EXAM PAPERS PRACTICE

AQA A Level Biology

Topic 7

Genetics, populations, evolution and ecosystems

Topic	Understand	Memorise	Practise
7.1 Inheritance			
7.2 Populations			
7.3 Evolution may lead to speciation			
7.4 Populations in ecosystems			
Required practical 12			

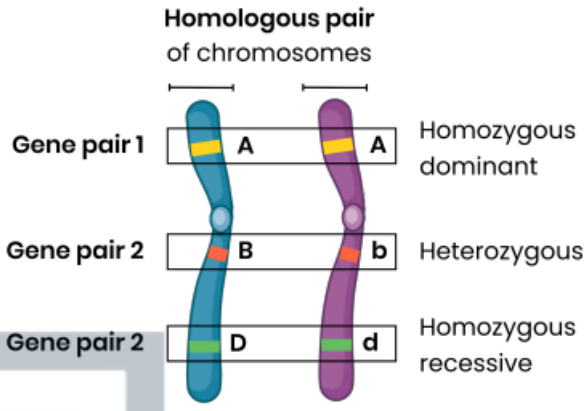
7.1 Inheritance

What is meant by the term genotype?

Genetic constitution of an organism

What is meant by the term phenotype?

The **expression** of this **genetic constitution** (genotype) and its **interaction** with the **environment**



What are alleles and how do they arise?

Variations of a particular **gene** (same locus) → arise by **mutation** (changes in DNA **base sequence**)

How many alleles of a gene can be found in diploid organisms?

- **2** as diploid organisms have **2 sets of chromosomes** (chromosomes are found in homologous pairs)
  - But there may be **many** (more than 2) alleles of a single gene in a population

Describe the different types of alleles

Dominant allele	**Always** expressed (shown in the phenotype)
Recessive allele	Only expressed when **2 copies** present (**homozygous recessive**) / **NOT** expressed when dominant allele present (heterozygous)
Codominant alleles	**Both** alleles expressed / contribute to phenotype (if inherited together)

What is meant by the terms homozygous and heterozygous?

Homozygous	Alleles at a specific **locus** (on each homologous chromosome) are the **same**
Heterozygous	Alleles at a specific **locus** (on each homologous chromosome) are **different**

What do monohybrid and dihybrid crosses show?

- **Monohybrid cross** - inheritance of **one** phenotypic characteristic coded for by a **single gene**
- **Dihybrid cross** - inheritance of **two** phenotypic characteristics coded for by **two different genes**

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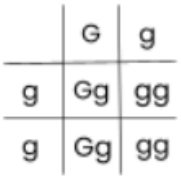
Worked example: monohybrid cross (basic)

The **dominant** allele for the grey gene (**G**) in horses results in a coat colour turning progressively **grey**.

The **recessive** allele (**g**) results in the normal coat colour being maintained (**non-grey** phenotype).

A **non-grey** female is crossed with a **heterozygous** male.

Draw a genetic diagram to show the expected **ratio** of **phenotypes** in the offspring.

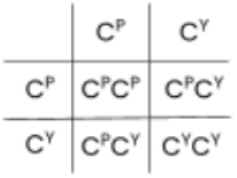
Parental phenotypes	Non-grey	Grey
Parental genotypes	gg	Gg
Gamete genotypes	g (and g)	G and g
Genetic diagram		
Offspring genotypes	Gg, gg	
Offspring phenotypes	Grey, non-grey	
Ratio	1:1	

Worked example: monohybrid cross with multiple alleles

In one snail species, shell colour is controlled by a gene with **3 alleles**. The shell may be **brown**, **pink** or **yellow**. The allele for **brown** (C^B) is **dominant** to the other two alleles. The allele for **pink** (C^P) is **dominant** to the allele for yellow (C^Y).

A cross between two **pink-shelled** snails produced only **pink-shelled** and **yellow-shelled** snails.

Use a genetic diagram to explain why.

Parental phenotypes	Pink-shelled	Pink-shelled
Parental genotypes	C^PC^Y	C^PC^Y
Gamete genotypes	C^P and C^Y	C^P and C^Y
Genetic diagram		
Offspring genotypes and phenotypes	C^PC^P, C^PC^Y - pink-shelled C^YC^Y - yellow-shelled	

Worked example: monohybrid cross with codominance and multiple alleles

The inheritance of the ABO **blood groups** in humans is controlled by **three alleles** of a single gene, I^A, I^B and I^O. The alleles **I^A** and **I^B** are **codominant**, and the allele **I^O** is **recessive to I^A** and **recessive to I^B**.

Two **heterozygous** parents plan to have a child. One has **blood group A** and the other has **blood group B**.

Use a genetic diagram to show all the possible **genotypes** and the **ratio** of **phenotypes** expected in their offspring.

Parental phenotypes	Blood group A	Blood group B
Parental genotypes	I^AI^O	I^BI^O
Gamete genotypes	I^A and I^O	I^B and I^O
Genetic diagram		
Offspring genotypes	I^AI^B, I^AI^O, I^BI^O, I^OI^O	
Offspring phenotypes	AB, A, B, O	
Ratio	1:1:1:1	

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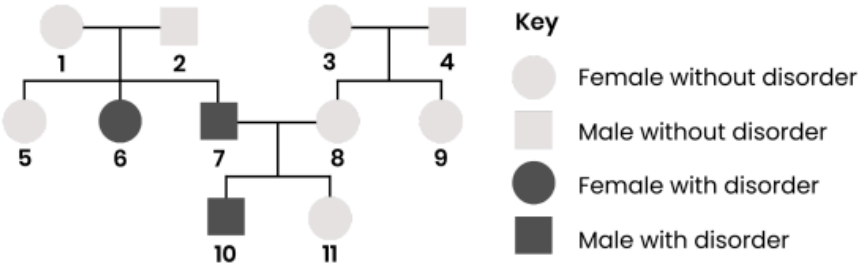
Worked example: monohybrid cross using a pedigree diagram

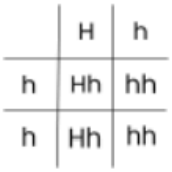
The figure shows the inheritance of a **genetic disorder** in a family.

