

INBREEDING **

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Abstract: The objective of this paper is to present to scientific and professional public the most common forms of inbreeding appearing or carried out with different kinds of domestic animals aimed to enhancement of the population production capabilities. In this way, by following the change of certain productive, reproductive and other characteristics, the kind of the inbreeding that gives the most favourable effects will be established. Thus such characteristics would be additionally enhanced at given domestic animals population.

Herewith are described modern methods determining direct relationships, collateral relationships and inbreeding coefficient.

Key words: breeding, relationships, ascendants, descendants

Introduction

When animals in certain inter-relationship are mating it is known as inbreeding. It means that *parentage or ascendants to the certain level have to be known*, based on which it can be established whether there is a inter-relationship between the mating animals. Level of relationship depends on the size of population and number of ascendants' generations. In bisexual organism populations each animal has two parents, 4 grandfathers and grandmothers, 8 great grandfathers and great grandmothers, etc., and t generation has 2^t ascendants, *Falconer*, (1961).

Based on the aforementioned one can see that at even small number of generations creating particular ascendants of all existing animals of a population number of existing ascendants becomes larger than one population can contain. For example, an individual in 30 generation contain ascendants' population of more than 87 million head. Therefore it is

important to know the number of ascendants in previous generations in order to expect certain level of inbreeding.

To present interrelationships *Walsh genealogy chart*, developed by *De Chapeaurouge*, with particular focus on inbreeding studies. Establishment and marking of inbreeding was performed in different ways, but most frequently marking was done with **Lehndorff's blood share method, ascendant removes, free generations, etc.** However, it has been established that those methods are inadequate for genetic research since they do not provide any numerical value.

Pearl and Križenecki (1921) tried to express level of interrelationship numerically, but they did not take genetic base.

Nowadays, **interrelation coefficient and inbreeding coefficient** are in use. They were inaugurated by *Wright* (1921). At first *Wright* defined inbreeding coefficient as correlation between coupling gametes i.e. gene values. According to *Malecot* (1961) definition inbreeding coefficient is likelihood for two genes at the same location to be of the same origin. In this context, same origin means that both genes are copies of the same gene of a common ascendant. Therefore, significant outcome for two animals having common ascendant is that they can carry characteristics of a gene that existed in the ascendant. In case of mating such two animals, they carry on such characteristics further on their descendants. Offspring produced through process of inbreeding might have two genes that were separated in preceding generation. Such genes are *identical by the origin*. Identity of two or more genes by the descendants is measured by the inbreeding coefficient. However, identity of allele genes could be *functional*, i.e. when two identical genes lack phenotypic differentiation and therefore have the same allele status. Animal that is carrier of such genes for any characteristic is homozygotic in pure meaning of the word. It is important to mention that in phenotypic effect there are no differences between genes whose identity is based in origin or those generated via status.

Relationship between parents and descendants in terminology **PAF analysis** in genetics is based on observation of gametes and zygotes as variables having being allocated values in line with their genetic structure, and is related to the additive gene effects. In genotype analysis of these relations genotypic variable is given value 1 if it contains gamete of gene A_1 , and $\mathbf{g} = \mathbf{0}$ if contains gene A_2 . Thus, zygote variable can have 2, 1 or 0 of A_1 genes what depends on genetic structure that might be A_1A_1 , A_1A_2 and A_2A_2 *Li* (1964). Since constitution of gamete is defined by the one contained in parents, it depends on the parents' genetic structure whether one parent (in

spermatogenesis or oogenesis) will produce the same or different types of gametes through a process of random separation. This analysis is based on Mendel's concept that every animal receives a half genes from father and another half from mother. Therefore relationship between one parent and descendant is $\frac{1}{2}$, between grandson and grandfather $\frac{1}{4}$ etc. *Li* (1964), *Begg* (1959), and others.

