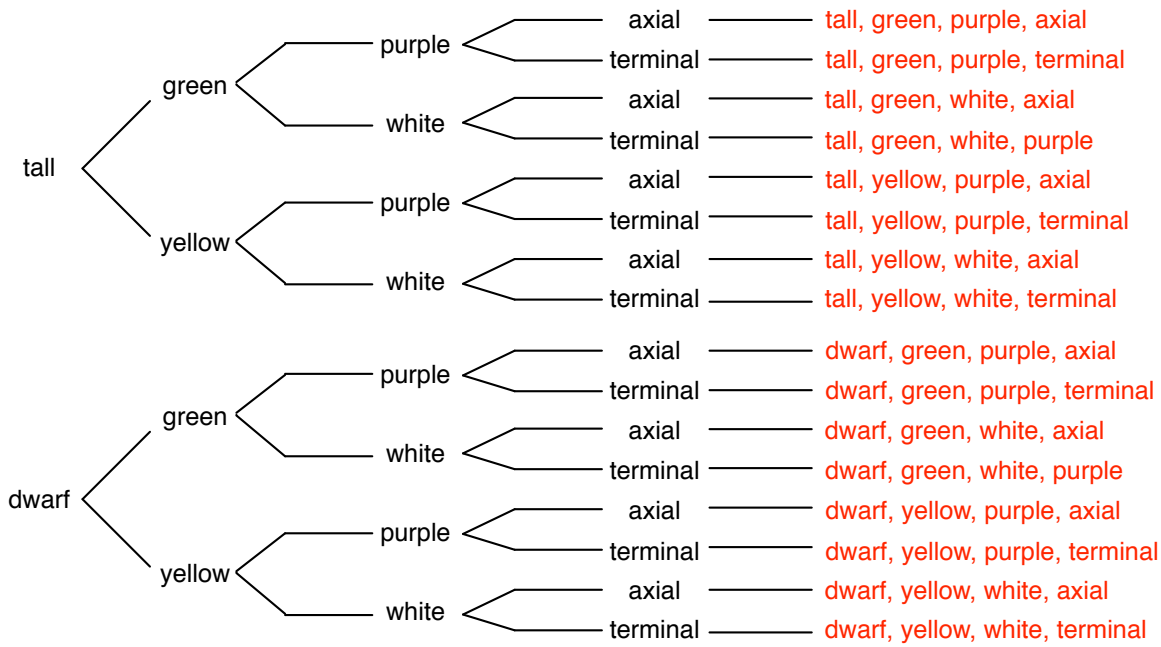
Aa Tt × *Aa Tt* → 3/4 *A*– (achoo) : 1/4 *aa* (non-achoo) and 3/4 *T*– (trembling) : 1/4 *tt* (non-trembling).

The probability that a child will be *A*– (and have achoo syndrome) is independent of the probability that it will lack a trembling chin, so the probability of a child with achoo syndrome but without trembling chin is 3/4 *A*– × 1/4 *tt* = **3/16**.

b. The probability that a child would have neither dominant trait is 1/4 *aa* × 1/4 *tt* = **1/16**.

24. The F_1 must be heterozygous for all the genes because the parents were pure-breeding (homozygous). The appearance of the F_1 establishes that the dominant phenotypes for the four traits are tall, purple flowers, axial flowers and green pods.

a. From a heterozygous F_1 × F_1, both dominant and recessive phenotypes can be seen for each gene. Thus, you expect 2 × 2 × 2 × 2 = 16 different phenotypes when considering the four traits together. The possibilities can be determined using the product rule with the pairs of phenotypes for each gene, because the traits are inherited independently. Thus: [tall : dwarf] × [green : yellow] gives [tall green : tall yellow : dwarf green : dwarf yellow] × [purple : white] gives [tall green purple : tall yellow purple : dwarf green purple : dwarf yellow purple : tall green white : tall yellow white : dwarf green white : dwarf yellow white] × [terminal : axial] which gives **tall green purple terminal : tall yellow purple terminal : dwarf green purple terminal : dwarf yellow purple terminal : tall green white terminal : tall yellow white terminal : dwarf green white terminal : dwarf yellow white terminal : tall green purple axial : tall yellow purple axial : dwarf green purple axial : dwarf yellow purple axial : tall green white axial : tall yellow white axial : dwarf green white axial : dwarf yellow white axial**. The possibilities can also be determined using the branch method shown on the next page, which might in this complicated problem be easier to track



b. Designate the alleles: *T* = tall, *t* = dwarf; *G* = green; *g* = yellow; *P* = purple, *p* = white; *A* = axial, *a* = terminal. The cross *Tt Gg Pp Aa* (an F_1 plant) × *tt gg pp AA* (the dwarf parent) will produce 2 phenotypes for the tall, green and purple genes, but only 1 phenotype (axial) for the fourth gene or 2 × 2 × 2 × 1 = **8 different phenotypes**. The first 3 genes will give a 1/2 dominant : 1/2 recessive ratio of the phenotypes (for example 1/2 *T* : 1/2 *t*) as this is in effect a test cross for each gene. Thus, **the proportion of each phenotype in the progeny will be 1/2 × 1/2 × 1/2 × 1 = 1/8.**

Using either of the methods described in part (a), **the progeny will be 1/8 tall green purple axial : 1/8 tall yellow purple axial : 1/8 dwarf green purple axial : 1/8 dwarf yellow purple axial : 1/8 tall green white axial : 1/8 tall yellow white axial : 1/8 dwarf green white axial : 1/8 dwarf yellow white axial**.