Person **7** and person **8** plan to have another child. Determine the probability that the child will be a **male** who has the disorder. Use the symbol **H** for the **dominant** allele and **h** for the **recessive** allele.



In this example, we first have to use the pedigree diagram to work out whether the disorder was caused by a **dominant or recessive allele**. Since two parents without the disorder had a child with the disorder, it is caused by a **recessive allele**.

We also need to use the diagram to work out the genotypes of 7 and 8 (parents). Since 7 has the disorder, he must be **homozygous recessive**. 8 doesn't have the disorder so must have at least **one dominant allele**. Since 7 and 8 have a child with the disorder, 8 must be **heterozygous** to have passed on the recessive allele.

Parental phenotypes	With disorder	Without disorder
Parental genotypes	hh	Hh
Gamete genotypes	h (and h)	H and h
Genetic diagram		
Offspring genotypes	Hh, hh	
Offspring phenotypes	With disorder, without disorder	
Probability	½ male, ½ have disorder → ½ x ½ = ¼ (or 0.25) male with disorder	

Explain the evidence from a pedigree diagram which would show that the allele for [named phenotype] is dominant

- [Named phenotype] parents **[n & n]** have child **[n] WITHOUT** [named phenotype]
- So both parents **[n & n]** must be **heterozygous / carriers** of **recessive allele**
  - If it were recessive, **all** offspring would have [named phenotype]

Explain the evidence from a pedigree diagram which would show that the allele for [named phenotype] is recessive

- Parents **[n & n] WITHOUT** [named phenotype] have child **[n] WITH** [named phenotype]
- So both parents **[n & n]** must be **heterozygous / carriers** of **recessive allele**

Worked example: dihybrid cross (basic)

Note - if the two genes are on two **different chromosomes** (the genes are **not linked**), an allele from one pair of chromosomes can enter a gamete with either allele from the other pair. This is due to **independent segregation** of homologous chromosomes during meiosis. For example, If an adult had the genotype AaBb, the possible gamete genotypes are: Ab, AB, ab and aB.

In fruit flies, the allele for **grey** body (**G**) is **dominant** to the allele for **ebony** body (**g**) and the allele for **normal** wings (**N**) is **dominant** to the allele for vestigial wings (**n**). These genes are **not linked**.

Vestigial-winged flies, **heterozygous** for **grey** body colour, were crossed with **ebony**-bodied flies, **heterozygous** for **normal** wings.

Complete the genetic diagram to show all the possible **genotypes** and the **ratio** of **phenotypes** expected in the offspring of this cross.

Parental phenotypes	Grey body, vestigial wings	Ebony body, normal wings
Parental genotypes	Ggnn	ggNn
Gamete genotypes	Gn and gn	gN and gn
Genetic diagram		

	gN	gn
Gn	GgNn	Ggnn
gn	ggNn	ggnn

Offspring genotypes	GgNn, Ggnn, ggNn, ggnn
Offspring phenotypes	Grey, normal; grey, vestigial; ebony, normal; ebony, vestigial
Ratio	1:1:1:1

Note - although in this example there are only two gamete genotypes for each parent, there could be **up to 4** if a parent is **heterozygous for both genes.** Just add extra columns / rows to the punnett square.

Worked example: dihybrid cross with codominance

In a species of flowering plant, the **T** allele for **tallness** is **dominant** to the **t** allele for **dwarfness**. In the same species, two alleles **C^R (red)** and **C^W (white)** code for the colour of flowers.

When homozygous red-flowered plants were crossed with homozygous white-flowered plants, all the offspring had **pink** flowers. A **dwarf, pink-flowered** plant was crossed with a **heterozygous tall, white-flowered** plant.

Complete the genetic diagram to show all the possible **genotypes** and the **ratio** of **phenotypes** expected in the offspring of this cross.

Parental phenotypes	Dwarf, pink-flowered	Tall, white-flowered
Parental genotypes	ttC^RC^W	TtC^WC^W
Gamete genotypes	tC^R and tC^W	TC^W and tC^W
Genetic diagram		
Offspring genotypes	TtC^RC^W, ttC^RC^W, TtC^WC^W, ttC^WC^W	
Offspring phenotypes	Tall pink, dwarf pink, tall white, dwarf white	
Ratio	1:1:1:1	

	TC^W	tC^W
tC^R	TtC^RC^W	ttC^RC^W
tC^W	TtC^WC^W	ttC^WC^W

What is a sex-linked gene?

A gene with a **locus** on a **sex-chromosome** (normally **X**)

Explain why males are more likely to express a recessive X-linked allele

This assumes **males** are **XY** and **females** are **XX**, as in humans. In some organisms, it is swapped. In these cases, females (XY) would be more likely to express a recessive X-linked allele.

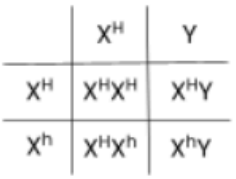
- **Females (XX)** have **2 alleles** → only express recessive allele if **homozygous recessive** / can be **carriers**
- **Males (XY)** have **1 allele** (inherited from mother) → recessive allele **always** expressed

Worked example: monohybrid cross with sex-linkage

A single gene that's carried on the **X chromosome** controls the presence of hair on the skin of cattle. Its **dominant** allele causes **hair** to be present and its **recessive** allele causes **hairlessness**.

A male and a female with **hair** have **two hairless female** offspring.

What is the **probability** that their next calf born is **hairless**?

Parental phenotypes	Female with hair	Male with hair
Parental genotypes	X^HX^h	X^HY
Gamete genotypes	X^H and X^h	X^H and Y
Genetic diagram		
Offspring genotypes	X^HX^H, X^HX^h, X^HY, X^hY	
Offspring phenotypes	Female with hair (2), male with hair, male hairless	
Probability	0.25 / 25% / ¼ / 1 in 4	

Worked example: monohybrid cross with sex-linkage and codominance

A gene on the **X chromosome** controls fur colour in cats. The allele **G** codes for **ginger** fur and the allele **B** codes for **black** fur. These alleles are **codominant**. **Heterozygous** females have patches of both so their phenotype is described as **tortoiseshell**.

