Biology Assignment

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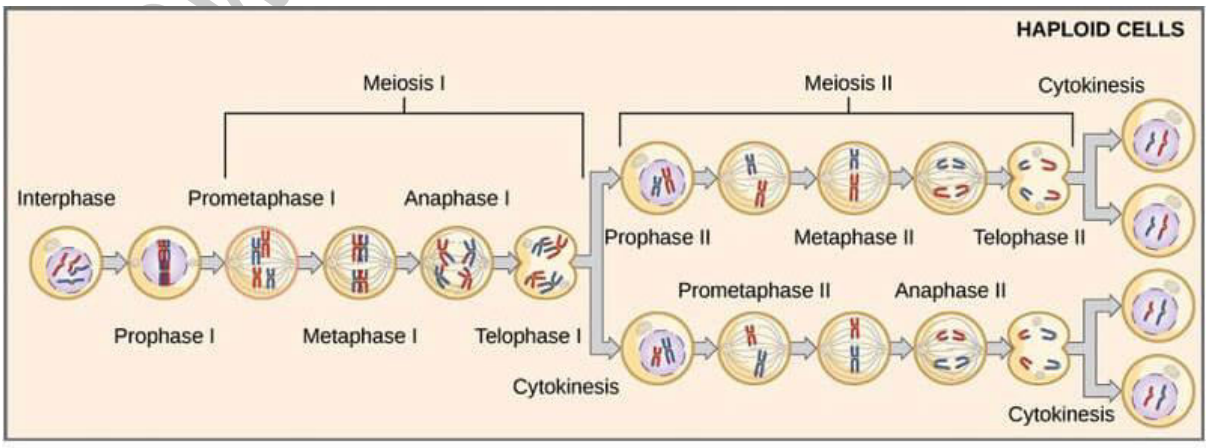
1.0. Biological Significance of Meiosis

Meiosis is essential to biological survival. It is a type of cell division whose primary role is to produce gametes (sperm and egg in mammals). In meiosis, every parent cell divides twice to contain half the genetic information. Meiosis results in the reduction from diploid (two sets of chromosomes) to haploid (one set of chromosomes). According to Holliday (1984), in meiosis, there is a reduction from the normal somatic number of 46 chromosomes to 23 chromosomes. There is an initial DNA replication process followed by two nuclear divisions (meiosis I and meiosis II) (O'Connor, 2008). Both divisions have four stages, including prophase, metaphase, anaphase and telophase, as evident in the following Figure 1. In prophase 1 (in meiosis I), the starting cell is diploid. At this stage, there is pairing up of homologous chromosomes and exchange of fragments through cross-over. In metaphase I, the homologous pairs line up at the metaphase plate. In anaphase I, there is separation of the homologues pairs to opposite ends of the cell. Telophase I involves the newly formed cells becoming haploid, every chromosome having two non-identical sister chromatids (Bernstein and Bernstein, 2013). also has four stages. In prophase II (in meiosis II), the cells are in the haploid condition. The chromosomes condense at this stage. In the metaphase II stage, the chromosomes line up at the metaphase plate. In anaphase II, the sister chromatids separate to opposite ends of the cell, and in telophase II, every chromosome has a single chromatid through decondensation (Moens, 2012). This essay highlights the biological significance of meiosis across both divisions.

Figure 1: Meiosis I and II



Source: Rye et al. (2016)

Meiosis I is different from mitosis in that there is homologous chromosome pairing, reciprocal recombination and release of sister chromatic cohesion. Crossing over or reciprocal recombination is essential during meiosis as it can account for genetic variation. This occurs during the pachytene stage of prophase I of meiosis. In eukaryotes, every cell has two versions of the gene, referred to as alleles. Every parent contributes one allele to the offspring. During meiosis I, the recombination results in the new arrangement of maternal and paternal alleles on the same chromosome (Terasawa et al., 2007).

