

## Hardy-Weinberg Equilibrium:-

G.H. Hardy and W. Weinberg (1908) independently proposed Hardy-Weinberg law of Equilibrium to define the genetic structure of gene pool of a population and describe the gene and genotype frequencies in it.

The law states that the relative frequencies of alleles of various genes in a large, randomly mating, non evolving population tend to remain constant generation after generation in the absence of evolutionary force.

Thus, this principle models a population without evolution under the following conditions;

1. No mutation
2. No Immigration / Emigration
3. No Natural Selection
4. No sexual selection
5. A large population

But there are number of forces which can disrupt the Hardy-Weinberg equilibrium. These are, mutations, natural selection, non-random mating, genetic drift, gene flow etc. For instance, mutations disrupt the equilibrium of allele frequencies by introducing new alleles into a population. Similarly, natural selection and non-random mating disrupt the Hardy Weinberg equilibrium because they result in change in gene frequencies and alteration in gene/allele frequencies also occur because of genetic drift and gene flow. Because all of these disruptive forces commonly occur in nature, the Hardy-Weinberg equilibrium rarely applies in reality.

## Hardy - Weinberg Equations and Analysis

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According to the Hardy-Weinberg principle, the variable 'P' often represents the frequency of a particular allele, usually dominant and 'q' represents the frequency of recessive allele.

For example, assume that "p" represents the frequency of dominant allele "Y" for yellow pods and "q" represents the frequency of recessive allele "y" for green pods. If p and q are the only two possible alleles for this characteristic, then the sum of the frequencies must add up to 1 or 100%. We can also write this as  $p + q = 1$ . If the frequency of the Y allele in the population is 0.6, then we know that the frequency of the y allele is 0.4.

From the Hardy-Weinberg principle and the known allele frequencies, we can also find the genotypic frequencies. Since each individual carries two alleles per gene (Y or y), the genotypic frequencies can also be determined. If two alleles are drawn at random from the gene pool, the probability of each genotype can be determined.

As cited above, three genotype possibilities are PP (YY), producing yellow peas; Pq (Yy), also yellow or qP (yY), also yellow or qq (yy), producing green peas. The frequency of homozygous pp individual is  $p^2$ , the frequency of heterozygous pq individuals

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is  $2pq$  and the frequency of homozygous  $qq$  individual is  $q^2$ . If  $p$  and  $q$  are the only two possible alleles for a given trait in the population, these genotypes frequencies will sum to  $p^2 + 2pq + q^2 = 1$

Thus, the possible genotypes are homozygous dominant ( $YY$ ), heterozygous ( $Yy$ ) and homozygous recessive ( $yy$ ). For example, in a garden of 100 pea plants, 86 might have yellow peas and 14 have green peas. We don't know ~~exactly~~ how many are homozygous dominant ( $YY$ ) or heterozygous ( $Yy$ ), but we know that 14 of them are homozygous recessive ( $yy$ ).

Therefore, by knowing the recessive phenotype and thereby the frequency of that genotype (14 out of 100 individuals or 0.14), we can calculate the number of other genotypes. If  $q^2$  represents the frequency of homozygous recessive plants, then  $q^2 = 0.14$ . Therefore,  $q = 0.4$  as  $p + q = 1$ ,

$$\text{then, } 1 - 0.4 = p$$

$$\Rightarrow 0.6 = p.$$

The frequency of homozygous dominant plants  $p^2$  is  $(0.6)^2 = 0.36$ . Out of 100 individuals, there are 36 homozygous dominant ( $YY$ ) plants. The frequency of heterozygous plants is ( $2pq$ ) is  $2(0.6)(0.4) = 0.48$ .

Therefore, 48 out of 100 plants are heterozygous yellow ( $Yy$ )

## Applications of Hardy-Weinberg →

The genetic variation of natural populations is constantly changing because of genetic drift, mutation, migration and natural and sexual selection. The Hardy-Weinberg principle gives scientists a mathematical baseline of a non-evolving population to which evolving populations can be compared. By recording allele frequencies over time and then calculating the expected frequencies based on Hardy-Weinberg values, scientists can hypothesize the mechanisms driving the population's evolution.