A **tortoiseshell female** was crossed with a **black male**.

Use a genetic diagram to show all the possible **genotypes** and the **ratio** of **phenotypes** expected in the offspring of this cross.

Parental phenotypes	Tortoiseshell female	Black male
Parental genotypes	X^GX^B	X^BY
Gamete genotypes	X^G and X^B	X^B and Y
Genetic diagram		
Offspring genotypes	X^GX^B, X^BX^B, X^GY, X^BY	
Offspring phenotypes	Tortoiseshell female, black female, ginger male, black male	
Ratio	1:1:1:1	

Worked example: dihybrid cross with sex linkage

In fruit flies, a gene for **body colour** has a **dominant** allele for **grey** body (**G**) and a **recessive** allele for **black** body (**g**). A gene for **eye colour** has a **dominant** allele for red eyes (**R**) and a recessive allele for white eyes (**r**) and is located on the **X chromosome**.

A **heterozygous grey-bodied, white-eyed** female fly was crossed with a **black-bodied, red-eyed** male fly. Complete a genetic diagram to show all the possible **genotypes** and the **ratio** of **phenotypes** expected in the offspring from this cross.

Parental phenotypes	Grey-bodied, white-eyed female	Black-bodied, red-eyed male
Parental genotypes	GgX^rX^r	ggX^RY
Gamete genotypes	GX^r and gX^r	gX^R and gY
Genetic diagram		
Offspring genotypes	GgX^RX^r, ggX^RX^r, GgX^rY and ggX^rY	
Offspring phenotypes	Grey-bodied red-eyed female, black-bodied red-eyed female, grey-bodied white-eyed male, Black-bodied white-eyed male	
Ratio	1:1:1:1	

	gX^R	gY
GX^r	GgX^RX^r	GgX^rY
gX^r	ggX^RX^r	ggX^rY

Explain the evidence from a pedigree diagram which would show that the allele for [named phenotype] on the X-chromosome is recessive

- **Mother [n] WITHOUT** [named phenotype] has child **[n] WITH** [named phenotype]
- So mother **[n]** must be **heterozygous / carrier** of **recessive allele**

Explain the evidence from a pedigree diagram which would suggest that [named recessive phenotype] is caused by a gene on the X chromosome

Only **males** tend to have [named recessive phenotype].

Explain the evidence from a pedigree diagram which would show that the gene for [named phenotype] is not on the X chromosome

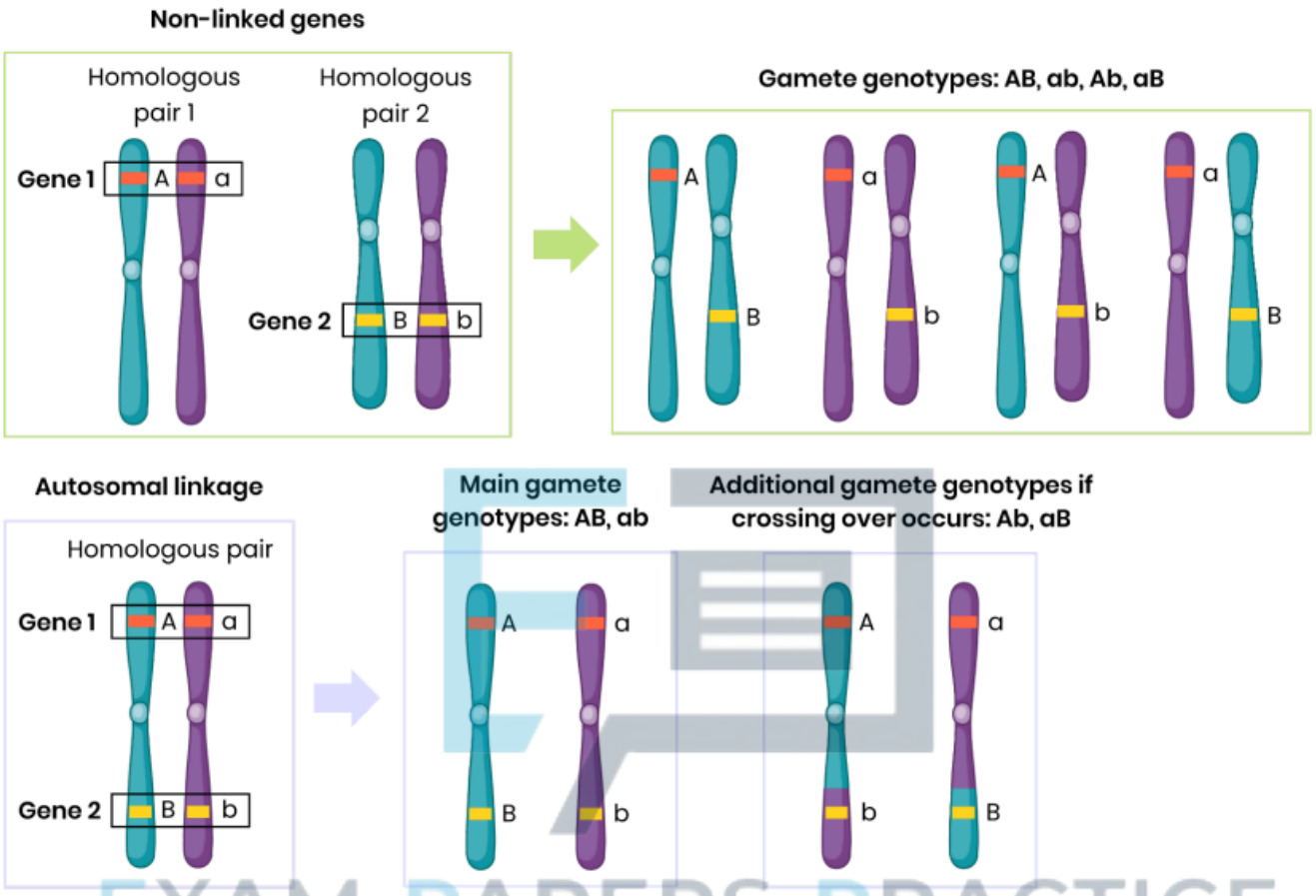
- [Named phenotype] **father [n]** has **daughter [n] WITHOUT** [named phenotype]
- **Father [n]** would **pass on allele** for [named phenotype] on **X chromosome** so daughter **[n]** would **have** [named phenotype]

  OR
- [Named phenotype] **mother [n]** has **son [n] WITHOUT** [named phenotype]
- **Mother [n]** would **pass on allele** for [named phenotype] on **X chromosome** so son **[n]** would **have** [named phenotype]

Note - this assumes **males** are **XY** and **females** are **XX**, as in humans. There has been a question previously about birds where males are XX and females are XY. In this case, **swap** father for mother and son for daughter.

