

## Mating system

**Random mating:** It is the mating in which the male can mate any female in the experimental group or population. This method generally maintains the genetic diversity in the population.

**Assortive mating:** It is the mating which depend on phenotype there are two types of Assortive mating:

1- Positive Assortive mating : is mating in which similar individuals within a group are mated. They may be alike phenotypically, e.g. the heaviest individuals within a flock.

2- Negative assortive mating: individuals more distantly related either genotypically or phenotypically are mated. An example of phenotypic dissimilarity would be mating two groups within a population that have the highest and the lowest body weights.

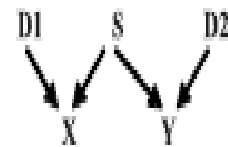
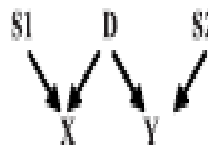
## Concept of Relationship

It's the degree of genetic similarity or correlation between two individual have common pedigree. Those individual may carrying the same gene due to their relationship , if the fathers genotype was Aa his son will carry one of these genes, so the relationship supposed to be 0.5 because the son will has the half of his fathers genes .

### The Relationship patterns

1- **Direct Relationship** : Relationship between fathers and sons.

2- **Indirect Relationship** : relationship between brothers as full sibs or half sibs

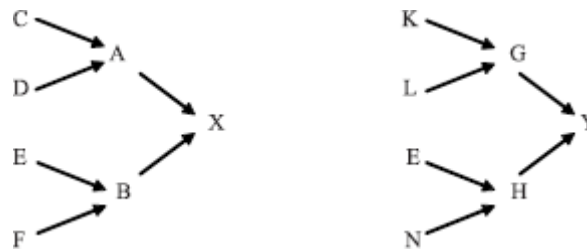


For brothers ,the possibility of obtaining the same genes through father are 0.5 for each , so the genetic similarity will be  $0.5 \times 0.5 = 0.25$  for the half sibs , but in full sibs it will  $(0.5 \times 0.5) + (0.5 \times 0.5) = 0.5$

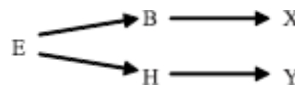
Relationship coefficient Calculation:

- 1- Determine the arrows between the individual and his father or grandfather then apply the equation  $(1/2)^n$  . n= arrows number
- 2- In case distant relationship between two individuals(X and Y), determine all arrows which lead to each of them by their common fathers, then we calculate the Relationship coefficient using :  $R= (1/2)^n$ .
- 3- Summation (adding up) all possible similarity of common different parents by the equation:  $R_{XY} = \Sigma(1/2)^n$ .

**Example:** Find the relationship coefficient between the individuals X and y from the following pedigree records .



Summarize the above chart in a simple one

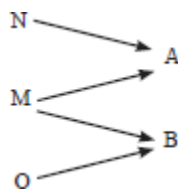


$$R_{XY} = \Sigma (1/2)^n = (1/2)^4 = 1/16$$

**Example 2:** Calculate relationship coefficient between A and B from the following pedigree record?



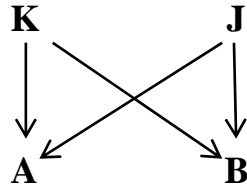
We can draw the chart in a simple way:



The possibility to be similar due to common father M:

$$R_{AB} = \sum (1/2)^2 = 1/4$$

**Example 3:** From the following chart calculate the relationship coefficient between A and B ( $R_{AB}$ ).



**Solution:** There are two common parents K and J .

So the possibility to be similar due to k:

$$B \longleftarrow K \longrightarrow A \quad = (1/2)^2 = 1/4$$

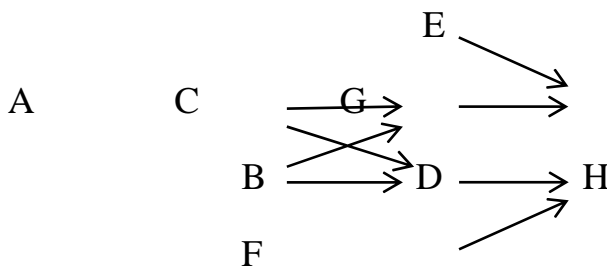
The possibility to be similar due to J

$$B \longleftarrow J \longrightarrow A \quad = (1/2)^2 = 1/4$$

The Summation of similarity probabilities are

$$R_{AB} = 1/4 + 1/4 = 1/2$$

**Example:** From the following chart calculate  $R_{CD}$  ,  $R_{GH}$  ,  $R_{ED}$ .



1- **Calculation of  $R_{CD}$ :** The common father is **A** , The possible similarity between C and D :

$$C \longleftarrow 1 \text{---} A \text{---} 2 \longrightarrow D \quad (1/2)^2 = 1/4$$

The second common father is **B** , The possible similarity between C and D :

$$C \longleftarrow 1 \text{---} B \text{---} 2 \longrightarrow D \quad (1/2)^2 = 1/4$$

$$R_{CD} = 1/4 + 1/4 = 1/2$$

2- **Calculation of  $R_{GH}$** : The common parents for ( G, H ) are A and B

The similarity which obtained from the father A:-

$$G \longleftarrow C \longleftarrow A \longrightarrow D \longrightarrow H = (1/2)^4 = \mathbf{1/16}$$

The similarity which obtained from the father B:-

$$G \longleftarrow C \longleftarrow B \longrightarrow D \longrightarrow H = (1/2)^4 = \mathbf{1/16}$$

$R_{GH}$  represent adding up of the degrees of similarity which have been obtained from parents A and B:-

$$R_{GH} = 1/16 + 1/16 = 2/16 = \mathbf{1/8}$$

3-  $R_{ED} = 0$  .Because there is no relationship between them.

## SEX CHROMOSOMES SYSTEMS

**XX-XY** are the sex chromosomes in **human** and mammalian, in this system (XX) is the female sex chromosomes. (XY) is the male sex chromosomes, that make male responsible for progeny sex determination.

**ZZ-ZW** are the sex chromosomes in **poultry**, (ZZ) is the male chromosomes .(ZW) are the female chromosomes which make female responsible for progeny sex determination.

**XX-XO** are the sex chromosome in **insects** , XX female chromosomes and the XO is male chromosomes

### SEX LINKED INHERITANCE IN POULTRY

Sex linked traits is the traits which affected by genes located on sex chromosome (Z) ,their effect appears in one gender, this is because there are no alleles on the unreal chromosome (W) in females .

*Genetic behavior and the economic importance of gender-related traits:*

#### **1- Barred feathers trait:**

This trait of plumage is common in the Plymouth Rock strain, its appear due to dominance sex-linked gene, Symbolizes B. The economic importance of this trait when the proper mating is applied, the sex of hatching chicks can be distinguished, we can keep females for the purpose of producing eggs and dispose of the males. The following example illustrates the mating of unbarred males with barred females

Parents	barred females	unbarred males
Genotype	$Z^B W$	$Z^b Z^b$
Gametes	$Z^B$ $W$	$Z^b$
F1	$Z^B Z^b$	$Z^b W$
	barred males	unbarred females

We note that mothers trait transported to her males chicks, and fathers trait transported to his females chicks. This type of genetic behavior for sex-linked traits called **CRISSCROSS INHERITANCE**.

NOW the question is: Can we take advantage of this gene in the second generation (F2)? Homework

**2-Sex-linked slow feathering trait:**

In the poultry strains, there is a difference in feathers growth speed, which are classified into two types, rapid feathering and slow feathering, due to the action of a sex-linked gene, the slow feathering gene is dominant on the allele of fast feathering gene. The differences in these genes are observed between the chicks at the age of ten days, the birds which carried fast feathering gene are characterized by the clear rapid growth of wings feathers, as well as tail feathers, which are approximately 2 centimeters in length (at 10 days). The slow feathers chicks do not show tail feathers growth, and the wings feathers are much shorter than individuals of fast feathering gene.

