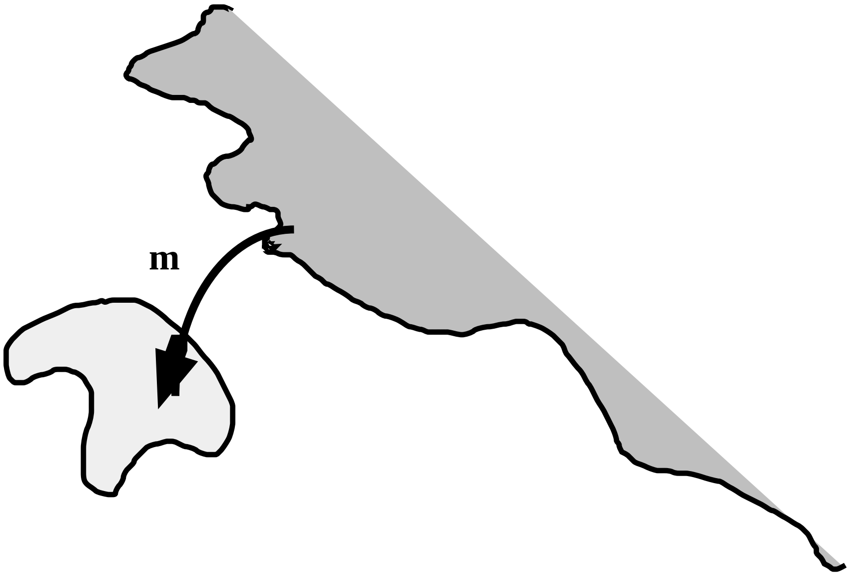
# Mendelian Genetics in Populations II: Migration, Genetic Drift, and Nonrandom Mating

## I. Migration

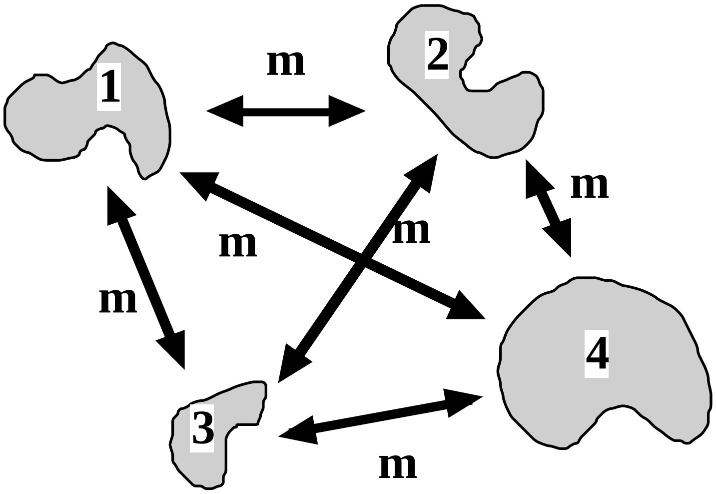
A. Definition: the movement of individuals (or gametes) among populations. If populations have different allele frequencies it will homogenize the frequencies among the populations.

B. Types of Models

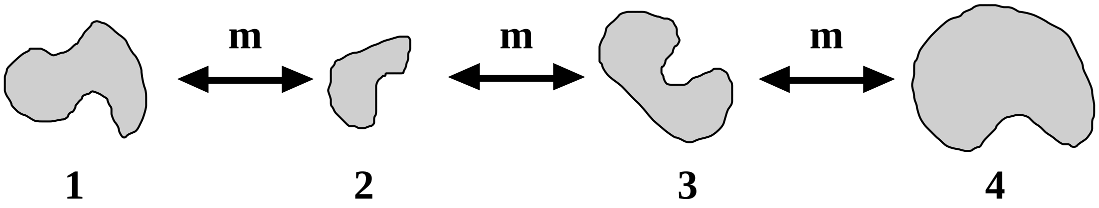
2. Continent-island model – effectively one-way movement from the large continent to the small island