Explain how autosomal linkage affects inheritance of alleles

- **Two genes** located on **same autosome** (non-sex **chromosome**)
- So **alleles** on same chromosome **inherited together**
  - Stay together during independent segregation of homologous chromosomes during meiosis
- But **crossing over** between homologous chromosomes can create **new combinations of alleles**
  - If the genes are **closer together** on an autosome, they are **less likely** to be split by crossing over



Worked example: autosomal linkage

In fruit flies, the genes for body colour and for wing development are **not** on the sex chromosomes. The allele for **grey** body colour, **G**, is **dominant** to the allele for **black** body colour, **g**. The allele for **long** wings, **L**, is **dominant** to the allele for **short** wings, **l**.

A cross was carried out between flies with **grey** bodies & **long** wings (**heterozygous** for both genes) and flies with **black** bodies & **short** wings.

The result of this cross was **225** offspring with a **grey** body & **long** wings and **220** with a **black** body & **short** wings. Explain these results.

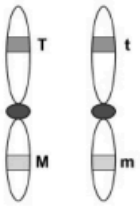
- The two genes are **linked / autosomal linkage**
- **No crossing over** occurs / genes are close together
- So **only GL** and **gl gametes** produced / **no Gl** and **gL gametes** produced / **no GgII** and **ggLl** offspring produced

Worked example: autosomal linkage

In tomato plants, the genes for height and for the type of leaf are on the **same homologous pair of chromosomes**. The allele **T**, for a **tall** plant, is **dominant** to the allele **t**, for a **dwarf** plant. The allele **M**, for **normal** leaves, is **dominant** to the allele **m**, for **mottled** leaves.

Phenotype of offspring	Number of offspring
Tall plants and normal leaves	1850
Tall plants and mottled leaves	63
Dwarf plants and normal leaves	52
Dwarf plants and mottled leaves	579

Crosses were carried out between plants **heterozygous** for both genes. The position of the two alleles for both genes was the **same** in each parent plant as shown in the diagram.



Explain the results in the table. Give the **expected ratio of phenotypes** if the genes for height and type of leaf were on **different homologous pairs of chromosomes**.

- Genes are **linked** (so mainly TM and tm gametes are produced)
- **Crossing over** has occurred
- So **few Tm** and **tM gametes** produced / **fewer tall, mottled** and **dwarf, normal** offspring produced
- If not linked (use punnett square) - **9:3:3:1** (tall, normal : tall, mottled : dwarf normal : dwarf, mottled)

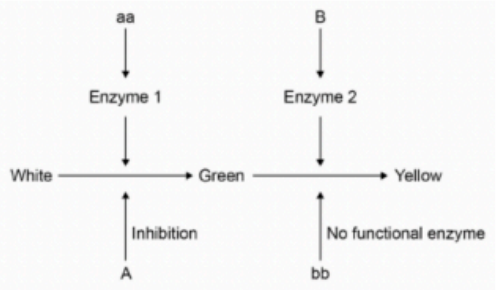
What is epistasis?

Interaction of (products of) non-linked genes where one **masks / suppresses** the expression of the other.

Worked example: dihybrid cross with epistasis

The inheritance of fruit colour in summer squash plants is controlled by two genes that are **not linked**, A and B. Each gene has two alleles. The diagram shows the **interaction** of these two genes.

Complete the genetic diagram to show all the possible genotypes and the ratio of phenotypes expected in the offspring of this cross.



Parental genotypes	**aabb**	**AaBb**
Gamete genotypes	ab (and ab)	AB, ab, aB, Ab
Genetic diagram		

	AB	Ab	aB	ab
ab	AaBb	Aabb	aaBb	aabb

Offspring genotypes	AaBb, Aabb, aaBb, aabb
Offspring phenotypes	White (x2), yellow, green
Ratio	2:1:1

Describe when a chi-squared (X^2) test can be used

- When determining if **observed results** are **significantly different** from **expected results (frequencies)**
  - Eg. comparing the **goodness of fit** of observed **phenotypic ratios** with expected ratios
- Data is **categorical** (can be divided into **groups** eg. phenotypes)

Suggest why in genetic crosses, the observed phenotypic ratios obtained in the offspring are often not the same as the expected ratios

- Fusion / fertilisation of gametes is **random**
- Autosomal **linkage** / epistasis / sex-linkage
- **Small** sample size → not **representative** of whole population
- Some genotypes may be **lethal** (cause death)

Describe how a chi-squared value can be calculated

$$\chi^2 = \sum \frac{(O-E)^2}{E}$$

O = frequencies observed

E = frequencies expected (multiply total n with each expected ratio as a fraction)

Describe how a chi-squared value can be analysed

1. Number of **degrees of freedom** = **number of categories - 1** (eg. 4 phenotypes = 3 degrees of freedom)
2. Determine **critical value** at **p = 0.05** (5% probability) from a table
3. If X^2 value is **[greater / less]** than critical value at $p < 0.05$
   - Difference **[is / is not] significant** so **[reject / accept]** null hypothesis
   - So there is **[less / more]** than **5%** probability that **difference** is due to chance

