- C1. Genetic recombination is a term that refers to a new combination of alleles in an offspring. Crossing over is a physical event that involves the exchange of pieces of genetic material between two chromosomes.
- C2. An independent assortment hypothesis is used because it enables us to calculate the expected values based on Mendel's ratios. Using the observed and expected values, we can calculate whether or not the deviations between the observed and expected values are too large to occur as a matter of chance. If the deviations are very large, we reject the hypothesis of independent assortment.
- C3. Mitotic recombination is crossing over between homologous chromosomes during mitosis in somatic cells. Mitotic recombination is one explanation for a blue patch. Following mitotic recombination, the two chromosomes carrying the *b* allele could segregate into the same cell and produce the blue color. Another reason could be chromosome loss; the chromosome carrying the *B* allele could be lost during mitosis.
- C4.



If the chromosomes labeled 2 and 4 move into one daughter cell, that will lead to a patch that is albino and has long hair. The other cell will receive chromosomes 1 and 3, which will produce a patch that has dark, short hair.

- C5. A.1 and 4
  - B. 2 and 3
  - C. 2 and 4, or 3 and 1
- C6. A single crossover produces A B C, A b c, a B C, and a b c.
  - A. Between 2 and 3, between genes *B* and *C*
  - B. Between 1 and 4, between genes A and B
  - C. Between 1 and 4, between genes *B* and *C*
  - D. Between 2 and 3, between genes A and B
- C7. There are 7 chromosomes per haploid genome. If we divide 20,000 by 7, there are about 2,857 genes per chromosome, on average.
- C8. The likelihood of scoring a basket would be greater if the basket was larger. Similarly, the chances of a crossover initiating in a region between two genes is proportional to the size of the region between the two genes. There are a finite number (usually a few) that occur between homologous chromosomes during meiosis, and the likelihood that a crossover will occur in a region between two genes depends on how big that region is.
- C9. If there are seven linkage groups, this means there are seven chromosomes per set. The sweet pea is diploid, meaning it has two sets of chromosomes. Therefore, the sweet pea has 14 chromosomes in leaf cells.
- C10. The pedigree suggests a linkage between the dominant allele causing nail-patella syndrome and the  $I^B$  allele of the ABO blood type gene. In every case, the individual who inherits the  $I^B$  allele also inherits this disorder.
- C11. There are four phenotypic categories for the F<sub>2</sub> offspring: brown fur, short tails; brown fur, long tails; white fur, short tails; and white fur, long tails. The recombinants are brown fur, long tails and white fur, short tails. The F<sub>2</sub> offspring will occur in a 1:1:1:1 ratio if the two genes are not linked. In other words, there will be 25% of each of the four phenotypic categories. If the genes are linked, there will be a lower percentage of the recombinant offspring.
- C12.<u>Ass-1 43 Sdh-1 5 Hdc 9 Hao-1 6 Odc-2 8 Ada-1</u>
- C13. We use the product rule. The likelihood of a double crossover is  $0.1 \times 0.1$ , which equals 0.01, or 1%. The likelihood of a triple crossover is  $0.1 \times 0.1 \times 0.1 = 0.001$ , or 0.1%. Positive interference would make these values lower.

- C14. The inability to detect double crossovers causes the map distance to be underestimated. In other words, there are more crossovers occurring in the region than we realize. When we have a double crossover, we do not get a recombinant offspring (in a dihybrid cross). Therefore, the second crossover cancels out the effects of the first crossover.
- C15. The map distance between genes *A* and *B* would appear to be greater than between *C* and *D* because of the higher rate of crossing over. We would obtain more recombinant offspring with regard to genes *A* and *B*, so the computed map distance would be higher, even though the physical distance between *A* and *B*, and between *C* and *D*, is identical.
- C16. The key feature is that all the products of a single meiosis are contained within a single sac. The spores in this sac can be dissected out, and then their genetic traits can be analyzed individually. In fungi, the traits most commonly analyzed are nutritional growth requirements (as described in Chapter 5), as well as pigmentation and antibiotic resistance.
- C17. A tetrad contains four spores; an octad contains eight. In a tetrad, meiosis produces four spores. In an octad, meiosis produces four cells, and then they all go through mitosis to double the number to eight cells.
- C18. In an unordered ascus, the products of meiosis are free to move around. In an ordered octad (or tetrad), they are lined up according to their relationship to each other during meiosis and mitosis. An ordered octad can be used to map the distance between a single gene and its centromere.
- C19. It could be a 2:2:2:2 or a 2:4:2 arrangement.
- C20. They would be higher with respect to gene *A*. First-division segregation patterns occur when there is not a crossover between the centromere and the gene of interest. Since gene *A* is closer to the centromere compared to gene *B*, it would be less likely to have a crossover between gene *A* and the centromere. This would make it more likely to observe first-division segregation.