Chapter 8

Evolution of Populations

TB Ch. 16, p. 393

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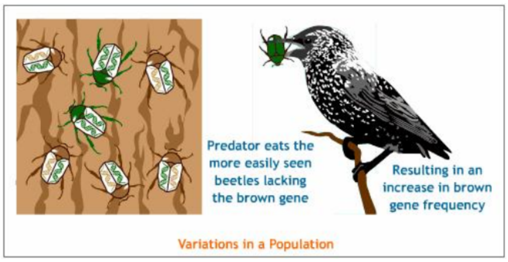
Genes and variation

Darwin's theories were published long before Mendel's work allowed us to understand inheritance. The two weren't linked until the 1930's.

Today, we understand genes, nucleotides, mutations,the double helix model of DNA, variety and change are all linked.



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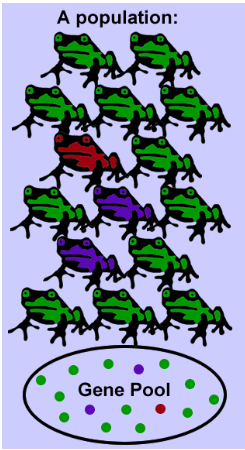
Population

Evolution never acts on individuals, but rather on population groups.

Genetic variety is studied in a population.

A population is a group of interbreeding organisms from the same species that live in the same geographical area.

Interbreeding leads to members sharing common genes. These members belong to the same *gene pool*.



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Causes of genetic variety

There are 2 main causes:

1) Mutations:
- caused by a mistake when replicating DNA, exposure to harmful chemicals or exposure to radiation.
- mutations that affect fitness affect evolution.

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2) Gene shuffling:
- each chromosome moves independently during meiosis and can result in 8.4 million different combinations!
- Add to this the process of crossing over and the possibilities are practically endless!

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Today, evolution is understood to the change in *relative frequency* of a particular allele in a gene pool.

The relative frequency of an allele is a measure of how often a particular allele occurs in a gene pool when compared to another allele from the same gene.

Relative frequency:

B - 40%
b - 60%

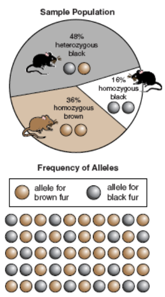

Figure 16 - 2, p. 394

When the relative frequency of a particular allele does not change, the population is said to be in *genetic equilibrium*.

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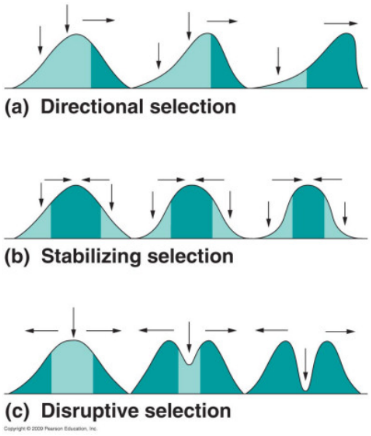

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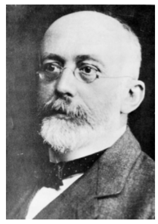
The Hardy-Weinberg Principle (TB p. 400)

In order to explain how evolution takes place, Hardy and Weinberg decided to find out what it takes for *no evolution* to take place.

Their principle states that allele frequencies in a population will remain constant (*genetic equilibrium*) unless one or more factors cause those frequencies to change.

Geoffrey Harold Hardy and Wilhelm Weinberg.

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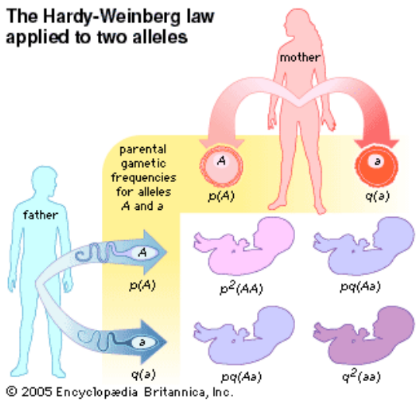

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In order for the Hardy-Weinberg Principle to be true:

1) Mating must be random
   - *cannot be dependant on choice for particular traits*
2) A large population is required
   - *lots of choice and chance for mating*
3) Organisms cannot leave the population, nor can they enter it.
   - *no new members, none leaving*
4) There can't be any mutations
   - *no new traits randomly introduced*
5) Natural selection must not take place.
   - *competition for resources cannot favor certain traits over others.*

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When the Hardy-Weinberg Principles applies (and it does, from time to time in certain populations, for an extended period of time), a formula can be used to determine the relative frequency of genotypes.

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

Where: p is the relative frequency of the dominant allele
q is the relative frequency of the recessive allele

The relative frequency of both alleles in a population must always equal 1 (which represents 100% of the population).

The three terms represent the three possible genotypes resulting from a monohybrid cross.

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

The three terms represent the three possible genotypes resulting from a monohybrid cross.

p^2 represents the frequency of homozygous dominant (ex: TT)

2 pq represents the frequency of heterozygous dominant (ex: Tt)

q^2 represents the frequency of homozygous recessive (ex: tt)

1 represents the sum of all genotype frequencies (100%)

If it helps, you can replace the letters p and q with the letters of teh dominant and recessive alleles of a trait.

ex: $T^2 + 2Tt + t^2 = 1$

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Let's try it!

In a population of randomly mating tomato plants in genetic equilibrium, the relative frequency of the trait for tomato size is as follows:

S = 0.8 (80%)
s = 0.2 (20%)

Using the Hardy-Weinberg equation:

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

$$S^2 + 2Ss + s^2 = 1$$

$$(0.8)^2 + 2(0.8)(0.2) + (0.2)^2 = 1$$

$$(0.64) + (0.32) + (0.04) = 1$$

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$$(0.64) + (0.32) + (0.04) = 1$$

These fractions can be converted to determine the frequency of each genotype in the population:

0.64 = 64% homozygous dominant (SS)

0.32 = 32% heterozygous dominant (Ss)

0.04 = 4% homozygous recessive (ss)

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