Exam insight: common mistakes ❌

Mistake	Explanation
"Only **genotype / genes / alleles** influence phenotype."	The environment affects **phenotype** too. This is a key part of the phenotype definition.
*Not matching offspring genotypes to their **phenotypes**.*	Some questions require you to link each offspring's genotype to its corresponding phenotype, either by **listing them in order** (see examples above), or **annotating** the Punnett square.
*Using **incorrect pairs of parents** when giving evidence from **pedigree diagrams** for alleles being dominant or recessive.*	These questions come up often but students find them very challenging. Use the **template answers** given and practice **applying** them to different examples of these questions.
*Omitting the **sex** of offspring when listing phenotypes of a cross involving **sex-linkage**.*	Crosses involving sex-linkage are the only ones that require the **sex of offspring** to be specified when listing **phenotypes**.
*Giving rote-learned ratios eg. **9:3:3:1** for every dihybrid cross.*	**Many factors influence** the ratio of phenotypes of offspring. It's best to calculate this yourself.

7.2 Populations

What is a population?

A group of organisms of the **same species** in one **area** at one **time** that can **interbreed**

What is a gene pool?

All the **alleles** of all the genes in a **population** at any one time

What is allele frequency?

Proportion of an **allele** of a gene in a **gene pool** (decimal or percentage)

What does the Hardy-Weinberg principle state and what are the conditions under which the principle applies?

- **Allele frequencies** will **not change** from **generation** to generation, given:
  - Population is **large**
  - No **immigration / emigration** (to introduce / remove alleles)
  - No **mutations** (to create new alleles)
  - No **selection** for / against particular alleles
  - Mating is **random**

This provides a **mathematical model**.

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What is the Hardy-Weinberg equation?

$p^2 + 2pq + q^2 = 1$

This can be used simultaneously with:

$p + q = 1$

- **p** = **frequency** of one (usually **dominant**) **allele** of the gene
- **q** = **frequency** of the other (usually **recessive**) **allele** of the gene
- p^2 = frequency of **homozygous** (usually **dominant**) **genotype**
- **2pq** = frequency of **heterozygous genotype**
- q^2 = frequency of **homozygous** (usually **recessive**) **genotype**

Note - if alleles are **codominant**, either can be assigned p and q.

Worked example: using the Hardy-Weinberg equation (basic)

The gene for the Rhesus blood group has two alleles. The allele for Rhesus **positive, R,** is **dominant** to that for **Rhesus negative, r.**

16% of the population of Europe is **Rhesus negative**. Use the Hardy-Weinberg equation to calculate the **percentage** of this population that you would expect to be **heterozygous** for the Rhesus gene.

Find q^2	q^2 = 16% = **0.16**
Find q	q = $\sqrt{0.16}$ = **0.4**
Find p	p = 1 - 0.4 = **0.6**
Find 2pq	2 x 0.4 x 0.6 = **0.48**
Convert	48%

Worked example: using the Hardy-Weinberg equation with codominance

In one species of flowering plant, two alleles C^R (**red**) and C^W (**white**) code for flower colour. When both are present, flowers are **pink**.

A population contained **9% red**-flowered plants. Use the Hardy-Weinberg equation to calculate the **percentage** of **pink-flowered** plants in this population.

Find q^2	q^2 = 9% = **0.09**
Find q	q = $\sqrt{0.09}$ = **0.3**
Find p	p = 1 - 0.3 = **0.7**
Find 2pq	2 x 0.3 x 0.7 = **0.42**
Convert	42%

Worked example: using the Hardy-Weinberg equation (more challenging)

In fruit flies, a gene for body colour has a **dominant** allele **G** (**grey**) for and a **recessive** allele **g** (**black**).

A population contained **64% grey**-bodied flies. Use the Hardy–Weinberg equation to calculate the **percentage** of flies **heterozygous** for this gene.

Find q^2	$p^2 + 2pq$ = 64% = **0.64** so q^2 = 1 - 0.64 = **0.36**
Find q	q = $\sqrt{0.36}$ = **0.6**
Find p	p = 1 - 0.6 = **0.4**
Find 2pq	2 x 0.6 x 0.4 = **0.48**
Convert	48%

Exam insight: common mistakes ❌

Mistake	Explanation
"A gene pool is all the **genes** in a population."	It is all of the **alleles** of all the genes in a population.
"A gene pool is all the alleles in a **species**."	It is all of the alleles of all the genes in a **population**.
*Using **'pq'** to calculate the frequency of the **heterozygous genotype**.*	The heterozygous phenotype is **'2pq'.** This represents **both ways** the two different alleles can be combined (eg. Aa and aA), effectively **doubling** the probability.
*Not being able to apply the Hardy-Weinberg formula when alleles are **codominant**.*	If alleles are codominant, **either** can be assigned p and q. The formula can be applied in the same way.
*Not **converting percentages to decimals** for Hardy-Weinberg calculations.*	Convert percentage allele frequencies to decimals by **dividing by 100** before using them in the formula.
*Confusing **allele frequency** with **homozygous genotype frequency**.*	Allele frequencies **'p'** and **'q'** represent the proportion of each allele in the population, while **'p^2'** and **'q^2'** indicate the proportion of individuals with homozygous genotypes (dominant and recessive, respectively).

7.3 Evolution may lead to speciation

Explain why individuals within a population of a species may show a wide range of variation in phenotype

- **Genetic factors**
  - **Mutations** = primary source of genetic variation
  - **Crossing over** between homologous chromosomes during **meiosis**
  - **Independent segregation** of homologous chromosomes during **meiosis**
  - **Random fertilisation** of gametes during sexual reproduction
- **Environmental factors** (depends on context - eg. food availability, light intensity)

What is evolution?

