Genetics Practice Problems – Answers

1.

To solve this problem, you need to first determine which phenotypes are parental (the highest in number) and which are recombinants (the lowest in number). In this case, the 5 purple-flowered short-petaled plants are recombinant, as are the 10 peach-flowered long-petaled plants. Remember, how many recombinants you have is indicative of how far apart your genes are. To find out a definite number of cM in between the genes, just add up the number of recombinants and divide by the total. In this case, your genes are 5 + 10 / 149 = 10 cM apart.

2.

To solve this question, you need to think of this like a puzzle. They give you the pieces, and you need to just put them in order. Let us draw it out.

A_____39_____C

A_____10_____E

D_2_B

B_____13_____C

D_____15_____C

E_____14_____D

E_____29_____C

A_____24_____D

The furthest apart must be the ones that are farthest apart on the gene (A and C). Notice that they are still under 50 cM. If they were more, we could not put this map together! Start there.

A_____39_____C

Then, start to step your way around. A and E are 10 cM apart, while E and C are 29 cM apart. This tells you that E is in the middle of A and C. Add that to the above figure.

A_____10_____E_____29_____C

Now let us place D. We know that D and C are 15 cM apart, and we also know that E and D are 14 cM apart. This places D in the middle of E and C. Draw it in.

A_____E_____14_____D_____15_____C

Now check your work, They also tell you that A and D are 24 cM apart. Go to the above drawings to see. Are they? They should be.

Lastly, you need to place B. You know that D and B are 2 cM apart and that C and B are 13 cM apart. This places B in between of D and C.

A_____E_____D__2__B_____13_____C

Remember, though, as the question states, we do not know where these genes are located with respect to the centromere (middle) of the chromosome. They did not give us enough information. Thus, we need to assume that the order is either AEDBC or CBDEA.

3.

The first thing you need to do is write out the genotypes of the cross they give you. Thus, you have a smooth yellow pea plant and a wrinkled green pea plant: SsRr x ssrr. You can easily solve this if you break out the alleles and look at them separately. You have a Ss x ss and then a Rr x rr. If you use a Punnett square for each set of alleles, you will find that you have ½ Ss and ½ ss as well as ½ Rr and ½ rr. It is now time to put them back together and solve for both alleles in the next generation:

½ Ss $\Big\langle$

    ½ Rr = ½ x ½ = ¼ RrSs

    ½ rr = ½ x ½ = ¼ rrSs

½ ss $\Big\langle$

    ½ Rr = ½ x ½ = ¼ Rrss

    ½ rr = ½ x ½ = ¼ rrss

Thus, your final ratio should be 1:1:1:1.

4.

This is known as a testcross. Whenever you have an unknown genotype, you cross it with a homozygous-recessive individual. Your phenotypic ratio in the offspring will tell you if you initially had a heterozygous individual or a homozygous-dominant individual to start with.

5.

Remember, this is a three-gene cross that was exhibited first in fruit flies. The parental genotypes are always the most common, and in this case, they are ABC and abc. The next frequent genotypes would be those that have undergone one crossover event (again, the further apart the genes, the more crossing over). These would be ABc and abC as well as Abc and aBC. Finally, the least common genotypes are those that have undergone a double crossover event; in this case, they are AbC and aBc.