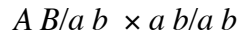


1. You perform the following cross and are told that the two genes are 10 m.u. apart.



Among their progeny, 10 percent should be recombinant ( $A b/a b$  and  $a B/a b$ ) and 90 percent should be parental ( $A B/a b$  and  $a b/a b$ ). Therefore,  $A B/a b$  should represent  $1/2$  of the parentals or 45 percent.

2. P  $A d / A d \times a D / a D$   
 F<sub>1</sub>  $A d / a D$   
 F<sub>2</sub> 1  $A d / A d$  phenotype: A d  
 2  $A d / a D$  phenotype: A D  
 1  $a D / a D$  phenotype: a D

3. P  $R S/r s \times R S/r s$

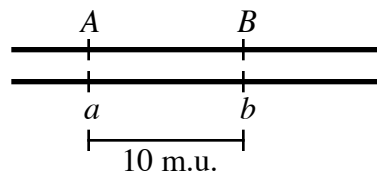
gametes  $1/2 (1 - 0.35) R S$   
 $1/2 (1 - 0.35) r s$   
 $1/2 (0.35) R s$   
 $1/2 (0.35) r S$

F<sub>1</sub> genotypes 0.1056  $R S/R S$  0.1138  $r s/r S$   
 0.1056  $r s/r s$  0.1138  $r s/R s$   
 0.2113  $R S/r s$  0.0306  $R s/R s$   
 0.1138  $R S/r S$  0.0306  $r S/r S$   
 0.1138  $R S/R s$  0.0613  $R s/r S$

F<sub>1</sub> phenotypes 0.6058 R S  
 0.1056 r s  
 0.1444 R s  
 0.1444 r S

5. Because only parental types are recovered, the two genes must be tightly linked and recombination must be very rare. Knowing how many progeny were looked at would give an indication of how close the genes are.
6. The problem states that a female that is  $A/a \cdot B/b$  is test crossed. If the genes are unlinked, they should assort independently and the four progeny classes should be present in roughly equal proportions. This is clearly not the case. The  $A/a \cdot B/b$  and  $a/a \cdot b/b$  classes (the parentals) are much more common than the  $A/a \cdot b/b$  and  $a/a \cdot B/b$  classes (the recombinants). The two genes are on the same chromosome and are 10 map units apart.

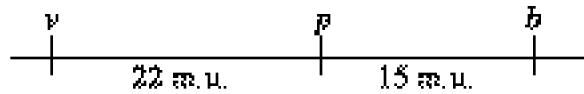
$$RF = 100\% \times (46 + 54)/1000 = 10\%$$



7. The cross is  $A/A \cdot B/B \times a/a \cdot b/b$ . The  $F_1$  would be  $A/a \cdot B/b$ .
- If the genes are unlinked, all four progeny classes from the test cross (including  $a/a ; b/b$ ) would equal 25 percent.
  - With completely linked genes, the  $F_1$  would produce only  $A B$  and  $a b$  gametes. Thus, there would be a 50 percent chance of having  $a b/a b$  progeny from a test cross of this  $F_1$ .
  - If the two genes are linked and 10 map units apart, 10 percent of the test cross progeny should be recombinants. Since the  $F_1$  is  $A B/a b$ ,  $a b$  is one of the parental classes ( $A B$  being the other) and should equal  $1/2$  of the total non-recombinants or 45 percent.
  - 38 percent (see part c)
8. Meiosis is occurring in an organism that is  $C d/c D$ , ultimately producing haploid spores. The parental genotypes are  $C d$  and  $c D$ , in equal frequency. The recombinant types are  $C D$  and  $c d$ , in equal frequency. Eight map units means 8 percent recombinants. Thus,  $C D$  and  $c d$  will each be present at a frequency of 4 percent, and  $C d$  and  $c D$  will each be present at a frequency of  $(100\% - 8\%)/2 = 46\%$ .
- 4 percent
  - 4 percent
  - 46 percent
  - 8 percent