This leads to different combinations of parental alleles in the offspring. From the Mendelian genetic perspective, a key biological significance of meiosis is the principle of independent assortment (Darlington, 1977). The chromosomes that result from meiosis can have a mix of traits from both parents. In human gametes, there are 23 chromosomes. Therefore, independent assortment leads to 223 or 8,388,608 combinations, creating significant genetic variability at the offspring level. Therefore, the key biological significance of meiosis is that it contributes to recombination-driven genetic diversity and natural selection (Maiato and Schuh, 2018). The chromosomal pairing is supported by the formation of synopsis and the chiasma, which help in cross-over and the exchange of large chromatic segments. The synaptonemal complex disappears after the exchange of genetic material. The primary reason for the formation of the synaptonemal complex is that it helps stabilise the homologues during the cross-over process (Zickler and Kleckner, 2015). According to Arkhipova and Meselson (2005), meiotic pairing and recombination evolved as a way to avoid the burden of non-allelic ectopic recombination in eukaryotes which may have had repetitive sequencies.

Another important biological significance of meiosis is its ability to repair genetic defects in the germline. Selection in the germline occurs from the mitotically dividing germ cells to recombination events during meiosis (Immler and Otto, 2018). Such selection events may have an effect on the heritability of specific alleles. The recombination process helps suppress recessive genes through the integration of dominant genes. As a result of meiosis, it is possible for a dominant allele in the end heterozygote to mask a recessive allele and ensure that the recessive phenotype is not transmitted (Benavente and Volff, 2009). For example, in sickle cell anaemia, if an individual has one dominant allele, they only act as carriers and do not have the

actual disease. According to Archetti (2003), recombination caused during the meiosis process is essential to spread the self-promoting genetic element to exploit DNA repair and associated gene conversion.

The third key biological significance of meiosis is its ability to contribute to the immortality of the germline. The process of meiosis is intended to transfer genetic material from one generation to the next indefinitely (Holliday, 1984). In contrast, in somatic cells, there is only a need for single generation transmission. Meiosis is regulated and the notion of regulation is different for different species. Meiosis can act as a survival mechanism for some eukaryotic species, like yeast. For such simple organisations, if there is a lack of nutrients, they enter meiosis (O'Connor, 2008). However, when there are favourable conditions, yeast reproduces asexually through mitosis. In yeast, the commitment to meiosis is attributed to the expected probability that during meiosis there will be four reproductive spores for every cell each with a novel genotype (Lopez-Maury et al., 2008). Therefore, meiosis is considered as a regulated and timed process which contributes to continued survival in other species.

In contrast, in most multicellular organisms, meiosis is restricted only to the germ cells. The timing of meiosis may vary across sexes. In male germ cells, meiosis occurs only after puberty. Only a few spermatogonia enter meiosis at any one time. Adult males have a large population of actively dividing spermatogonia which continue to act as a stem cell population (O'Connor, 2008). In contrast, in mammalian females, the oogonia stop dividing and enter meiosis within the fetal ovary. The germ cells that enter meiosis eventually become oocytes, which are the source of future eggs. Therefore, unlike males, females have a finite number of oocytes (Holliday, 1984). The regulation of meiosis is intended to support the sustenance of species and mediate biological reproduction.

Meiosis and syngamy are also linked to epigenetic reset. According to Gorelick and Carpinone (2009), meiosis allows for epigenetic resetting in eukaryotes. The authors reported that metazoan development is controlled as a result of meiosis, where epigenetic changes are irreversibility maintained through life, and is reset twice (n to 2n and 2n to n transitions). This process supports proper development and can ensure that parent-specific imprints are transmitted to the offspring (Lenormand et al., 2016).

Therefore, meiosis is key to the formation of gametes which can aid in sexual reproduction. Its biological significance also rests with its ability to activate genetic information, maintaining chromosomal integrity, addressing genetic repair and supporting recombination and natural selection. It also helps create genetic diversity through new combinations of traits and variations.

