Topic 10 – Genetics and Evolution (AHL)

10.1 - Meiosis

Nature of science:

Making careful observations—careful observation and record keeping turned up anomalous data that Mendel's law of independent assortment could not account for.

Thomas Hunt Morgan developed the notion of linked genes to account for the anomalies. (1.8)

∑ - Understandings:

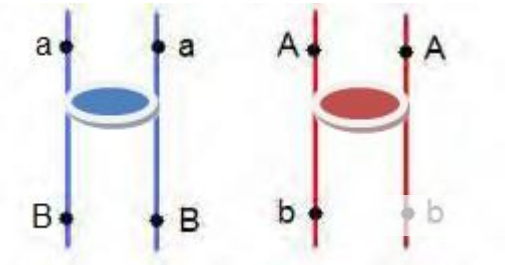
∑ - Chromosomes replicate in interphase before meiosis.

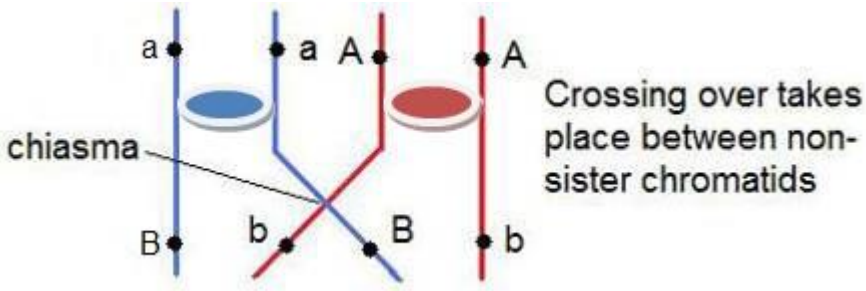
- During the S phase of the cell cycle, so that each chromosome has a copy of itself and consists of two sister chromatids.
- During meiosis I, chromosomes condense and synapse to form bivalents (homologous chromosomes are aligned next to each other).

∑ - Crossing over is the exchange of DNA material between non-sister homologous chromatids.

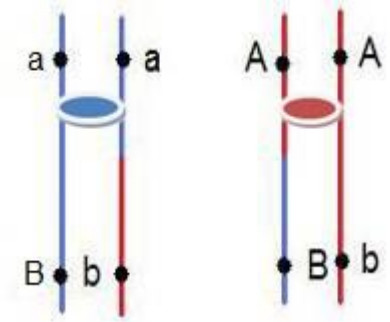
∑ - Crossing over produces new combinations of alleles on the chromosomes of the haploid cells.

- Crossing over occurs during prophase I of meiosis.

Diagram of Crossing-Over	Explanation of Crossing-Over
	• On the left is a pair of homologues (the blue ones are paternal and the red ones are maternal) • The loci for genes A and B are shown on both of the chromosomes • Gene A and B are linked genes because they are on the same chromosome • The chromosomes are held together by the centromere
	Non-sister chromatids can cross over. The point where they cross over is called thechiasma (plural



chiasmata). Crossing over can occur many times between the non-sister chromatids



- As seen on the left, part of the paternal chromatid is now attached to the maternal chromatid, and part of the maternal chromatid is now attached to the paternal chromatid
- This results in the exchange of alleles between the maternal and paternal chromatids contained on the swapped portions of the chromatids
- Hundreds of alleles can be exchanged through crossing over
- This formation of new combinations of alleles different than the parental chromosomes is called recombination

- **Crossing over only takes place some of the time between linked genes, therefore the parental combination in the gametes Ab and Ab will show up more often in the offspring, while ab and AB (recombinants) will show up with less frequency**
- **Start: AaBb and AAbb Result after crossing over: Aabb and AABb**

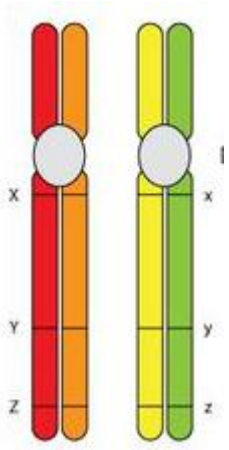
∑ - Chiasmata formation between non-sister chromatids can result in an exchange of alleles (see in picture above as well).

- Chiasmata are points where two homologous non-sister chromatids exchange genetic material during crossing over in meiosis.
- Chromosomes intertwine and break at the exact same positions in non-sister chromatids.
- The two chromosomes are now attached at the same corresponding positionon the non-sister chromatid.
- Many chiasmata can form between the chromatids.

- Once attached the non-attached portions of the chromatids actually repel each other.
- Chiasmata refer to the actual break of the phosphodiester bond during crossing over.
- The chiasmata are separated during anaphase 1 which can result in anexchange of alleles between the non-sister chromatids from the maternal and paternal chromosomes.

β - Skill: Drawing diagrams to show chiasmata formed by crossing over.

Draw diagrams to show chiasmata and the resulting chromosomes formed during crossing over.



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∑ - Homologous chromosomes separate in meiosis I.

