CAIE Biology A-level

Topic 16: Inherited change

Notes

Meiosis is a form of cell division that gives rise to **genetic variation**. The main role of meiosis is the **production of haploid gametes,** as cells produced by meiosis have half the number of chromosomes. **Reduction division** takes place where the chromosome number halves from diploid to **haploid**.

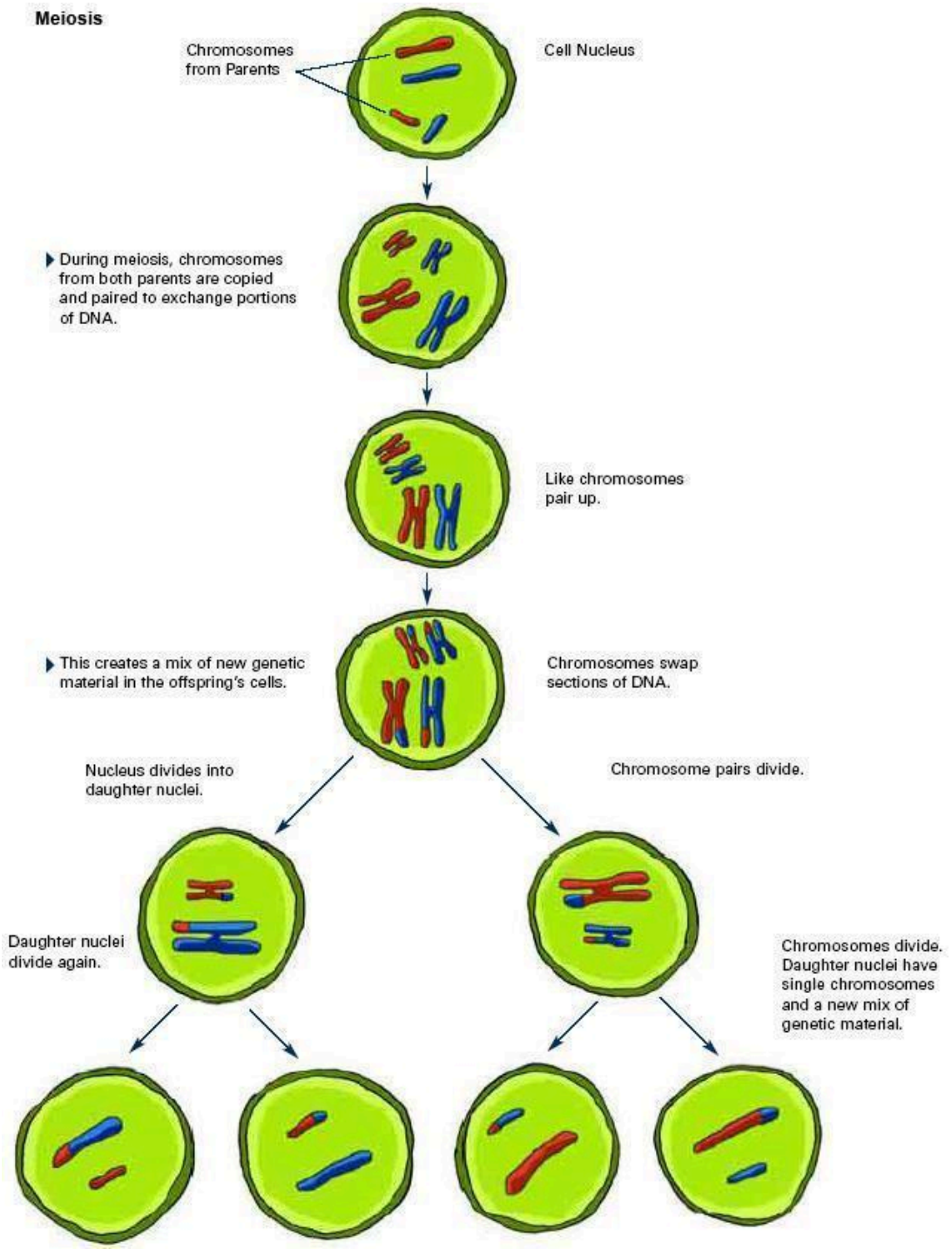

*Figure SEQ Figure * ARABIC 1 Biologypost - Meiosis*

Stages of Meiosis:

Interphase occurs before meiosis begins. During this phase, **DNA is replicated** so each chromosome consists of **two identical sister chromatids** joined at a **centromere**. The cell is **diploid** at this stage.