2.0. Explaining Inheritance Pattern Using Named Examples of Genetic Disorders

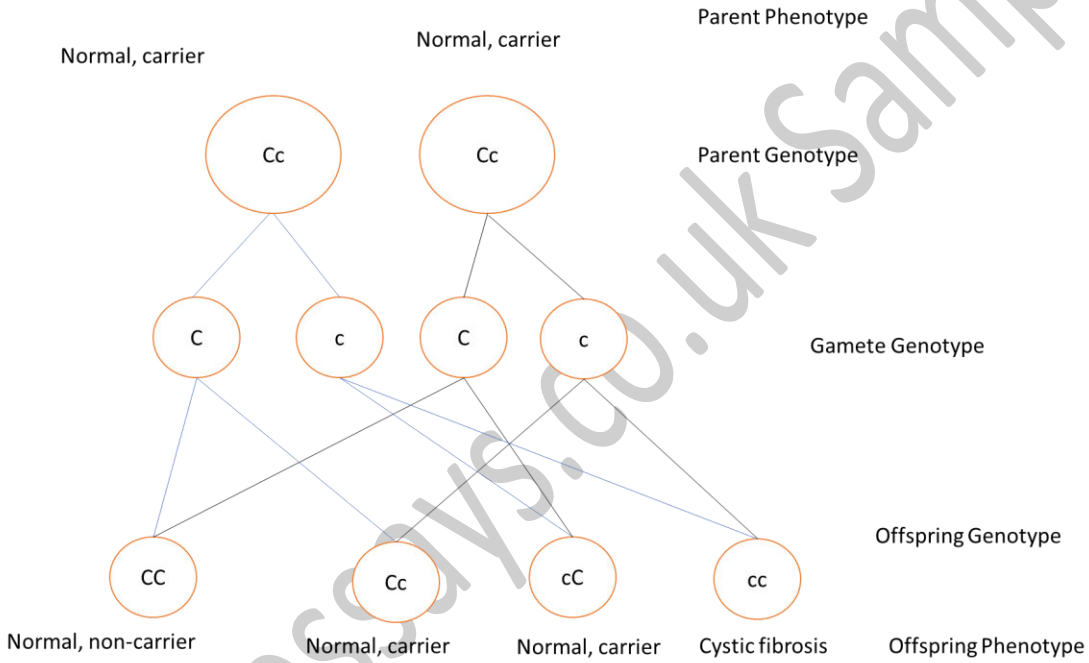
2.1. Autosomal Recessive Disorder

An autosomal recessive disorder occurs when a person has mutations or defects in both copies of a specific autosomal gene. This can lead to a loss of function, manifesting as a disease. If both copies of the gene have similar mutations, then the defect is homozygous (McKusick, 2014). However, if each gene has a different mutation, then the defect is compound heterozygous. In autosomal recessive disorders, both parents of the affected individual are often heterozygous carriers, having one copy of the normal gene and one copy of the gene with a specific mutation (Lewis, 2016). The autosomal recessive disorder that is considered in this essay is cystic fibrosis.

Cystic fibrosis (CF) occurs as a result of a loss of function mutation in the CFTR gene. The mutation of the CFTR gene leads to ineffective functioning of the CF transmembrane conductance regulator, leading to the build-up of mucus and lung infections (Ratjen and Doring, 2003). Mutation of the CFTR gene can be identified through genetic testing of expecting parents. According to Goldstein and Prystowsky (2017), a single genetic mutation is responsible for 70% of all cases of cystic fibrosis. It is caused by the deletion of three base pairs at codon 508 due to the loss of phenylalanine amino acid. This deletion is referred to as del508. The del508 mutation shows Mendelian inheritance wherein both parents are heterozygous for the del508 mutation. Therefore, there is a 25% chance that a child resulting from a pregnancy will have cystic fibrosis. However, as Lommatzch and Aris (2009) remark, not all parents have the same mutations: the child may inherit different mutations from both parents, which can have a differential impact on the CFTR gene. Goldstein and Prystowsky (2017) argued that these differences in mutation cause a spectrum of disease phenotypes to be observed. Also, Egan (2016) identified that there could

be a partial effect in some mutations which may create a CF phenotype along with other mutations. Such complexities across over 1,800 identified mutations linked to the CFTR gene create significant variability in how the mutation affects protein function and how its clinical phenotype is perceived. The following Figure 2 presents a genetic inheritance diagram for the pattern of inheritance of cystic fibrosis. 'C' refers to the dominant gene and 'c' the recessive gene. The parental phenotype, the gamete phenotype and the offspring genotype and phenotype are highlighted in the figure.