10. a. The three genes are linked.
- b. Comparing the parentals (most frequent) with the double crossovers (least frequent), the gene order is  $v p b$ . There were 2200 recombinants between  $v$  and  $p$ , and 1500 between  $p$  and  $b$ . The general formula for map units is

$$\text{m.u.} = 100\%(\text{number of recombinants})/\text{total number of progeny}$$
 Therefore, the map units between  $v$  and  $p = 100\%(2200)/10,000 = 22 \text{ m.u.}$ ,  
 and the map units between  $p$  and  $b = 100\%(1500)/10,000 = 15 \text{ m.u.}$   
 The map is



- c.  $I = 1 - \text{observed double crossovers}/\text{expected double crossovers}$   
 $= 1 - 132/(0.22)(0.15)(10,000)$   
 $= 1 - 0.4 = 0.6$
11. P  $a b c/a b c \times a^+ b^+ c^+/a^+ b^+ c^+$
- $F_1$   $a^+ b^+ c^+/a b c \times a^+ b^+ c^+/a b c$

F <sub>2</sub>	1364	$a^+ b^+ c^+$
	365	$a b c$
	87	$a b c^+$
	84	$a^+ b^+ c$
	47	$a b^+ c^+$
	44	$a^+ b c$
	5	$a b^+ c$
	4	$a^+ b c^+$

This problem is somewhat simplified by the fact that recombination does not occur in male *Drosophila*. Also, only progeny that received the  $a b c$  chromosome from the male will be distinguishable among the F<sub>2</sub> progeny.

- a. Because you cannot distinguish between  $a^+ b^+ c^+/a^+ b^+ c^+$  and  $a^+ b^+ c^+/a b c$ , use the frequency of  $a b c/a b c$  to estimate the frequency of  $a^+ b^+ c^+$  (parental) gametes from the female.

parentals	730	(2 × 365)
CO $a-b$ :	91	( $a b^+ c^+, a^+ b c = 47 + 44$ )
CO $b-c$ :	171	( $a b c^+, a^+ b^+ c = 87 + 84$ )
DCO:	$\frac{9}{1001}$	( $a^+ b c^+, a b^+ c = 4 + 5$ )

$$a-b: 100\%(91 + 9)/1001 = 10 \text{ m.u.}$$

$$b-c: 100\%(171 + 9)/1001 = 18 \text{ m.u.}$$

- b. Coefficient of coincidence = (observed DCO)/(expected DCO)  
 $= 9/[(0.1)(0.18)(1001)] = 0.5$

13. By comparing the most frequent classes (parental:  $+ v lg, b + +$ ) with the least frequent classes (DCO:  $+ + +, b v lg$ ) the gene order can be determined. The gene in the middle switches with respect to the other two, yielding the following sequence:  $v b lg$ . Now the cross can be written

$$P \ v b^+ lg/v^+ b lg^+ \times v b lg/v b lg$$

F <sub>1</sub>	305	$v b^+ lg/v b lg$	parental
	275	$v^+ b lg^+/v b lg$	parental
	128	$v^+ b lg/v b lg$	CO $b-lg$
	112	$v b^+ lg^+/v b lg$	CO $b-lg$
	74	$v^+ b^+ lg/v b lg$	CO $v-b$
	66	$v b lg^+/v b lg$	CO $v-b$
	22	$v^+ b^+ lg^+/v b lg$	DCO
	18	$v b lg/v b lg$	DCO

$$v-b: 100\%(74 + 66 + 22 + 18)/1000 = 18.0 \text{ m.u.}$$

$$b-lg: 100\%(128 + 112 + 22 + 18)/1000 = 28.0 \text{ m.u.}$$

c.c. = observed DCO/expected DCO =  $(22 + 18)/(0.28)(0.18)(1000) = 0.79$

15. a. The hypothesis is that the genes are not linked. Therefore, a 1:1:1:1 ratio is expected.

b.  $\chi^2 = (54-50)^2/50 + (47-50)^2/50 + (52-50)^2/50 + (47-50)^2/50$   
 $= 0.32 + 0.18 + 0.08 + 0.18 = 0.76$

c. With 3 degrees of freedom, the *p* value is between 0.50 and 0.90.