- During meiosis I, unlike mitosis homologous chromosomes separate to opposite poles; however, their sister chromatids remain attached to each other
- Homologous chromosomes can exchange material in a process called crossing over
- Meiosis I is considered reduction division because the chromosome number is reduced by half (2n -> n in humans)

∑ - Sister chromatids separate in meiosis II.

- During meiosis II sister chromatids separate (some are non-identical sister chromatids due to crossing over
- This type of separation is very similar to mitosis as the chromatids are separated from each other

∑ - Independent assortment of genes is due to the random orientation of pairs of homologous chromosomes in meiosis I.

- When Mendel first did his experiments on pea plants, he looked at the traits that were passed on from generation to generation. He did not know how the traits were inherited in terms of meiosis.
- We now know that independent assortment is an essential component in explaining how chromosomes align themselves during meiosis.
- It also explains how unlinked genes are passed on from generation to generation.
- As explained above, when homologues line up along the equatorial plate in metaphase I, the orientation of each pair of is random; meaning the maternal or paternal homologue can orient towards either pole.
- Also the orientation of how one set of homologues line up has no effect on how any of the other homologues line up.
- For example, if chromosome pair one is heterozygous for a certain trait, there is a 50% chance that the gamete will receive the dominant trait and a 50% chance that the gamete will receive the recessive trait.
- Also if chromosome pair five is heterozygous for a particular trait, again there is a 50% chance that the gamete will receive the dominant allele and a 50% chance that it will receive the recessive allele.
- Both of these homologues line up independently during meiosis and have no effect on which gamete the other alleles will end up in.

Guidance:

Diagrams of chiasmata should show sister chromatids still closely aligned, except at the point where crossing over occurred and a chiasma was formed

10.2 Inheritance

Nature of science:

Looking for patterns, trends and discrepancies—Mendel used observations of the natural world to find and explain patterns and trends. Since then, scientists have looked for discrepancies and asked questions based on further observations to show exceptions to the rules. For example, Morgan discovered non-Mendelian ratios in his experiments with *Drosophila*. (3.1)

∑ - Understandings:

∑ - Unlinked genes segregate independently as a result of meiosis.

- Mendel's law of independent assortment states allele pairs separate independently from other allele pairs during gamete formation (meiosis).
- Therefore, traits on different chromosomes are transmitted to the offspring independently of traits on other chromosomes.
- An exception to this rule is linked genes

β - Application: Completion and analysis of Punnett squares for dihybrid traits.

β - Skill: Calculation of the predicted genotypic and phenotypic ratio of offspring of dihybrid crosses involving unlinked autosomal genes.

- A dihybrid cross is a cross between two individuals that shows the inheritance of two different genes at the same time; usually involving unlinked autosomal genes.
- Genotype and phenotype are defined in topic 3.4.1.
- Note: The following example contains two unlinked genes, which means the genes are on different chromosomes. This means they follow Mendel's law of independent assortment.

Dihybrid Cross Example

- Since almost all examples look at Mendel's pea plants, for this example we will look at two traits in cats; hair length and color.
- If the question stated that short hair (S) is dominant over long hair (s) and black fur (B) is dominant over white fur (b), what would be the genotypic and phenotypic ratio of a cross between a short hair black cat that is homologous for these traits and a long hair white cat?

First, write out the cross: **SSBB x ssbb**

Next, write out the possible gametes: **SB and sb**

If both parents are homologous for both traits, you can probably just look at the question and determine the genotype and phenotype, as it will be heterozygous for both traits (SsBb), but let's look at the Punnett square as most questions require you to show your working

Next, put the possible gametes into a Punnett square

	sb	**sb**	**sb**	**sb**
SB	SsBb	SsBb	SsBb	SsBb
SB	SsBb	SsBb	SsBb	SsBb
SB	SsBb	SsBb	SsBb	SsBb
SB	SsBb	SsBb	SsBb	SsBb

The genotypic ratio is 16:0 or 1:0 - SsBb

The phenotypic ratio is the same 16:0 or 1:0 – Short hair Black cat

Dihybrid Example (2)

- Cross two heterozygous cats for hair length and color from the F1generation

First, write out the cross: **SsBb x SsBb**

Next, write out the possible gametes: **SB, Sb, sB and sb for both cats**

Next, put the possible gametes into a Punnett square

(The Punnett square shows all possible offspring genotypes from random fertilization)

	SB	**Sb**	**sB**	**sb**
SB	SSBB	SSBb	SsBB	SsBb
Sb	SSBb	SSbb	SsBb	Ssbb
sB	SsBB	SsBb	ssBB	ssBb
sb	SsBb	Ssbb	ssBb	ssbb

Next, count the different genotypes in the Punnett square (cross out after you count so you don't count twice)

1 SSBB : 2 SSBb : 2 SsBB : 4 SsBb : 1 SSbb : 2 Ssbb : 1 ssBB : 2 ssBb : 1 ssbb

****Make sure that you counted 16 possible combinations****

Genotypic ratio is **1:2:2:4:1:2:1:2:1 - SSBB : SSBb : SsBB : SsBb : SSbb : Ssbb : ssBB : ssBb : ssbb**

Phenotypic ratio is **9:3:3:1 – Short Hair black, short hair white, long hair black and long hair white**

****Note: The phenotypic ratio for a dihybrid heterozygous cross is always 9:3:3:1****

Question from previous IB exams (answer at the bottom of the webpage)

1 (a) A farmer has rabbits with two particular traits, each controlled by a separate gene. Coat colour brown is completely dominant to white. Tailed is completely dominant to tail-less. A brown, tailed male rabbit that is heterozygous at both loci is crossed with a white, tail-less female rabbit. A large number of offspring is produced

with only two phenotypes: brown and tailed, white and tail-less, and the two types are in equal numbers.