Stages of Meiosis	Description
Prophase I	**Chromosomes condense and become visible**. **Homologous chromosomes pair up** to form **bivalents**. **Crossing over** occurs between non-sister chromatids at **chiasmata**, resulting in **exchange of genetic material and increased genetic variation**. The **nuclear envelope breaks down and spindle fibres form**.
Metaphase I	Bivalents **line up randomly along the equator of the cell**. The **independent assortment** of homologous chromosomes **increases** genetic variation. Spindle fibres attach to centromeres.
Anaphase I	**Homologous chromosomes are pulled apart to opposite poles** by spindle fibres. Centromeres do not divide, so sister chromatids remain together. This stage results in **reduction division, halving the chromosome number**.
Telophase I and Cytokinesis	The cytoplasm **divides into two haploid cells**, each containing one chromosome from **each homologous pair**. Chromosomes still consist of two sister chromatids.
Prophase II	**Chromosomes condense** again, the **nuclear envelope breaks down**, and **new spindle fibres form** in each haploid cell.
Metaphase II	**Chromosomes line up along the equator of each cell**. Spindle fibres attach to the centromeres of sister chromatids.
Anaphase II	**Centromeres divide, and sister chromatids are pulled apart to opposite poles**. Each chromatid is now an individual chromosome.
Telophase II and Cytokinesis	**Nuclei reform and the cytoplasm divides**, producing **four genetically different haploid cells**. Each cell contains a single set of chromosomes, suitable for functioning as gametes.

Meiosis produces genetically different cells; genetic variation is achieved through:

- **Crossing over between non-sister chromatids** of homologous pairs - pairs of chromosomes line up and exchange some of their genetic material. This happens in prophase I.
- **Independent assortment of chromosomes** – various combinations of chromosome arrangements can occur in pairs of homologous chromosomes during meiosis I.

During **fertilisation,** the **random fusion** of gametes also increases genetic variation in offspring.

Genetic crosses are used to predict the ratios of inherited characteristics in a population.

Monohybrid Crosses:

- **Monohybrid crosses** are used to determine the outcome of **one gene**. There are **four** possible genotypes, giving a phenotypic ratio of **3:1**, where the dominant trait is more common. E.g. Crossing heterozygous green and yellow pea plants:

  G = green (dominant allele), g = yellow (recessive allele)

  (Gg x Gg)

	G	g
G	GG	Gg
g	Gg	gg

  The outcomes are GG, Gg, Gg and gg. As G is dominant, there is a 75% chance that offspring will be green and a 25% chance they will be yellow.

Dihybrid Crosses:

- **Dihybrid crosses** are used to determine the outcome of **two genes,** each of which have **two alleles**. This results in **16 outcomes.**

  E.g. Pea plants can be tall or short, and have purple or white flowers.

  P = purple, p = white
  T = tall, t = short

  Crossing two heterozygous parents (PpTt x PpTt):

	PT	Pt	pT	pt
PT	PPTT	PPTt	PpTT	PpTt
Pt	PPTt	PPtt	PpTt	Pptt
pT	PpTT	PpTt	ppTT	ppTt
pt	PpTt	Pptt	ppTt	pptt

  Assuming the genes assort independently, this results in a **9:3:3:1** ratio.

Sex-linked Crosses:

- **Sex-linked genes** are located on the **X chromosome** (the Y chromosome carries very few genes). Males are **XY** and females are **XX**, so males have **only one allele** for X-linked genes. **Recessive X-linked alleles** are more commonly expressed in males because there is **no corresponding allele on the Y chromosome** to mask them.

E.g. Red–green colour blindness

X^N = normal vision (dominant)
X^n = colour blindness (recessive)

Carrier female (X^NX^n) × normal male (X^NY)

	X^N	Y
X^N	X^NX^N	X^NY
X^n	X^NX^n	X^nY

Outcome: 50% of sons affected, 0% of daughters affected, 50% of daughters carriers

- Normal female (X^NX^N)
- Carrier female (X^NX^n)
- Normal male (X^NY)
- Colour-blind male (X^nY)

Codominance:

- **Codominance** occurs when **both alleles are expressed equally** in the heterozygote. Neither allele is dominant or recessive. The heterozygous phenotype shows **both traits at the same time**.
E.g. ABO blood groups

I^A and I^B = codominant alleles
i = recessive

Blood group A × blood group B (I^Ai x I^Bi)

	I^B	i
I^A	I^AI^B	I^Ai
i	I^Bi	ii

Outcome: 1 AB : 1 A : 1 B : 1 O. I^AI^B individuals express **both alleles equally**.

Blood group AB shows **both A and B antigens**, demonstrating codominance.

Autosomal linked genes:

- **Autosomal linked genes** are located on the **same autosome** and are therefore **inherited together**. Linked genes **do not assort independently**. Crossing over during **prophase I of meiosis** may separate linked genes, but this occurs **less frequently** than independent assortment.

  E.g. Gene A and gene B are on the same chromosome

  AB/ab × AB/ab

	AB	ab
AB	AB/AB	AB/ab
ab	AB/ab	ab/ab

  Outcome: Phenotypic ratios **do not follow 9:3:3:1.**

  Linked genes are inherited together unless separated by **crossing over**.

Chi-squared test

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

The **chi-squared test** is a **statistical** test which can be used to establish whether a difference between **observed and expected results** is small enough to occur purely due to chance.