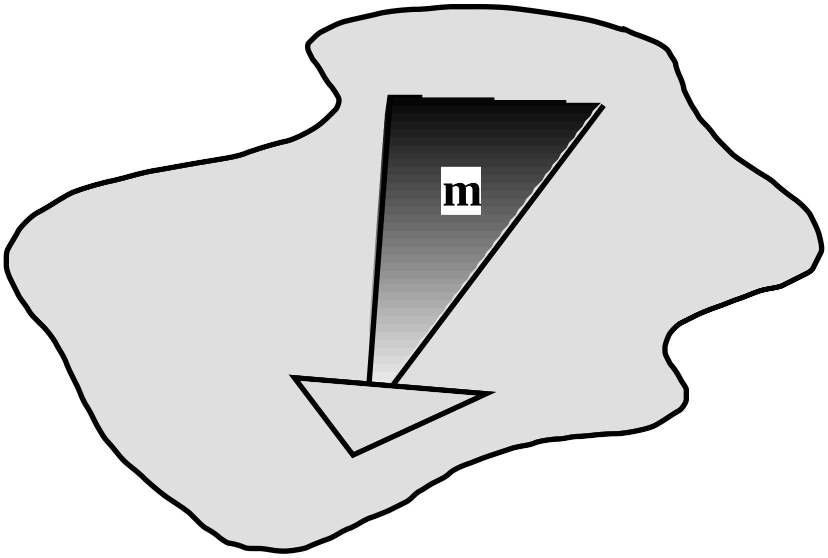
3. **Island model – movement is random among a groups of small populations**



4. **Stepping stone – each population received migrants from neighboring populations**



5. **Isolation by distance – gene flow occurs among local neighborhoods in a continuously distributed population.**



**C) Continent-island model with migration**

**$p_c$ = frequency of $A_1$ allele on the Continent**

**$p_i$ = frequency of $A_1$ allele on the island**

**$p_1'$ = the frequency of the $A_1$ allele in the next generation on the island**

**each generation (1 – m) of the individuals on the island were already on the island and m individuals migrated from the continent to the island.**