- **Change** in **allele frequency** over **time** / **many generations** in a population
- Occurring through the process of **natural selection**

Describe factors that may drive natural selection

- **Predation, disease** and **competition** for the means of survival
- These result in **differential survival** and **reproduction**, ie. natural selection

Explain the principles of natural selection in the evolution of populations

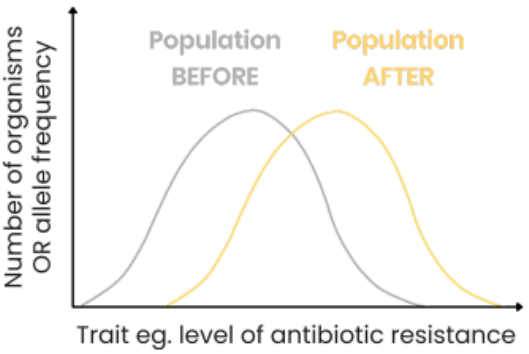
1. Mutations	**Random gene mutations** can result in [named] **new alleles** of a gene
2. Advantage	Due to [named] **selection pressure**, the new allele might **benefit** its possessor [explain why] → organism has a **selective advantage**
3. Reproductive success	Possessors are more likely to **survive** and have **increased reproductive success**
4. Inheritance	Advantageous allele is **inherited** by members of the next generation (**offspring**)
5. Allele frequency	Over **many generations**, [named] allele **increases** in **frequency** in the gene pool

Explain the effects of stabilising selection

- Organisms with alleles coding for **average / modal variations** of a trait have a **selective advantage** (eg. babies with an average weight)
- So **frequency of alleles** coding for **average** variations of a trait **increase** and those coding for **extreme** variations of a trait **decrease**
- So **range / standard deviation** is **reduced**

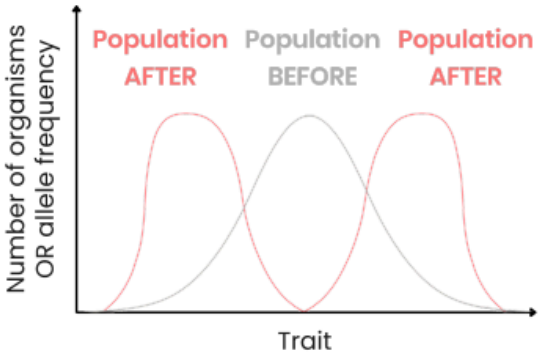
Explain the effects of directional selection

- Organisms with alleles coding for **one extreme variation** of a trait have a **selective advantage** (eg. bacteria with high resistance to an antibiotic)
- So **frequency of alleles** coding for this **extreme** variation of the trait **increase** and those coding for the other **extreme** variation of the trait **decrease**



Explain the effects of disruptive selection

- Organisms with alleles coding for **either extreme variation** of a trait have a **selective advantage**
- So **frequency of alleles** coding for **both extreme** variations of the trait **increase** and those coding for the **average** variation of the trait **decrease**
- This can lead to **speciation**

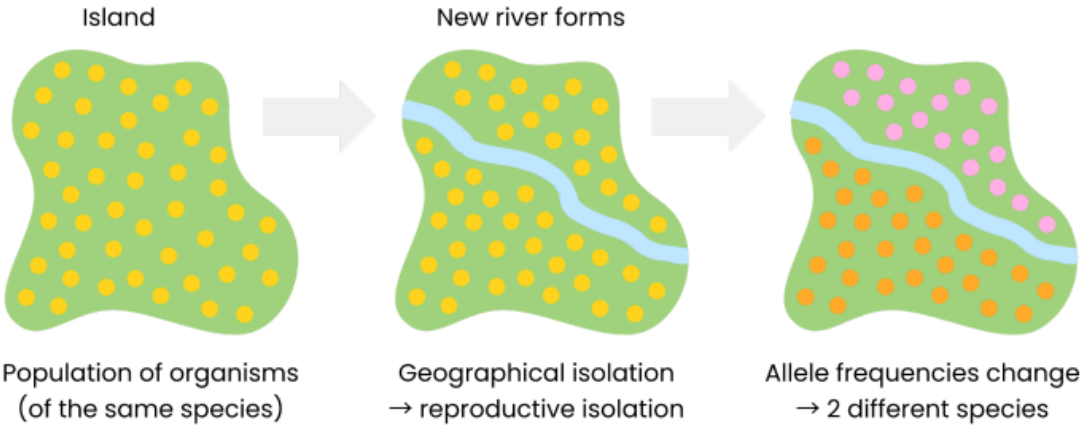


Describe speciation (how new species arise from existing species)

1. **Reproductive separation** of two populations (of the same species)
2. This can result in **accumulation of differences** in their **gene pools**
3. New species arise when these genetic differences lead to an inability of members of the populations to **interbreed** and produce **fertile offspring**

Describe allopatric speciation

1. Population is split due to **geographical isolation** (eg. new river formed)
2. This leads to **reproductive isolation**, separating **gene pools** by preventing **interbreeding / gene flow** between populations
3. Random **mutations** cause genetic variation within each population
4. **Different selection pressures** / environments act on each population
5. So **different advantageous alleles** are **selected for / passed on** in each population
6. So **allele frequencies** within each gene pool **change over many generations**
7. Eventually different populations **cannot interbreed to produce fertile offspring**



Describe sympatric speciation

1. Population is **not** geographically isolated
2. **Mutations** lead to **reproductive isolation**, separating **gene pools** by preventing **interbreeding / gene flow** within one population, eg.
   - Gamete incompatibility
   - Different breeding seasons (eg. different flowering times)
   - Different courtship behaviour preventing mating
   - Body shape / size changes preventing mating
3. **Different selection pressures** act on each population
4. So **different advantageous alleles** are selected for / passed on in each population
5. So **allele frequencies** within each gene pool **change over many generations**
6. Eventually different populations **cannot interbreed to produce fertile offspring**

Explain genetic drift and its importance in small populations

- **Genetic drift** = a mechanism of **evolution** in which **allele frequencies** in a population change over generations due to **chance**
- As some alleles are **passed onto offspring more / less often** by **chance**
  - **Regardless** of selection pressures and whether alleles give a **selective advantage**
- So strongest effects in **small populations** as **gene pool** is small and **chance** has a greater influence
  - Eg. when a population is sharply reduced in size (bottleneck effect)
  - Eg. when a small, new colony forms from a main population (founder effect)
- This can **reduce genetic diversity** - some alleles can become fixed or lost entirely