To take advantage of the sex-linked feathering gene for sexing newly hatching chicks, females carrying dominance gene that responsible for slow feathering (K) are mating with males of fast feathering gene (k) :

Parents	female (slow)	×	males(fast)
Genotype	$Z^KW$		$Z^kZ^k$
Gametes	$Z^K$ $W$		$Z^k$
F1	$Z^KZ^k$		$Z^kW$
	Slow males		fast females

What happen in next generation?

The advantage of early sexing is to keep females for egg production and discard the males or raising as broiler for meat production.

### 3-Sex-Linked Dwarfism (dw) :

Some types of chickens have a pair of sex-linked recessive genes (dw) that affect the growth of the body in older ages and was denote that it leads to a small size of the body compared to individuals carrying the dominant gene (DW), which leads to a normal growth of the body. It was observed that the males carrying the pure genetic makeup of the mutated gene were 40% less weight than the natural ones. The females carrying the same genetic makeup were approximately 30% less weight than the normal females, so they will save the place and feed. But there is no negative effect of this gene on the reproductive efficiency of males or the production of eggs in females. On the other hand, the effect of recessive gene on body weight does not appear until the age of eight weeks, so it cannot be used to distinguish the chick at hatching time. Recently, poultry breeding and improvement workers have begun to benefit from the dwarf gene by reducing the amount of feed consumed by the herds of meat-chicken mothers. Natural growth offspring can be obtained from mating dwarf mothers with natural males as described in the following mating:

Parents	Dwarf Females	Normal Males
Genotypes	$Z^{dw}W$	$Z^{DW}Z^{DW}$
F1	$Z^{DW}W$	$Z^{DW}Z^{dw}$
	Normal Females	Normal Males

What happen in next generation ?

### Silver and Gold Feather

It's widely used in egg type chicken. The silver and gold color is a description of the down feathers of white and brown chicken , we can benefit from this sex-linked trait in chicks sexing at the age of one day as follows:

Parents	silver females × golden males	
genotypes	$Z^S W$	$Z^s Z^s$
gametes	$Z^S$ $W$	$Z^s$

F1 silver males  $Z^S Z^S$

$Z^S W$  golden females

**Sex-limited traits:**

Are traits expressed in only one sex, although the genes are present in both. examples are plumage patterns in birds—in many species, the male is brightly colored—and horns found only in males of certain sheep species. Milk yield in mammals is expressed phenotypically only in females.

**Sex-influenced, or sex-conditioned, traits**

Appear in both sexes but occur in one sex more than the other. Pattern, or premature, baldness in human beings is an example of a sex-influenced trait. In women, it is usually expressed as a thinning of hair rather than as balding. Apparently testosterone, the male hormone, is required for the full expression of the allele.



## Gene Frequency:

Percentage of the number of loci occupied by a particular allele to all locations occupied by that gene. If there are number  $N$  of animals, the number of sites per gene in this group is  $2N$ . Usually, denotes the gene A frequency by the character  $q_A$ , and the allele a  $(1-q_A)$ . You can calculate the frequency of the gene by using the following equation:

$$q_A = \frac{2(\text{Animals of AA alleles}) + \text{Animales of Aa alleles}}{2(\text{number of all animales})}$$

If we have 50 animals distributed according to the genetic makeup as follows: 23 AA , 15 Aa , 12 aa , so they will have 100 loci for this gene , the number of loci occupied by the allele A:

$$A = 2 \times 23 + 15 = 61$$

While the number of loci occupied by the allele a :

$$a = 2 \times 12 + 15 = 39$$

$$\text{The allele A frequency : } \frac{61}{100} = 0.61$$

$$\text{The allele a frequency : } \frac{39}{100} = 0.39$$

$$0.61 + 0.39 = 1 \text{ (Note that the total frequency is 1)}$$

If there is more than 2 allele for specific gene the frequency of each allele will be the percentage of that allele to the entire number of all the alleles, and the total frequency must be One (1).