**$p_1'$ = the $A_1$ allele frequency originally on the island plus any $A_1$ alleles that came in with the migrants**

$$= (1 - m)p_1 + mp_c$$

**and**

**$\Delta p = m(p_c - p_i)$**

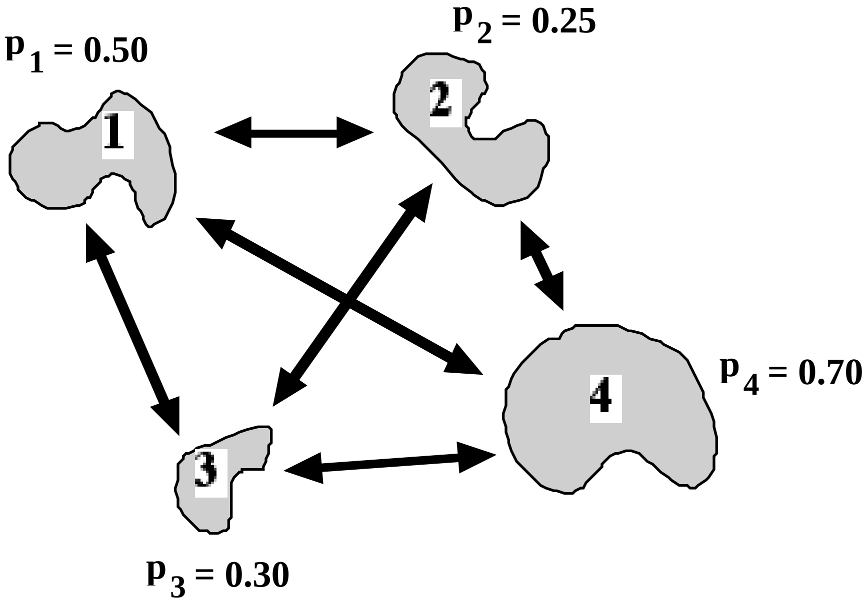
**So…**

**if $p_c > p_i$ then $\Delta p$ is positive and the $F(A_1)$ on the island increases**

**if $p_c < p_i$ then $\Delta p$ is negative and the $F(A_1)$ on the island decreases**

**only when $p_c = p_i$ does the allele frequency not change**

**D) Island model with migration**



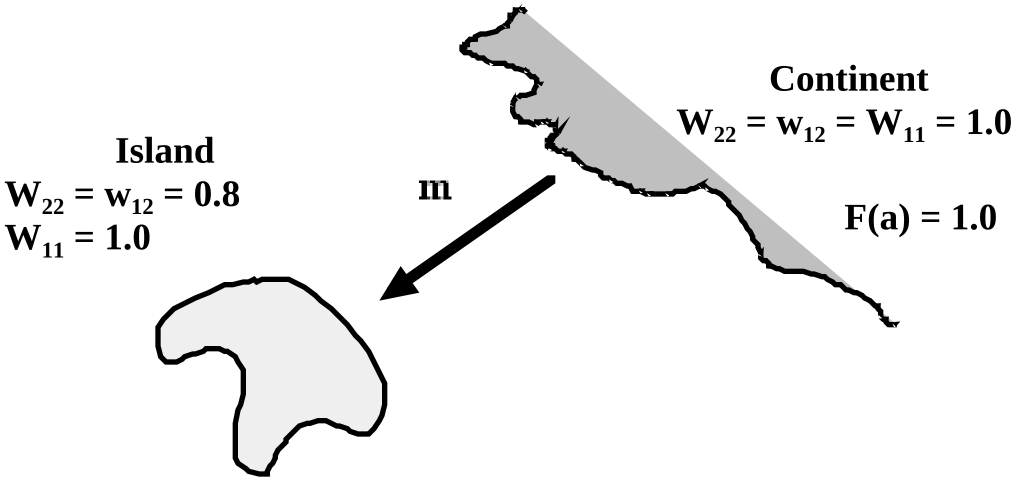
**Population 2 receives $A_1$ alleles from everyone**
**Population 4 gives $A_1$ alleles to everyone**
**Population 1 receives from 4 but gives to 2 and 3**
**Population 3 gives to 2 but receives from others**

**$\Delta p = 0$ when the allele frequency in all populations**

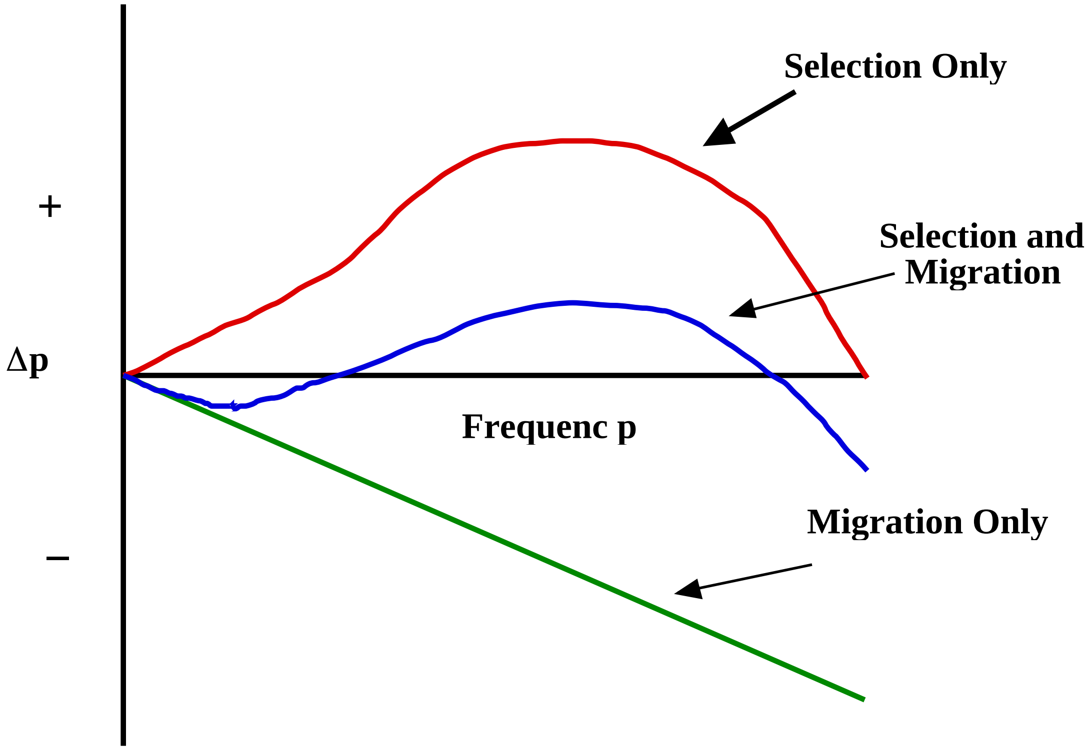
$$= \frac{p_1 + p_2 + p_3 + p_4}{4} = \bar{p}$$

## E) Migration and Selection – Continent-Island model

| Genotype | AA | Aa | aa |
|---|---|---|---|
| Fitness | 1 | 0.8 | 0.8 |



$$\hat{q} \quad \frac{mq_c}{s}$$



## II) Genetic Drift

A) When a new population is started from a small number of individuals it is likely, by chance alone, that the allele frequency of the new population is different from the source population.

B) Random change in allele frequency over generations due to gamete sampling effect caused by small population size.