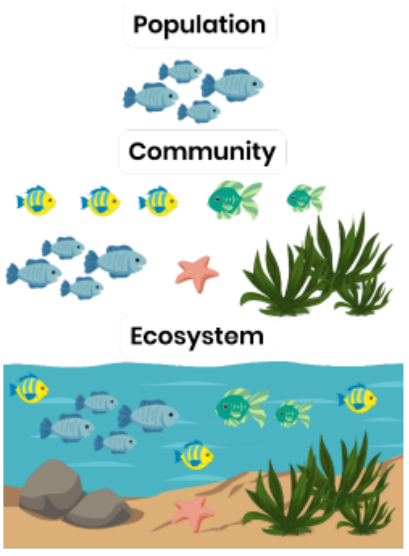
Exam insight: common mistakes ❌

Mistake	Explanation
"**Speciation** and **natural selection** are causes of genetic variation."	Speciation and natural selection **act on / require** existing genetic variation, but don't cause genetic variation.
"If I repeat the **generic answer** about natural selection, I'll get full marks."	Exam questions are almost always **application** based. Use information provided to **link** your answer to the question.
*Forgetting to mention **mutations** in an answer about natural selection.*	Mutations result in new **alleles** of genes, enabling natural selection to occur. This mark is commonly missed.
"Selection pressures eg. exposure to antibiotics **cause** mutations."	Mutations happen **continuously** and **randomly**.
"Reproductive isolation occurs at the **end** of allopatric speciation."	Geographical isolation **leads to reproductive isolation**. This then allows differences in gene pools to accumulate.
"**Organisms adapt** to their environments."	Whole **populations** adapt to their environment over **many generations**, not the organisms themselves. Organisms that happen to be **better adapted** are **more likely to survive and reproduce**.

7.4 Populations in ecosystems

What is a community?

All the **populations** of **different species** living in the same **place** (habitat) at the same **time.**



What is an ecosystem?

A **community** and the **non-living (abiotic)** components of its environment.

Ecosystems can range in size from **very small** to **very large**. They are **dynamic** systems (populations rise / fall over time).

What is a niche?

- The specific **role** of a **species** within its **habitat**, eg. what it eats, where and when it feeds
- Governed by its **adaptation** to both **abiotic** (non-living) and **biotic** (living) conditions

Explain the advantage of species occupying different niches

- **Less competition** for food / resources
- If two species tried to occupy the same niche, one would **outcompete** the other

What is carrying capacity?

The **maximum** (stable) **population size** of a species that an **ecosystem** can support.

List the factors that influence carrying capacity

Abiotic factors	Eg. light intensity, temperature, soil pH & mineral content, humidity
Interactions between organisms	a. **Interspecific competition** - between organisms of **different species** b. **Intraspecific competition** - between organisms of the **same species** c. **Predation** (predators kill and eat other animals, called prey)

Explain how abiotic factors may affect population size / carrying capacity

- If conditions **favourable**, organisms **more likely** to **survive & reproduce** → **increasing** carrying capacity
- Eg. increasing **light intensity** increases rate of **photosynthesis** in **plants**
  - This **increases** carrying capacity of a **variety** of **plant** species
  - So increases the number and **variety** of **habitats**, **niches** and **food sources** for animals
  - So **increasing** carrying capacity of a variety of **animal** species

Explain how interspecific competition may affect population size

- **Reduces [named resource]** available to both species, **limiting** their chances of **survival** & **reproduction**
  - So **reduces population size** of both species
- If one species is **better adapted,** it will **outcompete** the other
  - So **population size** of **less well adapted species declines**, potentially leading to **extinction**

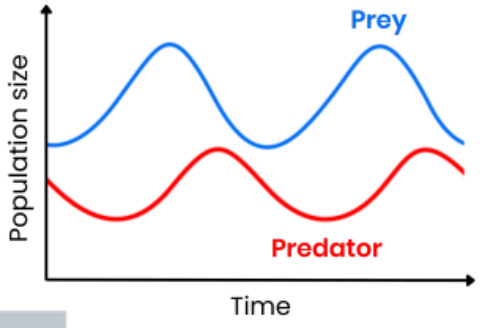
Explain how intraspecific competition may affect population size

1. As population size **increases,** resource availability per organism **decreases**, so **competition increases**
   - So chances of **survival & reproduction decrease** → population size **decreases**
2. As population size **decreases,** resource availability per organism **increases**, so **competition decreases**
   - So chances of **survival & reproduction increase** → population size **increases**

Explain the changes which occur in populations of predators & prey

Populations **fluctuate** in **cycles**, the **predator** population peaking **after** the prey (lag time):

1. **Prey** population **increases** so **predators** have **more food**
   - So **more predators** survive & reproduce
2. **Predator** population **increases** so **more prey killed & eaten**
   - So **less prey** survive & reproduce
3. **Prey** population **decreases** so **predators** have **less food**
   - So **less predators** survive & reproduce
4. **Predator** population decreases so **less prey killed & eaten**
   - So **more prey** survive & reproduce (cycle repeats)



Describe how the size of a population of slow-moving or non-motile organisms can be estimated

1. Divide area into a **grid / squares** eg. place **2 tape measures** at right angles
2. Generate a pair of **coordinates** using a **random number generator** (eg. on a calculator)
3. Place a **quadrat** here and count **number / frequency** of [named species]
4. **Repeat** a **large number** of times (10 or more) and calculate a **mean** per quadrat
5. **Population size** = (**total** area of habitat **/ quadrat** area) **x mean** per quadrat

Describe how the mark-release-recapture method can be used to estimate the size of a population of motile organisms

- **Capture** sample of species, **mark** and **release**
- Ensure marking is **not harmful** / does **not affect survival**
- Allow **time** for organisms to randomly **distribute** before collecting **second sample**
- Population = **(number in sample 1 x number in sample 2) / number marked in sample 2**

Note - marking doesn't have to be physical. It could be recording the base sequence, for example. Recapturing an organism with an identical base sequence would show the organism has been caught ('marked') before.