Figure 2: Cystic fibrosis inheritance



From the above figure one can conclude that there is a 25% chance of every pregnancy leading to cystic fibrosis. There is also a 50% chance that the offspring will be a carrier of the CFTR gene. The following table presents the Punnett square for cystic fibrosis diagnosis.

Table 1: Punnett square for cystic fibrosis

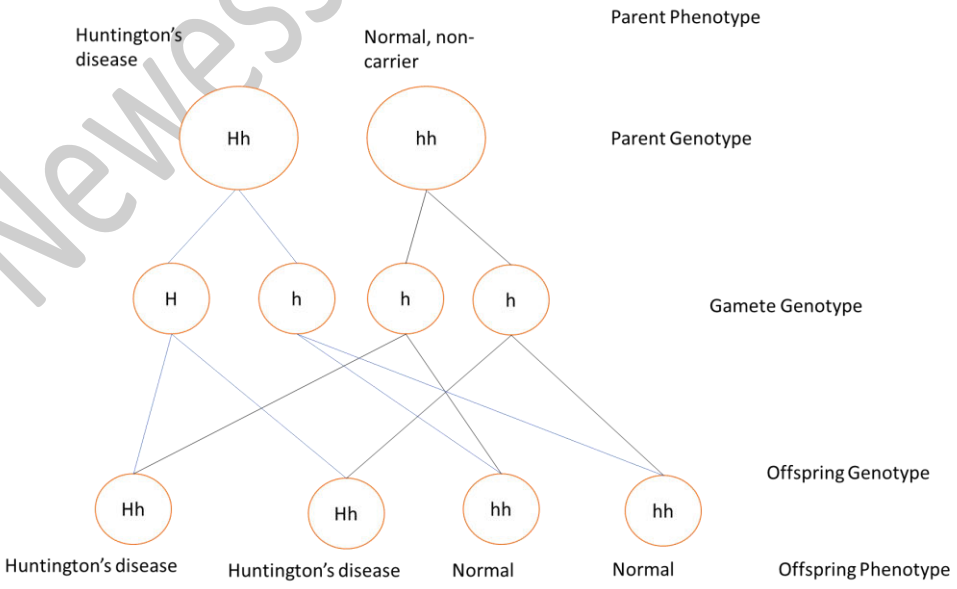
		Parent 1	
Parent 2		C	C
	C	CC	Cc
	c	Cc	Cc

2.2. Autosomal Recessive Condition

An autosomal dominant disorder occurs as a result of the mutation of a dominant gene located on a chromosome. In such disorders, just one mutated gene is enough to cause the disease. An example of a dominant autosomal disorder is Huntington's disease (Meyers, 2004). Huntington's disease is a type of genetic disorder which can be passed from the parent to the offspring through specific inheritance. If the individual has one copy of the mutant gene, it can cause the disorder. The mutant gene is the HTT gene. Huntington's disease is a neurodegenerative disorder where the basal ganglia and cerebral cortex are affected (Bates et al., 2014). Children of HD gene carriers have a 50% chance of inheriting the gene. The gene is located on chromosome 4p 16.3. The mutation associated with Huntington's disease is an increase in the number of nucleic acids (i.e. insertion). There is repetition of three nucleic acids (C, A and G) in the first exon of the HTT gene. The CAG triplet is repeated 20–40 times. The number of CAG repeats causes variations in the clinical phenotype of the disease (Burgunder, 2014). The age of onset of the disease and the number of CAG repeats can cause variations in symptomology.

The following Figure 3 presents the gamete diagram for inheritance of Huntington's disease. From the figure, it is observed that there is a 50% chance of disease in the offspring if one of the parents has the disease.

Figure 3: Huntington's disease genetic diagram (one parent has the disease)



The following Figure 4 presents a genetic diagram of the Huntington's inheritance pattern if both parents have the disease. If both parents have Huntington's, there is a 75% chance that any child from any pregnancy will have Huntington's.