25. For each separate cross, determine the number of genes involved. Remember that 4 phenotypic classes in the progeny means that 2 genes control the phenotypes. Next, determine the phenotypic ratio for each gene separately. A 3:1 monohybrid ratio tells you which phenotype is dominant and that both parents were heterozygous for the trait; in contrast, a 1:1 ratio results from a testcross where the dominant parent was heterozygous.

a. There are 2 genes in this cross (4 phenotypes). One gene controls purple : white with a monohybrid ratio of 94 + 28 = 122 purple : 32 + 11 = 43 white or ~3 purple : ~1 white. The second gene controls spiny : smooth with a monohybrid ratio of 94 + 32 =126 spiny : 28 + 11 = 39 smooth or ~3 spiny : ~1 smooth. Thus, designate the alleles ***P* = purple, *p* = white; *S* = spiny, *s* = smooth**. This is a straightforward dihybrid cross: ***Pp Ss* × *Pp Ss* → 9 *P–* *S–* : 3 *P–* *ss* : 3 *pp* *S–* : 1 *pp* *ss***.

b. The 1 spiny : 1 smooth ratio indicates a test cross for the pod shape gene. Because all progeny were purple, at least one parent plant must have been homozygous for the *P* allele of the flower color gene. **The cross was either *PP Ss* × *P– ss* or *P– Ss* × *PP ss*.**

c. This is similar to part (b), but here all the progeny were spiny so at least one parent must have been homozygous for the *S* allele. The 1 purple : 1 white test cross ratio indicates that **the parents were either *Pp S–* × *pp SS* or *Pp SS* × *pp S–*.**

d. Looking at each trait individually, there are 89 + 31 = 120 purple : 92 + 27 = 119 white. A 1 purple : 1 white monohybrid ratio denotes a test cross. For the other gene, there are 89 + 92 = 181 spiny : 31 + 27 =58 smooth, or a 3 spiny : 1 smooth ratio indicating that the parents were both heterozygous for the *S* gene. **The genotypes of the parents were *pp Ss* × *Pp Ss*.**

e. There is a 3 purple : 1 white ratio among the progeny, so the parents were both heterozygous for the *P* gene. All progeny have smooth pods so the parents were both homozygous recessive *ss*. **The genotypes of the parents are *Pp ss* × *Pp ss*.**

f. There is a 3 spiny : 1 smooth ratio, indicative of a cross between heterozygotes (*Ss* × *Ss*). All progeny were white so the parents must have been homozygous recessive *pp*. **The genotypes of the parents are *pp Ss* × *pp Ss*.**

26. Three characters (genes) are analyzed in this cross. While we can usually tell which alleles are dominant from the phenotype of the heterozygote, we are not told the phenotype of the heterozygote (that is, the original pea plant that was selfed). Instead, use the monohybrid phenotypic ratios to determine which allele is dominant and which is recessive for each gene. Consider height first. There are 272 + 92 + 88 + 35 = 487 tall plants and 93 + 31 + 29 + 11 = 164 dwarf plants. This is a ratio of ~3 tall : ~1 dwarf, indicating that **tall is dominant**. Next consider pod shape, where there are 272 + 92 + 93 + 31 = 488 inflated pods and 88 + 35 + 29 + 11 = 163 flat pods, or approximately 3 inflated : 1 flat, so **inflated is dominant**. Finally, consider flower color. There were 272 + 88 + 93 + 29 + 11 = 493 purple flowers and 92 + 35 + 31 + 11 = 169 white flowers, or ~3 purple : ~1 white. Thus, **purple is dominant**.

27. Diagram each of these crosses, remembering that you were told that tiny wings = *t,* normal wings = *T,* narrow eye = *n,* and oval (normal) eye = *N*. You thus know that one gene determines the wing trait and one gene determines the eye trait, and you further know the dominance relationship between the alleles of each gene.