Explain how the mark release recapture equation can be derived

This is for your **understanding** only. Assuming the **proportion** of **marked individuals** in the **second sample** reflects the **proportion** of the **entire first sample** in the **population**, the following formula can be derived:

$$\frac{\text{Number (marked) in sample 1}}{\text{Total population size}} = \frac{\text{Number marked in sample 2}}{\text{Total number in sample 2}}$$

This just needs to be **rearranged** to get the formula for population size.

Worked example: mark-release-recapture

A student **collected 17 lizards** and marked them before releasing them back into the same area. Later, she collected **20 lizards, 10 of which were marked.** Calculate the number of lizards in this area.

$(17 \times 20)/10 = \underline{34}$

What assumptions does the mark-release-recapture method make?

1. **Sufficient time** for marked individuals to **mix / distribute evenly** within the population
2. **Marking not removed** and doesn't affect chances of **survival / predation**
3. Limited / no **immigration / emigration**
4. No / few **births / deaths / breeding** / change in population size (or birth & death rate are equal)

Suggest why the mark-release-recapture method can produce unreliable results in very large areas

- Unlikely that organisms will **distribute randomly / evenly**
- Less chance of **recapturing** organisms (that were marked initially)

Describe and explain how primary succession occurs

Succession = change in a **community** over **time** due to change in abiotic factors / species

1. **Colonisation** by **pioneer species** (first to colonise)
2. Pioneer species (and other species at each stage in succession) **change abiotic conditions**
   - Eg. they die and decompose, forming **soil** which retains water (humus / organic matter)
3. So environment becomes **less hostile / more suitable** for **other species with different adaptations AND** less suitable for previous species, so better adapted species **outcompete** previous species
4. As succession goes on, **biodiversity increases**
5. **Climax community** reached - **final stable** community (no further succession)

Describe features of a climax community

- **Same species** present / **stable community** over a long time
- **Abiotic** factors (fairly) **constant** over time
- **Populations** (fairly) **stable** (around carrying capacity)

Explain how conservation of habitats involves management of succession

- Further succession can be **prevented** to **stop** a **climax community** forming
  - By **removing** or **preventing growth** of species associated with later stages eg. by allowing **grazing**
- This **preserves** an ecosystem at a certain point / in its current stage of succession (plagioclimax)
- So early species are **not outcompeted** by later species and **habitats / niches** are not lost

Describe the conflict between human needs and conservation as well as the importance of managing this

- Human demand for natural resources (eg. timber) is leading to **habitat destruction / biodiversity loss**
- **Conservation** is needed to protect **habitats / niches / species / biodiversity**
- Management of this conflict maintains the **sustainability of natural resources**
  - Meeting current needs **without compromising the ability of future generations to meet theirs**

Students should be able to **evaluate evidence** and **data** concerning **issues** relating to the **conservation** of species and habitats and consider **conflicting evidence**.

Exam insight: common mistakes ❌

Mistake	Explanation
"Climate is an abiotic factor."	Give a specific example eg. **light intensity** or **temperature**.
"Quadrats are randomly placed."	This is true, but you need to describe a method for this. Random coordinates can be generated using a **random number generator**. You also need to specify that a **large number** of quadrats are used.
*Describing how to calculate the **mean number of organisms per quadrat**, instead of the total population size.*	Many students suggest 'scaling up' from the mean number without giving any detail on how this would be achieved. Population size = (**total** area of habitat **/ quadrat** area) **x mean** per quadrat
*Not mentioning allowing sufficient **time** for organisms to disperse in the mark-release-recapture method.*	Sufficient time allows organisms to naturally **redistribute** within the area being sampled, ensuring a **representative** second sample for accurate population estimates.
*Giving the **incorrect equation** for mark-release-recapture.*	The best way to learn the equation is by **understanding** how it is derived. This is explained in the notes above.
Mixing up speciation and succession.	**Succession** is the change in a community over time, whereas **speciation** is how new species arise from existing species.
*Not referring to an increase in **biodiversity** during succession.*	As succession progresses, biodiversity tends to **increase** as the variety of species present increases.

Required practical 12

Investigation into the effect of a **named environmental factor** on the **distribution** of a given species.

Describe how you could investigate the effect of an environmental factor on the distribution of a species in a habitat (random sampling in two areas)

1. Divide **two areas** into **grids / squares** eg. place **2 tape measures** at right angles
2. Generate a pair of **coordinates** using a **random number generator** (eg. on a calculator)
3. Place a **quadrat** here and count **number / frequency** of [named species]
    - **Standardise** this eg. only count it if it is more than half in the quadrat
4. **Repeat** a **large number** of times (10 or more) and calculate a **mean** per quadrat for both areas
5. Measure **environmental factor** in each area eg. take soil moisture readings with a soil moisture meter

Common questions:

Suggest why percentage cover may be used rather than frequency.	• Too **difficult** to count individual organisms / individual organisms are **too small** to count
Explain why random sampling is used.	• To avoid sampling **bias**
Explain the importance of a large sample size.	• Minimises the effect of **anomalies** • Ensures sample is **representative** of the population
Describe how you could decide the number of quadrats that should be used in order to collect representative data.	• Calculate a **running mean** • When enough quadrats, this shows **little change** • Enough to carry out a **statistical test**

Describe how you could investigate the effect of a factor on the distribution of a species in a habitat (systematic sampling)

1. Place a **transect** line (tape measure) across an area with an **environmental gradient** eg. tree to full sun
2. Place **quadrats** at **regular intervals** eg. 1m (until end of transect) and record the **number** of organisms of [named species] and [named **environmental factor**] eg. light intensity using a light meter
3. **Repeat** in other parallel areas and calculate **mean** number of plants at each point along the transect

Common questions:

Explain the limitations of using systematic sampling to estimate the population of a species in a field.	• Not appropriate unless there is an **environmental gradient** • Transects run in **one direction**, but to cover the entire field, they would need placing in multiple directions
Which statistical test should be used to determine the relationship between abundance and an environmental factor?	• **Correlation coefficient** eg. Spearman's rank