Understandings:

1. Explain how unlinked genes segregate independently.

- We know that the genes on non-sister chromatids segregate independently. In other words, the genes on each chromosome are completely unlinked.

The genes on blue chromosome and red chromosome are completely independent. Therefore, when they align on the equator, the genes (basically the whole chromosome) segregate independently.

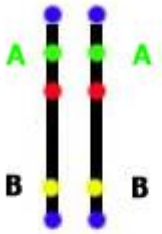
However, when the genes are on the same chromosome, say, two genes that we want to compare are both on the blue large chromosome; they do not usually segregate independently (it is in fact impossible to segregate independently). The only case when they can segregate independently is when there is crossing over taking place that moves one of the genes to another chromosome. The further away the genes are from each other, the higher chance of only 1 getting crossed over.

2. Explain the theory that genes on the same chromosome might actually be linked.

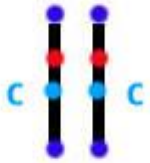
- When genes' locations, or loci, are situated on the same chromosome, we call them linked.

Essentially, there are two places where genes can be located: sex chromosome or autosome. Therefore, we have two types of linkages: sex-linkage or autosomal gene linkage.

This is a simple illustration of what it means to be linked.



A and B are linked



A and C are not linked

3. State that variation can be discrete or continuous.

- When we talk about genetic variations, the variations can be either discrete or continuous.

An example of discrete variation is blood type, where we only can have AB, A, B or O.

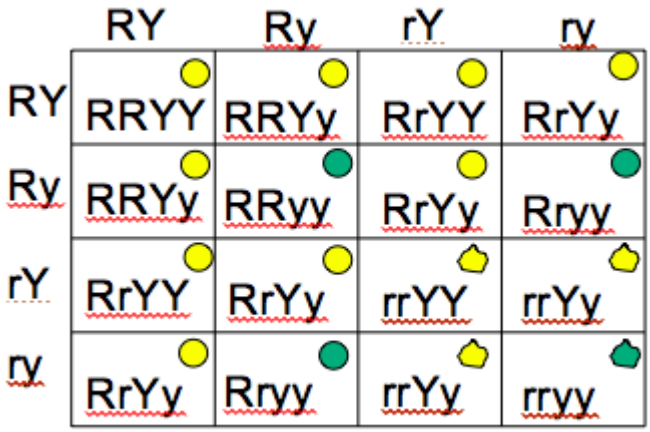
An example of continuous variation is height, where people can vary over continuous range.

4. Explain that polygenic phenotypes are likely to show continuous variations.

- Up to now, we have looked at discrete variations. Continuous variations are a bit more complex.

First of all, polygenic phenotype just means when there are many genes that affect the phenotype. Thus we are not simply talking about Mendelian inheritance where things are "either-or" and monohybrid.

We are now dealing with appearances that are affected by more than 2 unlinked genes.



This diagram is an example of dihybrid crossing.

We will have a phenotypic ratio of 9:3:3:1. Graphing this will give us the normal distribution.

5. Use chi-squared on data for dihybrid crosses.

- Chi-squared is basically testing for the association between two things. Before, we did it in ecology where we test association between two species. Now, we are testing the association between the breeding phenotypes and offspring phenotypes to verify the independent assortment.

This is how to do perform it:

1. Calculate the expected frequency. Say, if the theoretical result is 9:3:3:1 of certain phenotypes and we have done 190 trials, we expect 106.5 : 35.6 : 35.6 : 11.9.

2. Make a contingency (probability) table. Looks something like this:

	Phenotype 1	Phenotype 2	Phenotype 3	Phenotype 4	Total
Observed	111	37	34	8	190
Expected	106.5	35.6	35.6	11.9	190

3. Calculate degrees of freedom. Degree of freedom is the total number of classes minus 1. In this case it is 4-1.

4. Find the critical region in chi-squared table with significance level of 0.05 or 5%. If the chi value gets over the critical value, it means that there is a large discrepancy between observed and expected values. Now, depending on what your hypothesis was, you may or

may not accept the hypothesis from the obtained chi-squared value.

5. Calculate X-squared as:

$$X^2 = \sum \frac{(observed\ value - expected\ value)^2}{expected\ value}$$

In this case we get 1.56. This value is less than the critical value thus observed value is close to hypothesis. Hence we conclude they are independent, since that was our initial hypothesis.