C) Assumptions

1) Population size does not change over generations (this has been true all along).

2) Populations size is limited (i.e., not infinite; 100’s of individuals or less).

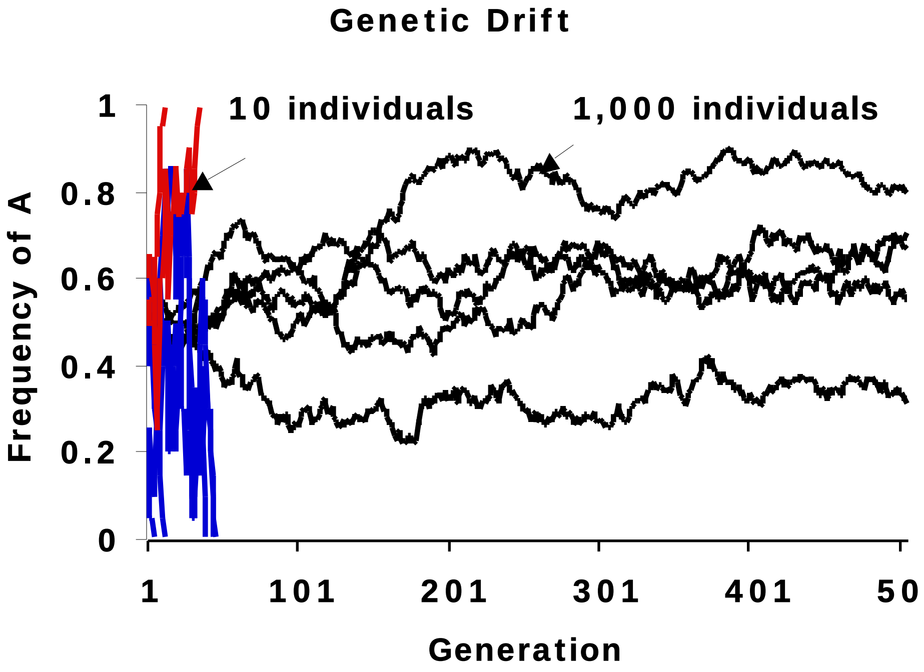
3) All other Hardy-Weinberg Assumptions

D) Effects of Genetic Drift

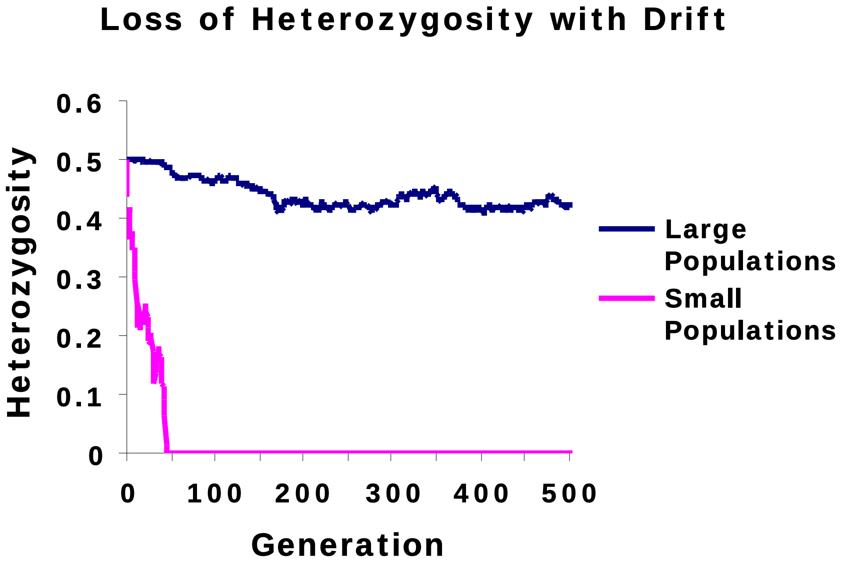
1) Each population changes differently.

2) Given enough time, genetic drift can change the frequency of an allele even in large populations.

3) More rapid and dramatic effect in small populations than in large.



