

# Mendels law of heredity biology essay

[Science](#), [Biology](#)



Introduction Genetics is a science in which hereditary characteristics are studied, looking at how certain traits are passed between generations and also the composition of DNA, consequently the study of genetics comprises all living things (Robinson, T. R. 2010).

1.) Mendel's Law of Heredity The first law is the law of segregation, this suggesting that in the creation of gametes, paired factors that determine visible characteristics are separated so only one of the pair is received by the gamete (Hickman JR. C. P. et al. 2011. A.). The second law is the law of independent assortment which states that during meiosis, genes that are positioned on different pairs of homologous chromosomes assort themselves independently (Hickman JR. C. P. et al. 2011. A.). Mendel's research shows that when selectively breeding pea plants, certain individualities would become apparent without the blending of parent characteristics for example pea flowers would be either white or purple and any intermediate colour did not appear (O'Neil, D. 2012). For every investigation conducted there will be a variety of possible outcomes, referred to as the 'sample space' and to determine this a Punnett square is used, these allow us to view all possible genotypes that may occur and the number of ways in which each genotype can be created (Duncan, S. 2012). A monohybrid cross (figure 1) allows for the analysis of one gene at a time whereas the dihybrid square (figure 2) allows for two genes to be studied simultaneously consequently the terms monohybrid and dihybrid refer to the number of genes being analysed (Mauseth. J. D. 2009). With G being the dominant allele and g recessive, we can see in figure 1 a phenotype ratio of 3: 1 (GG, Gg, Gg : gg). In figure 2, we can see in the second generation there is a ratio of 9: 3: 3: 1.

2.) F2 Genotype Ratio Below I have produced a Punnett

square showing all possible outcomes of the mating between a boar homozygous for curly tails and white bristles, and a sow homozygous for straight tails and black bristles. In this example:-Straight tails are recessive to curly - straight (ss) curly (SS)-Black bristles are dominant to white - black (BB) white (bb). Therefore the boar = SSbb and the sow = ssBB. The results are a 9: 3: 3: 1 ratio meaning:•9/16 chance the offspring will have curly tails and black bristles,•3/16 chance the offspring will have curly tails and white bristles,•3/16 chance the offspring will have straight tails and black bristles,•1/16 chance the offspring will have straight tails and white bristles.

3.) Homogametic and Heterogametic Sex Homogametic sex describes the sex of a species in which the same sex chromosomes are possessed, for example within humans, the female is classed as the homogametic sex as all females have two X-chromosomes therefore during gamete production the egg cells will contain the same X-chromosome (Biology Online. 2011. A). In other species such as reptiles and birds, the homogametic sex is the male as they have two Z sex chromosomes and any gamete produced will only contain the Z sex chromosome (Biology Online. 2011. B). Heterogametic sex describes the species in which the sex chromosomes differ and can therefore produce two different gametes, for example in mammals this would be the male as they produce both X and Y gametes whereas in reptiles and birds this would be the female (Allaby, M. 2009). The evolutionary value of sexual reproduction is that of necessity in some, to further the existence of a species. One notion is that sex introduces variability, meaning there are more likely to be surviving offspring if a variety of types is produced rather than more of the same. Organisms constantly have to improve to escape

predators, avoid disease and catch prey, in other words, "survival of the fittest" - Red Queen Hypothesis (Errub, B & Thompson, B. 2003). Inheritance of certain characteristics depends upon the sex of the offspring and also the parent carrying the gene. Most commonly these sex-linked traits in humans are colour blindness and haemophilia (Hickman JR. C. P. et al. 2011. A.). Males tend to be primarily affected by sex-linked traits as they have one copy of the X chromosome, females can be affected but only if they have two copies of the X chromosome and are homozygous to the trait (Unknown. 2000). As an example (Fig. 3), if a mother is a carrier of the gene yet the father is normal then the trait will appear in half of their sons and none of their daughters. If on the other hand the father is colour blind and the mother is a carrier, half of both their sons and daughters will be colour blind (Hickman JR. C. P. et al. 2011. A.). 5.) Mutations A gene mutation is a chemophysical change that modifies the base sequences within DNA (Hickman JR. C. P. et al. 2011. A.). Mutations can be inherited from a parent and in this instance are referred to as hereditary mutations, alternatively they can develop during a lifetime from environmental factors (i. e. radiation from the sun) or during cell division if a mistake is made whilst the DNA is replicating. In this circumstance they are referred to as acquired (or somatic) mutations (Genetics Home Reference. 2013). A mutated gene will continue to replicate its new structure and these can be harmful, advantageous or neutral mutations. In the instance of helpful mutations, these can be of great importance to the evolutionary process, providing new possibilities and allowing natural selection to build its own variations (Hickman JR. C. P. et al. 2011). a.) Frame Shift Mutation - This type of mutation directly affects the

