

# Unit 7 | Population Genetics



# Population Genetics

Analysis of genetic composition of populations and the evolutionary forces that promote changes; it connects evolutionary processes with concepts of genetic inheritance

# Estimation of Frequencies

**Allelic frequency:** proportion of alleles of a particular locus in a population under study.

**Genotypic frequency:** proportion of different genotypes for a particular locus in a population under study.

# Estimation of Frequencies

## MN group phenotypes

- 50 Individuals MM
- 20 Individuals MN
- 30 Individuals NN
- 100 TOTAL

## Allelic frequencies

$$frec(M) = \frac{(2 \times 50) + 20}{200} = 0.6$$

$$frec(N) = \frac{(2 \times 30) + 20}{200} = 0.4$$

## Genotypic frequencies

$$frec(MM) = \frac{50}{100} = 0.5$$

$$frec(MN) = \frac{20}{100} = 0.2$$

$$frec(NN) = \frac{30}{100} = 0.3$$

# Estimation of Frequencies

**Problem 1.** In a human population of 1200 individuals, analysis for the MN system blood group revealed the existence of 365 M individuals, 556 MN individuals and 279 N individuals. What are the genotypic and allelic frequencies in this population for the MN locus?

$$D = \text{Frequency of the } L^M L^M \text{ genotype} = 365/1200 = 0.304$$

$$H = \text{Frequency of the } L^M L^N \text{ genotype} = 556/1200 = 0.463$$

$$R = \text{Frequency of the } L^N L^N \text{ genotype} = 279/1200 = 0.233$$

$$p = 0.304 + 1/2 \cdot 0.463 = 0.5355$$

$$q = 0.233 + 1/2 \cdot 0.463 = 0.4645$$

[Remember that  $p + q = 1$ , and that  $q = 1 - p$ ].

# Hardy-Weinberg Equilibrium

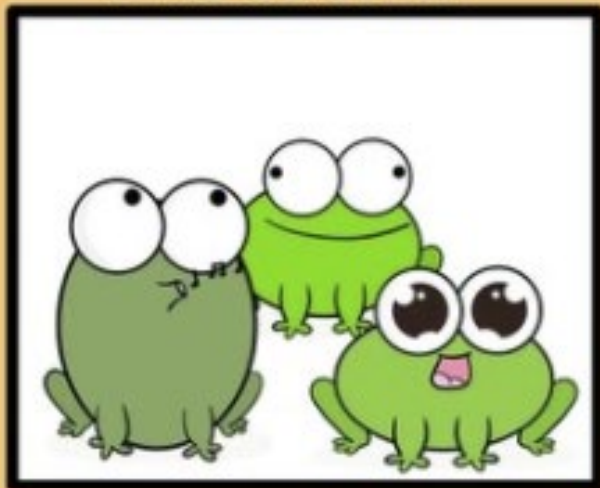
**Natural Population:** group of individuals belonging to the same species that live in the same geographic area and are able to reproduce among them

**Panmictic Population:** is a theoretical concept of population where the number of individuals is infinite and the mating is random (*panmixia/panmixis*)

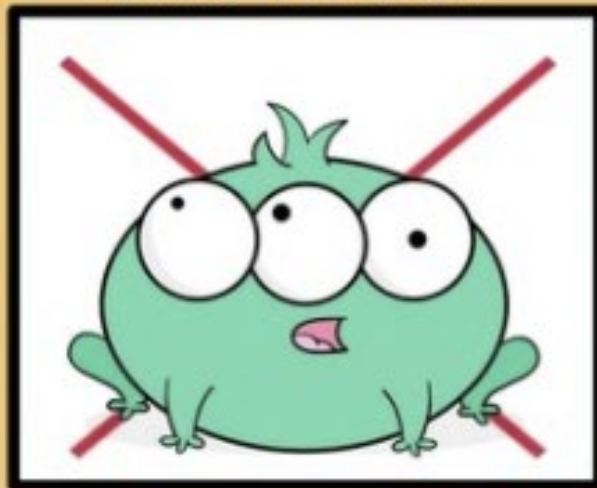
*The population is the unit of evolution*