d. Between 50 percent and 90 percent of the time values this extreme from the prediction would be obtained by chance alone.

e. Accept the initial hypothesis.

f. Because the  $\chi^2$  value was insignificant, the two genes are assorting independently. The genotypes of all individuals are

P  $dp^+/dp^+ ; e/e \times dp/dp ; e^+/e^+$

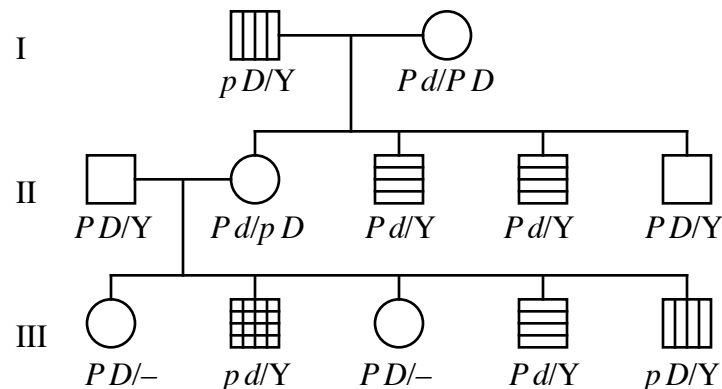
F<sub>1</sub>  $dp^+/dp ; e^+/e$

tester  $dp/dp ; e/e$

progeny	long, ebony	$dp^+/dp ; e/e$
	long, gray	$dp^+/dp ; e^+/e$
	short, gray	$dp/dp ; e^+/e$
	short, ebony	$dp/dp ; e/e$

19. a. Note that only males are affected by both disorders. This suggests that both are X-linked recessive disorders. Using *p* for protan and *P* for non-protan, and *d* for deutan and *D* for non-deutan, the inferred genotypes are listed on the pedigree below. The Y chromosome is shown, but the X is represented by the alleles carried.

b. Individual II-2 must have inherited both disorders in the trans configuration (on separate chromosomes). Therefore, individual III-2 inherited both traits as the result of recombination (crossing-over) between his mother's X chromosomes.



- c. Because both genes are X-linked, this represents crossing-over. The progeny size is too small to give a reliable estimate of recombination.

22. a. If the genes are unlinked, the cross becomes

$$P \quad \text{hyg/hyg ; her/her} \times \text{hyg}^+/\text{hyg}^+ ; \text{her}^+/\text{her}^+$$

$$F_1 \quad \text{hyg}^+/\text{hyg} ; \text{her}^+/\text{her} \times \text{hyg}^+/\text{hyg} ; \text{her}^+/\text{her}$$

$$F_2 \quad \begin{array}{ll} 9/16 & \text{hyg}^+/- ; \text{her}^+/- \\ 3/16 & \text{hyg}^+/- ; \text{her/her} \\ 3/16 & \text{hyg/hyg} ; \text{her}^+/- \\ 1/16 & \text{hyg/hyg} ; \text{her/her} \end{array}$$

So only  $1/16$  (or 6.25 percent) of the seeds would be expected to germinate.

- b. and c. No. More than twice the expected seeds germinated so assume the genes are linked. The cross then becomes

$$P \quad \text{hyg her/hyg her} \times \text{hyg}^+ \text{her}^+/\text{hyg}^+ \text{her}^+$$

$$F_1 \quad \text{hyg}^+ \text{her}^+/\text{hyg her} \times \text{hyg}^+ \text{her}^+/\text{hyg her}$$

$$F_2 \quad 13 \text{ percent} \quad \text{hyg her/hyg her}$$

Because this class represents the combination of two parental chromosomes, it is equal to

$$\text{and} \quad p(\text{hyg her}) \times p(\text{hyg her}) = (1/2 \text{ parentals})^2 = 0.13$$

$$\text{parentals} = 0.72 \quad \text{so recombinants} = 1 - 0.72 = 0.28$$

Therefore, a test cross of  $\text{hyg}^+ \text{her}^+/\text{hyg her}$  should give

$$\begin{array}{ll} 36\% & \text{hyg}^+ \text{her}^+/\text{hyg her} \\ 36\% & \text{hyg her/hyg her} \\ 14\% & \text{hyg}^+ \text{her/hyg her} \\ 14\% & \text{hyg her}^+/\text{hyg her} \end{array}$$

and 36 percent of the progeny should grow (the  $\text{hyg her/hyg her}$  class).