(i) Deduce the pattern of inheritance of these traits. (2)

(ii) State both parents' genotypes and the gametes that are produced by each during the process of meiosis.

Male genotype:

Female genotype:

Male gametes:

Female gametes:

(2)

(iii) Predict the genotypic and phenotypic ratios of the F2 generation. Show your working. (2)

2) In *Zea mays*, the allele for coloured seed (C) is dominant over the allele for colourless seed (c). The allele for starchy endosperm (W) is dominant over the allele for waxy endosperm (w). Pure breeding plants with coloured seeds and starchy endosperm were crossed with pure breeding plants with colourless seeds and waxy endosperm.

(a) State the genotype and the phenotype of the F1 individuals produced as a result of this cross. (2)

(b) The F1 plants were crossed with plants that had the genotype c c w w. Calculate the expected ratio of phenotypes in the F2 generation, assuming that there is independent assortment. Use the space below to show your working.

Expected ratio: (3)

(Do this part after you do the section on linked genes) The observed percentages of phenotypes in the F2 generation are shown below.

coloured starchy	37%	colourless starchy	14%
coloured waxy	16%	colourless waxy	33%

The observed results differ significantly from the results expected on the basis of independent assortment.

(c) State the name of a statistical test that could be used to show that the observed and the expected results are significantly different.(1)

(d) Explain the reasons for the observed results of the cross differing significantly from the expected results.(2)

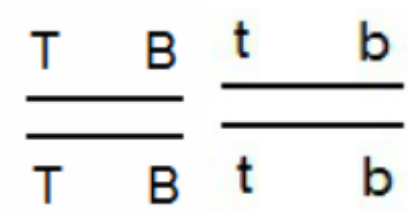
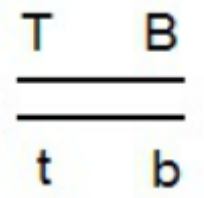
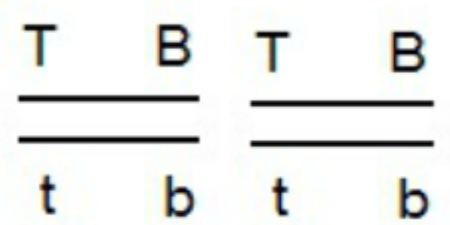
∑ - Gene loci are said to be linked if on the same chromosome.

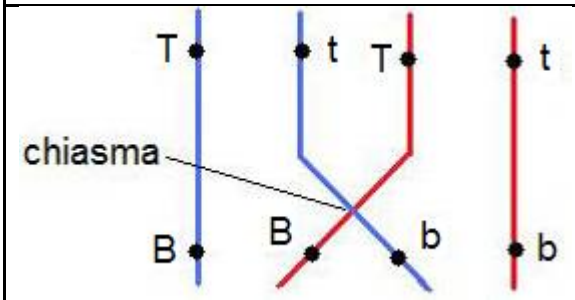
- Any genes that are found on the same chromosome and are therefore more likely to be inherited together are considered to be linked.
- When these genes (alleles) are inherited together as a group, they are considered to be a part of the same linkage group.

β - Skill: Identification of recombinants in crosses involving two linked genes.

Please look at the diagram in 10.1 to see the cross between two linked genes

- In a cross between two true breeding or homozygous parents the following would be the genotypes of the cross: **TTBB x ttbb.**
- On an exam if the genes are linked the genotypes would be represented as follows:

Diagrams	Explanation of Recombinants
	• The genotypes represented on the left show that T and B are on the same chromosome with one pair on the maternal chromosome and one pair on the paternal chromosome • The horizontal line represents the homologous chromosomes • The same can be said about the alleles t and b
	• The resulting cross should show that all the offspring are heterozygous for the traits • As the genes are linked T and B will go into the same gamete as will t and b, resulting in the heterozygous TtBb
	• If we now crossed the two heterozygous offspring TtBb the cross would be represented by the symbols on the left • Since the genes are linked T and B and t and b chromatids should be inherited together • The resulting gametes would

	contain <u>TB and tb alleles</u>, therefore the majority of the offspring will be <u>TTBB, TtBb and ttbb</u> • This <u>does not follow</u> Mendel's law off independent assortment because the genes are on the same chromosomes
	• However, crossing over can occur between the non-sister chromatids during prophase I of meiosis resulting in offspring with different genotypes • The gametes Tb and tB could also occur with crossing over, resulting in the <u>recombinant offspring TtBB and TTBb</u> • <u>Recombinants have different alleles combinations than either of the parents</u>
$\frac{T\ B}{t\ B}$ $\frac{T\ b}{t\ b}$	• The recombinants would be represented by the symbols on the left • TB, Tb, and tB would now be the new linked alleles for the next generation

∑ - Variation can be discrete or continuous.