# ASSUMPTIONS OF HARDY-WEINBERG EQUILIBRIUM

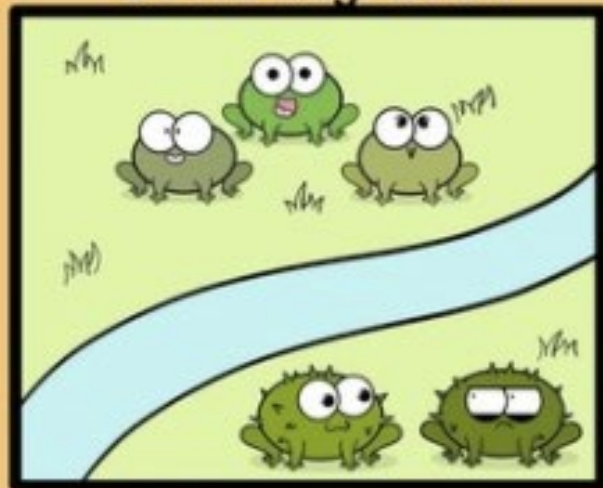
1. No Selection



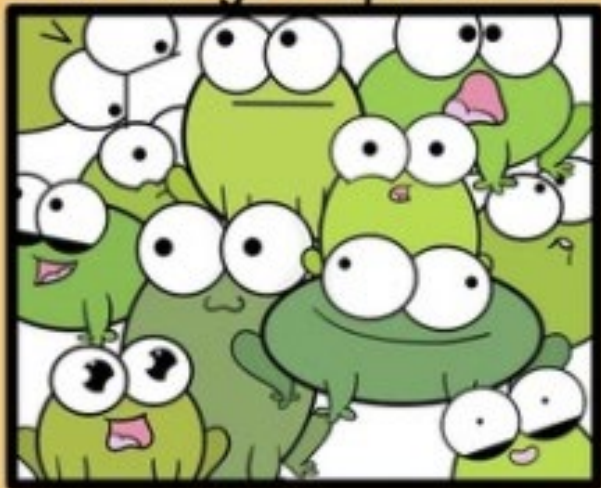
2. No Mutation



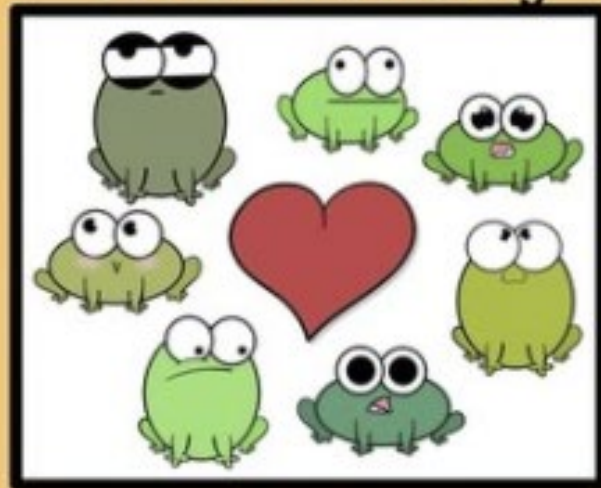
3. No Migration



4. Large Population



5. Random Mating

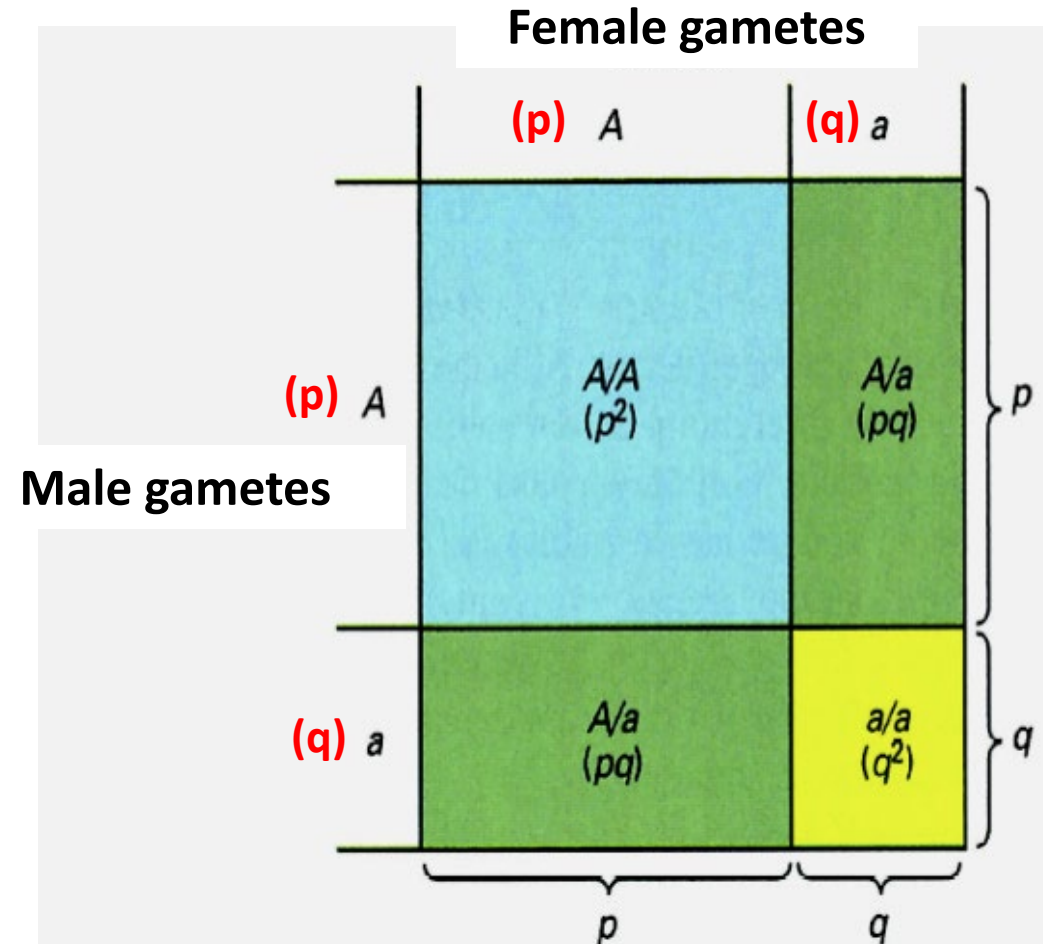


# Hardy-Weinberg Equilibrium

$$(p + q) = 1$$

$$(p + q)^2 = 1$$

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





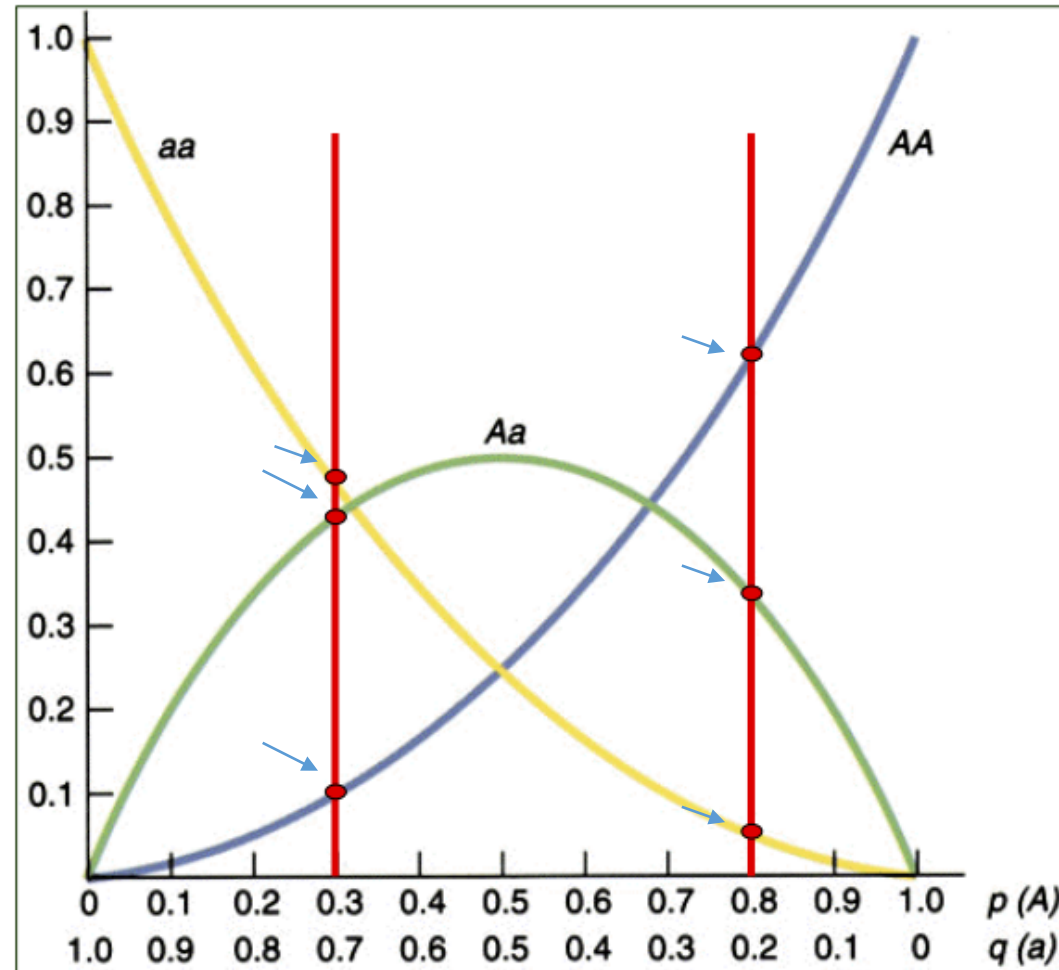
# Hardy-Weinberg Equilibrium

$p = 0.3$   
 $q = 0.7$

$$p^2 = 0.09$$

$$2pq = 0.42$$

$$q^2 = 0.49$$



$p = 0.8$   
 $q = 0.2$

$$p^2 = 0.64$$

$$2pq = 0.32$$

$$q^2 = 0.04$$

# Hardy-Weinberg Equilibrium

**Problem 2.** In a human population in Hardy-Weinberg equilibrium, the frequency of individuals affected by an autosomal recessive disease is 4 per 10000 individuals. What would be the allelic and the genotypic frequencies in this population?