Level of interrelationship, expressed by inbreeding coefficient, is comparison between the tested population and some specific or basic population or breed. Without such relation calculation is irrelevant. It means that inbreeding coefficient becomes relevant just in case certain timeline in past is specified beyond which no tracing of ascendants will be performed, and in which all existing genes in the given population have to be considered as independent, meaning not identical by descendants. Such timeline is presented through *basic population*, and as definition reads its' inbreeding coefficient is *zero*. Inbreeding coefficient of a following generation indicates a size of a dispersive process that develops from basic population and compares interrelationship level of tested animals with those of basic population. However, in spite the fact it is always considered, relation with the basic population is not always clearly defined. The main biological effect of inbreeding is decrease of hetero-zygotes. A coefficient of inbreeding indicates a level of this effect, and it is defined as average decrease of heterozygote, in percents (or vice versa – increase of homozygote) in tested animal, in comparison with average animals of the same breed or basic population in the furthest generation pedigree studied. If the starting point was a population of a breed that contained 50 % of heterozygote, Figure 1 shows decrease of heterozygote in following generations depending on the mating system intended for inbreeding.

To increase level of homozygote for 20 % it is necessary to make 8 generation of continuous mating of half-brothers with half-sisters. Four generations of continuous mating of brothers and sisters increase homozygote for 30 % *Lörtshher* (1947) etc.

Important note in regard to the coefficient of inbreeding gave *Begg* (1959). He, as well as some other authors, claims that inbreeding is computed according to the previously mentioned method, not taking into account in which particular allele occurred increase of homozygote, or which have become a homozygote.

Relationship coefficient and inbreeding coefficient are calculated for characteristics that depend on additive genes and for the traits that are gender hereditary. Those coefficients are not an absolute measure but relative

values. However, they are still exact and comparable measure for the strength of implemented inbreeding and increase of homozygote in breeding or population, in cases where no selection is being performed.

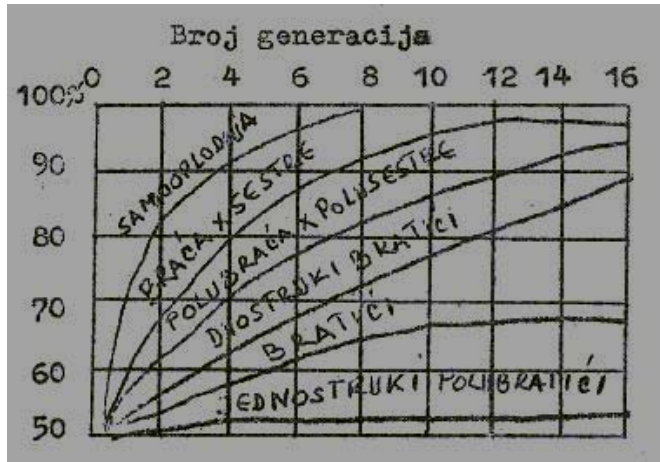


Figure 1. Increase of homozygous state through generations at different mating systems.

Calculation of direct relationships

Relationship between individuals could be either direct or collateral. Direct relationship calculation is used for assessment of a relative matching of descendant genotype and genotype of one of its ascendants. The calculation is performed as follows:

$$R_{XA} = \sum (1/2)^n \sqrt{1 + F_A / 1 + F_X}$$

Where

R_{XA} = Relationship coefficient of descendant X and ascendant A,

Σ = sum in case the remove appears more than once,

n = number of generations from X to A,

F_A = inbreeding coefficient ascendant A,

F_X = inbreeding coefficient descendant X.

Calculation of a relationship coefficient *includes* generations of ascendants, and *excludes* generations of descendant. $\sqrt{1 + F_A / 1 + F_X}$ means correction in the formula. If ascendant and descendant are not inbred i.e. when $F_A = F_X = 0$, calculation of direct relationship between certain

ascendant and descendant is done in the following way: $\Sigma (1/2)^n$, which is system for calculation of “Blood”. share Expression “blood” is used here following the traditional breeders terminology, although the blood as such has no function in inheritance process. Each embryo produces own blood and no blood transfers directly from parents to descendant. Therefore, term “blood” corresponds to hereditary traits.