- If variation is discrete it is controlled by alleles of a single gene or a small number of genes. The environment has little effect on this type of variation.
- In this case you either have the characteristic or you don't. Cystic fibrosis is a good example for this; either you have cystic fibrosis or you don't. Blood groups are another example of this type of variation. You are either blood type A, B, AB or O, there is no blending of these traits.
- Chi-squared calculations work well when using examples with discrete variation
- In continuous variation there is a complete range of phenotypes that can exist from one extreme to the other. Height is an example of continuous variation as there is a wide assortment of heights of individuals.
- Continuous variation is the combined effect of many genes (known as polygenic inheritance) and is often significantly affected by environmental influences. Skin colour is another example of continuous variation.

∑ - The phenotypes of polygenic characteristics tend to show continuous variation.

β - Application: Polygenic traits such as human height may also be influenced by environmental factors.

- When one gene controls the expression of a trait, the number of phenotypes that are expressed is limited to the dominant phenotype or recessive phenotype.
- If there is co-dominance, this adds another possible phenotype that can be expressed.
- With polygenic inheritance when two or more genes control the expression of a phenotype many possible phenotypes can exist.
- As the amount of genes that control one trait increase, the number of phenotypes increases to a point where it is impossible to determine the genotype by just observing the phenotype.
- Each additional gene has an additive affect, increasing the phenotypes. This is called continuous variation.
- For example, people's skin color varies dramatically around the world, between people of different races and within the same race. The multiple genes affect the intensity of the pigments in the skin.
- Another example is human height, which varies from person to person within the same race, and varies between different races. Height shows continuous variation.
- If you graphed the frequency of the occurrence of different phenotypic variations in a population, there should be a normal distribution.
- Continuing with human height, there will be some really tall people and some really short people, but the majority of people will be average height (normal distribution).
- As the number of genes that control a certain trait increases, the closer the distribution of the phenotypes represents a normal distribution.

∑ - Chi-squared tests are used to determine whether the difference between an observed and expected frequency distribution is statistically significant.

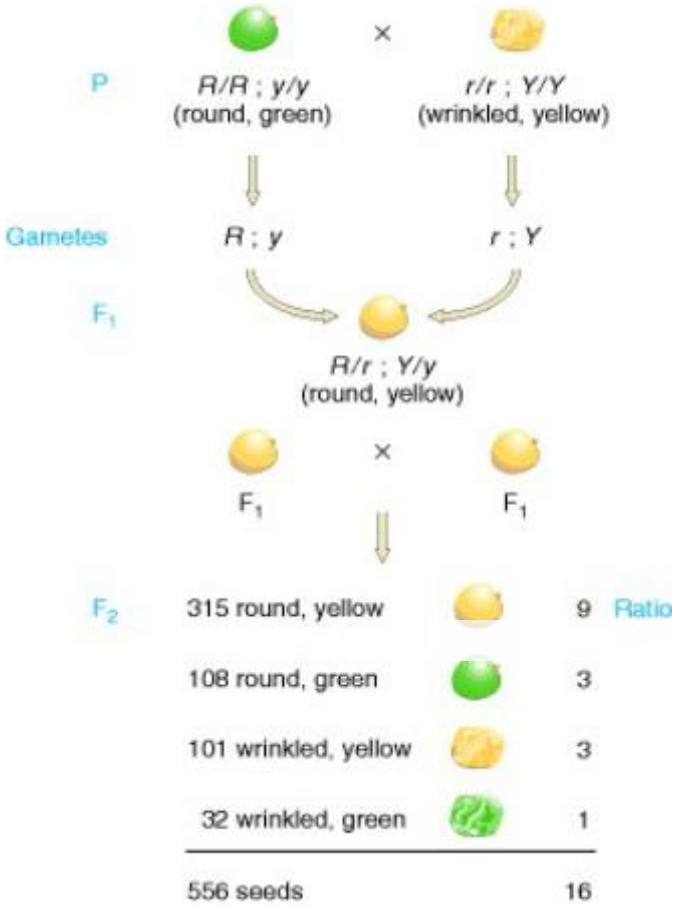
- A chi-square test is a statistical test that can be used to determine whether observed frequencies are significantly different from expected frequencies
- These statistical tests enable us to compare observed and expected frequencies empirically and to decide if the results we see are statistically significant. Statistical significance in this case implies that the differences are not due to chance alone, but instead may be caused by other factors at work.
- This is the formula for a chi-squared test

$$X^2 = \sum \frac{(o-e)^2}{e}$$

- What it basically means is the sum of the (observed minus the expected) squared, divided by the expected. This value is then compared to a critical value from a chi-squared table (similar to a t-table) to determine if the numbers we see are due to random factors. This is useful in determining if the results from a dihybrid genetic cross are due to independent assortment.

β - Skill: Use of a chi-squared test on data from dihybrid crosses.