**4) Heterozygosity is always reduced**



**and in general** $H_{t+1} = (1 - \frac{1}{2N})H_t$ **where H is the heterozygosity and N is the population size.**

**5) Even large populations go to fixation after enough time.**

**6) The probability that a given allele is the one that drifts to fixation is equal to its frequency in the population.**

## III) The Genetically Effective Population Size ($N_e$)

**A) Generally the census size (N) of a population is not equal to the number of adults contributing genes to the next generation.**

**B) Definition: The number of individuals in an ideal population in which the rate of drift (as measured by the loss of heterozygosity) is the same as the observed population.**

**C) Causes of** $N_e \neq N$

**1) variation in number of offspring from one individual to the next**

**2) Unequal number of females and males**

3) overlapping generations (i.e., matting between parents as well as offspring)

4) Fluctuations in Population Size (i.e., Bottleneck)

| Generation | Census Size |
|---|---|
| 1 | 100 |
| 2 | 150 |
| 3 | 25* |
| 4 | 150 |
| 5 | 125 |
| Average | 110 |

* = bottleneck – drastic reduction in population size.

$N_e$ = harmonic mean of census size

70

## IV) Rate of Evolution by Genetic Drift

A) Neutral Evolution Rate (k) is the rate at which a population fixed for one allele is fixed for a new allele.

B) Components of Neutral Evolution

1) Mutation Rate (μ) – the rate at which new alleles are created. Mutation only creates new alleles. Generally $10^{-3}$ to $10^{-9}$ mutations per gene per generation.

2) Genetically Effective Population Size Number of Alleles (i.e., $2N_e$).

## C) Calculation of the Neutral Evolutionary Rate

**The rate at which new alleles in a population is the number of alleles in the population times the rate at which they mutate = $2N_e\mu$**

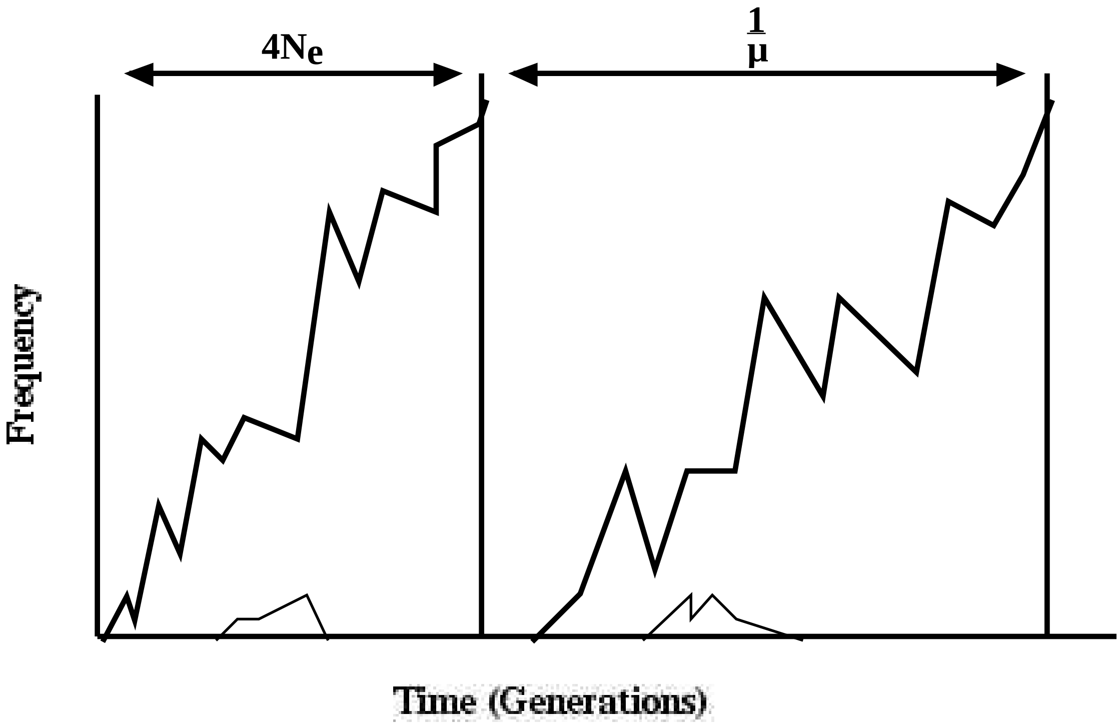
**The probability of fixation of a new allele is equal to its frequency in the population = $\frac{1}{2N_e}$**