28. a. The cross is  $A \cdot \text{arg-1} \times a \cdot \text{arg-1}^+$ . Use the classification of asci in part (17) above. First decide if the two genes are linked by using the formula  $\text{PD} \gg \text{NPD}$ , when the genes are linked, while  $\text{PD} = \text{NPD}$  when they are not linked.  $\text{PD} = 127 + 2 = 129$  and  $\text{NPD} = 125 + 4 = 129$ , which means that the two genes are not linked. Alternatively,

$$\text{RF} = 100\%(\frac{1}{2} \text{ T} + \text{NPD})/\text{total asci}$$

$$= 100\%[(1/2)(100 + 36 + 6) + (125 + 4)]/400 = 50\%.$$

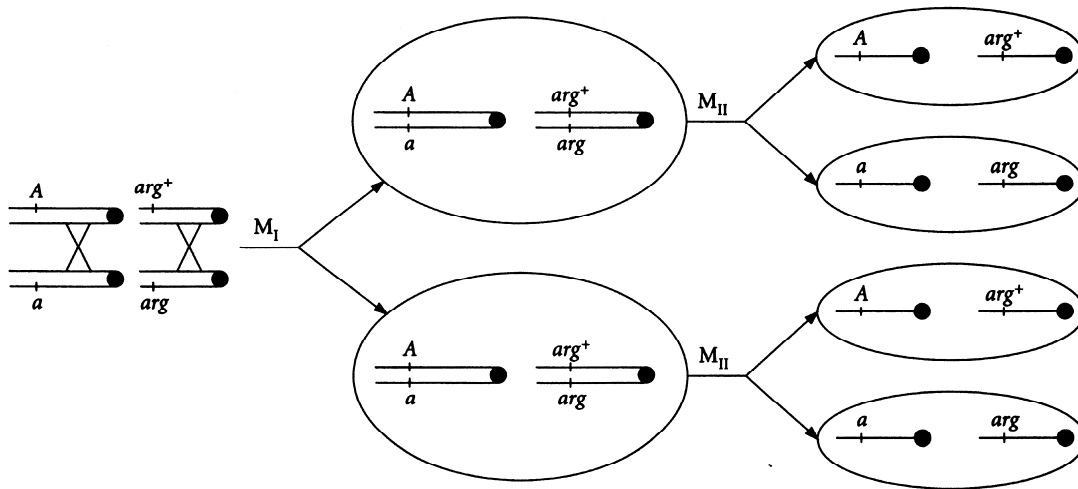
Next calculate the distance between each gene and its centromere using the formula  $RF = 100\%(1/2 \text{ number of tetrads exhibiting } M_{II} \text{ segregation})/(\text{total number of asci})$ .

$$\begin{aligned} A\text{-centromere} &= 100\%(1/2)(36 + 2 + 4 + 6)/400 \\ &= 100\%(24/400) = 6 \text{ m.u.} \end{aligned}$$

$$\begin{aligned} arg^+\text{-centromere} &= 100\%(1/2)(100 + 2 + 4 + 6)/400 \\ &= 100\%(56/400) = 14 \text{ m.u.} \end{aligned}$$



- b. Class 6 can be obtained if a single crossover occurred between chromatids 2 and 3 between each gene and its centromere.