- For an example let's use Mendel's results from his pea plant crosses
- When he did a dihybrid cross between two heterozygotes RrYy x RrYy, the expected phenotypic ratio due to independent assortment would be 9:3:3:1. Look at the chart below to see his actual results.



So the Ho (null hypothesis) would be the results are due to independent assortment and the Ha (alternative hypothesis) would be that the alleles do not assort independently and the results are due to ……gene linkage.

	Round Yellow	Round Green	Wrinkled Yellow	Wrinkled Green	Total
Observed (o)	315	108	101	32	556
Expected (e)	(9/16) x 556 = 312.75	(3/16) x 556 = 104.25	(3/16) x 556 = 104.25	(1/16) x 556 = 34.75	556

(315-312.75)^2/(312.75) + (108-104.25)^2/(104.25) + (101-104.25)^2/(104.25) + (32-34.75)^2/(34.75)= **0.47**

$X^2 = 0.47$

- The degrees of freedom would be (number of classes – 1), therefore 4-1 = 3
- So now you would look at the chi-squared table below and find out where 0.47fits for the degrees of freedom of 3

TABLE IV

Chi-Square (χ^2) Distribution

Degrees of Freedom	Area to the Right of Critical Value p 0.99	0.975	0.95	0.90	0.10	0.05	0.025	0.01
1	—	0.001	0.004	0.016	2.706	3.841	5.024	6.635
2	0.020	0.051	0.103	0.211	4.605	5.991	7.378	9.210
3	0.115	0.216	0.352	0.584	6.251	7.815	9.348	11.345
4	0.297	0.484	0.711	1.064	7.779	9.488	11.143	13.277
5	0.554	0.831	1.145	1.610	9.236	11.071	12.833	15.086

- As you can see from the table above the critical value at the 0.05 level of significance is 7.815.
- What the p-value of 0.05 or 5% indicates is the probability of getting the results you did (or more extreme results) given that the null hypothesis is true.
- If the calculated value is above or equal to **7.815** then we reject the Ho and accept the HA that the alleles in question are linked.
- However, since our chi-squared value of **0.47** is way less than this value (it has a p-value of 0.90 or 90%) we accept the Ho that the results that Mendel saw were due to independently assortment of the alleles. We can also see why some people think his results were just a little too good.

Try this next question on your own and calculate the chi-squared value to determine if the values are due to independent assortment.

1. The trait for tall pea plants is (T) and the trait for short pea plants is (t). The trait for smooth peas is (S) and the trait for wrinkled is (s). Two heterozygote plants are crossed yielding an F1 generation with 612 tall plants with smooth peas, 95 tall plants with wrinkled peas, 115 short plants with wrinkled peas and 395 short with smooth peas. Calculate the chi-squared coefficient to determine if the results seen are due to independent assortment.

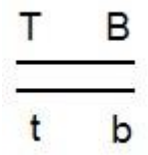
β - Application: Morgan's discovery of non-Mendelian ratios in *Drosophila.*

- Read through the following slide show and write down five interesting aspects regarding Morgan's discovery of non-Mendelian ratios.
- http://www.dnaftb.org/10/animation.html

Guidance:

• Alleles are usually shown side by side in dihybrid crosses, for example, TtBb.

In representing crosses involving linkage, it is more common to show them as vertical pairs, for example:



• This format will be used in examination papers, or students will be given sufficient information to allow them to deduce which alleles are linked.

Theory of knowledge:

• 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?

Utilization:

• An understanding of inheritance allowed farmers to selectively breed their livestock for specific characteristics.

Answers

(1) (i) autosomal;

linked genes / linkage;

together on same chromosome;

as they did not separate / segregate; 2

(ii) *Accept any letters for the alleles of the two genes.*

male genotype is BbTt / $\frac{BT}{bt}$ and female genotype is bbtt / $\frac{bt}{bt}$;

Reject Bb,Tt and bb, tt.

male gametes: BT and bt / BT and bt *female gametes*: (all) bt / bt; 2 max

(iii) BbTt / $\frac{BT}{bt}$ and bbtt / $\frac{bt}{bt}$;

1 / ½ / 50% brown tailed : 1 / ½ / 50% white tail-less; 2

2. (a) C c W w;
all are coloured starchy; 2

(b) gametes are C W, C w, c W, c w and c w;
F2 genotypes are CcWw, Ccww, ccWw and ccww;
1 coloured starchy: 1 coloured waxy: 1 colourless starchy: 1 colourless waxy; 3
Phenotypes must be unambiguously indicated, but not necessarily on the line.

(c) chi-squared test 1

(d) (autosomal) linkage (*reject sex linkage*) / genes are on the same chromosome / genes do not assort independently;
coloured starchy and colourless waxy are parentals / coloured waxy and colourless starchy are the recombinants;
recombinants produced by crossing over; 2 max

[8]

10.3 Gene pools and speciation

Nature of science:

Looking for patterns, trends and discrepancies—patterns of chromosome number in some genera can be explained by speciation due to polyploidy. (3.1)

Understandings:

∑ - A gene pool consists of all the genes and their different alleles, present in an interbreeding population.