In cross 1, all of the parents and offspring show the tiny wing phenotype so there is no variability in the gene controlling this trait, and all flies in this cross are *tt*. Note that the eye phenotypes in the offspring are seen in a ratio of 3 oval : 1 narrow. This phenotypic monohybrid ratio means that both parents are heterozygous for the gene (*Nn*). Thus **the genotypes for the parents in cross 1 are: *tt Nn* ♂ × *tt Nn* ♀.**

In cross 2 consider the wing trait first. The female parent is tiny (*tt*) so this is a test cross for the wings. The offspring show both tiny and normal in a ratio of 82 : 85 or a ratio of 1 tiny : 1 normal. Therefore the normal male parent must be heterozygous for this gene (*Tt*). For eyes the narrow parent is homozygous recessive (*nn*) so again this is a test cross for this gene. Again both eye phenotypes are seen in the offspring in a ratio of

1 oval : 1 narrow, so the oval female parent is a *Nn* heterozygote. Thus **the genotypes for the parents in cross 2 are: *Tt nn* ♂ × *tt Nn* ♀.**

Consider the wing phenotype in the offspring of cross 3. Both wing phenotypes are seen in a ratio of 64 normal flies : 21 tiny or a 3 normal : 1 tiny. Thus both parents are *Tt* heterozygotes. The male parent is narrow (*nn*), so cross 3 is a test cross for eyes. Both phenotypes are seen in the offspring in a 1 normal : 1 narrow ratio, so the female parent is heterozygous for this gene. **The genotypes of the parents in cross 3 are: *Tt nn* ♂ × *Tt Nn* ♀.**

When examining cross 4 you notice a monohybrid phenotypic ratio of 3 normal : 1 tiny for the wings in the offspring. Thus both parents are heterozygous for this gene (*Tt*). Because the male parent has narrow eyes (*nn*), this cross is a test cross for eyes. All of the progeny have oval eyes, so the female parent must be homozygous dominant for this trait. Thus **the genotypes of the parents in cross 4 are: *Tt nn* ♂ × *Tt NN* ♀.**

28. **a.** Analyze each gene separately: *Tt* × *Tt* will give 3/4 *T*– (normal wing) offspring. The cross *nn* x *Nn* will give 1/2 *N*– (normal eye) offspring. To calculate the probability of the normal offspring apply the product rule to the normal portions of the monohybrid ratios by multiplying these two fractions: 3/4 *T*– × 1/2 *N*– = 3/8 *T*– *N*–. Thus **3/8 of the offspring of this cross will have normal wings and oval eyes**.

b. Diagram the cross:

Tt nn ♀ × *Tt Nn* ♂ → ?

Find the phenotypic monohybrid ratio separately for each gene in the offspring. Then multiply these monohybrid ratios to find the phenotypic dihybrid ratio. A cross of *Tt* × *Tt* → 3/4 *T*– (normal wings) : 1/4 *tt* (tiny wings). For the eyes the cross is *nn* × *Nn* → 1/2 *N*– (oval) : 1/2 *nn* (narrow). Applying the product rule gives 3/8 *T*– *N*– (normal oval) : 3/8 *T*– *nn* (normal narrow) : 1/8 *tt N*– (tiny oval) : 1/8 *tt nn* (tiny narrow). When you multiply each fraction by 200 progeny you will see **75 normal oval : 75 normal narrow : 25 tiny oval : 25 tiny narrow**.

29. **a.** **The protein specified by the pea color gene is an enzyme called Sgr,** which is required for the breakdown of the green pigment chlorophyll. (See Fig. 2.20b on p. 29.)

b. **The *y* allele could be a null allele** because it does not specify the production of any of the Sgr enzyme.

c. The *Y* allele is dominant because in the heterozygote, **the single *Y* allele will lead to the production of some Sgr enzyme,** even if the *y* allele cannot specify any Sgr. **The amount of the Sgr enzyme made in heterozygotes is sufficient for yellow color.**

d. **In *yy* peas, the green chlorophyll cannot be broken down,** so this pigment stays in the peas, which remain green in color.

e. If the amount of Sgr protein is proportional to the number of functional copies of the gene, then *YY* homozygotes should have twice the amount of Sgr protein as do *Yy* heterozygotes. Yet both *YY* and *Yy* peas are yellow. These observations suggest

that **half the normal amount of Sgr enzyme is sufficient for the pea to break down enough chlorophyll that the pea will still be yellow.**

f. Just as was seen in part (e), for many genes (including that for pea color), half the amount of the protein specified by the gene is sufficient for a normal phenotype. Thus, in most cases, even if the gene is essential, heterozygotes for null alleles will survive. **The advantage of having two copies of essential genes is then that even if one normal allele becomes mutated (changed) so that it becomes a null allele, the organism can survive because half the normal amount of gene product is usually sufficient for survival.**

g. **Yes, a single pea pod could contain peas with different phenotypes** because a pod is an ovary that contains several ovules (eggs), and each pea represents a single fertilization event involving one egg and one sperm (from one pollen grain). If the female plant was *Yy*, or *yy*, then it is possible that some peas in the same pod would be yellow and others green. For example, fertilization of a *y* egg with *Y* pollen would yield a yellow pea, but if the pollen grain was *y*, the pea would be green. However, a pea pod could not contain peas with different phenotypes if the female plant was *YY*, because all the peas produced by this plant would be yellow.

h. **Yes, it is possible that a pea pod could be different in color from a pea growing within it.** One reason is that, as just seen in part (g), a single pod can contain green and yellow peas. But a more fundamental reason is that one gene controls the phenotype of pea color, while a different gene controls the separate phenotype of pod color.