29. Before beginning this problem, classify all asci as PD, NPD, or T and determine whether there is  $M_I$  or  $M_{II}$  segregation for each gene:

type	Asci type						
	1	2	3	4	5	6	7
gene a	PD	NPD	T	T	PD	NPD	T
gene b	I	I	I	II	II	II	II

If  $PD \gg NPD$ , linkage is indicated. The distance between a gene and its centromere =  $100\% (1/2)(M_{II})/\text{total}$ . The distance between two genes =  $100\% (1/2T + NPD)/\text{total}$ .

**Cross 1:**  $PD = NPD$  and  $RF = 50\%$ ; the genes are not linked.

$a$ -centromere:  $100\% (1/2)(0)/100 = 0$  m.u. Gene  $a$  is close to the centromere.

$b$ -centromere:  $100\% (1/2)(32)/100 = 16$  m.u.

**Cross 2:** PD  $\gg$  NPD; the genes are linked.

$a$ - $b$ :  $100\% [1/2(15) + 1]/100 = 8.5$  m.u.

$a$ -centromere:  $100\% (1/2)(0)/100 = 0$  m.u. Gene  $a$  is close to the centromere.

$b$ -centromere:  $100\% (1/2)(15)/100 = 7.5$  m.u.

**Cross 3:** PD  $\gg$  NPD; the genes are linked.

$a$ - $b$ :  $100\% [1/2(40) + 3]/100 = 23$  m.u.

$a$ -centromere:  $100\% (1/2)(2)/100 = 1$  m.u.

$b$ -centromere:  $100\% (1/2)(40 + 2)/100 = 21$  m.u.

**Cross 4:** PD  $\gg$  NPD; the genes are linked.

$a$ - $b$ :  $100\% [1/2(20) + 1]/100 = 11$  m.u.

$a$ -centromere:  $100\% (1/2)(10)/100 = 5$  m.u.

$b$ -centromere:  $100\% (1/2)(18 + 8 + 1)/100 = 13.5$  m.u.

**Cross 5:** PD = NPD (and RF = 49%); the genes are not linked.

$a$ -centromere:  $100\% (1/2)(22 + 8 + 10 + 20)/99 = 30.3$  m.u.

$b$ -centromere:  $100\% (1/2)(24 + 8 + 10 + 20)/99 = 31.3$  m.u.

These values are approaching the 67 percent theoretical limit of loci exhibiting  $M_{II}$  patterns of segregation and should be considered cautiously.

**Cross 6:** PD  $\gg$  NPD; the genes are linked.

$a$ - $b$ :  $100\% [1/2(1 + 3 + 4) + 0]/100 = 4$  m.u.

$a$ -centromere:  $100\% (1/2)(3 + 61 + 4)/100 = 34$  m.u.

$b$ -centromere:  $100\% (1/2)(1 + 61 + 4)/100 = 33$  m.u.

These values are at the 67 percent theoretical limit of loci exhibiting  $M_{II}$  patterns of segregation and therefore both loci can be considered unlinked to the centromere.

**Cross 7:** PD  $\gg$  NPD; the genes are linked.

$a$ - $b$ :  $100\% [1/2(3 + 2) + 0]/100 = 2.5$  m.u.

$a$ -centromere:  $100\% (1/2)(2)/100 = 1$  m.u.

$b$ -centromere:  $100\% (1/2)(3)/100 = 1.5$  m.u.

**Cross 8:** PD = NPD; the genes are not linked.

$a$ -centromere:  $100\% (1/2)(22 + 12 + 11 + 22)/100 = 33.5$  m.u.

$b$ -centromere:  $100\% (1/2)(20 + 12 + 11 + 22)/100 = 32.5$  m.u.

Same as cross 5.

**Cross 9:** PD  $\gg$  NPD; the genes are linked.

$a$ - $b$ :  $100\% [1/2(10 + 18 + 2) + 1]/100 = 16$  m.u.