- A species is generally considered a group of potentially interbreeding populations that have a common gene pool and are reproductively isolated from other species
- A gene pool is the set of all genes, including all the different alleles, in any interbreeding population, usually of a particular species

∑ - Evolution requires that allele frequencies change with time in populations.

- Evolution is the cumulative change in allele frequency or heritable characteristics in a population over time
- The cumulative change can occur as a result of genetic mutations and selective pressures which favour certain heritable characteristics over other less favourable characteristics
- These populations have to be reproductively isolated, thus preventing gene flow between populations
- If a population that has a certain allele or characteristic is quite small, random events such as disease or natural disasters can cause a drastic drop in this particular allele

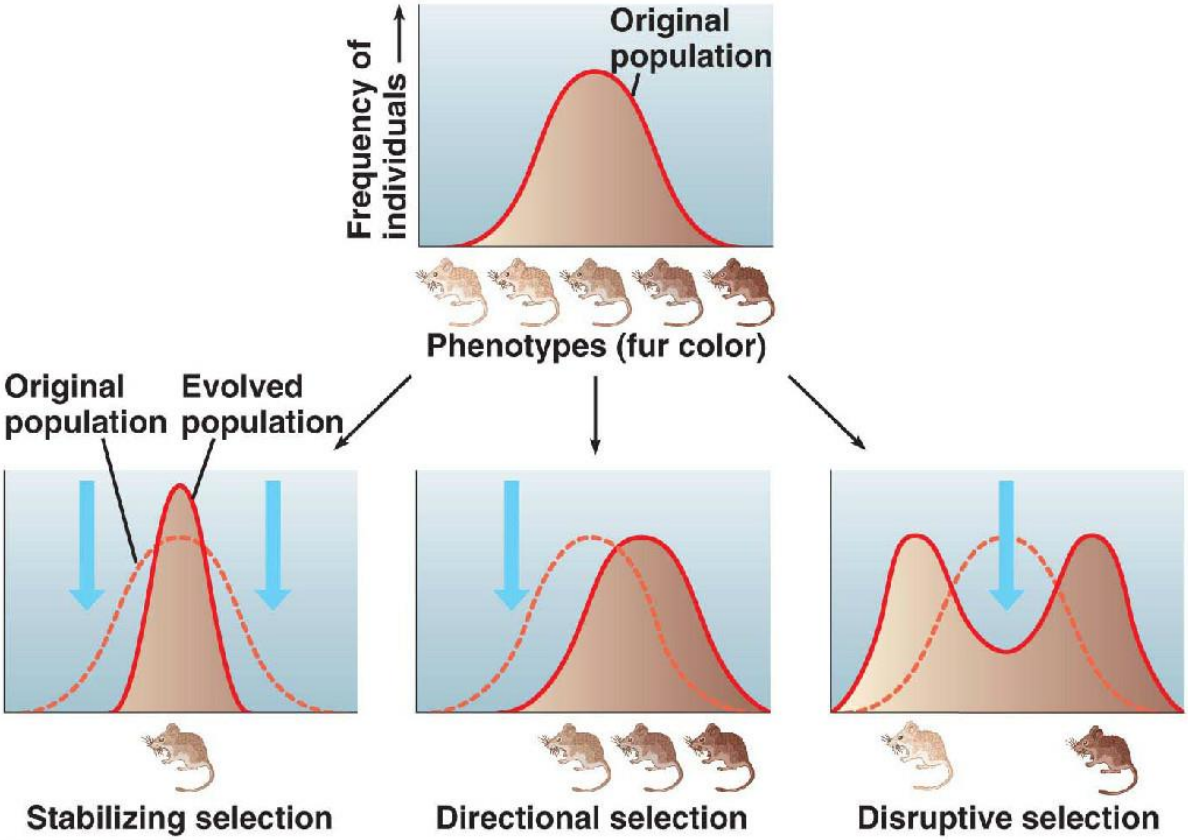
β - Application: Identifying examples of directional, stabilizing and disruptive selection.

Directional Selection:
Selection that removes individuals from one end of a phenotypic distribution and thus causes a shift in the distribution towards the other end. This occurs when natural selection favours one extreme end of the continuous variation of phenotypes. Over time, the favoured extreme will become more common and the other extreme will be less common or lost. For example, dark mice are favoured because they live in an area that favours that phenotype.

Stabilizing Selection:
A type of selection that removes individuals from both ends of a phenotypic distribution, thus maintaining the same distribution mean. This occurs when natural selection favours the intermediate phenotypes. Over time, the intermediate states become more common and each extreme variation will become less common or lost.

Same mouse example where medium coloured fur is favoured over dark or light fur colour.

Disruptive Selection:
A type of selection that removes individuals from the center of a phenotypic distribution and thus causes the distribution to become bimodal. This occurs when natural selection favours both ends of the phenotypic variation. Over time, the two extreme variations will become more common and the intermediate states will be less common or lost. Disruptive selection can lead to two new species. Light coloured and dark coloured mice might live in an environment with patches of light and dark vegetation making it hard for predators to spot those colours, while the middle coloured mouse doesn't blend into either background.