The frequency of sick people is 4 per 10000 inhabitants. Thus:

$$q^2 = \text{frequency of recessive homozygotes} = 4/10000 = 0.0004;$$

$$q = \text{frequency of the allele } a = 0.02 \left( \sqrt{0.0004} \right)$$

And, therefore,  $p$  (frequency of the  $A$  allele) would be:  $1 - q = 1 - 0.02 = 0.98$

With these allelic frequencies, the equilibrium genotypic frequencies would be:

$$p^2 = \text{frequency of } AA = 0.9604$$

$$2pq = \text{frequency of } Aa = 0.0392$$

$$q^2 = \text{frequency of } aa = 0.0004$$

# Evolutionary Factors

**Systematic deviation of H-W equilibrium:** direction and scale of change are predictable

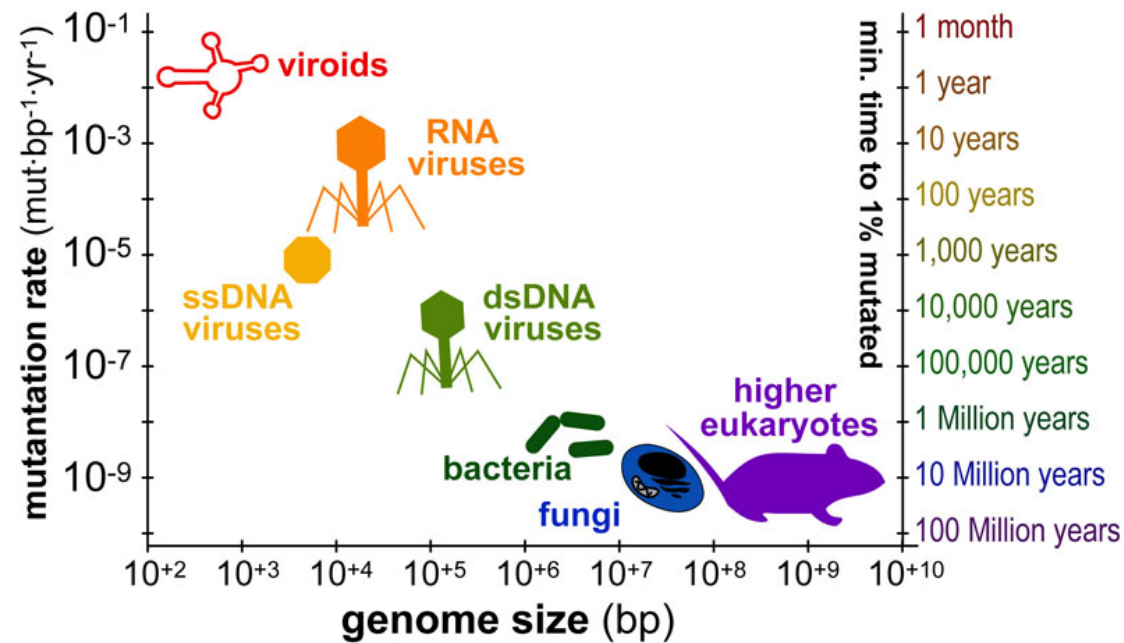
- **Mutation**
- **Selection** (differential reproductive success | fitness)
- **Migration**

**Random deviation of H-W equilibrium:** direction of change is not predictable and the change of allelic frequencies is random

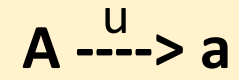
- **Genetic drift**
- **Endogamy** (consanguinity)

# Mutation

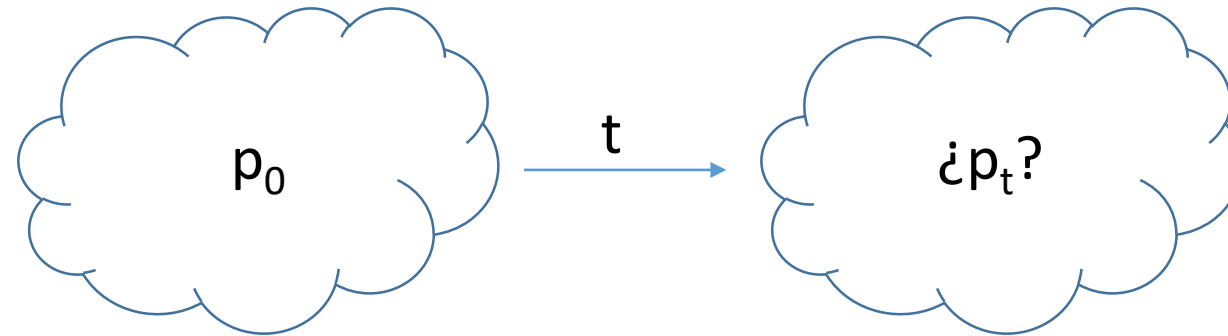
- Primary source of variation
- Changes allelic frequencies (some alleles change to different allelic forms)
- Generally, its influence on allelic frequencies is low



# Mutation



New allelic  
variants  
appear



$$p_1 = p_0 - p_0 u$$



$$p_t = p_0 (1-u)^t$$

# Mutation

**Problema 3.** At a certain locus the mutation rate of  $A \rightarrow a$  is  $10^{-6}$ , the rate of reverse mutation being negligible. What will be the frequency of A after 10, 100 and 100,000 generations of mutation, if we start from an initial frequency of 0.5?

$$p_t = p_0 (1 - u)^t$$

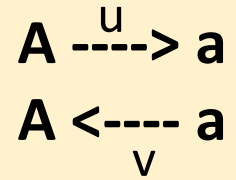
Therefore, in the problem at hand, given that  $p_0 = 0.5$  and  $u = 10^{-6}$ , after 10 generations, the frequency of A will be:

$$p_{10} = 0.5 (1 - 10^{-6})^{10} = 0.499995$$

$$\text{In 100 generations: } p_{100} = 0.5 (1 - 10^{-6})^{100} = 0.4999995$$

$$\text{In 100,000 generations: } p_{100,000} = 0.5 (1 - 10^{-6})^{100,000} = 0.4524$$

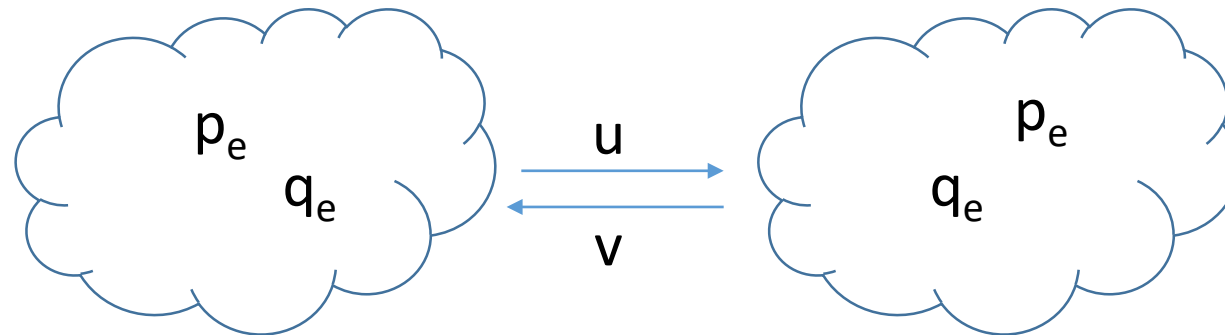
# Mutation



Mutation rates  
(direct & reverse)