- It can be used if the **sample size** is sufficiently large, that is over 20. It can only be used for **discontinuous variation** data in the form of raw counts.
- The chi-squared test can be used to determine whether the **null hypothesis** is correct or not. The null hypothesis is the assumption that there is no difference between observed and expected results.
- The value obtained is compared to the **critical value**. In a case where the value obtained is less than the critical value, the null hypothesis is accepted as the difference is considered to be due to chance and is not significant.
- In a case where the chi value is greater than critical value, the null hypothesis is rejected. This means that the difference between observed and expected results is significant and is not due to chance.
- The number of degrees of freedom can be calculated by using the formula: $v = c - 1$

Mutations

Mutations are changes in the sequence of nucleotides in DNA molecules. Gene mutations are a result of substitution, deletion, or insertion of nucleotides. Insertion and deletion of nucleotides typically result in a frameshift, altering the entire subsequent polypeptide sequence. Mutations can also have **neutral effects** (mutation causes no change to the organism). For example, this often happens if the mutation occurs in **a non-coding region** of DNA. A mutation can also be neutral if a change in the protein's tertiary structure does not affect its function.

Some mutations are beneficial, for instance, humans developed **trichromatic vision** through a mutation. Harmful mutations include the **CFTR gene** mutation which causes **cystic fibrosis.**

Conditions caused by gene mutations:

Human condition	Effect of mutation on genotype	Effect of mutation on phenotype
Albinism	The **TYR gene** is responsible for the production of **tyrosinase**. This is the enzyme that controls melanin production. If a **mutation** in the TYR gene occurs, tyrosinase production is hindered resulting in the person developing albinism.	Albinism is a result of a mutation in a gene that causes the production of melanin. This causes **little or no melanin to be produced**, resulting in light hair and skin colour, and vision impairment.
Sickle cell anaemia	The **HBB gene** is responsible for producing a protein which is a subunit of haemoglobin. If a mutation occurs in the HBB gene, then the red blood cell's **haemoglobin** will be altered leading to sickle cell anaemia.	Caused by a **missense mutation** in the β-haemoglobin gene. This causes **red blood cells to become sickle shaped**. Sickle cells carry less oxygen and can block blood vessels.
Haemophilia	Haemophilia A is an **X-linked recessive disorder** only affecting **males** - caused by a mutation in the F8 gene, leading to a deficiency of clotting **factor VIII.**	It is when a person's blood does not clot normally due to the lack of a blood-clotting factor. If this is not treated, it can lead to prolonged bleeding which can be fatal.
Huntington's disease	Huntington's is caused by a mutation to the HTT gene. The **HTT gene** codes for a protein called **huntingtin** which plays a role in normal functioning of neurones.	It leads to the **degeneration of nerve cells** in the brain, causing cognitive and movement problems.

Controlling gene expression

Gene expression can be controlled at the transcriptional, post-transcriptional, translational and post-translational levels.

An example of transcriptional control is **the lac operon**, which is a length of DNA composed of structural genes and control sites which controls the expression of **β-galactosidase** responsible for hydrolysis of lactose in E. coli. The operon consists of:

- a **promoter region** which is the binding site for RNA polymerase to initiate transcription
- an **operator region** where the inhibitor binds
- **structural genes** which give rise to 3 products; β-galactosidase, lactose permease and another enzyme.

The **inhibitor** is coded for by a regulator gene, located outside the operon which binds to the operator region.

In a case where the concentration of glucose is high and the concentration of lactose is low, the transcription of the structural genes is inhibited due to binding of the **repressor** to the operator region. However, in a case where the concentration of glucose is low and concentration of lactose is **high, lactose binds the repressor,** thus causing the shape of its active site to change, therefore making it ineffective. This means that it can no longer bind to the operator region and transcription of the structural genes takes place.

Gene expression can also be controlled by **transcription factors**. Transcription factors are proteins that bind to DNA, and have the ability to switch genes on and off. They do so through interaction with the promoter sequence of DNA to either initiate or inhibit transcription.

Gene expression is controlled at the post-transcriptional level by **editing of the primary mRNA transcript**, during which the non-coding regions called **introns are** removed, thus creating a mature transcript consisting only of protein-producing regions known as **exons.**

Gibberellin is a plant hormone that controls plant growth and seed germination by controlling the production of amylase. It does this by breaking down **DELLA**, a **repressor protein** which inhibits the binding of a transcription factor to the gene promoter region. As a result, the transcription factor can bind and transcription of the gene can occur which increases the synthesis of amylase. The height of plants is controlled by whether the active form of gibberellin is present, which is determined by the plant's genes: if the **dominant allele (Le)** is present, gibberellin is active and the plant grows tall, if the **recessive allele (le)** is present in the homozygous state, a **non-functioning** gibberellin enzyme is coded for, thus the plant remains short.