Percentage of hereditary from the given source is satisfactory measure of direct relationship. Since each of bisexual individuals receives 50 % of hereditary material from father, and 50 % from mother means that direct relationship between son X and father A 50 %, i.e.

$$R_{XA} = \Sigma (1/2)^n = (1/2)^1 = 50 \%$$

Calculation of collateral relationship

Collateral relatives are brothers and sisters, half-brothers and half-sisters, single nephews, double nephews and other relatives in population. In this case percent of hereditary material is not adequate measure for collateral relationship, thus it is calculated by the following formula:

$$R_{BC} = \Sigma (1/2)^{n+n'} (1 + F_A) / \sqrt{(1 + F_B) \cdot (1 + F_C)}$$

The symbols in this formula have the following meaning:

R_{BC} = relationship coefficient between animals **B** and **C**,

n = number of generations between animal **B** and common ascendant,

n' = number of generations between animal **C** and common ascendant,

F_A = common ascendant **A** inbreeding coefficient

F_B = inbreeding coefficient of animal **B**,

F_C = inbreeding coefficient of animal **C**,

Σ = sum, in case of multiple relationship with a common ascendant or a number of common ascendants.

Expression $(1 + F_A)$ means correction for common ascendant inbreeding, which in fact *increases homozygote* indicated in expression $\Sigma (1/2)^{n+n'}$. Expression $\sqrt{(1 + F_B) \cdot (1 + F_C)}$ also means correction of the original formula which is cautiously constructed to create measurement of the level of relationship based on relationship coefficient up to which similar gamete pairs of akin animals are found. In fact this means that relationship coefficient is measurement that indicates how high could be the share of the

same genes present in the two akin individuals, **B** and **C**, from common ascendant. If we disregard inbreeding of common ascendant (F_A) and animals for which relationship coefficient (F_B i F_C) is calculated i.e. when $F_A = F_B = F_C = 0$, then formula for calculation of relationship coefficient:

$$R_{BC} = \sum (1/2)^{n+n'}$$

As calculation example we can take pedigrees of animals shown at Figure 2.

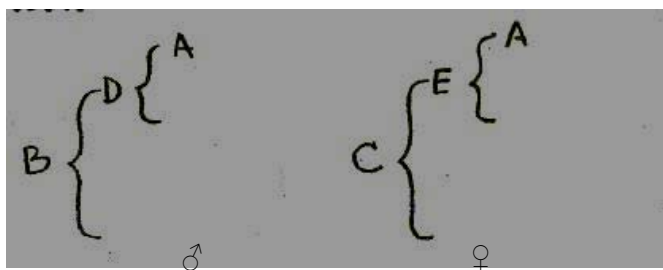


Figure 2. Pedigrees of animals **B** and **C** having common grandfather **A**.

The first step in calculation of relationship coefficient is to compute number of generations between an ascendant and descendants. Example given in Figure 2. shows that animals **B** and **C**, having common grandfather **A**, have higher level of interrelationships than average animals of their breed. In order to establish relationship level between animals **B** and **C** it is necessary to count generations from common ascendant **A** to his descendants **B** and **C**. *In this calculation generation of a common ascendant is not considered. However, generations of animals for which the relationship is calculated (in this case **B** and **C**) are taken into account.* Therefore *R i c e et al.* (1959) says that key **for relationship measuring is number of generations between two animals** whose lineages are studied, and their common ascendant(s). In this specific case common ascendant **A** is 2 generations apart from descendant **B** and 2 generations from **C**, therefore:

$$R_{BC} = \sum (1/2)^{n+n'} = \sum (1/2)^{2+2} = (1/2)^4 = 1/16 = 0,0625$$

$$0,0625 \times 100 = 6,25 \%$$

This simply means that approximately 6,25 % of genes of animals **B** and **C** are more similar than any other two animals selected from a breed.

There is a *relationship between animals **B** and **C** regardless whether those two animals will mate or not.* In this specific case they are half-

nephews. The more distant relationship between the animals, or the more distant common ascendant is from its descendants, relationship coefficient is of lower value.

Calculation of inbreeding coefficient

Inbred descendants are produced through mating of related animals. Calculation of inbreeding is done according to the following formula:

$$F_X = \Sigma (1 / 2)^{n+n'+1} (1 + F_A)$$

Symbols have the following meaning:

F_X = inbreeding coefficient of animal **X**,

n = number of generations between animal **X** and common ascendant **A**, paternal line,

n' = number of generations between animal **X** and common ascendant **A**, maternal line,

F_A = inbreeding coefficient common ascendant **A**, when it alone is inbred,

Σ = sum, in case of multiple inbreeding on same or more common ascendants.