**The rate that new alleles will be come fixed in the population (k) is equal to the number of new alleles times the probability that they will go to fixation**

$$k = 2N_e\mu\frac{1}{2N_e} = \frac{2N_e\mu}{2N_e}$$

$$k = \mu$$

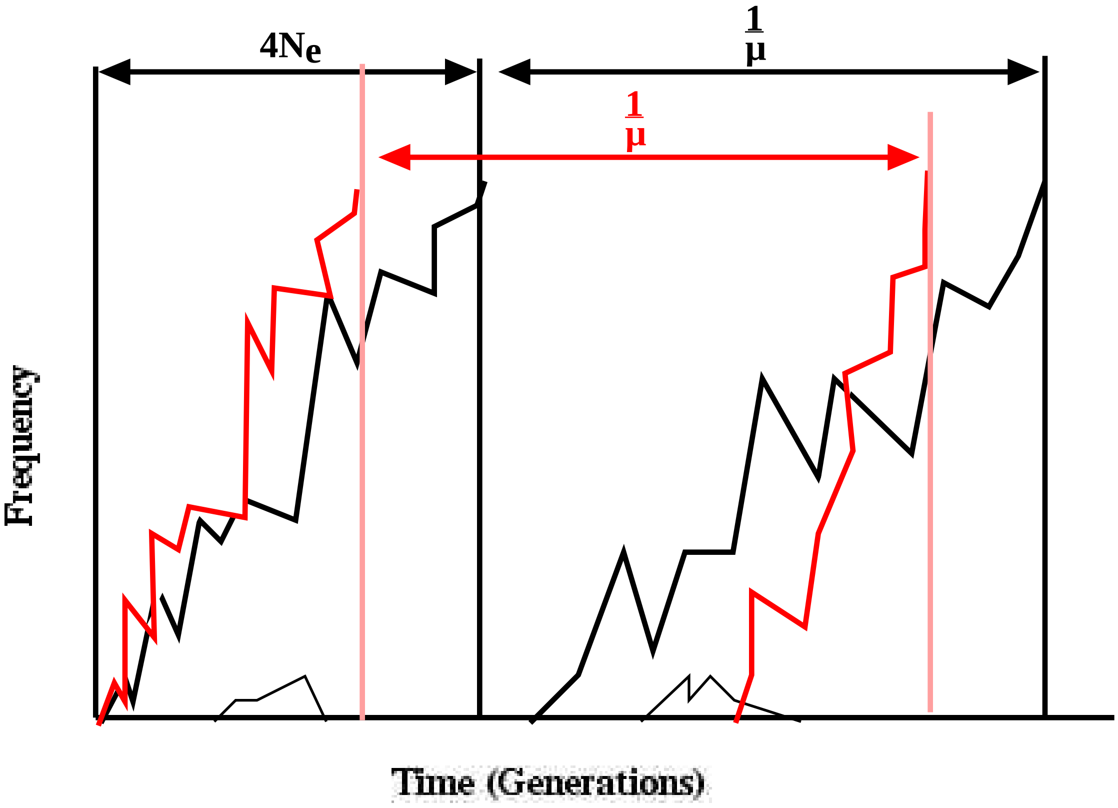
**The rate of neutral evolution is the mutation rate**



### D) Population Size and the Neutral Evolutionary Rate (k)

1) **k is independent of population size – although the time it takes a new allele goes to fixation is shorter in smaller populations (i.e., $4N_e$) the rate at which new alleles arise (i.e., $2N\mu$) is slower. The faster fixation rate and the slower origination rate cancel each other out.**

2) **Effect of population size**



## V) Nonrandom Mating

**A) Types of Nonrandom mating – nonrandom mating is when individuals select a mate based on their genotype and can take many forms.**

1) **Positive Assortative mating – mating with similar genotype (e.g., AA prefers AA, Aa prefers Aa, and aa prefers aa)**

**2) Negative Assortative Mating – mating with dissimilar genotypes (e.g., AA prefers aa, etc.)**

**3) Inbreeding – mating among relatives. Most extreme form is selfing (common in plants).**

**B) General setup – s is the probability of selfing and t is the probability of outcrossing, U, V, and W are the frequency of the genotypes AA, Aa and aa respectively.**

|  |  |  |  | Offspring |  |  |
|---|---|---|---|---|---|---|
| $P_1$ | X | $P_2$ | Frequency | AA | Aa | aa |
| AA |  | AA | $sU + tU^2$ | $sU + tU^2$ | — | — |
| AA |  | Aa | 2tUV | tUV | tUV | — |
| AA |  | aa | 2tUW | — | 2tUW | — |
| Aa |  | Aa | $sV + tV^2$ | $1/4(sV + tV^2)$ | $1/2(sV + tV^2)$ | $1/4(sV + tV^2)$ |
| Aa |  | aa | 2tVW | — | tVW | tVW |
| aa |  | aa | $sW + tW^2$ | — | — | $sW + tW^2$ |
|  |  |  |  | U’ | V’ | W’ |