Figure 4: Huntington's disease genetic diagram (both parents have the disease)

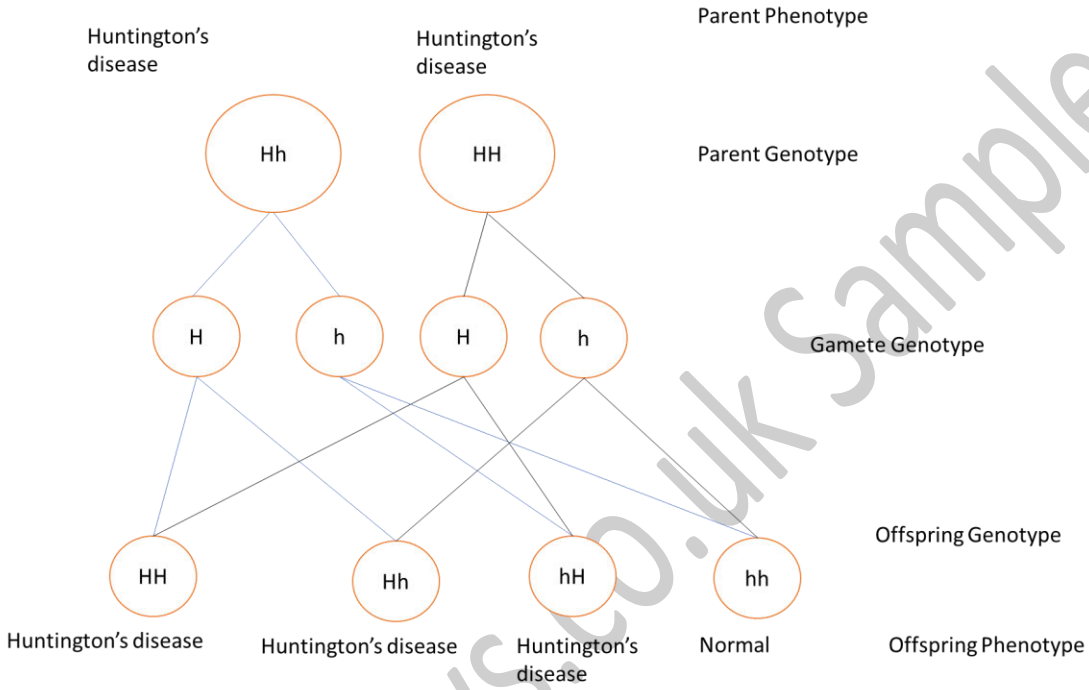


Table 2: Punnett square for Huntington's disease

If one parent has Huntington's disease		Parent 1	
Parent 2		H	H
	h	Hh	hh
	h	hH	Hh
If both parents have Huntington's disease		Parent 1	
Parent 2		H	H
	H	HH	Hh
	h	hH	Hh