As an example for calculation of inbreeding coefficient we'll take that we paired animal **B** with animal **C**, whose relationship is showed in Figure 2. Arrow-shaped pedigree, that is constructed on basis of classic genealogy chart or genealogy created with braces is the best way to present common ascendants, since *common ascendant and animal for which the inbreeding coefficient is being calculated close routes by which the relationships from mother's and father's line are calculated* (see Figure 3.).

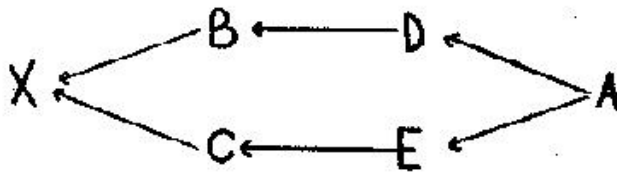


Figure 3. Arrow-shaped pedigree

Calculation of inbreeding is based on probability that animals **D** and **E** inherit the same allele from parent **A** in amount of $\frac{1}{2}$. The same time, probability to inherit different allele is $\frac{1}{2}$. If common ascendant **A** is inbred

it is expressed as $(1 + F_A)$, which means that it is likely that based on previous inbreeding one allele is identical. Based on the aforementioned the overall probability that animals **D** and **E** receive the same genes by origin will be expressed by the following formula $1 / 2 (1 + F_A)$. Further probability that **D** will transmit received gene onto **B** is $1/2$. The same probability applies onto transmission of this gene from **E** onto **C**. If between animal **X** and its ascendant **A** there are more generations than it is shown at Figure 3 then the same likelihood for farther ascendants in the chain of calculation between **X** and **A**. In the aforementioned case common ascendant has not been inbred, i.e. $F_A = 0$, therefore inbreeding coefficient equals to:

$$F_X = \Sigma (1 / 2)^{n+n'+1} (1 + F_A) = \Sigma (1 / 2)^{2+2+1} (1 + 0) = (1 / 2)^5 = 1 / 32 = 0,03125$$

$$0,03125 \times 100 = 3,125 \%$$

When animal **X** is inbred 3,125 %, than it means that 3,125 % more of its pairs are homozygotic, than in case of animals that are not inbred.

As it was seen, when calculating inbreeding coefficient for animal **X**, common ascendant is considered just once with the lines drawn from him to his descendants. Those lines present paths for genes transmission. When calculating a number of generations between common ascendant and animal for which inbreeding coefficient is calculated then generations of common ascendant and that animal are excluded.

If in lineage of an animal the same common ascendant appears more than once then calculation of inbreeding coefficient should be performed in a way that inbreeding is calculated only once per path route. In a process of calculation of relationship value of each path means contribution to the total value of an inbreeding coefficient. The same happens if the animal is inbred from more than one common ascendants. This means that all calculated values of inbreeding are added to the common amount.

Relationship coefficient and inbreeding coefficient are *statistical values*. When calculating those values no selection impact is taken into consideration. On the other side, logical conclusion of the inbreeding calculation is that the value of the inbreeding coefficient is based on the relationship level of the parents of inbred animal.

In order to follow further calculations of relationship and inbreeding coefficients please see the table of exponential values from $1 / 2$.

$(1 / 2)^2 = 1 / 4 = 25,0 \%$	$(1 / 2)^6 = 1 / 64 = 1,5625 \%$
$(1 / 2)^3 = 1 / 8 = 12,5 \%$	$(1 / 2)^7 = 1 / 128 = 0,78125 \%$
$(1 / 2)^4 = 1 / 16 = 6,25 \%$	$(1 / 8)^8 = 1 / 256 = 0,390625 \%$
$(1 / 2)^5 = 1 / 32 = 3,125 \%$	$(1 / 2)^9 = 1 / 512 = 0,1953125 \%$

Table 1. Exponential values from $1 / 2$.