Good video on directional, stabilizing and disruptive selection https://www.youtube.com/watch?v=vCHdT9MWIaA

∑ - Reproductive isolation of populations can be temporal, behavioural or geographic.

- Reproductive Isolation - https://www.youtube.com/watch?v=EmtIofdeUbc
- Reproductive isolation of populations occurs when barriers or mechanisms prevent two populations from interbreeding, keeping their gene pools isolated
- There are different types of reproductive isolation including temporal, behavioural, and geographic

Temporal Isolation

- Individuals of different populations do not mate because they are active at different times of day and/or different times of the year, or they breed or reach sexual maturity at different times
- Some examples include flowers such as orchids and frogs in North America
- Three tropical orchid species of the genus Dendrobium each flower for only a single day; the flowers open at dawn and wither by nightfall. Flowering occurs in response to certain meteorological stimuli, such as a sudden storm on a hot day. The same stimulus acts on all three species, but the lapse between the stimulus and flowering is 8 days in one species, 9 in another, and 10 or 11 in the third. Fertilization between orchids is impossible because, at the time the flowers of one species open, those of the other species have already withered or have not yet matured(http://www.britannica.com/EBchecked/topic/197367/evolution/49880/The-origin-of-species#ref311674)

- Five frog species of the genus Rana differ in the time of their peak breeding activity.
- Wood Frogs and Leopard Frogs breed at different times in the spring

Wood frog
(*Rana sylvatica*)
It usually mates in late March or early April when water temperature is about 7.2°C (45°F)

Leopard frog
(*Rana pipiens*)
It usually mates in mid-April when water temperature is 12.8°C(55°F)

Behavioural Isolation

- In most animal species, members of the two sexes must first search for each other and come together.
- Two populations may share a habitat and breed at similar times, but animals especially may have different courtship rituals

- During these complex courtship rituals, the male often takes the initiative and the female responds, which leads to additional actions by the male and responses by the female.
- After a successful courtship, copulation or sexual intercourse (or, in the case of some aquatic organisms, release of the sex cells for fertilization in the water) takes place.
- An animal that does not recognize another animal's courtship ritual or is not attracted to the courtship display, will be unlikely to breed with that individual.

An example of this is the Western Grebe of North America

- The dark-phase and light-phase Western Grebes occupy the same habitat and breed at similar times, yet maintain their color forms by differing sets of courtship behaviors (probably learned).

Video on the mating of the Western Grebe in Oregon https://www.youtube.com/watch?v=ZbRrxw-H6xA

Geographical Isolation

- Geographic isolation can lead to allopatric speciation if the separation is maintained for many generations.
- Allopatric speciation occurs when populations are completely separated from one another by geographical barriers such as the formation of a river or separate lakes, rise of a mountain, or migration to an island

There are many examples of geographic isolation.