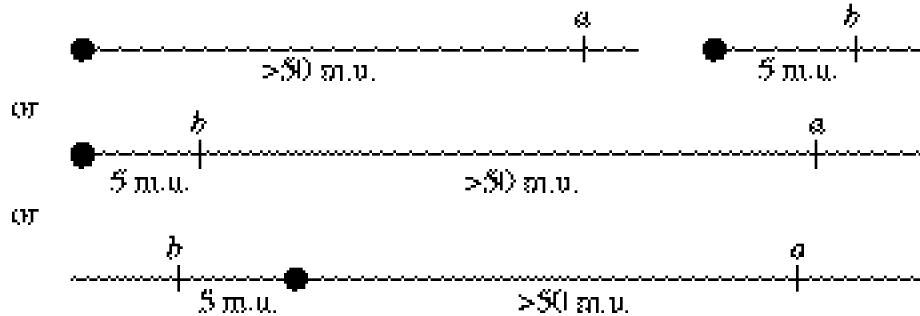
$a$ -centromere:  $100\% (1/2)(18 + 1 + 2)/100 = 10.5$  m.u.

*b*-centromere:  $100\% (1/2)(10 + 1 + 2)/100 = 6.5 \text{ m.u.}$

**Cross 10:** PD = NPD; the genes are not linked.

*a*-centromere:  $100\% (1/2)(60 + 1 + 2 + 5)/100 = 34 \text{ m.u.}$

*b*-centromere:  $100\% (1/2)(2 + 1 + 2 + 5)/100 = 5 \text{ m.u.}$



**Cross 11:** PD = NPD; the genes are not linked.

*a*-centromere:  $100\% (1/2)(0)/100 = 0 \text{ m.u.}$

*b*-centromere:  $100\% (1/2)(0)/100 = 0 \text{ m.u.}$

35. The gene order is *a c b d*.

Recombination between *a* and *c* occurred at a frequency of

$$100\%(139 + 3 + 121 + 2)/(669 + 139 + 3 + 121 + 2 + 2,280 + 653 + 2,215) \\ = 100\%(265/6,082) = 4.36\%$$

Recombination between *b* and *c* in cross 1 occurred at a frequency of

$$100\%(669 + 3 + 2 + 653)/(669 + 139 + 3 + 121 + 2 + 2,280 + 653 + 2,215) \\ = 100\%(1,327/6,082) = 21.82\%$$

Recombination between *b* and *c* in cross 2 occurred at a frequency of

$$100\%(8 + 14 + 153 + 141)/(8 + 441 + 90 + 376 + 14 + 153 + 64 + 141) \\ = 100\%(316/1,287) = 24.55\%$$

The difference between the two calculated distances between *b* and *c* is not surprising because each set of data would not be expected to yield exactly identical results. Also, many more offspring were analyzed in cross 1. Combined, the distance would be

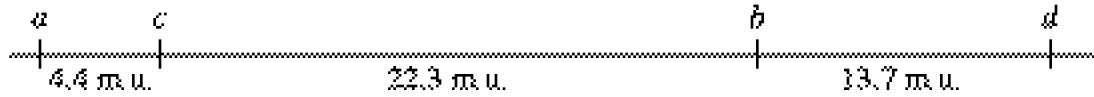
$$100\%[(316 + 1,327)/(1,287 + 6,082)] = 22.3\%$$

Recombination between *b* and *d* occurred at a frequency of

$$100\%(8 + 90 + 14 + 64)/(8 + 441 + 90 + 376 + 14 + 153 + 64 + 141) \\ = 100\%(176/1,287) = 13.68\%$$

The general map is:





37. a. To obtain a plant that is  $a b c/a b c$  from selfing of  $A b c/a B C$ , both gametes must be derived from a crossover between  $A$  and  $B$ . The frequency of the  $a b c$  gamete is

$$\frac{1}{2} p(\text{CO } A-B) \times p(\text{no CO } B-C) = \frac{1}{2}(0.20)(0.70) = 0.07$$

Therefore, the frequency of the homozygous plant will be  $(0.07)^2 = 0.0049$

- b. The cross is  $A b c/a B C \times a b c/a b c$ .

