The Hardy-Weinberg principle states that a population's allele and genotype frequencies will remain constant in the absence of evolutionary mechanisms. The Hardy-Weinberg principle models a population without evolution under the following conditions:

1. No mutations. The gene pool is modified if mutations alter alleles or if entire genes are deleted or duplicated.

2. Random mating. If individuals mate preferentially within a subset of the population, such as their close relatives (inbreeding), random mixing of gametes does not occur, and genotype frequencies change.

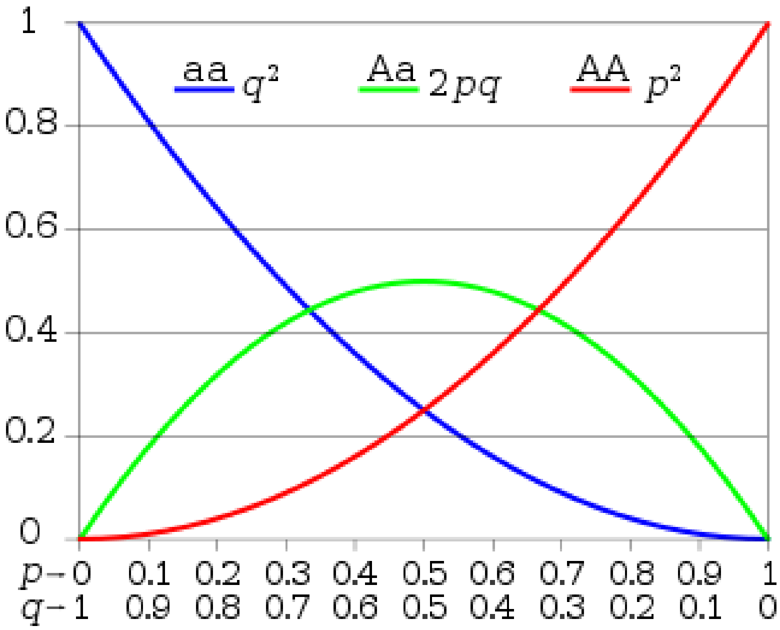
3. No natural selection. Differences in the survival and reproductive success of individuals carrying different genotypes can alter allele frequencies.

4. Extremely large population size. The smaller the population, the more likely it is that allele frequencieswill fluctuate by chance from one generation to the next (a process called genetic drift).

5. No gene flow. By moving alleles into or out of populations, gene flow can alter allele frequencies.

Although no real-world population can satisfy all of these conditions, the principle still offers a useful model for population analysis.

Applications of Hardy-Weinberg



Hardy–Weinberg proportions for two alleles: the horizontal axis shows the two allele frequencies p and q and the vertical axis shows the expected genotype frequencies. Each line shows one of the three possible genotypes.

The Hardy-Weinberg Equation

To estimate the frequency of alleles in a population, we can use the Hardy-Weinberg equation. According to this equation:

p = the frequency of the dominant allele (represented here by *A*)

q = the frequency of the recessive allele (represented here by *a*)

For a population in genetic equilibrium:

$p + q = 1.0$ (The sum of the frequencies of both alleles is 100%.)

$(p + q)^2 = 1$

so

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

The three terms of this binomial expansion indicate the frequencies of the three genotypes:

p^2 = frequency of *AA* (homozygous dominant)

$2pq$ = frequency of *Aa* (heterozygous)

q^2 = frequency of *aa* (homozygous recessive)

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

p^2 = dominant homozygous frequency (AA)

$2pq$ = heterozygous frequency (Aa)

q^2 = recessive homozygous frequency (aa)

Genetic drift is the change in the frequency of an existing gene variant in a population due to random sampling of organisms. The alleles in the offspring are a sample of those in the parents, and chance has a role in determining whether a given individual survives and reproduces.

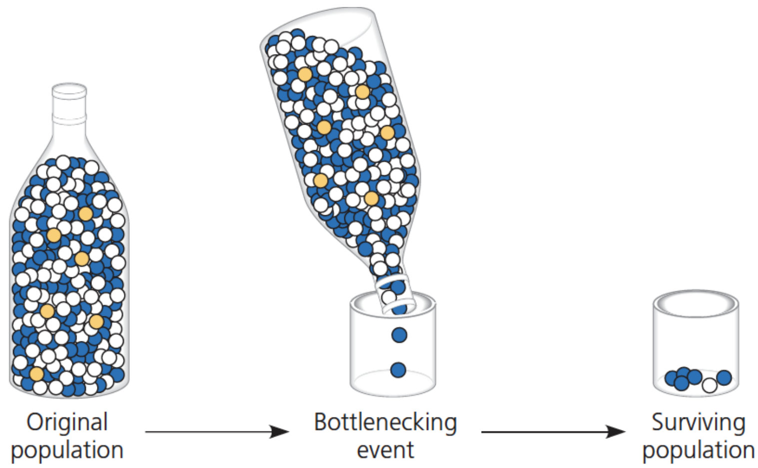
- Genetic drift is a mechanism of evolution in which allele frequencies of a population change over generations due to chance (sampling error).
- Genetic drift occurs in all populations of non-infinite size, but its effects are strongest in small populations.
- Genetic drift can have major effects when a population is sharply reduced in size by a natural disaster (**bottleneck effect**) or when a small group splits off from the main population to find a colony (**founder effect**).

There are two mechanisms which cause **genetic drift**:

The Bottleneck Effect

A sudden change in the environment, such as a fire or flood, may drastically reduce the size of a population. A severe drop in population size can cause the bottleneck effect, so named because the population has passed through a "bottleneck" that reduces its size

The bottleneck effects. *Shaking just a few marbles through the narrow neck of a bottle is analogous to a drastic reduction in the size of a population. By chance, blue marbles are overrepresented in the surviving population and gold marbles are absent.*



The Founder Effect

When a few individuals become isolated from a larger population, this smaller group may establish a new population whose gene pool differs from the source population; this is called the founder effect. The founder effect might occur, for example, when a few members of a population are blown by a storm to a new island. Genetic drift, in which chance events alter allele frequencies, will occur in such a case if the storm indiscriminately transports some individuals (and their alleles), but not others, from the source population.

References

- NCERT Books
- Cambell Biology

[The information, including the figures, are collected from the above references and will be used solely for academic purpose.]