30. If the alleles of the pea color and pea shape genes inherited from a parent in the P generation always stayed together and never separated, then the gametes produced by the doubly heterozygous F_1 individuals in Fig. 2.15 on p. 25 would be either *Y R* or *y r*. (Note that only two possibilities would exist, and these would be in equal frequencies.) On a Punnett square (male gametes shaded in blue, female gametes in red):

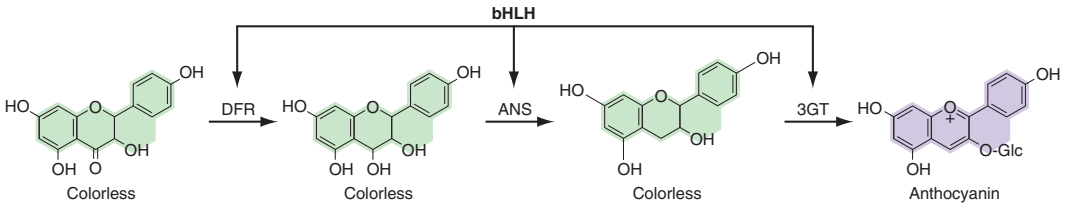
	Y R ½	*y r* ½
Y R ½	*YY RR* ¼	*Yy Rr* ¼
y r ½	*Yy Rr* ¼	*yy rr* ¼

Thus **the genotypic ratios of the F_2 progeny would be ¼ *YY RR*, ½ *Yy Rr*, and ¼ *yy rr*. The phenotypic ratios among the F_2 progeny would be ¾ yellow round and ¼ green wrinkled.** These results make sense because if the alleles of the two genes were always inherited as a unit, you would expect the same ratios as in a monohybrid cross.

31. Similar to what you saw in Fig. 2.20 on p. 29, **the most likely biochemical explanation is that the dominant allele *L* specifies functional G3βH enzyme, while the recessive allele *l* is incapable of specifying any functional enzyme** (in

nomenclature you will see in later chapters, *l* is a *null allele*). The functional enzyme can synthesize the growth hormone gibberellin, so plants with the *L* allele are tall. **Even half the normal amount of this enzyme is sufficient for the tall phenotype, explaining why *L/l* heterozygotes are tall.**

32. *Note:* Your copy of the text might be missing the key figure referred to in this Problem. That figure follows here:



a. As in Problem 31 above, **the dominant allele *P* most likely specifies a functional product (in this case, the protein bHLH), while the recessive *p* allele cannot specify any functional protein.** The fact that the hybrid is purple (as shown on Fig. 2.8 on p. 19) indicates that half the normal amount of active bHLH protein is sufficient for purple color.

b. **Yes, flower color could potentially be controlled by genes specifying the enzymes DFR, ANS, or 3GT in addition to the gene specifying the bHLH protein.** Alleles specifying functional enzymes would yield purple color, while those that could not produce functional enzymes would cause white color. It is likely that the alleles for purple would be dominant.

Section 2.3

33. a. **Recessive** - two unaffected individuals have an affected child (*aa*). Therefore the parents involved in the consanguineous marriage must both be carriers (*Aa*).

b. **Dominant** - the trait is seen in each generation and every affected person (*A*–) has an affected parent. Note that III-3 is unaffected (*aa*) even though both his parents are affected; this would not be possible for a recessive trait. The term "carrier" is not applicable, because everyone with a single *A* allele shows the trait.

c. **Recessive** - two unaffected, carrier parents (*Aa*) have an affected child (*aa*), as in part (a).

34. a. Cutis laxa must be a recessive trait because affected child II-4 has normal parents. Because II-4 is affected she must have received a disease allele (*CL*) from both parents. The mother (I-3) and the father (I-4) are both heterozygous (CL^+ *CL*). **The trait is thus recessive.**

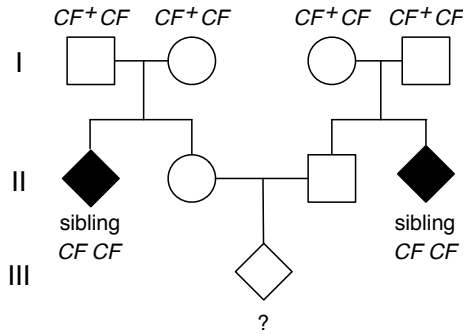
b. You are told that this trait is rare, so unrelated people in the pedigree, like I-2, are almost certainly homozygous normal (CL^+ CL^+). Diagram the cross that gives rise to II-2: *CL CL* (I-1) × CL^+ CL^+ (I-2) → CL^+ *CL*. Thus **the probability that II-**