Prior to construction of an arrow-shaped pedigree it is necessary to study classic pedigree, and establish whether there is one or more common ascendants. Common ascendant is any animal that appears at least once on mother's and at least once on father's line. A pedigree can contain one or more common ascendant. The same common ascendant can appear two or more times from mother's or father's line. This can happen with different common ascendants. In case one or more common ascendants are established in a pedigree then each of them needs to be marked with adequate symbol (Δ , \blacktriangle , \blacktriangledown , \blacktriangleright , \blacktriangleleft , \blacksquare , — , * etc.), capital or small letter or Arabic number. It is recommendable to determine two signs, one of which would serve for marking male, and another one for marking female animals (e.g. \square = male, and \blacksquare = female animals). Construction of arrow-shaped diagram is based on the principle that male ascendants are placed on the right side and female ascendants on the left side of a diagram. Common ascendant is placed within the most distant generation where it is registered in classic pedigree.

From the pedigree carrier to the paternal common ascendant successive sequence of generations are drawn as a **s o l i d** lines. In this manner number of generations between pedigree carrier and paternal or maternal common ascendant can be counted. Common ascendant is exclusively the one that closes path route of the paternal pedigree carrier to the common ascendant, and then from maternal line to the pedigree carrier. When calculating the inbreeding coefficient the entire circle can be calculated only once. However, if on paternal line there is only one path, and there are two or more paths on maternal line the calculation will be performed in the way to include paternal path as many times as many different paths on maternal line are there. All the calculations represent individual inbreeding coefficient contribution which is result of adding up all values pursuant to the instruction explaining mode of marking and calculation. The other uncommon ascendants' paths that are not on the direct path through generations are represented with **b r o - k e n** lines.

There should be other books along with the pedigree which would serve as source of information on productive and reproductive characteristics, and also breeding values, breed type etc.

Analysis of a classic pedigree and arrow-shaped diagram gives opportunity to establish the following:

1. Whether all ascendants in the pedigree belong to the same or different breeds.

2. If ascendants belong to different breeds then breeding construction for the pedigree carrier can be established along with type of applied crossing.
3. Whether it is regular or irregular type of mating. Members of the same generation are mating in regular type of mating, whereas in irregular type of mating a sire mates with members of different generations.
4. Along with the calculated inbreeding coefficient, type of applied inbreeding can be determined, e.g. incest, narrow or moderate mating of relatives.
5. By knowing size of population one can assess whether it is intended inbreeding method or forced inbreeding, which is likely to happen in smaller populations. When partners for creation of the new generation are being selected based on the production traits, during the process of the sire selection and dam allocation it often happens that some kind of inbreeding can not be avoided
6. Through pedigree analysis it is possible to follow a course of breeding of population.
7. Effect of inbreeding onto productive features (regression or indifference in production level), vitality of animals, and presence of harmful genes has to be separately assessed and compare with the type of inbreeding and its level.

The following Figures show relationship schemes and inbreeding in forms of classic and arrow-shaped pedigrees, in order to get better idea about the coefficient calculation and types of common ascendants in different relationships.

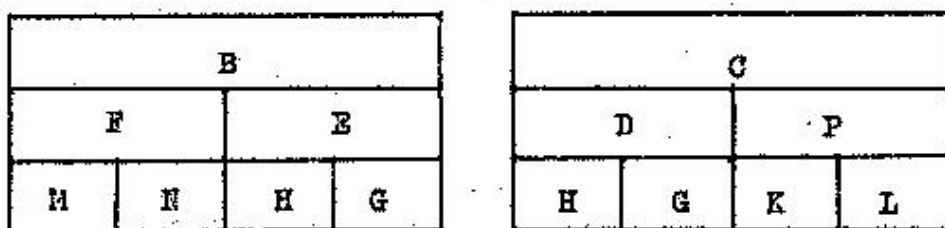


Figure 4. Classic pedigree of nephews. $R_{BC} = 12,5\%$.