**C) Pure Selfing (s = 1.0, t = 0.0):**

|  |  |  |  | Offspring |  |  |
|---|---|---|---|---|---|---|
| $P_1$ | X | $P_2$ | Frequency | AA | Aa | aa |
| AA |  | AA | $sU + tU^2$ | $sU + tU^2$ | — | — |
| AA |  | Aa | 2tUV | tUV | tUV | — |
| AA |  | aa | 2tUW | — | 2tUW | — |
| Aa |  | Aa | $sV + tV^2$ | $1/4(sV + tV^2)$ | $1/2(sV + tV^2)$ | $1/4(sV + tV^2)$ |
| Aa |  | aa | 2tVW | — | tVW | tVW |
| aa |  | aa | $sW + tW^2$ | — | — | $sW + tW^2$ |
|  |  |  |  | U’ | V’ | W’ |

**U’ = U + 1/4V        V’ = 1/2V        W’ = W + 1/4V**

**p’ = U’ + 1/2V’ = U + 1/4V + 1/4V = U + 1/2V = p**

## D) Effects of Inbreeding

1) Allele frequencies stay the same over time (i.e., nonrandom mating does not itself result in evolution).

2) Genotype frequencies change with the frequency of heterozygotes decreasing every generation.

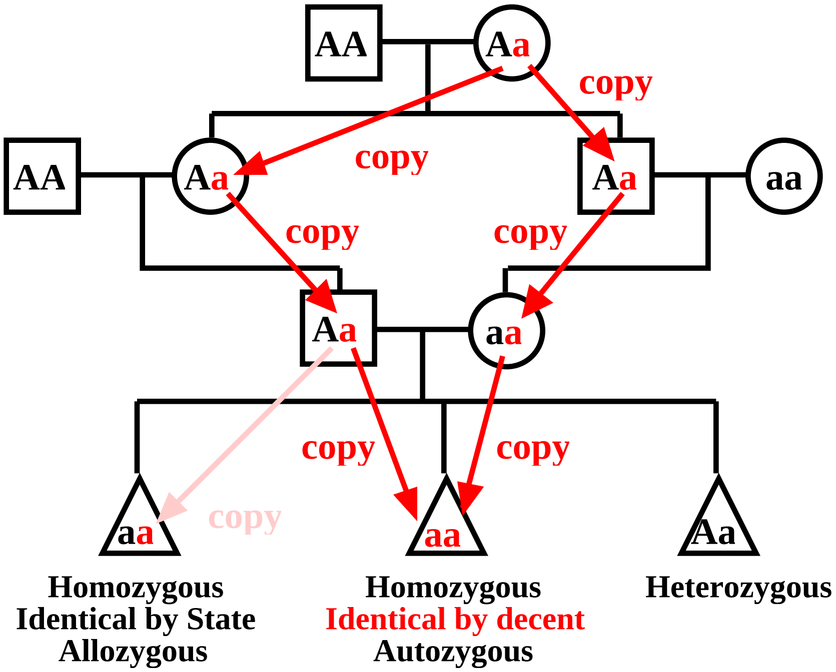
3) Population is not in Hardy-Weinberg Equilibrium

4) Inbreeding Depression – as homozygosity increases rare, recessive deleterious alleles are brought into homozygous state and reduce fitness.

5) Outbreeding Depression

## E) Inbreeding Coefficient (F)

1) Definition – the probability that two alleles in an individual (or two gametes that are uniting to form a zygote) are identical by decent (IBD).



## 2) Genotype and Allele Frequencies with Inbreeding

**$F$ = Probability that two gametes are Autozygous**
**$1 - F$ = Probability that two gametes are Allozygous**

**$F(A) = p$**
**$F(a) = q$**

**Probability of AA and Allozygous**

$$= p^2 (1 - F)$$

**Probability of AA and Autozygous**

$$= pF$$

| Genotype | Allozygous | | Autozygous | Frequency |
|---|---|---|---|---|
| AA | $p^2(1 - F)$ | + | $pF$ | U |
| Aa | $2pq(1 - F)$ | | | V |
| AA | $q^2(1 - F)$ | + | $qF$ | W |

**Note: $0 \leq p$ and $q \leq 1$ and $0 \leq F \leq 1$ so homozygotes are always increasing in frequency and heterozygote is always decreasing**

$$H_{t+1} = H_t(1 - F)$$

**Note: The allele frequency, however, is not changing.**

$$\begin{aligned} p' &= U + 1/2V \\ &= p^2(1 - F) + pF + pq(1 - F) \\ &= [p^2(1 - F) + qp(1 - F)] + pF \\ &= p(1 - F)(p + q) + pF \\ &= p(1 - F) + pF \\ &= p - pF + pF \\ &= p \end{aligned}$$