2 is a carrier is very close to 100%. (In Chapter 21 you will find the definition of a term called the *allele frequency;* if the value of the allele frequency in the population under study is known, you can calculate the very low likelihood that II-2 is a carrier.)

c. As described in part (a) both parents in this cross are carriers: CL^+ *CL* × CL^+ *CL*. II-3 is not affected so he cannot be the *CL CL* genotype. Therefore there is a 1/3 probability that he is the CL^+ CL^+ genotype and a **2/3 probability that he is a carrier (CL^+ *CL*).**

d. As shown in part (b), II-2 must be a carrier (CL^+ *CL*). In order to have an affected child II-3 must also be a carrier. The probability of this is 2/3 as shown in part (c). The probability of two heterozygous parents having an affected child is 1/4. Apply the product rule to these probabilities: 1 probability that II-2 is CL^+ *CL* × 2/3 probability that II-3 is CL^+ *CL* × 1/4 probability of an affected child from a mating of two carriers = 2/12 = **1/6**.

35. Diagram the cross! In humans this is usually done as a pedigree. Remember that the affected siblings must be *CF CF*.



a. **The probability that II-2 is a carrier is 2/3**. Both families have an affected sibling, so both sets of parents (that is, all the people in generation I) must have been carriers. Thus, the expected genotypic ratio in the children is 1/4 affected : 1/2 carrier : 1/4 homozygous normal. II-2 is NOT affected, so she cannot be *CF CF*. Of the remaining possible genotypes, 2 are heterozygous. There is therefore a 2/3 chance that she is a carrier.

b. **The probability that II-2 × II-3 will have an affected child** is 2/3 (the probability that the mother is a carrier as seen in part [a]) × 2/3 (the probability the father is a carrier using the same reasoning) × 1/4 (the probability that two carriers can produce an affected child) **= 1/9**.

c. The probability that both parents are carriers and that their child will be a carrier is 2/3 × 2/3 × 1/2 = 2/9 (using the same reasoning as in part [b], except asking that the child be a carrier instead of affected). However, it is also possible for CF^+ CF^+ × CF^+ *CF* parents to have children that are carriers. Remember that there are two possible ways for this particular mating to occur: homozygous father × heterozygous mother or vice versa. Thus the probability of this sort of mating is 2 × 1/3 (the probability that a particular parent is CF^+ CF^+) × 2/3 (the probability that

the other parent is *CF*$^+$ *CF* × 1/2 (the probability such a mating could produce a carrier child) = 2/9. **The probability that a child could be carrier** from either of these two scenarios (where both parents are carriers or where only one parent is a carrier) is the sum of these mutually exclusive events, or 2/9 + 2/9 **= 4/9**.

36. **a.** Because the disease is rare the affected father is most likely to be heterozygous (*HD HD*$^+$). **There is a 1/2 chance that the son** inherited the *HD* allele from his father and **will develop the disease.**

b. **The probability of an affected child is:** 1/2 (the probability that Joe is *HD HD*$^+$) × 1/2 (the probability that the child inherits the *HD* allele if Joe is *HD HD*$^+$) = **1/4**.

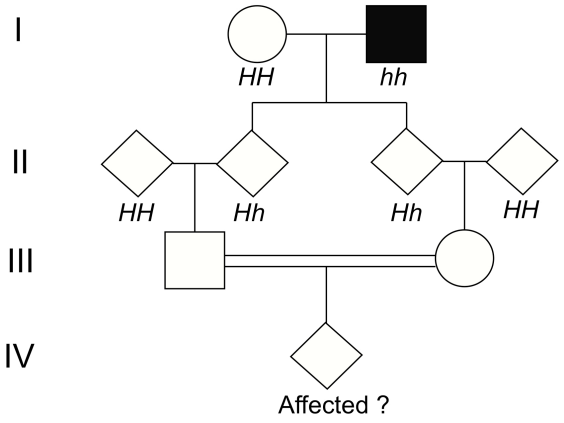
37. **The trait is recessive** because pairs of unaffected individuals (I-1 × I-2 as well as II-3 × II-4) had affected children (II-1, III-1, and III-2). There are also two cases in which an unrelated individual must have been a carrier (II-4 and either I-1 or I-2), so **the disease allele appears to be common in the population.**

38. **a.** **The inheritance pattern seen in Fig. 2.22 on p. 32 could be caused by a rare dominant mutation**. In this case, the affected individuals would be heterozygous (*HD*$^+$ *HD*) and the normal individuals would be *HD*$^+$ *HD*$^+$. Any mating between an affected individual and an unaffected individual would give 1/2 normal (*HD*$^+$*HD*$^+$) : 1/2 affected (*HD*$^+$ *HD*) children. **However, the same pattern of inheritance could be seen if the disease were caused by a common recessive mutation**. In the case of a common recessive mutation, all the affected individuals would be *HD HD*. Because the mutant allele is common in the population, most or even all of the unrelated individuals could be assumed to be carriers (*HD*$^+$ *HD*). Matings between affected and unaffected individuals would then also yield phenotypic ratios of progeny of 1/2 normal (*HD*$^+$ *HD*) : 1/2 affected (*HD HD*).

b. Determine the phenotype of the 14 children of III-6 and IV-6. If the disease is due to a recessive allele, then III-6 and IV-6 must be homozygotes for this recessive allele, and all their children must have the disease. If the disease is due to a dominant allele, then III-6 and IV-6 must be heterozygotes (because they are affected but they each had one unaffected parent), and 1/4 of their 14 children would be expected to be unaffected.