2.3. Sex Linked Condition

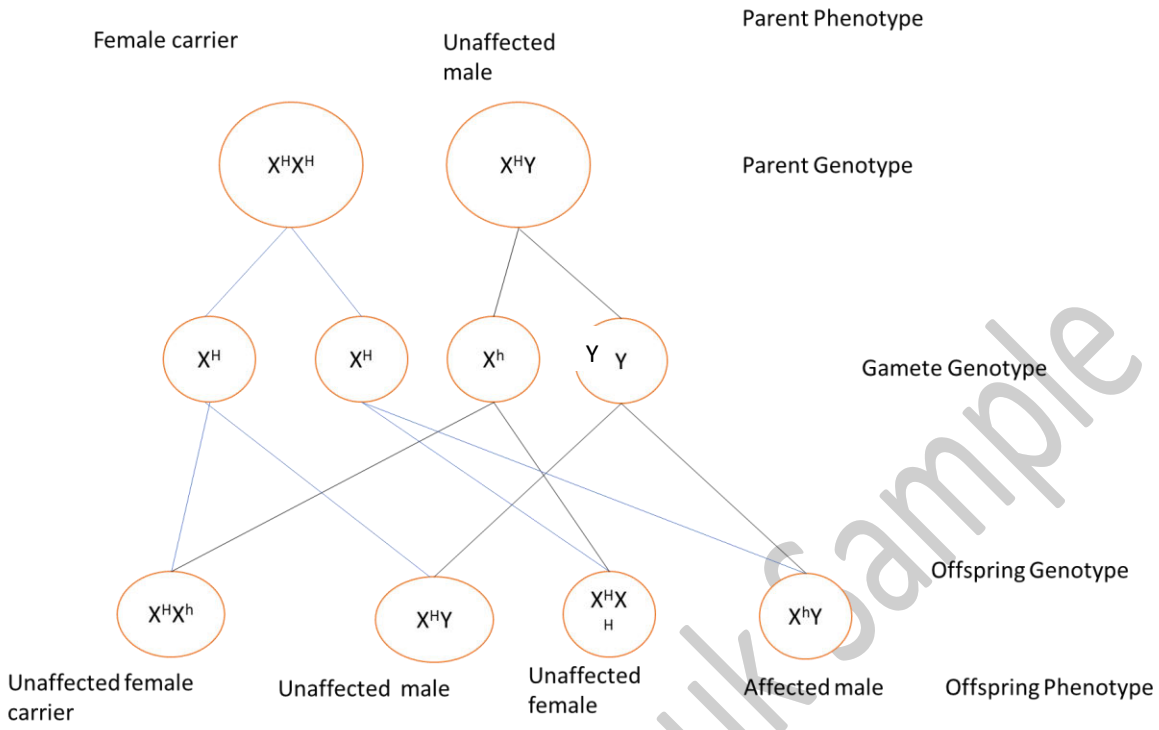
Haemophilia is an inherited blood disorder. In patients with haemophilia, the blood does not clot properly. Therefore, there can be challenges of spontaneous bleeding and injuries. Haemophilia is a result of low levels of Factor VIII or Factor IX. The lower the amount of these factors in the blood, the more likely that the patient will have serious health issues. Haemophilia A denotes low levels of Factor VIII and haemophilia B denotes low levels of Factor IX. The abnormal gene responsible for haemophilia is carried on the X chromosome. Therefore, it is an X-linked recessive pattern disease. In haemophilia patients, there is mutation in the F8 or F9 gene (Cahill and Colvin, 1997). In the F8 gene, there is intron 22 inversion linked to point mutation or small rearrangements. There are over 1,200 mutations linked to F8 or F9 genes, causing various levels of phenotypic severity (Bowen, 2002).

The presence of haemophilia varies according to the sex of the parent who carries the gene. Men have one X chromosome and one Y chromosome. If the abnormal F8 or F9 gene is present, it leads to haemophilia in the individual as there is no other X chromosome with a different dominant allele. In contrast, when a woman carries a haemophilia gene, they could act as a carrier (Prasad, 2018). Since they have two X chromosomes, the non-mutated F8 or F9 allele will produce the required Factor VIII or IX.

The pattern of inheritance varies based on gender. Affected males with haemophilia cannot transfer the abnormal gene to their sons, while all daughters of men with haemophilia will be carriers of the disease. However, the daughters may have the disease only if the mother is also a carrier of haemophilia. Similarly, a woman can pass the recessive haemophilia gene to her son or her daughter.

