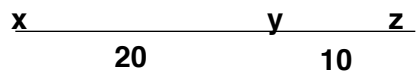


Question 1 (6 pts):

Your poli sci roommate does not believe all this mumbo jumbo about genetics. He says that there is no way for you to predict the phenotypes of offspring from the following cross.

$$\begin{array}{ccc} \underline{x-} & \underline{y-} & \underline{z-} \\ + & + & + \end{array} \quad \times \quad \begin{array}{ccc} \underline{x-} & \underline{y-} & \underline{z-} \\ x- & y- & z- \end{array}$$

You look up on wikipedia that the x, y, and z genes are all linked. Also, x is 20 map units from y, and y is 10 map units from z. The gene order is x, y, z. Fill out the table below for numbers of offspring with each phenotype (Total offspring = 1000).



Recombination between x and y should occur with a frequency of 0.2 and between y and z with a frequency of 0.1.

However, recombination will also occur between both as double recombinants. This will occur with a frequency of $0.2 * 0.1 = 0.02$

Phenotype	Number of offspring
x y z	360
+ + +	360
x y +	40
+ + z	40
x + +	90
+ y z	90
x + z	10
+ y +	10

Therefore, if we account for double recombinants:

$$\begin{aligned} \text{freq}(xy) &= 0.2 - 0.02 = 0.18 \\ \text{freq}(yz) &= 0.1 - 0.02 = 0.08 \end{aligned}$$

Multiply 1000 by expected freq. and divide by 2 to account for both classes:

$$\begin{aligned} n(xy) &= (1000 * 0.18) / 2 = 90 \\ n(yz) &= (1000 * 0.08) / 2 = 40 \end{aligned}$$

$$n(\text{double recombinants}) = 1000 * 0.02 = 20.$$

Finally, we can calculate parental: Probability of not having a recombinant between x and y (0.8), and probability of not having a recombinant between y and z (0.9). Therefore, the probability of both is $0.8 * 0.9 = 0.72$ or 720/1000

Question 2 (2 pts each):

You perform a selection for mutant *Arabidopsis* plants that can grow in the presence of high salt. You get four mutants (m1-m4). To determine how many genes are mutated, you perform complementation tests and get the following results when plants are grown on high salt.

	m1	m2	m3	m4
m1	Dead	Alive	Dead	Alive
m2	Alive	Dead	Alive	Dead
m3	Dead	Alive	Dead	Alive
m4	Alive	Dead	Alive	Dead

(a) You were lucky that your results were interpretable. What should you have done first?

Check whether the mutant phenotypes are dominant or recessive. If the phenotype is dominant, then you might be confused about a failure to complement.

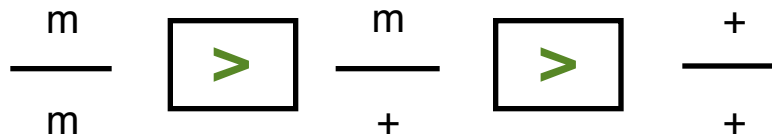
(b) How many genes are there?

Question 3 (2 pts each):

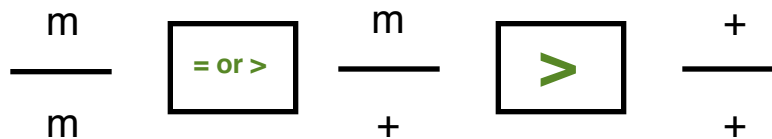
For the following questions, write the phenotypic relationships that would show the mutation effect in the boxes.

Use > or < symbols to denote when mutant phenotypes will be worse or better (or = equal).

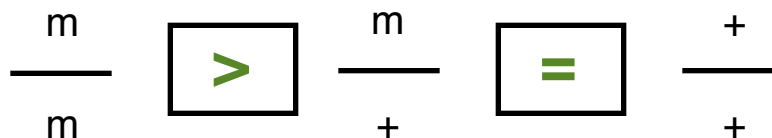
(a) Hypermorph (increase in wild-type function)



(b) Neomorph (altered function)



(c) Hypomorph (partial loss of gene function)

**Question 4 (2 pts each):**

(a) In a regulatory pathway, if the mutant phenotype of the gene *studying* is masked by the mutant phenotype of the gene *playing*, then what can we conclude about the order of action for those two genes?

Playing is downstream of or in parallel to studying.

Studying → Playing

(b) In a biosynthetic pathway where precursor is converted to A and then A converted to B, mutant1 builds up compound A and mutant2 builds up compound B. Which compound would build up in the double mutant?

Compound A

Precursor → A → B