To calculate the progeny frequencies, note that the parentals are equal to all those that did not experience a crossover. Mathematically this can be stated as

$$\begin{aligned} \text{parentals} &= p(\text{no CO } A-B) \times p(\text{no CO } B-C) \\ &= (0.80)(0.70) = 0.56 \end{aligned}$$

Because each parental should be represented equally

$$\begin{aligned} A b c &= \frac{1}{2}(0.56) = 0.28 \\ a B C &= \frac{1}{2}(0.56) = 0.28 \end{aligned}$$

As calculated above, the frequency of the  $a b c$  gamete is

$$\frac{1}{2} p(\text{CO } A-B) \times p(\text{no CO } B-C) = \frac{1}{2}(0.20)(0.70) = 0.07$$

as is the frequency of  $A B C$ .

The frequency of the  $A b C$  gamete is

$$\frac{1}{2} p(\text{CO } B-C) \times p(\text{no CO } A-B) = \frac{1}{2}(0.30)(0.80) = 0.12$$

as is the frequency of  $a B c$ .

Finally, the frequency of the  $A B c$  gamete is

$$\frac{1}{2} p(\text{CO } A-B) \times p(\text{CO } B-C) = \frac{1}{2}(0.20)(0.30) = 0.03$$

as is the frequency of  $a b C$ .

So for 1,000 progeny, the expected results are

$A b c$	280
$a B C$	280
$A B C$	70
$a b c$	70
$A b C$	120
$a B c$	120

<i>A B c</i>	30
<i>a b C</i>	30

- c. Interference =  $1 - \text{observed DCO}/\text{expected DCO}$   
 $0.2 = 1 - \text{observed DCO}/(0.20)(0.30)$

$$\text{observed DCO} = (0.20)(0.30) - (0.20)(0.20)(0.30) = 0.048$$

The *A-B* distance = 20% = 100% [ $p(\text{CO } A-B) + p(\text{DCO})$ ].  
 Therefore,  $p(\text{CO } A-B) = 0.20 - 0.048 = 0.152$

Similarly, the *B-C* distance = 30% = 100% [ $p(\text{CO } B-C) + p(\text{DCO})$ ]  
 Therefore,  $p(\text{CO } B-C) = 0.30 - 0.048 = 0.252$

$$\begin{aligned} \text{The } p(\text{parental}) &= 1 - p(\text{CO } A-B) - p(\text{CO } B-C) - p(\text{observed DCO}) \\ &= 1 - 0.152 - 0.252 - 0.048 = 0.548 \end{aligned}$$

So for 1,000 progeny, the expected results are

<i>A b c</i>	274
<i>a B C</i>	274
<i>A B C</i>	76
<i>a b c</i>	76
<i>A b C</i>	126
<i>a B c</i>	126
<i>A B c</i>	24
<i>a b C</i>	24

42. Crossing-over occurs 8 percent of the time between *w* and *s*, which means it does not occur 92 percent of the time. Crossing-over occurs 14 percent of the time between *s* and *e*, which means that it does not occur 86 percent of the time.

- a. and b. The frequency of parentals =  $p$  (no crossover between either gene)

$$\begin{aligned} &= p(\text{no CO } w-s) \times p(\text{no CO } s-e) = (0.92)(0.86) \\ &= 0.791 \end{aligned}$$

or

$$1/2(0.791) = 0.396 \text{ each}$$

- c. and d. The frequency that will show recombination between *w* and *s* only

$$= p(\text{CO } w-s) \times p(\text{no CO } s-e) = (0.08)(0.86) = 0.069$$

or

$$1/2(0.069) = 0.035 \text{ each}$$

- e. and f. The frequency that will show recombination between *s* and *e* only

$$= p(\text{CO } s-e) \times p(\text{no CO } w-s) = (0.14)(0.92) = 0.128$$

or

$$1/2(0.128) = 0.064 \text{ each}$$

- g. and h. The frequency that will show recombination between *w* and *s* and *s* and *e*

$$\begin{aligned} &= p(\text{CO } w-s) \times p(\text{CO } s-e) = (0.08)(0.14) = 0.011 \\ \text{or} & \\ & \frac{1}{2}(0.011) = 0.006 \text{ each} \end{aligned}$$