

GENETIC DRIFT

(A destabilising factor of genetic equilibrium)

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DEFINITION

- Genetic drift is defined as a phenomenon of chance (random) deviation in allele frequencies due to sampling error, most often observed in **small populations**.
- This concept was proposed by Sewall Wright (1951) and hence, it is also known as **Sewall Wright effect**.
- Genetic drift can also arise either through the **founder effect** or a **bottleneck effect** in the large populations.
- In the founder effect, a **new colony** is formed by a small number of individuals derived from a large parent population.
- In the bottleneck effect, a large population undergoes a **drastic reduction** (temporarily) due to some calamities.
- As a result, some alleles of the main population may be *missing* and other may be disproportionately represented in the new population, causing a change in the **gene pool**.
- Genetic drift, therefore, leads to elimination of an allele and fixation of other allele in the population by **chance alone** *irrespective of the effect of natural selection*, even alleles of potentially great benefit get “nipped in the bud” by genetic drift.

Extent of deviation in allele frequency

- If given pair of parents in a population have a small number of offspring, then the frequency of alleles will deviate by an estimate of *standard deviation* (σ) from its previous generation.
- Standard deviation (σ) = $\sqrt{\frac{pq}{2N}}$ for diploid parents (N is the number of parents, and p and q are the initial frequency of two alleles)
- For a large population when N = 5000 and p and q are both equal to 0.5, then,

$$\sigma = \sqrt{\frac{0.5 \times 0.5}{2 \times 5000}} = 0.005$$

- The mean value of alleles in such a population, therefore, will vary around 0.5 ± 0.005 , i.e. between *0.495 and 0.505* (i.e. almost no deviation).
- If there are only 2 parents in the population and the allele frequency remains the same, then,

$$\sigma = \sqrt{\frac{0.5 \times 0.5}{2 \times 2}} = 0.25$$

The mean value of alleles in such a population, therefore, will vary around 0.5 ± 0.25 , i.e. between 0.25 and 0.75.

- Again, if the population of next generation remains small and begins with these 2 allele frequencies (0.25 and 0.75) then,

$$\sigma = \sqrt{\frac{0.25 \times 0.75}{2 \times 2}} = 0.22$$

The following generation may have the frequency of the allele reduced to 0.25 ± 0.22 , i.e. between 0.03 (**almost zero**) to 0.47 or may be increased to 0.75 ± 0.22 , i.e. between 0.53 to 0.97 (**almost one**).

- For example, if a population has only one pair of heterozygous parents (Aa × Aa), and they produced only 2 offspring, the allele frequency in the subsequent generation will depend upon the possible genotype of the two offspring.

Aa × Aa

Possible genotypes of two offspring	Probability	Allele frequency	
		A	a
AA and AA	$(1/4)(1/4) = 1/16$	1.0	0.0
aa and aa	$(1/4)(1/4) = 1/16$	0.0	1.0
AA and aa	$2(1/4)(1/4) = 2/16$	0.5	0.5
Aa and Aa	$(2/4)(2/4) = 4/16$	0.5	0.5
AA and Aa	$2(1/4)(2/4) = 4/16$	0.75	0.25
Aa and Aa	$2(1/4)(2/4) = 4/16$	0.25	0.75

- As shown in the table, the new allele frequency would be altered dramatically in 10 of 16 times, and even in 2 of 16 times, either A or a allele would be eliminated in a single generation.

Example of genetic drift in human population

- Pingelap atoll in the Pacific Ocean has been devastated in past by typhoons and famine and in 1780, there were only 30 Pingelapese surviving.
- Today there are less than 2000 inhabitants and 4-10% of them are affected by an autosomal recessive disorder **achromatopsia** (blind from infancy).
- It was found that one of the 30 survivors was a chief who was heterozygous for the disorder. Assuming that he was the only carrier in the founder population, the initial gene frequency was $1/60 = 0.016$ (1.6%).
- About 7% of the current population is affected (homozygous recessive), so the frequency of the allele in the present population is $\sqrt{0.07} = 0.26$ or 26%.
- The increase in gene frequency from 1.6% to 26% is caused by genetic drift alone.

Importance of genetic drift

- Genetic drift is a **random** process and is, therefore, **non-directional**.
- Irrespective of the effect of an allele on the reproductive success of individuals, genetic drift may ultimately lead to elimination of one allele with the fixation of other allele ($p=0$ and $q = 1$ or vice-versa)
- Genetic drift, therefore, tends to reduce the amount of genetic variation within the population.
- It can, however, increase variation within the species as small isolated populations may develop characteristics atypical of the main population (i.e. become more widely divergent from the parent population).
- As the drift may cause drastic change in the gene pool of resulting population compared to the original one, which in turn in due course of time may leads to origin of new races/ species.