Applications and skills:

1. Be able to use Punnett squares for dihybrid traits.
- It is exactly the same as for monohybrid crosses. The only "difficulty" is when determining their possible gametes. However, it is easy. Before, we had a gamete with only 1 allele. Now we have a gamete with 2 alleles.

Let's say the parent has QqTT. What will their gametes be?

Simply, put the first allele as reference.

Q = QT and QT.

q = qT and qT.

So those are the four gametes!

Then once you have the alleles, just combine them with the other parent gametes.

3. Explain Morgan's discovery on sex-linkage.
- Morgan used fruit flies *Drosophila* to experiment the inheritance. What he considered was eye colour red and white. As he predicted, red eyes were dominant and white recessive and the ratio supported his predictions.

However, he was surprised that all white-eyed flies were males. Hence the sex and the eye colour did not assort independently. He came to the conclusion that the eye-colour must be sex-linked!

3. Explain how polygenic traits like human height might be influenced by environmental factors.
- Yes, we all know that nutrition and sports all affect the growth. Most of the polygenic traits are easily affected by environmental factors; hence blur the boundaries even more.

Intelligence, skin colour, height, muscle percentage, etc.

4. Make predictions of genotypes and phenotypes using Punnett squares of dihybrid crosses.

- I will answer the questions on page 447 in my book.

1(i). Male phenotype is brown, tailed both homozygous, hence genotype BBTT.

Female phenotype is white, tail-less, hence genotype bbtt.

	BT	Bt	bT	Bt
BT	BBTT	BBTt	BbTT	BbTt
Bt	BBTt	BBtt	BbTt	Bbtt
bT	BbTT	BbTt	bbTT	bbTt
bt	BbTt	Bbtt	bbTt	bbtt

Phenotype ratio: 9:3:3:1.

Genotype ratio: 1:2:1:2:4:2:1:2:1

(ii). This is the cross breed of BbTt and bbtt. It is already done above.

2. Genotypes are YYSS and yyss

	YS	YS	YS	YS
ys	YySs	YySs	YySs	YySs
ys	YySs	YySs	YySs	YySs
ys	YySs	YySs	YySs	YySs
ys	YySs	YySs	YySs	YySs

All are tall and smooth seeds. These were then bred together.

	YS	Ys	yS	ys
YS	YYSS	YYSs	YySS	YySs
Ys	YYSs	YYss	YySs	Yyss
yS	YySS	YySs	yySS	yySs
ys	YySs	Yyss	yySs	yyss

We have 16 outcomes total.

3 are tall with wrinkled seeds. Thus if we do 320, we would expect 60 to have that phenotype.

3. Genotypes are Wwgg and wwGg.

	Wg	Wg	wg	wg
wG	WwGg	WwGg	wwGg	wwGg
wg	Wwgg	Wwgg	wwgg	wwgg

wG	WwGg	WwGg	wwGg	wwGg
wg	Wwgg	Wwgg	wwgg	wwgg

Normal wings & normal body = 4
Vestigial wings & normal body = 4
Normal wings & ebony = 4
Vestigial wings & ebony = 4

Ratio is 1:1:1:1.

5. Identify recombinants.
- First of all, what are recombinants? This is nothing new actually. Basically, it is when the genotype of offspring is different from its parents. A recombinant can be due to meiosis, product of crossing over and also independent assortment but not mutation apparently. This means that the chromosomes formed has got new combinations of alleles compared to their parents.

Next question is how we can identify them. So, when we have 2 genes to consider, we are essentially dealing with 4 alleles. This is because for each gene, it has 1 allele from father and one from mother.

Now, if those 2 genes were on separate chromosomes, it will show an independent assortment with the ratio 9:3:3:1.

However, if the genes are on the same chromosomes, i.e. they are linked; the ratio will not be 9:3:3:1. A certain trait will appear more frequently. Such as, orange hair and freckles seems to come together, hence draw conclusion that they are linked.

6. Be able to use chi-squared. This skill is the same as number 5 in Understandings.
- Yes!

TOK:

1. The law of independent assortment was soon found to have exceptions when looking at linked genes. What is the difference between a law and a theory in science?