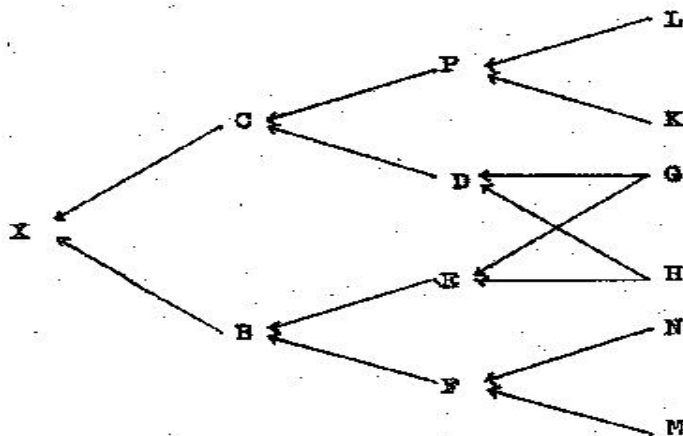


Figure 5. Arrow-shaped pedigree of individual X, result of single nephews mating.

$$F_X = 6,25 \%$$

Table 2. Calculation of inbreeding coefficient from nephews mating

Common Paternal path ascendant	Maternal path	$n+n^2+1$	F_A	Contribution $F_X - u$
G D - C	E - B	$(1/2)^5$	0	0,03125
H D - C	E - B	$(1/2)^5$	0	<u>0,03125</u>
				$\Sigma = 0,06250$

$$F_X = 0,0625 \times 100 = 6,25 \%$$

$$R_{BC} = 2F_X / \sqrt{(1 + F_B)(1 + F_C)}$$

Since in the particular case animals **B** and **C** are not inbred, then:

$F_B = F_C = 0$, than $R_{BC} = 2F_X = 2 \cdot 0,0625 = 0,125 \cdot 100 = 12,5 \%$.

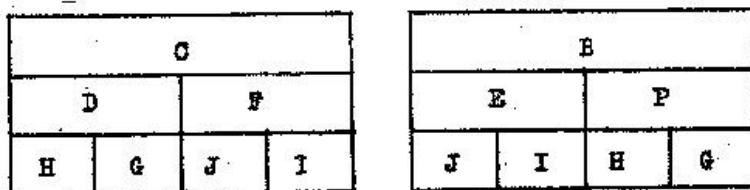


Figure 6. Classic pedigree of double nephews. $R_{BC} = 25 \%$.

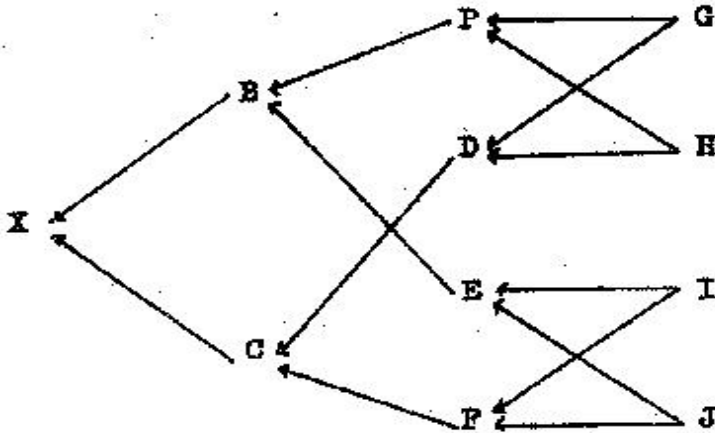


Figure 7. Arrow-shaped pedigree of individual X, result of a double nephews mating.

$$F_X = 12,5 \%$$

Table 3. Calculation of inbreeding coefficient based on mating of double nephews

Common Paternal path ascendant	Maternal path	$n+n'+1$	F_A	Contribution $F_X - u$
G P-B	C-D	$(1/2)^5$	0	0,03125
H P-B	C-D	$(1/2)^5$	0	0,03125
I E-B	C-F	$(1/2)^5$	0	0,03125
J E-B	C-F	$(1/2)^5$	0	0,03125
				$\Sigma = 0,12500$

$$F_X = 0,125 \times 100 = 12,5 \%$$

Relationship between half-brothers and inbreeding coefficient are shown in Figures 8 and 9.