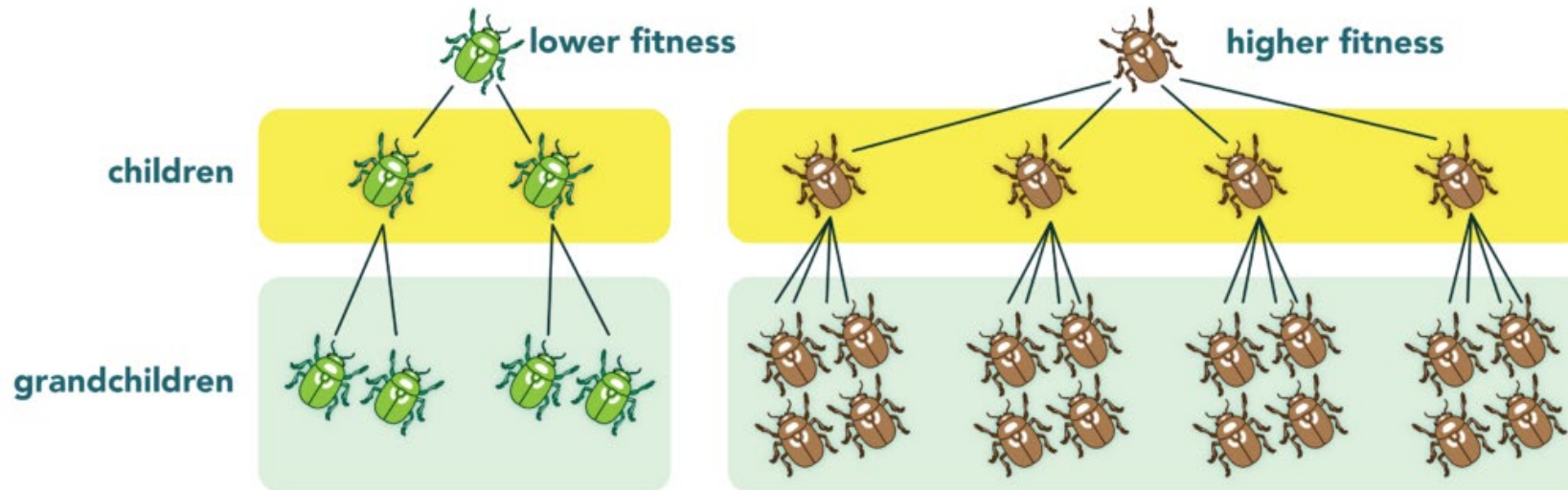
$$p_e = v/(u+v)$$

$$q_e = u/(u+v)$$



# Selection

- Represents differential reproduction of individuals
- Alleles with differential reproductive success (*fitness*)
- Relies on each environment
- Can cause drastic changes in allelic frequencies
- Is adaptative, reduces the genetic variability





# Selection

**w = fitness**

Estimation of reproductive success of a genotype ( $w = 1$  for the genotype with higher reproductive success. In proportion for the rest of genotypes)

**s = selection coefficient**

$$s = 1 - w$$

After one generation of selection, in a sufficiently large population and with random mating, if we apply the general model of natural selection, expected relative genotypic frequencies will be:

***Frequency of genotype AA:***  $p^2 w_{AA} / W$

***Frequency of genotype Aa:***  $2pqw_{Aa} / W$

***Frequency of genotype aa:***  $q^2 w_{aa} / W$

Where  $W$  (average fitness of all three genotypes)  
 $= p^2 w_{AA} + 2pqw_{Aa} + q^2 w_{aa}$

And, therefore,

$$p' = p^2 w_{AA} + 1/2 2pqw_{Aa}$$

$$q' = q^2 w_{aa} + 1/2 2pqw_{Aa}$$

# Selection

**Problema 4.** In a large population of insects with random mating, the progeny produced on average by individuals belonging to each of the three possible genotypic classes for a locus with two alleles (A and a) have been analyzed and the following results have been obtained:

Genotype	Average number of descendants
AA	150
Aa	120
aa	75

- a) What is the value of fitness in each case?  
 b) Being the frequency of allele A (p) equal to 0.6, what will be its frequency in the next generation?

Frequency of genotype AA:  $p^2 w_{AA}/W$   
 Frequency of the genotype Aa:  $2pq w_{Aa}/W$   
 Frequency of genotype aa:  $q^2 w_{aa}/W$

Where  $\bar{w}$  (average biological efficacy of the three genotypes) =  $p^2 w_{AA} + 2pq w_{Aa} + q^2 w_{aa}$   
 $= (0.6)^2 \times (1) + 2(0.6) \times (0.4) \times (0.8) + (0.4)^2 \times (0.5) = 0.36 + 0.384 + 0.08 = 0.824$

[Given that  $p = 0.6$  and  $q = 0.4$ ]

Thus:

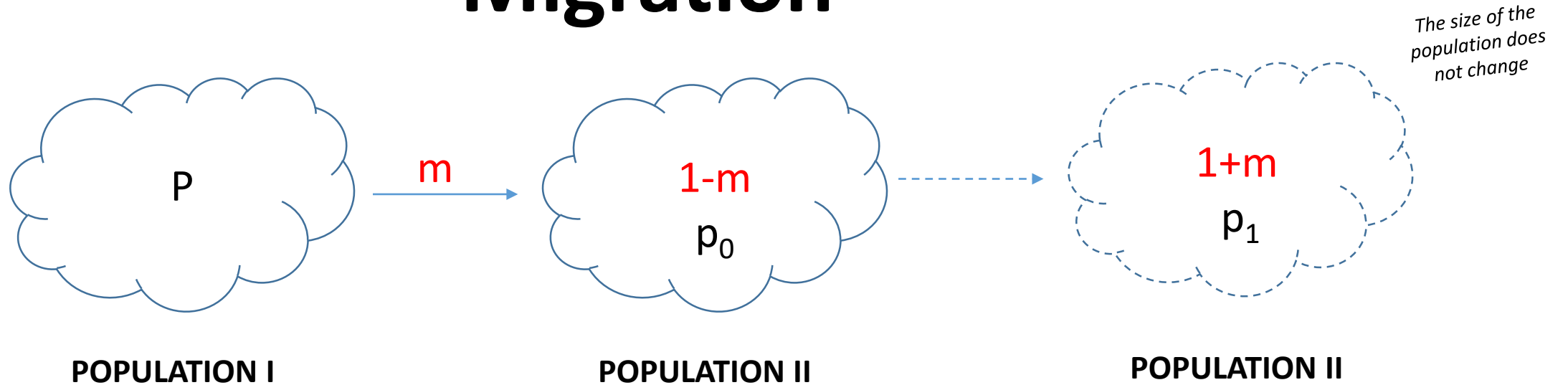
Frequency of genotype AA:  $p^2 w_{AA}/\bar{w} = 0.36/0.824 = 0.437$   
 Frequency of genotype Aa:  $2pq w_{Aa}/\bar{w} = 0.384/0.824 = 0.466$   
 Frequency of genotype aa:  $q^2 w_{aa}/\bar{w} = 0.08/0.824 = 0.097$