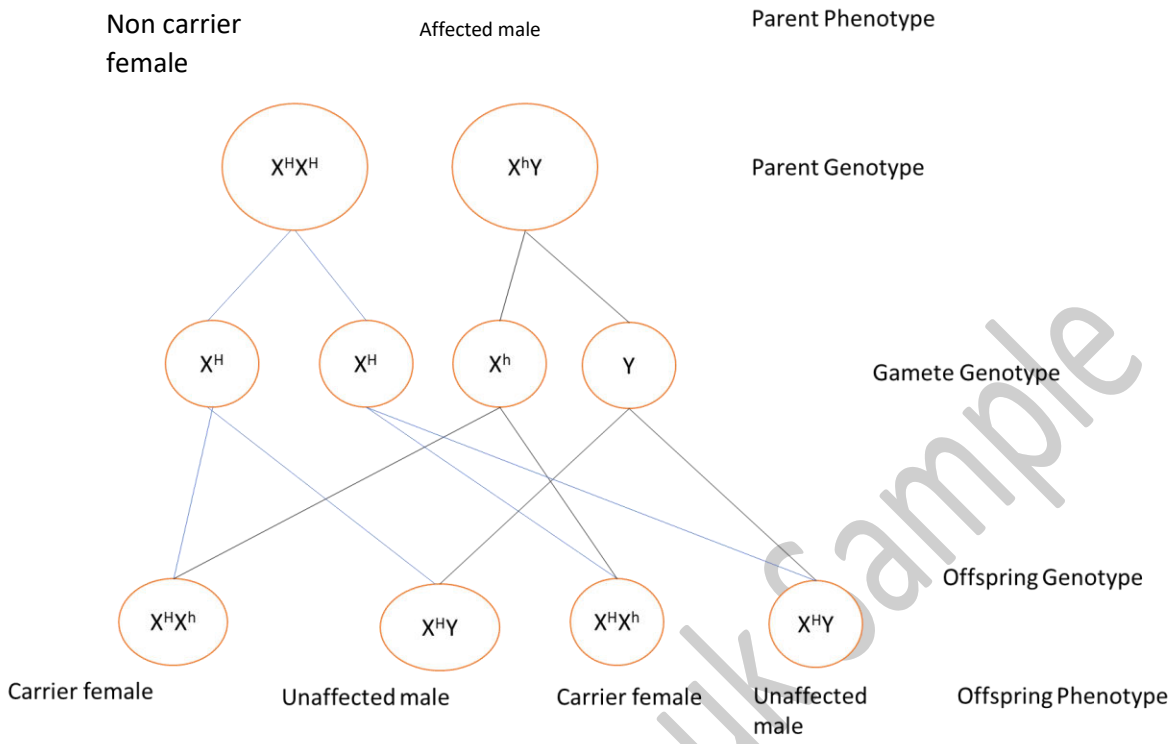
The following Figure 5 shows the inheritance of haemophilia from an unaffected female carrier and an unaffected male. There is a 25% chance that a progeny carries the disease.

Figure 5: Haemophilia – female carrier and unaffected male



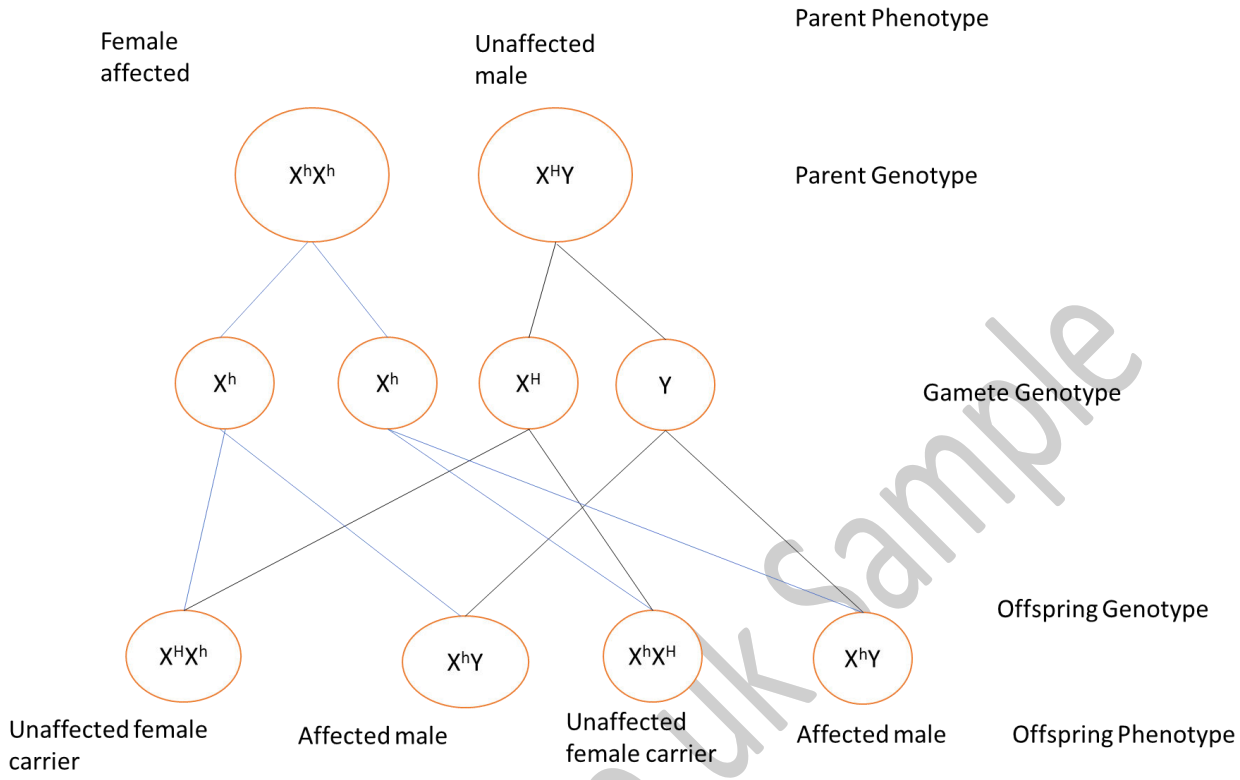
The following Figure 6 presents an assessment of haemophilia for a non-carrier female and an affected male. It is observed that 50% of offspring have a chance of being carriers for the recessive haemophilia gene.