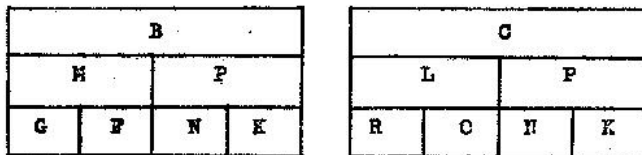


Figure 8. Classic pedigree of paternal half-brother and half-sister. $R_{BC} = 25 \%$.

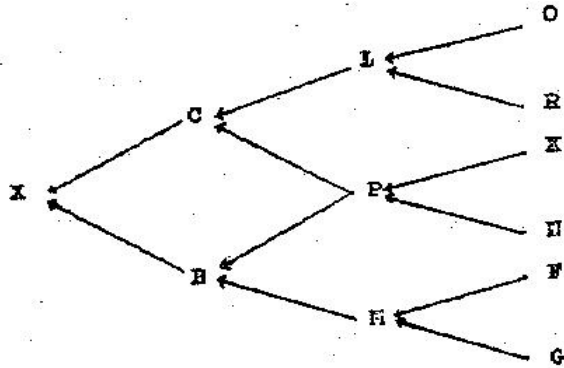


Figure 9. Arrow-shaped pedigree of individual X, result of mating of half-brother and half-sister.

$$F_X = 12,5 \%$$

Relationship between brothers, sisters or brother and sister and inbreeding coefficient when pairing brother and sister is showed in Figures 10 and 11.

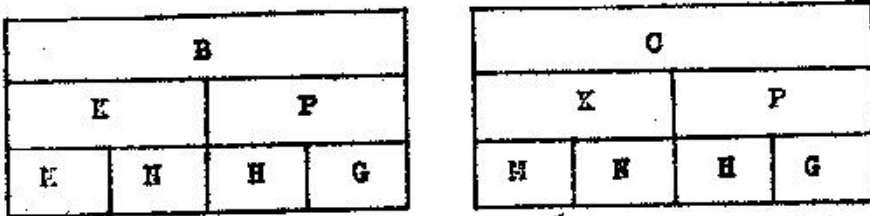


Figure 10. Classic pedigree between brothers. $R_{BC} = 50 \%$.

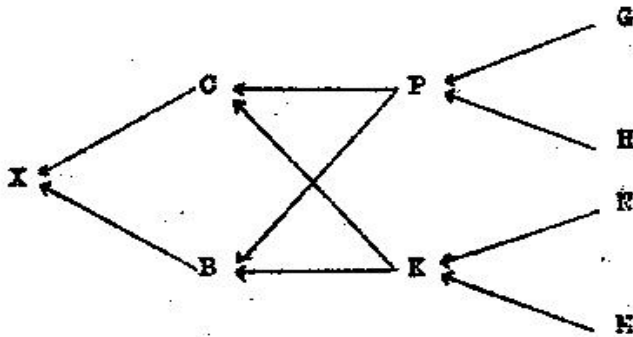


Figure 11. Arrow-shaped pedigree of individual X, result of mating of brother and sister.

$$F_X = 25 \%$$

Relationship between uncle (aunt) and niece (nephew) and inbreeding coefficient showed in Figures 12 and 13.



Figure 12. Classic pedigree of uncle (aunt) and niece (nephew). $R_{BC} = 25\%$.

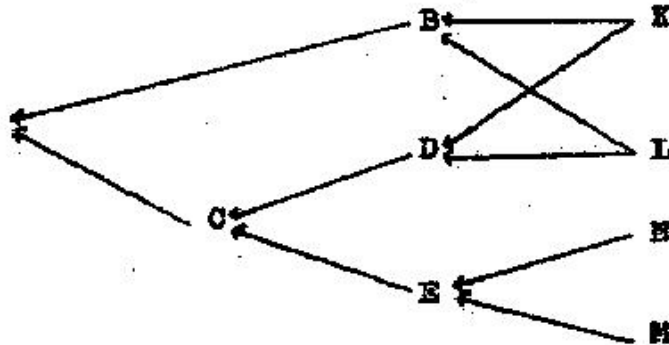


Figure 13. Arrow-shaped pedigree of individual X, result of mating of uncle (aunt) and niece (nephew). $F_X = 12,5\%$.