And, therefore,

$p = 0.437 + 1/2 \cdot 0.466 = 0.67$   
 $q = 0.097 + 1/2 \cdot 0.466 = 0.33$

Fitness of AA ( $w_{AA}$ ):  $150/150 = 1$   
 Fitness of Aa ( $w_{Aa}$ ):  $120/150 = 0.8$   
 Fitness of aa ( $w_{aa}$ ):  $75/150 = 0.5$

# Migration

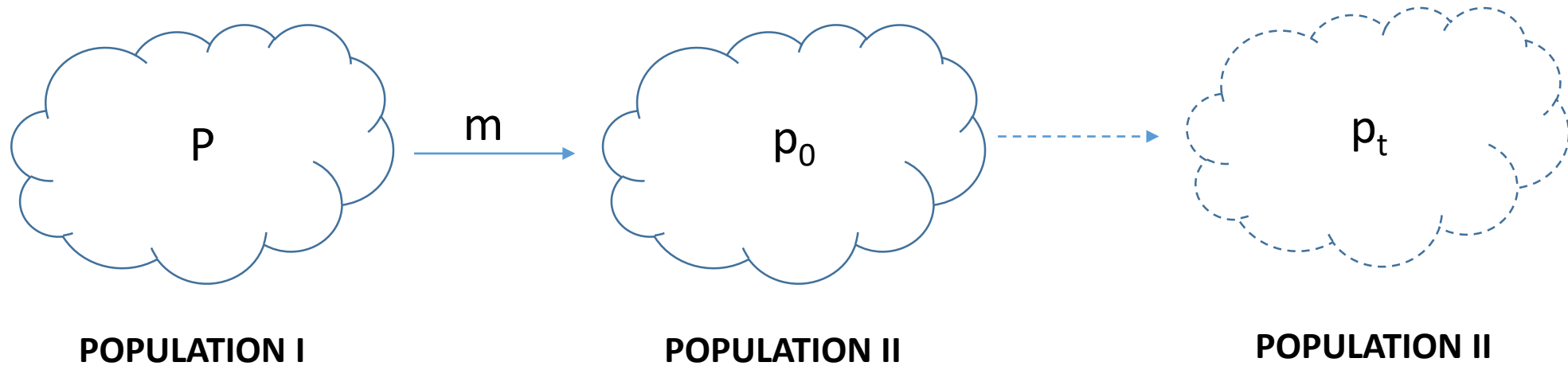


$$p_1 = (1 - m)p_0 + mP = p_0 - m(p_0 - P)$$

Original/initial  
situation of  
Population II

Migrating  
proportion from  
Population I

# Migration



Number of generations (t) needed for a particular change in frequencies due to migration:

$$(1 - m)^t = (p_t - P)/(p_0 - P)$$

# Migration

**Problema 5.** In a population that maintains its size constant over generations, the frequency of an allele at an autosomal locus at a given time is 0.4. The rate of migration into that population from a neighboring population where the frequency of that allele is 0.6 is 20%.

- a) What will be the frequency of this allele one generation later?
- b) And after 5 generations?
- c) Will there ever come a time when, under these conditions, the gene frequencies will not change?

$$a) p_1 = p_0 - m (p_0 - P) = 0,4 - 0,2 (0,4 - 0,6) = 0,44$$

$$b) (1 - m)^t = (p_t - P) / (p_0 - P) \rightarrow (1 - 0,2)^5 = (p_5 - 0,6) / (0,4 - 0,6) \rightarrow p_5 = 0,534$$

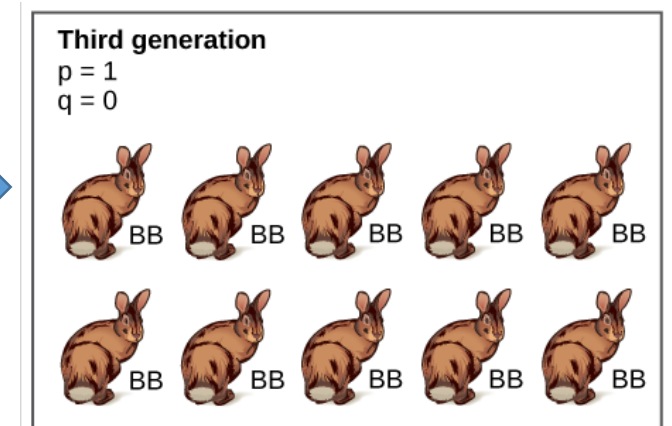
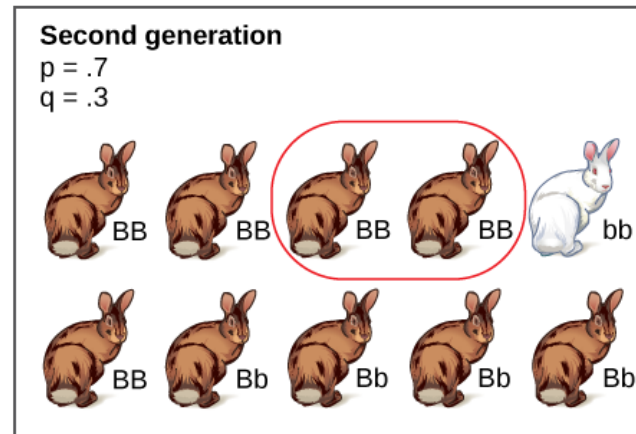
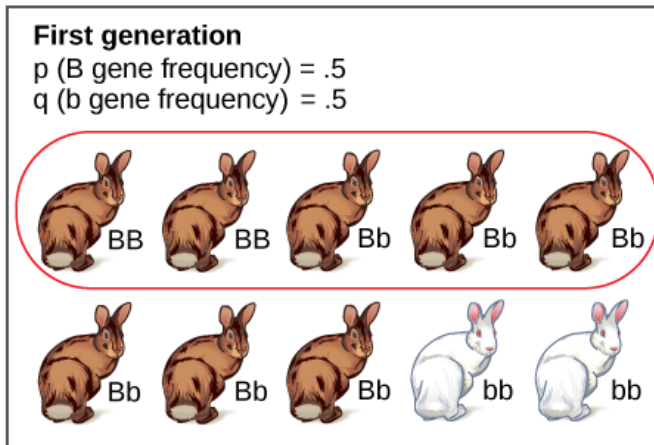
- c) Yes, when allelic frequencies of both populations are equal and reach 0.6 (allelic frequency of donor population). There is still gene flow but without modification of frequency.

# Genetic Drift

- It is the result of a random “sampling”.
- Allelic frequencies change randomly and the genetic composition of the new population can significantly change.
- Loss of variability.