For example Darwin's finches https://www.youtube.com/watch?v=mcM23M-CCog

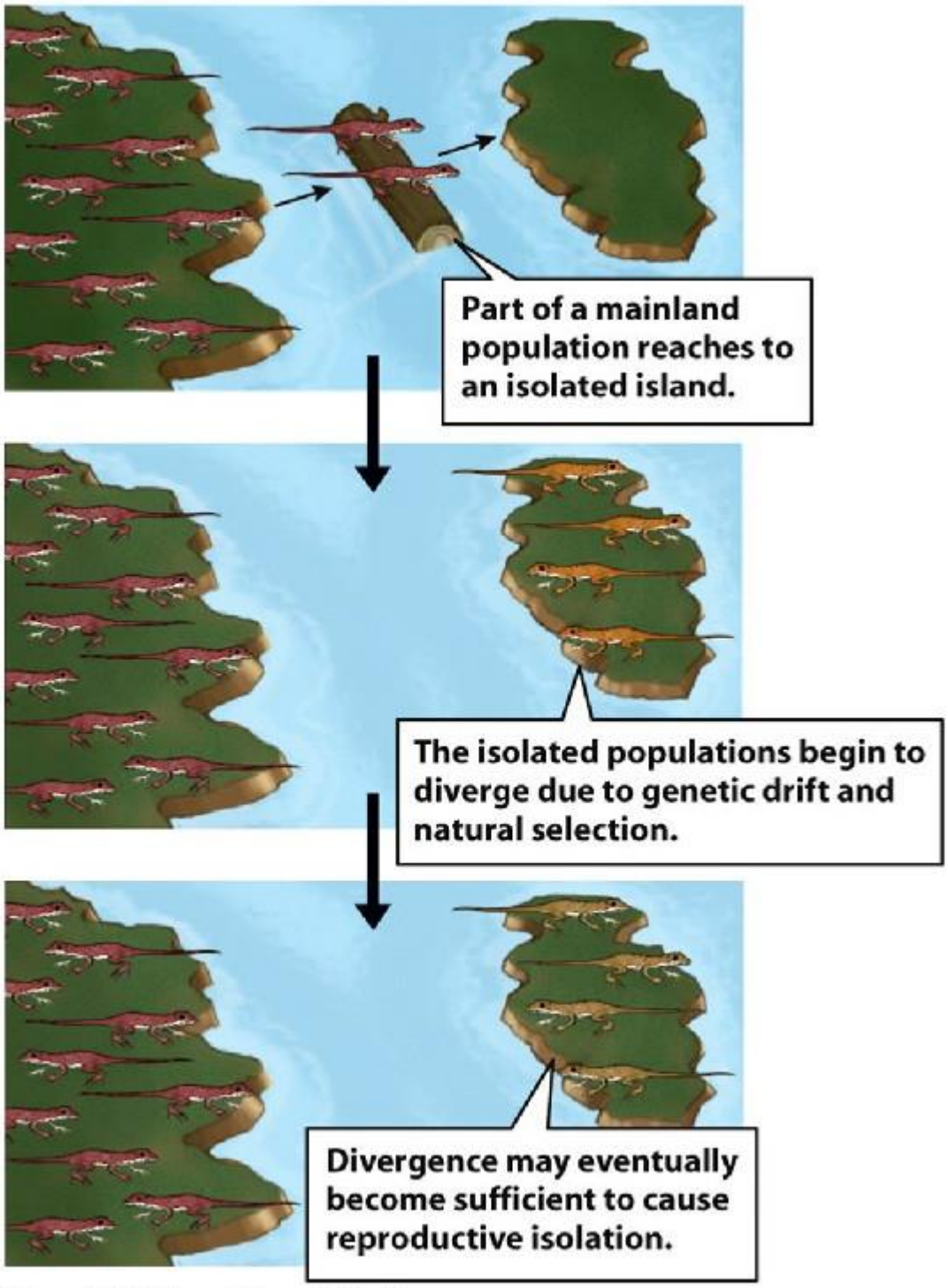


Figure 16-9 Biology: Life on Earth, 8/e

These are some other videos on speciation.

Crash course Speciation: https://www.youtube.com/watch?v=2oKlKmrbLoU

Video on Stickleback evolution https://www.youtube.com/watch?v=VE2q5IhjdYM

Do the data-based questions on page 456-458

β - Skill: Comparison of allele frequencies of geographically isolated populations.

Go to **http://alfred.med.yale.edu/** and search for a specific allele within a population

Answer the questions on page 460 regarding allele frequency

∑ - Speciation due to divergence of isolated populations can be gradual.

- Simply stated, speciation can occur gradually over long periods of time, with several intermediate forms in between species leading to today's current species. This can be seen by some of the more complete fossil records, like the whale.
- However, in some species, large gaps were evident for certain species in the fossil record. This could be explained by possible imperfections in the fossil record, or perhaps, these species have not been discovered yet.
- Another explanation is through abrupt speciation.

∑ - Speciation can occur abruptly.

- Formation of new species which is reproductively and ecologically isolated from the parental species.as a result of a genetic mutation such as a sudden change in chromosome number or constitution
- Genetic mutations such as non-disjunctions of an entire set of chromosomes can cause a doubling of chromosomes (polyploidy) resulting in a different species
- Also interbreeding of two genetically different organisms can produce hybrids which are generally infertile

Interesting article on Rainbow Trout http://www.kplu.org/post/scientists-washingtons-state-fish-has-remarkable-evolutionary-past

β - Application: Speciation in the genus *Allium* by polyploidy.

- The genus Allium comprises monocot flowering plants and includes the onion, garlic, chives, scallion, shallot, and the leek
- In many of these species of plants, chromosome doubling has occurred naturally and through hybridization or selective breeding to create a large number of different phenotypes. This results in a number of reproductively isolated but similar populations.
- Polyploidy increases allelic diversity and permits novel phenotypes to be generated. It also leads to hybrid vigour.
- Examples of this are seen in 7 natural populations Allium grayi that were examined in in Okayama Prefecture, Japan. They showed often tetraploid (2n=32) and pentaploid (2n=40) plants together in the 5 populations and hexaploid (2n=48) plants in the Kasaoka population. The hexaploid plant of the species was found for the first time in western-half part of Japan. Tetraploid plants were solely observed in the Oku population and only pentaploid plants were found in the Kuse population.

Guidance:

• Punctuated equilibrium implies long periods without appreciable change and short periods of rapid evolution.

Theory of knowledge:

• Punctuated equilibrium was long considered an alternative theory of evolution and a challenge to the long established paradigm of Darwinian gradualism. How do paradigm shifts proceed in science and what factors are involved in their success?

Utilization:

• Many crop species have been created to be polyploid. Polyploidy increases allelic diversity and permits novel phenotypes to be generated. It also leads to hybrid vigour.

Topic 1 - Cells
Topic 2 - Molecular Biology
Topic 3 - Genetics
Topic 4 - Ecology
Topic 5 - Evolution & Biodiversity
Topic 6- Human Health and Physiology
Topic 7 - Nucleic Acids (AHL)
Topic 8 - Respiration and Photosynthesis (AHL)
Topic 9 - Plant Biology (AHL)
Topic 10 - Genetics and Evolution (AHL)
10.1 - Meiosis
10.2 - Inheritance

10.3 - Gene Pools and Speciation
Topic 11 - Physiology (AHL)