Alternatively, you could look at the progeny of matings between unaffected individuals in the pedigree such as III-1 and an unaffected spouse. If the disease were due to a dominant allele, these matings would all be homozygous recessive × homozygous recessive and would never give affected children. If the disease is due to a recessive mutation, then many of these individuals would be carriers, and if the trait is common then at least some of the spouses would also be carriers, so such matings could give affected children.

39. Diagram the cross by drawing a pedigree:



a. Assuming the disease is very rare, the first generation is *HH* unaffected (I-1) × *hh* affected (I-2). Thus, both of the children (II-2 and II-3) must be carriers (*Hh*). Again assuming this trait is rare in the population, those people marrying into the family (II-1 and II-4) are homozygous normal (*HH*). Therefore, the probability that III-1 is a carrier is 1/2; III-2 has the same chance of being a carrier. **Thus the probability that a child produced by these two first cousins would be affected** is 1/2 (the probability that III-1 is a carrier) × 1/2 (the probability that III-2 is a carrier) × 1/4 (the probability the child of two carriers would have an *hh* genotype) **= 1/16 = 0.0625.**

b. If 1/10 people in the population are carriers, then the probability that II-1 and II-4 are *Hh* is 0.1 for each. In this case an affected child in generation IV can only occur if III-1 and III-2 are both carriers. III-1 can be a carrier as the result of 2 different matings: (i) II-1 homozygous normal × II-2 carrier or (ii) II-1 carrier × II-2 carrier. (Note that whether I-1 is *HH* or *Hh,* II-2 must be a carrier because of the normal phenotype (II-2 cannot be *hh*) and the fact that one parent was affected.) The probability of III-1 being a carrier is thus the probability of mating (i) × the probability of generating a *Hh* child from mating (i) + the probability of mating (ii) × the probability of generating an *Hh* child from mating (ii) = 0.9 (the probability II-1 is *HH*, which is the probability for mating [i]) x 1/2 (the probability that III-1 will inherit *h* in mating [i]) + 0.1 (the probability II-1 is *H,* which is the probability for mating [ii]) × 2/3 (the probability that III-1 will inherit *h* in mating [ii]; remember that III-1 is known not to be *hh*) = 0.45 + 0.067 = 0.517. The chance that III-2 will inherit *h* is exactly the same. **Thus, the probability that IV-1 is *hh*** = 0.517 (the probability III-1 is *Hh*) × 0.517 (the probability that III-2 is *Hh*) × 1/4 (the probability the child of two carriers will be *hh*) **= 0.067. This number is slightly higher than the answer to part (a), which was 0.0625, so the increased likelihood that II-1 or II-4 is a carrier makes it only slightly more likely that IV-1 will be affected.**

40. a. Both diseases are known to be rare, so normal people marrying into the pedigree are assumed to be homozygous normal. **Nail-patella (*N*) syndrome is dominant** because all affected children have an affected parent. **Alkaptonuria (*a*) is recessive** because the affected children are the result of a consanguineous mating between 2

unaffected individuals (III-3 × III-4). Because alkaptonuria is a rare disease, it makes sense to assume that III-3 and III-4 inherited the same *a* allele from a common ancestor. Genotypes: **I-1 *nn Aa*; I-2 *Nn AA* (or I-1 *nn AA* and I-2 *Nn Aa*); II-1 *nn AA*; II-2 *nn Aa*; II-3 *Nn A–*; II-4 *nn A–*; II-5 *Nn Aa*; II-6 *nn AA*; III-1 *nn AA*; III-2 *nn A–*; III-3 *nn Aa*; III-4 *Nn Aa*; III-5 *nn A–*; III-6 *nn A–*; IV-1 *nn A–*; IV-2 *nn A–*; IV-3 *Nn A–*; IV-4 *nn A–*; IV-5 *Nn aa*; IV-6 *nn aa*; IV-7 *nn A–*.**

b. The cross is *nn A–* (IV-2) × *Nn aa* (IV-5). The ambiguity in the genotype of IV-2 is due to the uncertainty of her father's genotype (III-2). His parents' genotypes are *nn AA* (II-1) × *nn Aa* (II-2) so there is a 1/2 chance III-2 is *nn AA* and a 1/2 chance he is *nn Aa*. Thus, for each of the phenotypes below you must consider both possible genotypes for IV-2. For each part below, calculate the probability of the child inheriting the correct gametes from IV-2 × the probability of obtaining the correct gametes from IV-5 to give the desired phenotype. If both the possible IV-2 genotypes can produce the needed gametes, you will need to sum the two probabilities.