Ex: **30**  $A_3A_2$ , **25**  $A_1A_3$  , **18**  $A_1A_2$  , **12**  $A_3A_3$ , **10**  $A_2A_2$ , **15**  $A_1A_1$

The total number of animals = 110

Number of the gene loci = 220

$$A_1 \text{ freq} = \frac{2(15)+25+18}{220} = \frac{73}{220} = 0.33$$

$$A_2 \text{ freq} = \frac{2(10)+30+18}{220} = \frac{68}{220} = 0.31$$

$$A_3 \text{ freq} = \frac{2(12)+25+30}{220} = \frac{79}{220} = 0.36$$

Example : In a herd of cows found the following phenotypic frequencies **16** black BB , **48** colored Bb , **36** white bb. What is the frequency in this group?

$$q_B = \frac{2(16)+48}{200} = 0.4$$

$$q_b = \frac{2^{(36)+48}}{200} = 0.6 \quad \text{or} \quad q_b = 1 - 0.4 = 0.6$$

The gene frequency of this group can be expressed as follows: (W 0.4+w 0.6). note , we can get the phenotypic distribution by squareness of the gene frequency

$$(W 0.4+w 0.6)^2 = 16WW + 48 Ww + 36 ww$$

### Factors Which Change Gene Frequency

The genes within the population genetic base remain constant from generation to other, but its frequency may change among individuals in each generation as a result of certain factors.

**1- Selection:** selection mains keep a specific group of males and females, using them as parents to produce next generation. It is the most important factor, lead to change the gene frequency used by the breeders to improve their animals production. For the purpose of clarifying the act of selection on gene frequency and changing the rate of production performance we assume:

Genotype	BB	Bb	bb
Freq.	720	960	320

In this flock the gene frequency of B is :

$$q_B = \frac{2(720)+960+0}{2 \times 2000} = 0.6$$

Suppose all individuals which produce 2 kg were excluded. So the gene frequency will be :

$$q_B = \frac{2(720)+960}{2 \times (720+960)} = 0.7$$

The selection resulted in a 0.1 increase in gene frequency

**2-Migration:** Migration means introducing new animals to the herd and mixing them with the original herd. So it has an active role in changing gene frequency when the migrated and the local animals have a different gene frequency. If we suppose that the gene frequency of specific gene is  $q_m$  and  $q_o$  of the immigrated and the original animals consequently , so the new gene frequency can be calculated by the equation :

$$q_1 = m (q_m - q_o) + q_o$$

( $q_1$  = new frequency,  $m$  = migrated animals percentage)

Example : Suppose that the original herd gene frequency is  $A = 0.3$  and the frequency in the migrated animals  $A = 0.4$ , if the migrated animals percentage was 20%, what is the new gene frequency in the mixed animals.

$$q_1 = m(q_m - q_0) + q_0$$

$$q_1 = 0.20(0.40 - 0.30) + 0.30 = 0.32$$

**3- Mutation:** Its defined as a genetic substance change that inherits from generation to generation. The mutation is also known as the change in the gene itself. Mutations are a very important factor in evolution over successive generations, but their value is simple for animal breeders because of their scarcity. The rate of mutation in the animal is estimated at 0,00001 or less. However, **the mutation is generally unimportant to the animal breeder because:**

- 1- Most mutation occur at a low rate.
- 2- Mutations are harmful or have little effect.
- 3- Most mutations are recessive genetic effect, so their effect disappear under dominant allele.

### References:

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2. Karvita B. Aluwalia, (2008), Genetics, 2<sup>nd</sup> ed.
3. Charlotte K. and Paul F. Lurquin, (2004), Genes and DNA, New York press.
4. Reference: [www.geneclinics.com](http://www.geneclinics.com)