5 rabbits reproduce

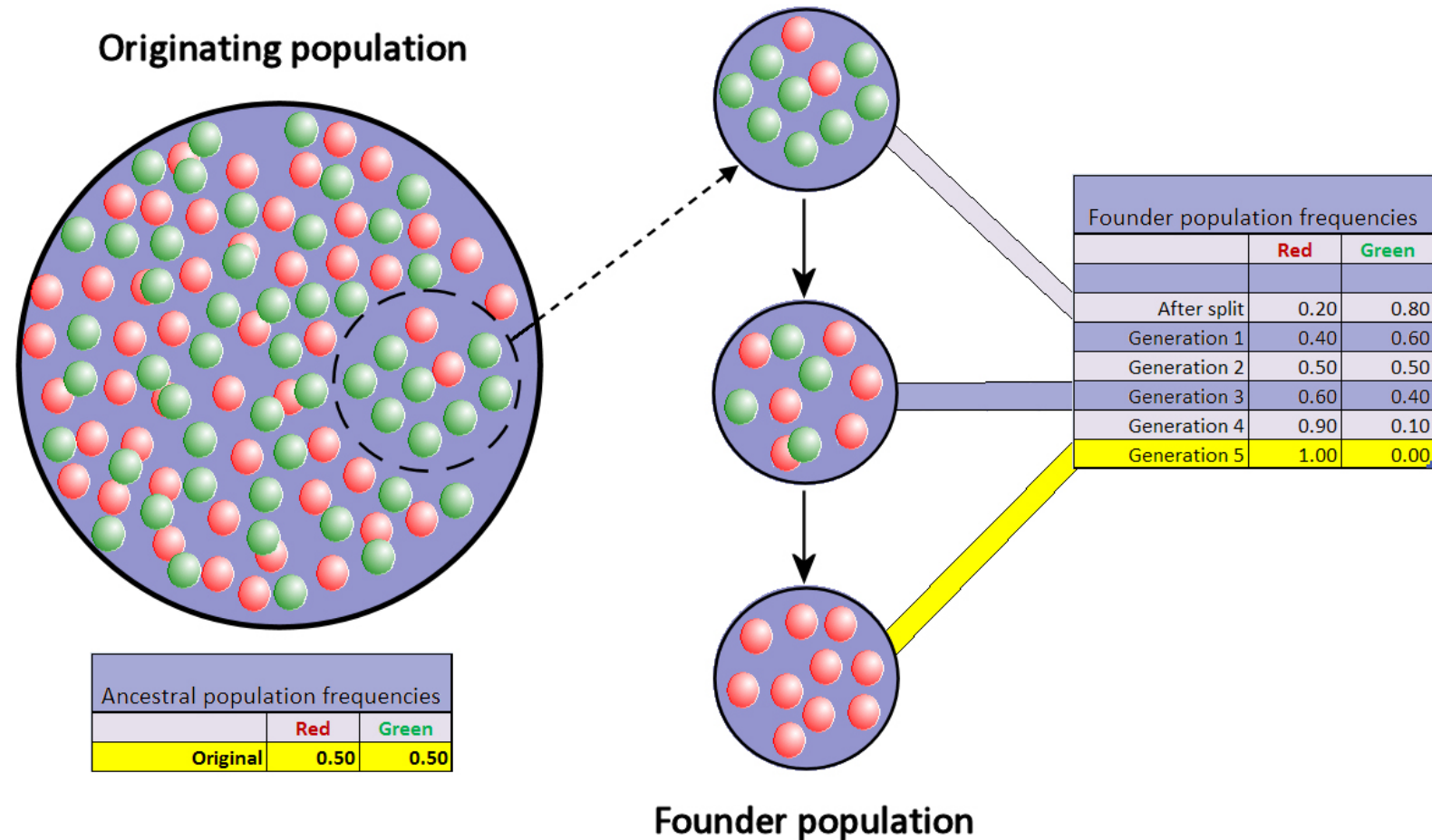
2 rabbits reproduce



Some  
beneficial  
alleles can  
disappear

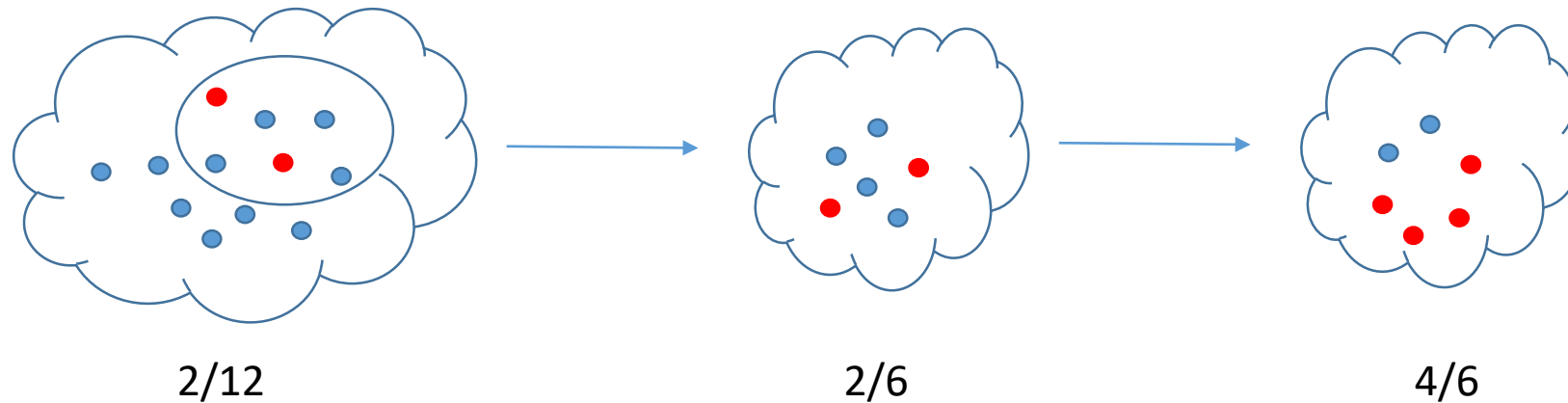
# Genetic Drift

- The effect is more drastic when the number of “sampled” individuals is low.