## 3) Calculating Inbreeding Coefficient

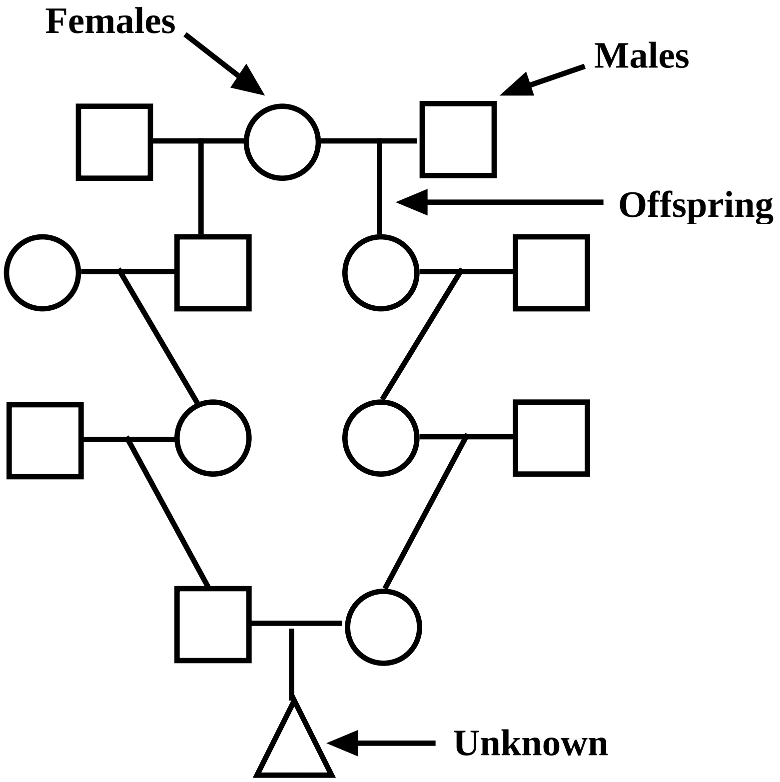
### a) Estimate based on heterozygote frequency

$$H_{obs} = H_{exp}(1 - F)$$

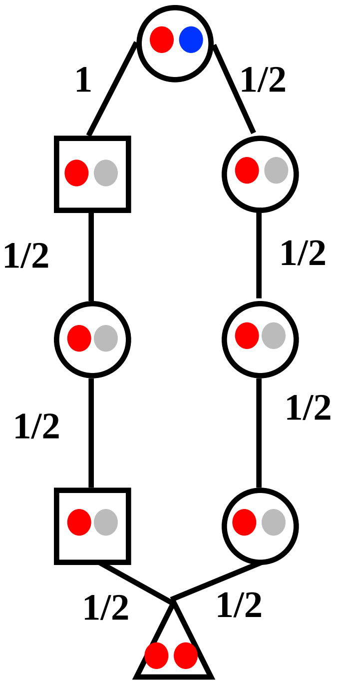
$$H_{obs} = H_{exp} - H_{exp} F$$

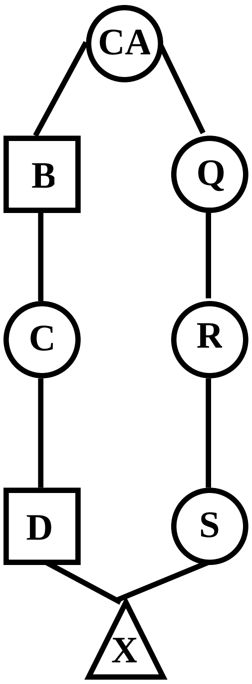
$$F = \frac{H_{exp} - H_{obs}}{H_{exp}}$$

### b) Directly from pedigree



**Simplified –**





**To have two autozygous gametes combine to produce individual X copies of one of the genes in the common ancestor (CA) must have been transmitted from B to C to D to X and from Q to R to S to X**

$$F_X = \left(\frac{1}{2}\right)^N (1 + F_{CA})$$

**Where N = the number of individuals in the chain starting from X going through the CA and back to X**

**or D => C => B => CA => Q => R => S**

$$F_X = \left(\frac{1}{2}\right)^7 (1 + F_{CA})$$

**Assuming $F_{CA} = 0$, $F_X = 0.008$**