For the child to have both syndromes (*N– aa*), IV-2 would have to contribute an *n a* gamete. This could only occur if IV-2 were *nn Aa*. The probability IV-2 is *nn Aa* is 1/4: For IV-2 to be *nn Aa,* III-2 would have had to be *nn Aa* and would also have had to give an *n a* gamete to IV-2. The probability of each of those events is 1/2, so the chance of both of them occurring is 1/2 × 1/2 = 1/4. (Note that we can assume that II-2 is *nn Aa* because III-3 must have given two of her children an *a* allele. Therefore, both II-2 and III-3 must be *nn Aa*.) *If* IV-2 is *nn Aa,* the chance that he would give a child an *n* a gamete is 1/2. The probability that IV-5 would supply an *N a* gamete is also 1/2. Thus, **the probability that the child would have both syndromes is 1/4 × 1/2 × 1/2 = 1/16.** There is no need to sum probabilities in this case because IV-2 cannot produce an *n a* gamete if his genotype is *nn AA*.

For the child to have only nail-patella syndrome (*N– A–*), IV-2 would have to provide an *n A* gamete and IV-5 an *N a* gamete. This could occur if IV-2 were *nn Aa*; the probability is 1/4 (the probability IV-2 is *Aa*) × 1/2 (the probability of an *A* gamete if IV-2 is *Aa*) × 1/2 (the probability of an *N a* gamete from IV-5] = 1/16. This could also occur if IV-2 were *nn AA*. Here, the probability is 3/4 (the probability IV-2 is *nn AA*) × 1 (the probability of an *n A* gamete if IV-2 is *nn AA*) × 1/2 (the probability of an *N a* gamete from IV-5) = 3/8. Summing the probabilities for the two mutually exclusive IV-2 genotypes, **the probability that the child of IV-2 and IV-5 would have only nail-patella syndrome** is 1/16 + 3/8 **= 7/16.**

For the child to have just alkaptonuria (*nn aa*), IV-2 would have to contribute an *n a* gamete. This could only occur if IV-2 were *nn Aa*. The probability IV-2 is *nn Aa* is 1/4, and the probability of receiving an *n a* gamete from IV-2 if he is *nn Aa* is 1/2. The probability that IV-5 would supply an *n a* gamete is also 1/2. Thus, **the probability that the child of IV-2 and IV-5 would have only alkaptonuria** is 1/4 x 1/2 x 1/2 **= 1/16.** There is no need to sum probabilities in this case because IV-2 cannot produce an *n a* gamete if his genotype is *nn AA*.

The probability of neither defect is 1 – (sum of the first 3) = 1 - (1/16 + 7/16 + 1/16) = 1 - 9/16 **= 7/16.** You can make this calculation because there are only the four possible outcomes and you have already calculated the probabilities of three of them.

41. Diagram the cross(es):

midphalangeal	×	midphalangeal	→	1853 midphalangeal : 209 normal
M?	×	*M*?	→	*M*? : *mm*

The following crosses are possible:

MM	×	*MM*	→	all *MM*
Mm	×	*MM*	→	all *M*-
MM	×	*Mm*	→	all *M*-
Mm	×	*Mm*	→	3/4 *M*- : 1/4 *mm*

The 209 normal children must have arisen from the last cross, so approximately 3 x 209 = 630 children should be their *M*- siblings. Thus, about 840 of the children or **~40% came from the last mating** and the other 60% of the children were the result of one or more of the other matings. This problem illustrates that much care in interpretation is required when the results of many matings in mixed populations are reported (as opposed to the results of matings where individuals have defined genotypes).

42. **a.** An equally likely possibility exists that any child produced by this couple will be affected (A) or unaffected (U) . For two children, the possibilities are: AA, AU, UA, UU. The case in which only the second child is affected is UA; this is one of the four possibilities so **the probability that only the second child is affected is 1/4.**

b. From the list just presented in part (a), you can see that there are two possibilities in which only one child is affected: AU and UA. The probability that either of these two mutually exclusive possibilities will occur is the sum of their independent probabilities: 1/4 + 1/4 = **1/2.**

c. From the list just presented in part (a), you can see that there is only one possibility in which no child is affected: UU. The probability of this event is **1/4.**

d. If this family consisted of 10 children, **the case in which only the second child out of 10 is affected** (that is, UAUUUUUUUU) **has a probability of $1/2^{10}$ = 1/1024 = ~0.00098.** This probability is based on the facts that each birth is an independent event, and that the chance of U and A are each 1/2. We thus use the product rule to determine the chance that each of those 10 independent events will occur in a particular way – a particular birth order.