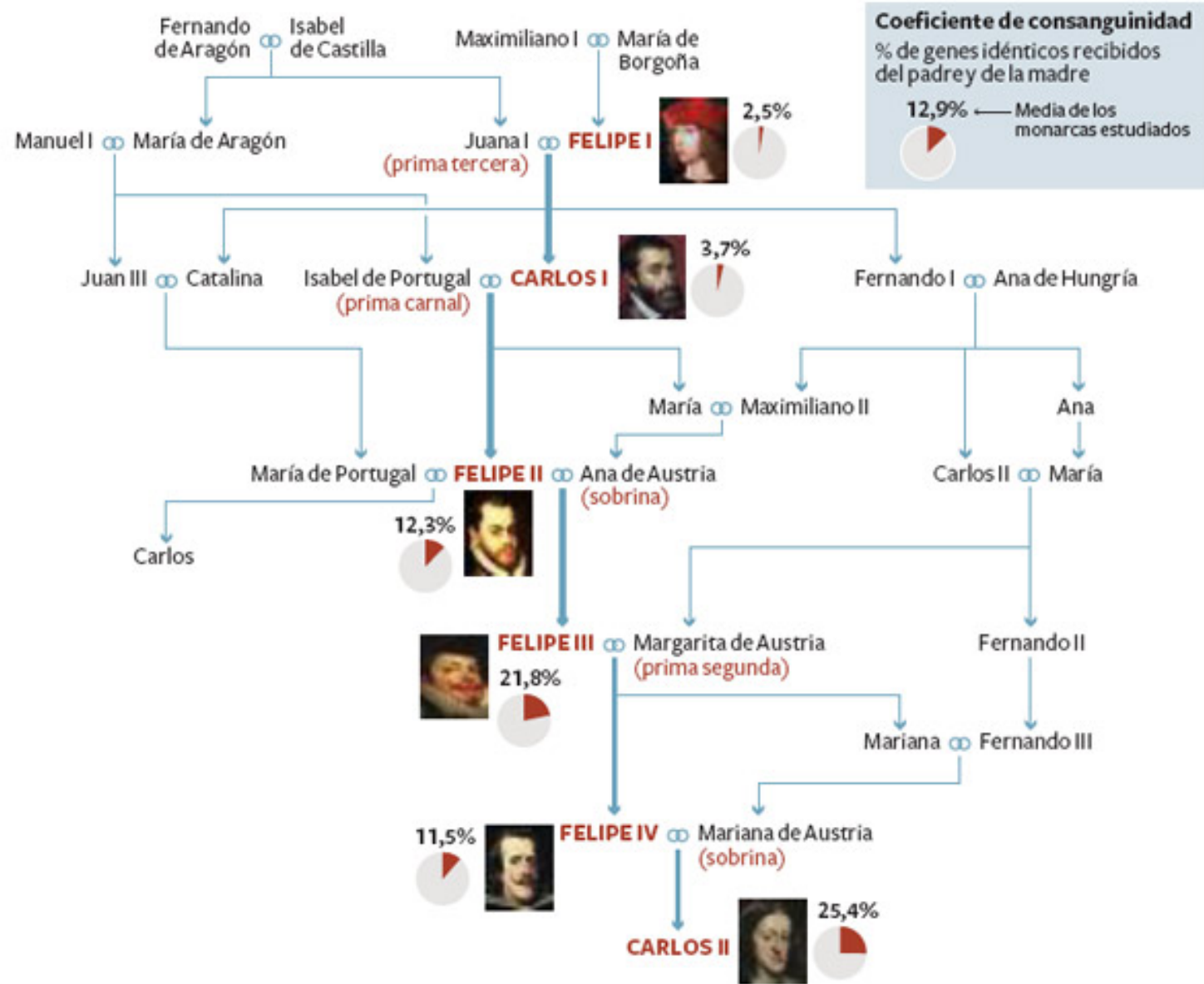
# Endogamy

- The cross between related individuals (endogamy) causes consanguinity
- Increases homozygosity and reduces genetic variability
- Reduces the adaptativity of individuals





# Genealogía de la casa de los Habsburgo en España



# Other H-W equilibrium deviations

**Sex-linked genes:** allelic frequencies are different in each sex. So it is the inheritance.

## *Equilibrium genotypic frequencies*

- Homogametic sex (XX|ZZ) coincident with those of autosomal genes, since an allele of each parental is inherited.
- Heterogametic sex (XY|ZW) coincident with  $p$  and  $q$  values, since there is only a single copy of this allele (corresponding to a single X|W chromosome).

# Sex determination XY

**Frequency of males with dominant phenotype** (*hemizygous* for dominant allele):  $p$

**Frequency of males with recessive phenotype** (*hemizygous* for recessive allele):  $q$

**Frequency of females with dominant phenotype:**  $p^2$

**Frequency of heterozygous females:**  $2pq$

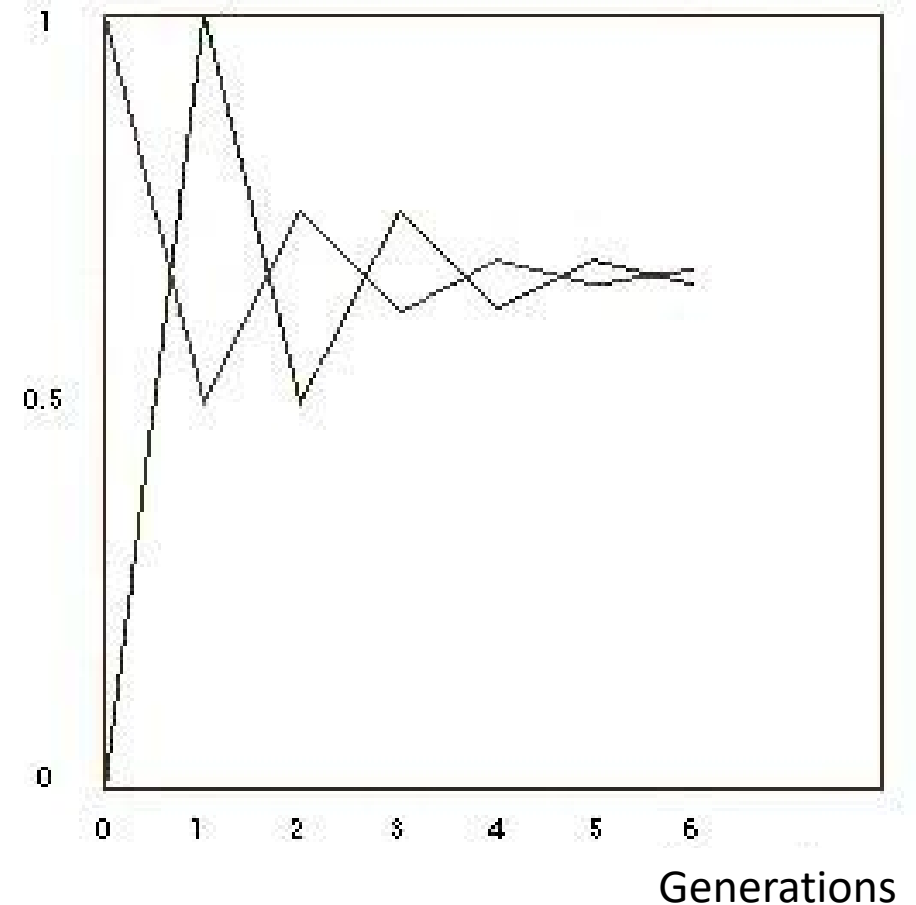
**Frequency of females with recessive phenotype:**  $q^2$

## Progress of allelic frequencies for a sex-linked gene

From a population of 100% normal men and 100% daltonic women, calculate the frequency of the allele responsible for daltonism after 6 generations.

