

Yo Frank, you trying to evolve today?

Lol nah

LS2201

Evolutionary Biology

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***The Horseshoe Crab**

445 Million Years of non-evolution

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II

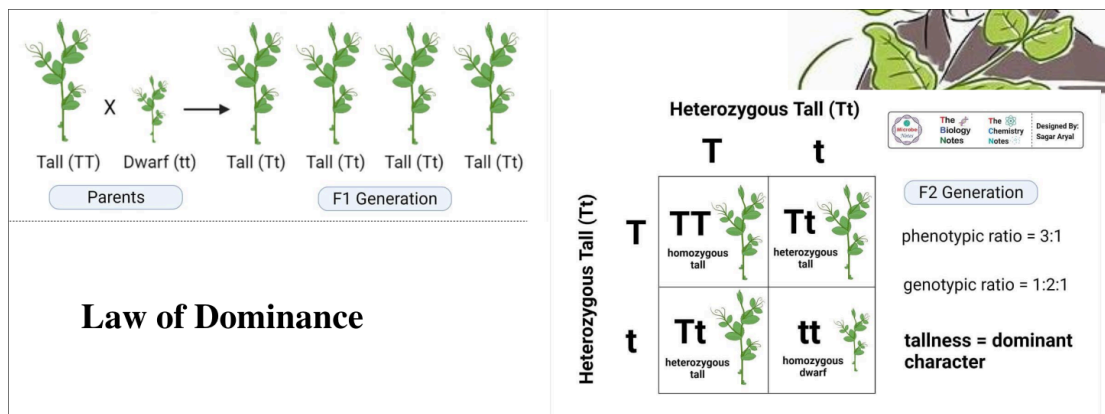
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1. Hardy Weinberg Equilibrium

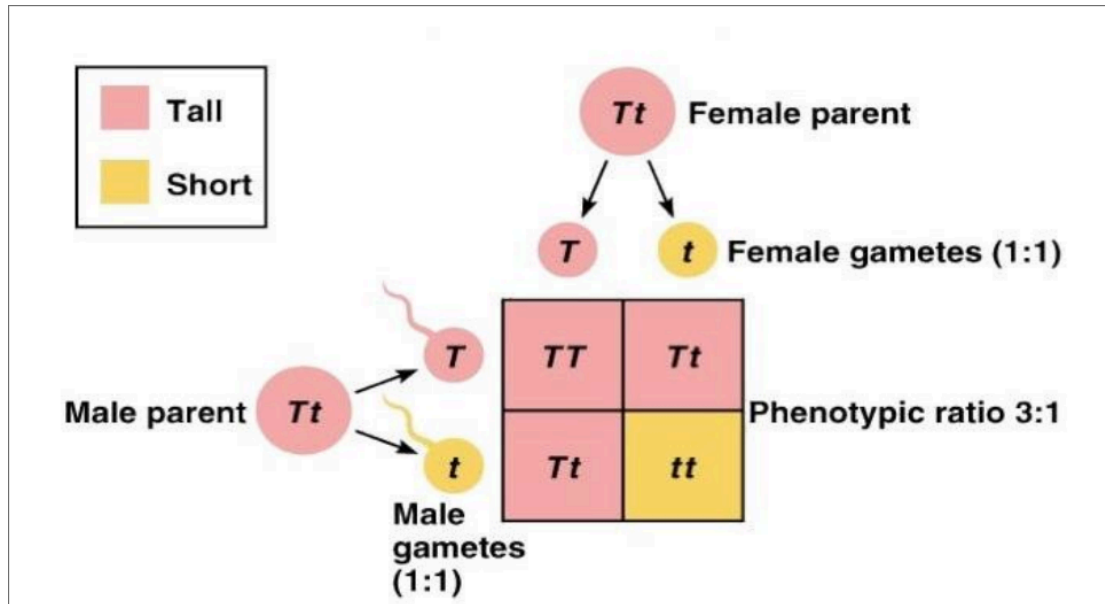
Mendelian Genetics

We start off with the three laws of Mendelian genetics, namely:

- *Law of Dominance* stating that the hybrid genotype in the F1 generation displays the phenotype of the dominant parent.



- *Law of Segregation* stating that when an organism makes gametes, each gamete receives just one gene copy, which is selected randomly.



- *Law of Independent Assortment* stating that for **dihybrid crosses**, genes of different traits can segregate independently during gamete formation.

1.1.1.1 Mendel and Darwin

After rediscovery of Mendel's work,

Biometricians	Mendelians
argued about the importance of continuous variation.	argued that most heritable characters were discontinuous.

Modern Synthesis

The Modern Synthetic Theory of Evolution (also called Modern Synthesis) merges the concept of Darwinian evolution with Mendelian genetics, resulting in a unified theory of evolution. It gave rise to a theory that emphasized the coaction of random mutation, selection, genetic drift, and gene flow ; also called the modern synthesis.

The theory gave a new definition of evolution as "the changes occurring in the allele frequencies within the populations," which emphasizes the genetic basis of evolution.

Features:

1. genetic variation is the source of phenotypic variation
2. this variation arises due to mutations that are random with respect to fitness
3. accumulated mutations selected over time are the basis of evolution within a taxon (gradualism)
4. adaptation is solely the result of natural selection
5. evolution occurs at the population level

Criticisms:

Is Evolution gradual, or does it proceed through a series of steps (punctuated equilibrium)?

Gradual transitions are by no means universally found in the fossil record. Intermediate stages in the evolution of many higher taxa are not known, and many closely related species in the fossil record are separated by smaller but nonetheless distinct gaps.

“Punctuated equilibria” refers to both a pattern of change in the fossil record and a hypothesis about evolutionary processes. Evolution often consists of long periods in which species exhibit little or no detectable phenotypic change, interrupted by **rapid shifts** from one such “equilibrium” state to another; that is, stasis that is “punctuated” by rapid change. They contrasted this pattern with what they called phyletic gradualism, the traditional notion of *slow, incremental change*.

The Population

A population refers to a group of sexually interbreeding or potentially interbreeding individuals.

Characteristics of a population:

1. Mendelian laws of transmission of genes apply.
2. It is usually local (deme)
3. All individuals have equal chance of mating with any other member of the opposite sex.
4. It has two attributes; **gene frequencies** and a **gene pool**.

Gene (allelic) frequencies are simply the proportion of the different alleles of a gene in a population.

The *gene pool* is the sum total of genes at all loci in every member of an interbreeding population. It can be considered as a gametic pool from which samples are drawn at random to form the zygotes of the next generation.

THE FALLBACK

In a Mendelian population, the dominant genotypes must also be dominant, or be present at a higher frequency in the population.

Is it the case?

Hardy Weinberg Equilibrium

In 1908, Hardy in England and Weinberg in Germany, disproved the argument that dominant alleles would dominate the population, following Mendelian inheritance.

=> **Statement:** *Gene frequencies are not dependent on dominance or recessivity, but are constant down the generations.*

An Example

Generation	OO	OG	GG
1	12	12	12
2	7	22	7
3	8	20	8

Let us say, frequency of O allele is p and frequency of G allele is q .

1. Generation 1:

$$OO = \frac{12}{36} = 0.33 \quad (1.1)$$

$$OG = \frac{12}{36} = 0.33 \quad (1.2)$$

$$GG = \frac{12}{36} = 0.33 \quad (1.3)$$

Hence,

$$p = \frac{24 + 12}{72} = 0.5 \quad (1.4)$$

$$q = \frac{24 + 12}{72} = 0.5 \quad (1.5)$$

2. Generation 2:

$$p = \frac{2 * 7 + 22}{72} = 0.5 \quad (1.6)$$

$$q = \frac{2 * 7 + 22}{72} = 0.5 \quad (1.7)$$

3. Generation 3:

$$p = \frac{2 * 8 + 20}{72} = 0.5 \quad (1.8)$$

$$q = \frac{[(2 * 8) + 20]}{72} = 0.5 \quad (1.9)$$

p and q , i.e., the gene or allelic frequencies remain unchanged across generations, though the genotypic frequencies may change. $p + q = 1$ and obviously, $(p + q)^2 = 1$

Inbreeding

Inbreeding occurs when individuals selectively mate with their relatives. In such cases, gene copies in uniting gametes are more likely to be identical by descent than if they joined at random.

Due to inbreeding, the frequency of each homozygous genotype increases and the frequency of heterozygotes decreases by the same amount. The frequency of heterozygotes is $H = H_0(1-F)$, where H_0 is the heterozygote frequency expected if the locus were in HWE, and F is the inbreeding coefficient.

Inbreeding coefficient (F) is the probability that an individual taken as random from the population will be autozygous.

In a completely outbred population, $F = 0$.

1. Self-fertilisation

The ways in which genotype frequencies change are easily seen if we envision mating between individuals only with their closest relatives—namely, themselves by self-fertilization.

The A_1A_1 can produce only A_1 eggs and A_1 sperm, and thus only A_1A_1 offspring; likewise, A_0A_0 individuals produce only A_0A_0 offspring. Heterozygotes produce A_1 and A_0 eggs in equal proportions, and likewise for sperm.

When these eggs and sperm join at random, $1/4$ of the offspring are A_1A_1 , $1/2$ are A_1A_0 , and $1/4$ are A_0A_0 . Thus the frequency of heterozygotes is halved in each generation, and eventually reaches zero. Conversely, F increases as inbreeding continues; in fact, F can be estimated by the deficiency of heterozygotes relative to the H-vV equilibrium value.

$$F = \frac{H_0 - H}{H_0} \quad (1.10)$$

Sex Linked Loci

Let us assume a mammal like species, where females are XX , and males are XY . Let us assume that our gene of interest lies on the X chromosome, and has two alleles A and B . Also, let us assume, that the overall frequency of A is p and B is q .

Now, since allelic frequencies in males and females (i.e., the probability of either A or B occurring) is same for both males and females,

for the male population, possible genotypes are A and B :

$$f_A = p \quad (1.11)$$

$$f_B = q \quad (1.12)$$

For the female population, since there are two X chromosomes, the possible gametes are AA , AB , and BB .

$$f_{AA} = p^2 \quad (1.13)$$

$$f_{AB} = 2pq \quad (1.14)$$

$$f_{BB} = q^2 \quad (1.15)$$

The frequency of the allele A in females of generation n necessarily determines $f(A)$ in males in generation $n+1$. The male $f(A)$ therefore “chases” the female $f(A)$ in the preceding generation until they reach approximate equality. Because each female in generation $n+1$ receives an X chromosome for each parent in generation n , the female $f(A)$ is the mean of the male and female $f(A)$ in the preceding generation.