In a family of ten children, 10 different outcomes (birth orders) exist that satisfy the criterion that only 1 child has the disease. Only the first child could have the disease, only the second child, only the third child, etc. :

1. **A**UUUUUUUUU
2. U**A**UUUUUUUU
3. UU**A**UUUUUUU
4. UUU**A**UUUUUU
5. UUUU**A**UUUUU
6. UUUUU**A**UUUU
7. UUUUUU**A**UUU
8. UUUUUUU**A**UU
9. UUUUUUUU**A**U
10. UUUUUUUUU**A**

We have already calculated that the chance of one of these outcomes in particular (#2) is 1/1024. As each of the 10 possibilities has the same probability, **the probability that only one child is affected would be 10 x (1/1024) = 10/1024 = ~0.0098.**

Only one possibility exists in which no child would be affected (UUUUUUUUUU), **and just like any other specific outcome, this one has a probability of 1/1024 = ~0.00098.**

e. One way to determine the probability that four children in a family of ten will have the disease is to write down all possible outcomes for the criterion, as we did above for the second answer in part (d). Then, also as we did above, sum their individual probabilities, each of which is $(1/2)^{10}$ just as before. If you start to do this……

1. **AAAA**UUUUUU
2. **AAA**U**A**UUUUU
3. **AAA**UU**A**UUUU
4. **AAA**UUU**A**UUU
5. **AAA**UUUU**A**UU
6. **AAA**UUUUU**A**U
7. **AAA**UUUUUU**A**
8. **AA**U**AA**UUUUU
9. **AA**U**A**U**A**UUU
10. **AA**U**A**UU**A**UU

etc.

…..you will realize fairly quickly that writing down every possible birth order in this case is quite a difficult task and you are likely to miss some outcomes. In short – this is not a good way to find the answer! For questions like this, it is far preferable to use a mathematical tool called the **binomial theorem** in order to determine the number of possible outcomes that satisfy the criterion. The binomial theorem looks like this:

P (**X** will occur **s** times, and **Y** will occur **t** times, in **n** trials) =

$$\frac{\mathbf{n}!}{\mathbf{s}! \times \mathbf{t}!} (\mathbf{p}^{\mathbf{s}} \times \mathbf{q}^{\mathbf{t}})$$

P = the probability of what is in parentheses
p = P(**X**)
q = P(**Y**)

X and **Y** are the only two possibilities, so **p** + **q** = 1.
Also, **s** + **t** = **n**.

Remember that **!** means *factorial*: for example, 5! = 5 × 4 × 3 × 2 × 1.

To apply the binomial theorem to the question at hand (assuming you can still remember what the question was!), we'll let **X** = a child has the disease (A), and **Y** = a child does not have the disease (U). Then, **s** = 4, **t** = 6, **n** = 10, **p** = ½, and **q** = ½. The answer to the question is then:

P (4 A and 6 U children out of 10) = $(10! / 4! \times 6!) (1/2^4 \times 1/2^6)$.

Notice that $(\mathbf{p}^{\mathbf{s}} \times \mathbf{q}^{\mathbf{t}}) = (1/2^4 \times 1/2^6) = 1/2^{10}$. This factor of the binomial theorem equation is the probability of each single birth order, as we saw previously in part (d) above. To get the answer to our question, we need to multiply this factor (the probability of each single birth order) by the number of different birth orders that satisfy our criterion. From the equation in the box above, this second factor is $[\mathbf{n}!/(\mathbf{s}! \times \mathbf{t}!)] = (10! / 4! \times 6!) = 210$. Thus, **the probability (P) of only 4 children having the disease in a family of 10 children is $1/2^{10} \times 210 \approx$ 21%.**

43. **In the case of cystic fibrosis, the alleles causing the disease do not specify active protein** [in this case, the cystic fibrosis transmembrane receptor (CFTR)]. Some *CF* disease alleles specify defective CFTR proteins that do not allow the passage of chloride ions, while other *CF* disease alleles do not specify any CFTR protein at all. As you will learn in a later chapter, such alleles are called *loss-of-function* alleles. In a heterozygote, the normal CF^+ allele still specifies active CFTR protein, which allows for the passage of chloride ions. Because the phenotype of the heterozygote is unaffected, the amount of active CFTR protein allows passage of enough chloride ions for the cells to function normally. Again as you will see, most loss-of-function alleles are recessive to normal alleles for similar reasons. (But it is important to realize that important exceptions are known in which loss-of-function mutations are actually dominant to normal alleles.)

In the case of Huntington disease, the disease-causing allele is dominant. The reason is that **the huntingtin protein specified by this *HD* allele has, in addition to its normal function** (which is not entirely understood), **a second function that is toxic to nerve cells.** This makes the *HD* disease allele a *gain-of-function* allele. The reason *HD* is dominant to HD^+ is that the protein specified by the disease allele will be toxic to cells even if the cells have normal huntingtin specified by the normal allele. Most (but again not all) gain-of-function mutations are dominant for similar reasons.