amino acid sequence by either the deleting or insertion of base nucleotides (Killeen, A. A. 2010). If this occurs with one or two nucleotides being added or removed then the sequence becomes disrupted and will be incorrectly read (Nature Education. 2012). Presuming our base sequence is; CGA - AUU - UUG - GCU - AGA - GGCA frame shift mutation will alter the sequence so it would then appear as; GAA - UUU - UGG - CUA - GAGb.) Mis-sense Mutation - An error within the DNA which causes the wrong amino acid to be combined into a protein, there may be no adverse effect from this although in some cases the protein could become non-functional (Austin, M. D. C. P. Unknown). Referring back to our base sequence, the presence of a mis-sense mutation would cause the following change as an example: CGA - AAU - UUG - GCU - AGA - GGCC.) Same Sense Mutation - An error again within the nucleotide sequence however the error does not change the function and it continues to code for the same amino acid (Toole, G. & Toole, S. 2008). 6.) Hardy Weinberg's Law.) Assumptions - Based on a specific set of assumptions as shown below, the law predicts the transmission of gene frequencies between generations (McClellan, P. 2007). • Mutation is not occurring - the definitive source of diversity within populations, this however tends to require interaction with other factors to enable an upset within the genetic equilibrium (Hickman JR. C. P. et al. 2011. B.). • Natural selection is not occurring - natural selection, otherwise known as 'survival of the fittest' where environmental pressures determine which species members will survive to reproduce and pass on their genes (Allaby, M 2009). • The population is infinitely large / Genetic Drift - changes which occur within gene frequency caused by chance factors, these are independent of natural

selection and mutation. The smaller reproductively isolated population have increased vulnerability to this (O'Neil, D. 2012. B).

- There is no migration in or out of the population / Gene Flow - The movement of genes between populations, causing an important source of genetic variation (The University of California Museum of Palaeontology. 2006).
- All members of the population breed
- All mating is entirely random
- Everyone produces the same number of offspring

b.) Hardy - Weinberg's formula and its components: Formula =  $p^2 + 2pq + q^2 = 1$  P is representative of the dominant allele (Hickman JR. C. P. et al. 2011. B.), for example in homozygous dominant individuals (BB) and also half of the alleles (Bb) in heterozygous individuals (O'Neil, D. 2012. A). q is representative of the recessive allele (Hickman JR. C. P. et al. 2011. B.), symbolising all alleles in homozygous recessive individuals (bb) and half the alleles (Bb) of heterozygous individuals (O'Neil, D. 2012. A). 2pq represents the predicted occurrence of heterozygous (Bb) individuals (O'Neil, D. 2012. A). Simply put;  $p^2$  (BB) + 2pq (Bb) +  $q^2$  (bb) = 1.

(.) Systemic Neurological Degeneration in Coatia.) Blood test results from 1800 coati show that 250 of the individuals have the condition Systemic Neurological Degeneration (SND), a condition caused by a recessive gene. Using Hardy - Weinberg's formula, we can calculate the number of heterozygous and homozygous individuals within the group;  $q = 250 \text{ coati with SND} / 1800 \text{ of coati initially tested} = 0.1$  ( $q^2 = 0.01$ )  $p = 1550 \text{ remaining coati} / 1800 \text{ initially tested} = 0.9$  ( $p^2 = 0.81$ )  $0.81 + 0.18 + 0.01 = 1$  ( $p^2 + 2pq + q^2 = 1$ ) Therefore the number of heterozygous dominant individuals is 0.18 (18%) and homozygous dominant individuals are 0.81 (81%).

b.) A Breeding Programme to Eradicate the SND Disorder - this could indeed prove very

effective. In sheep for example, closely related individuals are mated to increase the occurrence of similar genes being paired which is said to be crucial to the development of prepotent animals and also when making the effort to stabilise traits within a set of animals (Schoenian, S. 2011).