Figure 6: Haemophilia – non-carrier female and affected male



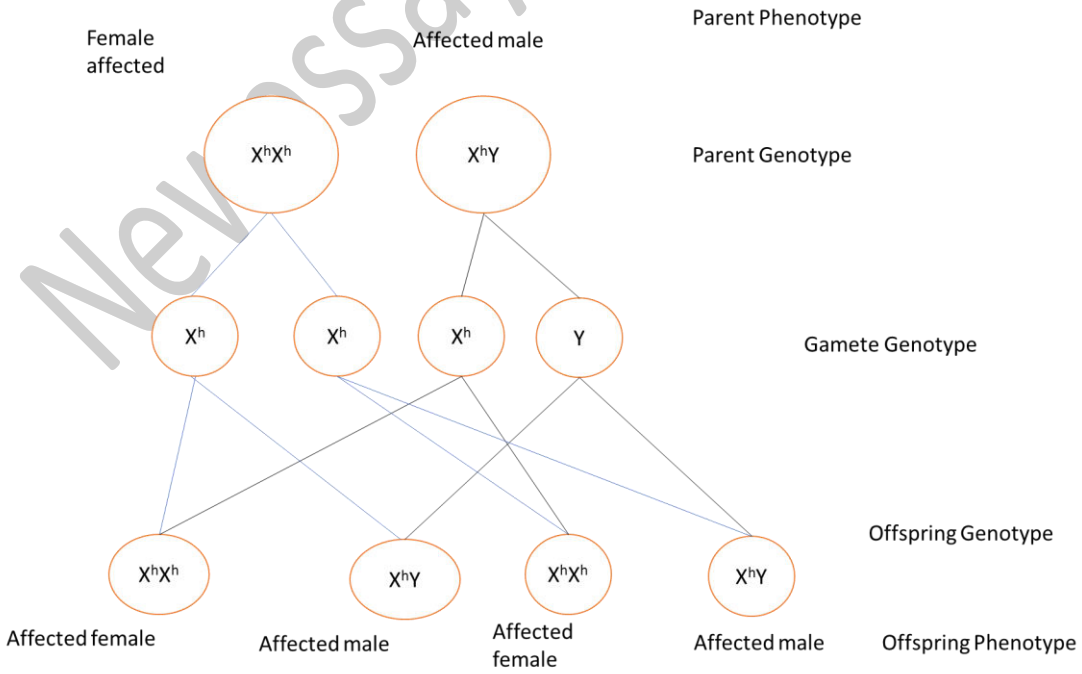
The following Figure 7 presents the genetic diagram for an affected female and an unaffected male with haemophilia. It is evident that 50% of offspring will be carriers (all female children) and 50% of offspring will have haemophilia (all male children).

Figure 7: Haemophilia – affected female and unaffected male



Finally, if an affected female and an affected male with haemophilia have children, all offspring will develop the disease.

Figure 8: Haemophilia – affected male and affected female



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