Relationship and inbreeding coefficient between grandfather (grandmother) and granddaughter (grandson) showed in Figures 14 and 15.

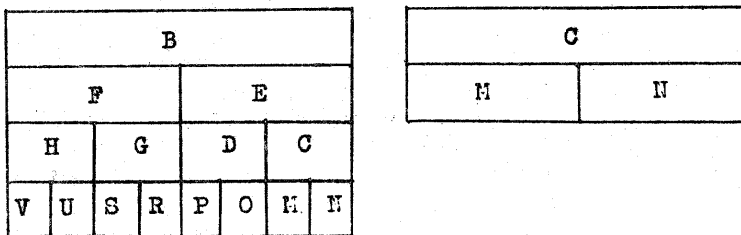


Figure 14. Classic pedigree of grandfather (grandmother) and granddaughter (grandson).

$R_{BC} = 25\%$.

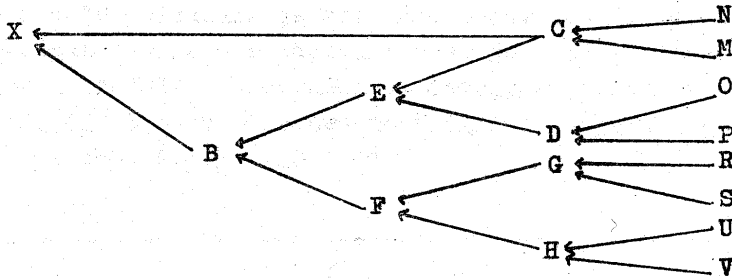


Figure 15. Arrow-shaped pedigree of individual X, result of mating of grandfather and granddaughter.

$$F_X = 12,5 \%$$

Relationship between parents and descendants and inbreeding coefficient shown in Figures 16 and 17.

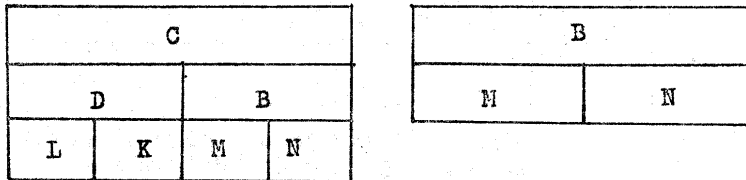


Figure 16. Classic pedigree of father and daughter. $R_{BC} = 50 \%$.

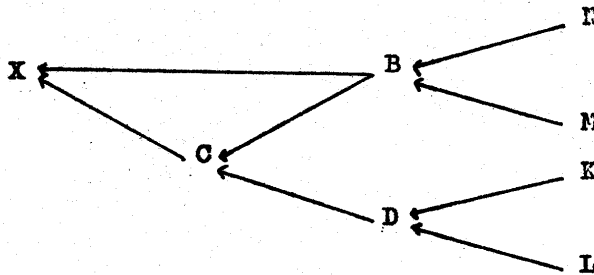


Figure 17. Arrow-shaped pedigree for an individual X, result of mating of father and daughter.

$$F_X = 25 \%$$

Conclusion

The Paper presents the most common forms of inbreeding, starting from simplest to most complex ones. Regular mating system with respective graphs is not presented in this Paper.

The intention of this Paper is to acquaint wider professional circle with start-up and implementation methods of inbreeding, and monitoring of researched characteristics effects through generations.

ODGOJ U SRODSTVU

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Rezime

Cilj ovog rada je predstavljanje naučnoj i stručnoj javnosti oblike odgoja u srodstvu koji su uobičajeni i koji se sprovode sa različitim vrstama domaćih životinja sa ciljem povećanja populacije sa odličnim proizvodnim kapacitetima. Na taj način, praćenjme promena u produktivnim, reproduktivnim i ostalim karakteristikama, uspostavlja se vrsta odgoja u srodstvu koja daje najpovoljnije dejstvo. Prema tome, takve karakteristike bi se dodatno poboljšale u datoj domaćoj populaciji.

Opisane su savremene metode kojima se određuje direktno srodstvo, kolateralno srodstvo i koeficijent odgoja u srodstvu.

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