Generation	XY	$X^dX^d$
G0	$q_x(0) = 0.00$	$q_{xx}(0) = 1.00$
G1	$q_x(1) = 1.00$	$q_{xx}(1) = 0.50$
G2	$q_x(2) = 0.50$	$q_{xx}(2) = 0.75$
G3	$q_x(3) = 0.75$	$q_{xx}(3) = 0.63$
G4	$q_x(4) = 0.63$	$q_{xx}(4) = 0.69$
G5	$q_x(5) = 0.69$	$q_{xx}(5) = 0.66$
G6	$q_x(6) = 0.66$	$q_{xx}(6) = 0.60$

Frequency  $q$



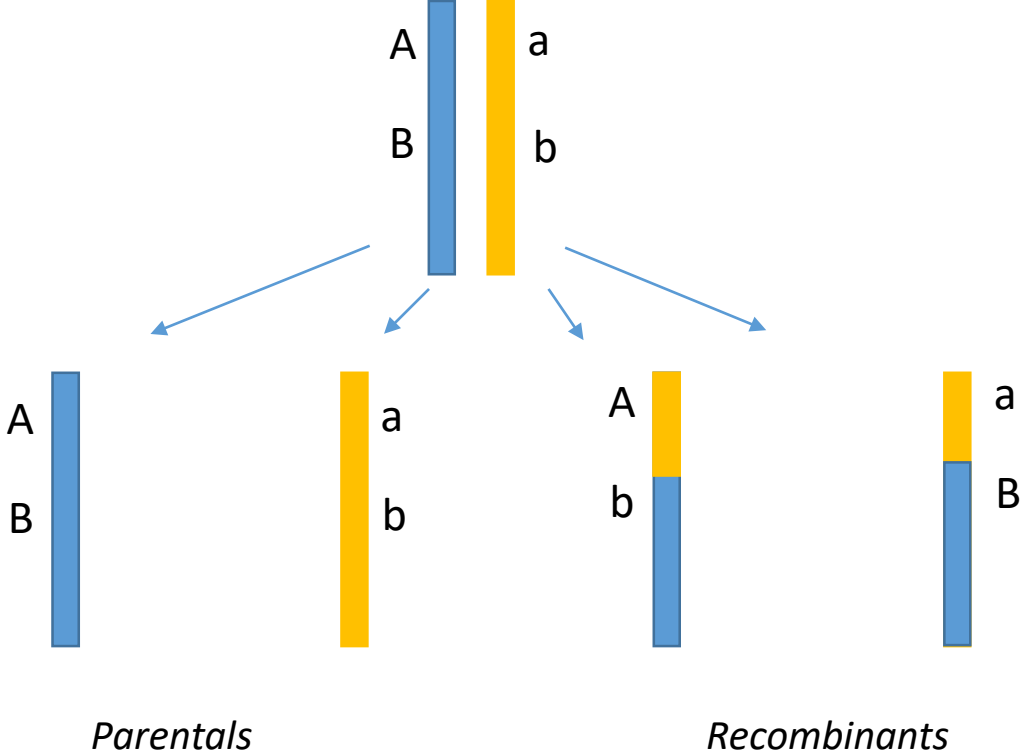
**Equilibrium is reached after several generations**

# Other H-W equilibrium deviations

**Linked genes:** equilibrium may not be reached (*linkage disequilibrium*)

**Alleles do not segregate independently (inherited together more often than expected)**

# Other H-W equilibrium deviations



Linkage

Independent segregation

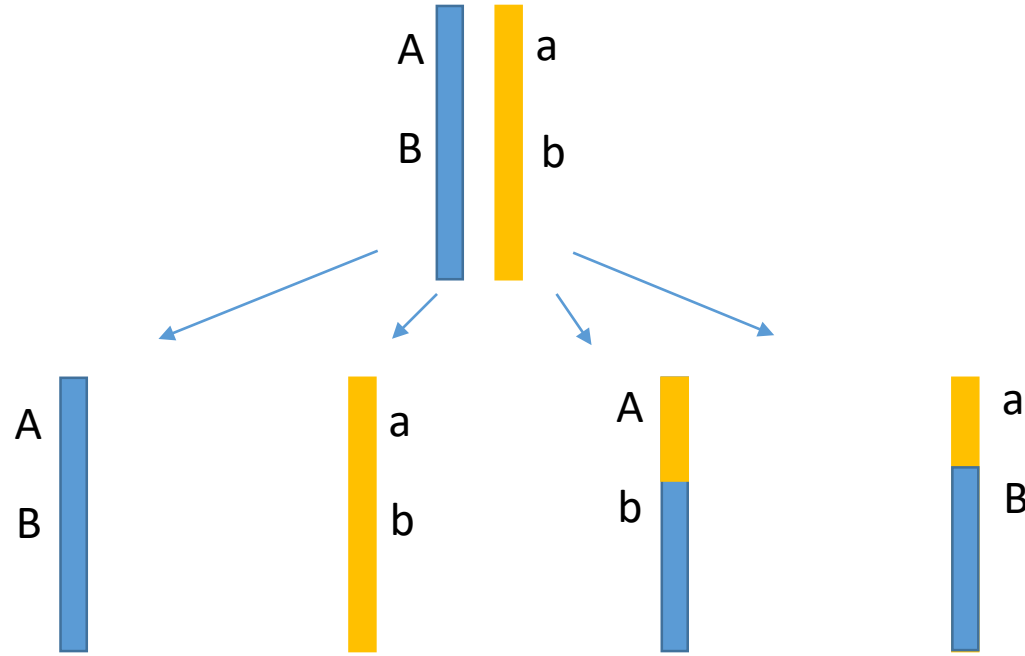
25%

25%

25%

25%

# Other H-W equilibrium deviations



$$D = F(AB) \times F(ab) - F(Ab) \times F(aB)$$

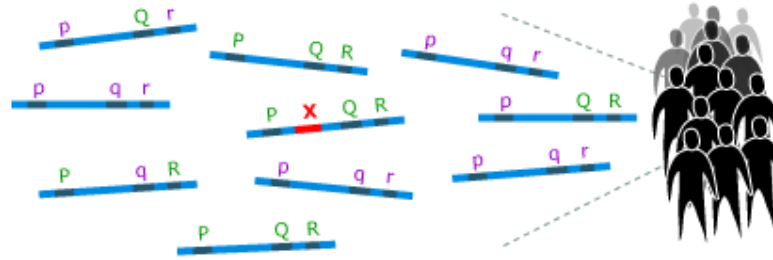
**D = 0** No linkage

**D > 0** More parentals than expected

**D < 0** More recombinants than expected

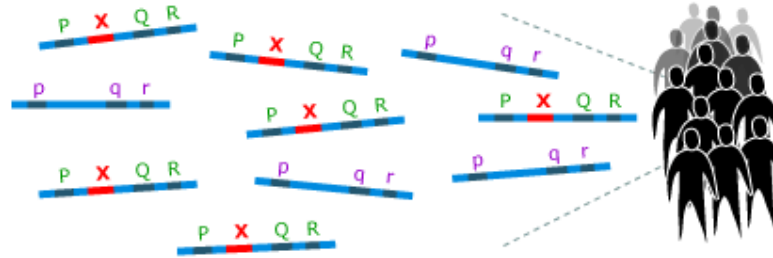
# Genetic Hitchhiking

A beneficial mutation (X) occurs on chromosome 4:



REPRODUCTION

Natural selection increases the frequency of the mutation X as well as the linked gene versions P, Q, and R:



REPRODUCTION with RECOMBINATION

Over time, recombination reduces the association between X and P, Q, and R:

