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INBREEDING**

R. Telalbašić[1]*, M. Baban[2], A. Rahmanović[1]

[1] Faculty of Agriculture and Food Science, Sarajevo, Bosnia and Herzegovina; [2] Agriculture Faculty, Osijek, Croatia
*Corresponding author: Refik Telalbašić: e-mail: refiktel@bih.net.ba
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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, descendents

Part II

Figure 18 shows classic pedigree of animal **X**, result of inbreeding where common ascendant is also result of inbreeding. Equivalent of arrow-shaped diagram is showed in Figure 19. Calculation of inbreeding coefficient is presented in the tables 4 and 5.

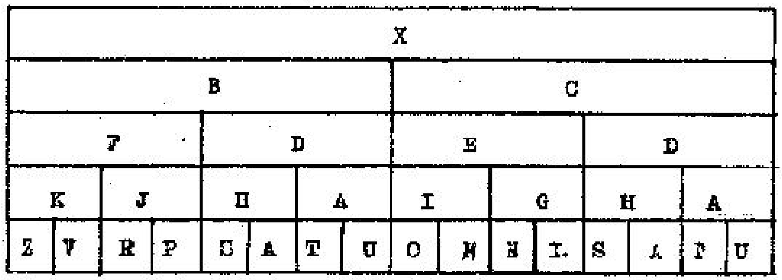


Figure 18. Classic pedigree of individual X, result of inbreeding where common ascendant is also inbred
Slika 18. Klasični pedigree individue X, kao rezultat parenja u srodstvu gde je zajednički predak takođe odgajan u srodstvu

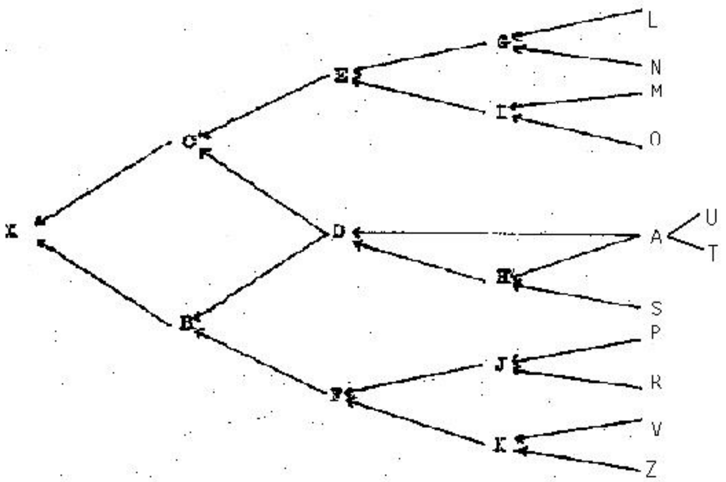


Figure 19. Equivalent arrow-shaped diagram of the pedigree shown in Figure 19
Slika 19. Ekvivalentni strelasti dijagram pedigree prikazanog na slici 19

Table 4. Calculation of inbreeding coefficient for common asscendant
Tabela 4. Kalkulacija koeficijenta odgoja u srodstvu za zajedničkog pretka

Common ascendant Zajednički predak	Paternal path Očinska linija	Maternal path Majčinska linija	n + n' + 1
A	–	H	$(1 / 2)^2$

$$F_A = (1 / 2)^2 = 0,25.$$

Table 5. Calculation of inbreeding coefficient for animal X
Tabela 5. Kalkulacija koeficijenta odgoja u srodstvu za grlo X

Common. ascendant Zajednički predak	Paternal path Očinska linija	Maternal path Majčinska linija	n+ n' + 1	F_A
D	C	B	$(1/2)^3$	0,25

$$F_X = \Sigma\,(1/2)^{n+n'+1}\,(1 + F_A) = \Sigma\,(1/2)^3\,(1 + 0{,}25) = 0{,}125 \cdot 1{,}25 = 15{,}625\ \%.$$

From the above calculation of the inbreeding coefficient it can be seen that common ascendant inbreeding increased the value of the inbreeding coefficient of animal **X**, i.e. increased probability for a gene from the common ascendant to transmit to descendant **X**. Individual **X** is result of mating of half brother with half-sister, and in this case value of the inbreeding coefficient is 12,5 %.

Calculation of inbreeding coefficient for an individual when both parents and common ascendant are inbred is presented in Figures 20 and 21 and tables 6, 7, 8 and 9.

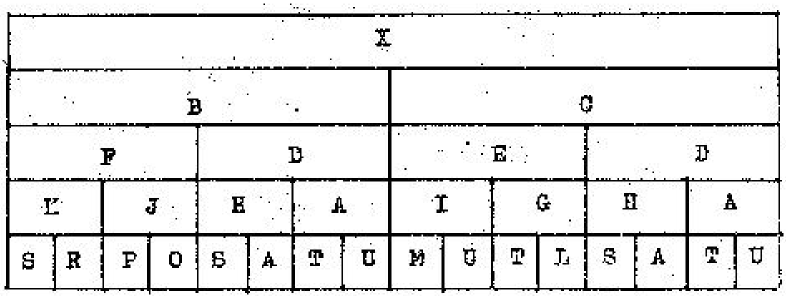


Figure 20. Classic pedigree of individual X, where both parents and common ascendant were inbred
Slika 20. Klasični pedigree grla X, gde su oba roditelja i zajednički predak odgojeni u srodstvu

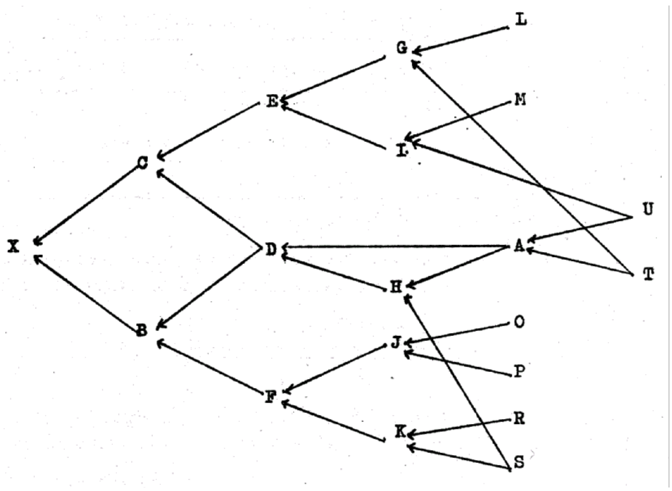


Figure 21. Equivalent arrow-shaped diagram of the pedigree shown in Figure 20
Slika 21. Ekvivalentni strelasti dijagram pedigree prikazanog na slici 20

Table 6. Calculation of inbreeding coefficient for common ascendant
Tabela 6. Kalkulacija koeficijenta odgoja u srodstvu za zajedničkog pretka

Common ascendant Zajednički predak	Paternal line Očinska linija	Maternal line Majčinska linija	n + n’ + 1	F_D
A	-	H	$(1/2)^2$	0,25

Table 7. Calculation of inbreeding coefficient for individual B
Tabela 7. Kalkulacija koeficijenta odgoja u srodstvu za individuu B

Common ascendant Zajednički predak	Paternal line Očinska linija	Maternal line Majčinska linija	n + n’ + 1	F_A	F_B
S	H – D	F – K	$(1/2)^5$	0	0,03125

Table 8. Calculation of inbreeding coefficient for individual C
Tabela 8. Kalkulacija koeficijenta odgoja u srodstvu za individuu C

Common ascendant Zajednički predak	Paternal line Očinska linija	Maternal line Majčinska linija	n + n’ + 1	F_A	Contribution F_X-u Doprinos F_X-u
U	A – D	E – I	$(1/2)^5$	0	0,03125
T	A – D	E – G	$(1/2)^5$	0	0,03125
			F_C = 0,06250		

Table 9. Calculation of inbreeding coefficient for individual X.
Tabela 9. Kalkulacija koeficijenta odgoja u srodstvu za individuu X

Common ascendant Zajednički predak	Paternal line Očinska linija	Maternal line Majčinska linija	n + n' + 1	F_A	Contribution F_X-u Doprinos F_X-u
D	C	B	$(1 / 2)^3$	0,25	0,1562500
S	H – D – C	B – F – K	$(1 / 2)^7$	0	0,0078125
			F_X = 0,1640625		

F_X = 0,1640625 × 100 = 16,40625

In the above example all elements for calculation of complete formula and relationship coefficient have been taken into consideration, i.e..

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

For **B** and **C** common ascendants are **S** and **D**. Therefore we get the following values:

$S = (1 / 2)^6$; $D = (1 / 2)^2$; $F_D = 0,25$; $F_B = 0,03125$ and **$F_C = 0,0625$**, thus

$R_{BC} = \Sigma\ (1 / 2)^6 + [\ (1 / 2)^2\ (1 + 0,25)] / \sqrt{}\ (1 + 0,03125)\ (1 + 0,0625) =$ 0,3137.

When relationship coefficient formula is applied, i.e. in case when inbreeding coefficient is calculated prior to calculation of relationship coefficient, we get the same result. In that case:

$$\mathbf{R_{BC} = 2F_X / \sqrt{}\ (1 + F_B)(1 + F_{C)} = 2\times\ 0,1640625 / \sqrt{}\ (1 + 0,03125)(1 + 0,0625) = 0,3137.}$$

The above examples indicate that value of relationship coefficient could be the same in spite the fact it was generated from different relationships. Therefore, Table 10 shows aggregate value of relationships that is equal to values of the relationship inbreeding coefficient.

Correlation between individuals lacking any common relationships is **0**. Relationship coefficient that indicates correlation between breeding values for two akin individuals can have value between **0** and **100**. Then one would ask a question, how much could be discrepancy from zero point in collateral relation, **R_{BC} = 0**, in order to consider mating as inbreeding? Any consequent mating leading to homozygous state are considered as inbreeding. Consequent mating of nephews is considered the most moderate form of mating **R_{BC} = 12,5 %**.

Therefore, mating of single half-nephews (only grandfather or grandmother is common) is a limit beyond which inbreeding starts.

Table 10. Relationship and respective values of the relationship coefficient and coefficient of inbreeding
Tabela 10. Odnos i respektivne vrednosti koeficijenta odnosa i koeficijenta odgoja u srodstvu

R e l a t i o n s h i p/O d n o s	R_{BC} %	F_X %
Identical twins/Identični blizanci	100	-
Parents – offspring, brothers-sisters	50	25
Roditelji – potomci, braća-sestre		
Grandfathers, grandmothers-granddaughters, grandsons, half-brothers -half-sisters, double nephews, uncle – nephew, nephew-aunt/ Babe, dede - unuci, unuke, polubraća – polusestre, dvostruki Bratanci, ujak/stric-sestrić/bratanac, bratanac-tetka	25	12,5
Nephews / bratanci/sestrići	12,5	6,25
Single half-nephews/ jednostruki polu bratanci/sestrići	6,25	3,125

Based on the aforementioned *Johansson (1961) and Lush (1945)* consider interval between **0** and **10 %** as minimum parameter, therefore term "inbreeding" is not used for cases of mating of individuals that are considerably less related than nephews.

As it was already stated, relationship coefficient and inbreeding coefficient are average statistical values. They do not indicate to what extent certain pair of genes is homozygote or heterozygote, but still it is valuable secondary tool for assessment of average heterozygote frequency and its changes within the inbred population. But, in order to use inbreeding coefficient as exclusive measure for showing contribution to higher level of homozygote there has to be effective measure from the moment of the increase occurrence. Therefore, a statement that inbreeding coefficient in a breed has increased for **10 %** is a non sense if one fails to state that value is calculated based on certain number of generations or that it is valid for definite time period. Consequently, inbreeding is measured versus some starting, basic population when inbreeding value was **0**. For that reason, generations or their number are the best measurement for presentation of changes in level of heterozygote within the population.

Presented systems for calculation of direct relationship coefficient, relationship coefficient for collateral relatives and inbreeding coefficient are presented for all members of the given population. Those methods are subject to slight change when calculation is mechanically processed *Wright (1921), Lush (1945), Crouden (1949), Emerik–Terill (1949), Döhring –Walter (1959)* and others.

Inbreeding coefficient for gender related genes

Study on hereditary of inbreeding coefficient for gender related genes has been thoroughly studied by *Wright (1921)* and *Li (1964)*. According to their observations formulas for relationship coefficient and inbreeding coefficient are related to traits linked to diploid autosomal loci. In order to follow hereditary gender related traits it is necessary to perform certain adjustments. This primarily applies on genetic structure of gender related chromosomes at male mammals because it is haploid, thus it does not have inbreeding coefficient for male animals. If common ascendant is male animal then it is considered that $\mathbf{F_A = 0}$. This, in fact means that constitution of the male is entirely defined by the constitution of his mother, i.e., gender related genes of spermatozoid produced by sexually mature male are identical to those in mothers egg. For that reason when tracing the chain path for calculation of inbreeding for gender related genes one male animal in that chain can be disregarded, and just number of female animals should be counted ($\mathbf{n_0}$). Therefore, the formula is:

$$\mathbf{F = \Sigma\ (1 / 2)^{n}{}_{0}\ (1 + F_A).}$$

In order to implement this formula, it is necessary to introduce the following rule: if for calculation of gender related traits there are two or more male animals in succession down the descendants line along chain junction than it can not any longer be considered chain junction (the second male in the chain received gender related traits from another female animal – mother, and not from the one whose path is followed). Thus, correlation **father – son = 0** for gender related genes, so one chain junction breaks. See example of calculation in Figure 22.

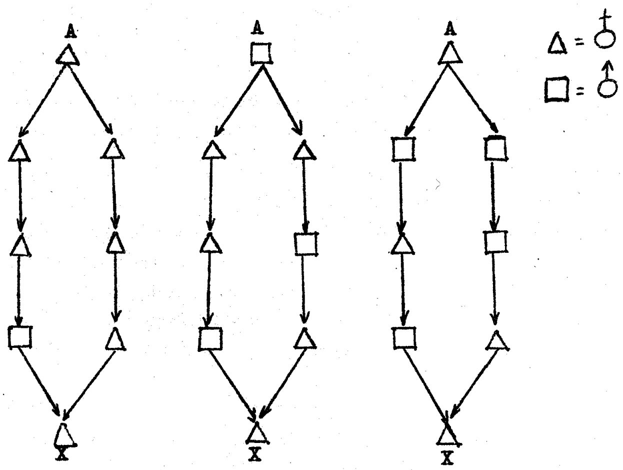


Figure 22. Inbreeding coefficient for gender related genes
Slika 22. Koeficijent odgoja u srodstvu za polno vezane gene

In case of diploid autosomal locus the value would be different from the one shown in Figure 22, and would be calculated according to the following formula: $\mathbf{F_X = \Sigma\ (1 / 2)^{n+n'+1}\ (1 + F_A)}$ and for the all three cases it would be : $\mathbf{F_X = \Sigma\ (n\ 1 / 2)^{3+3+1}\ (1 + F_A)}$.

Drawings and calculations taken over from *Li* (1964).

Changes in gene frequency as a consequence of inbreeding

Inbreeding has an impact onto decrease of heterozygote frequency, i.e. increase of homozygote classes. Taking that in a pan-mixture population lines are created and within them routine inbreeding is being applied then zygote frequency in overall population will be changed. If there are to alleles then the change in zygote frequency will look as follows:

Genotype Genotip	frequencies in basic population frekvencije u osnovnoj populaciji	frequency in inbred population frekvencije u populaciji odgojenoj u srodstvu
AA	$\mathbf{q^2}$	$\mathbf{q^2 + pqF}$
Aa	**2pq**	**2pq – 2pqF**
aa	$\mathbf{q^2}$	$\mathbf{q^2 + pqF}$

The same will happen on locus with multiple allele. **F re**presents inbred animals.

Reduction of heterozygous state, as seen, is related only to homozygote of the basic population. In case that within a population inbreeding coefficient is **25 %,** then ¼ of heterozygote locus in basic generation will become homozygote. For instance, if there were 1.000 heterozygote loci within the population then 750 genes will be heterozygote even after one generation mating of brothers and sisters.

Impact of inbreeding

It is generally known fact that inbred animals demonstrate decrease of all traits in living performance. Therefore inbreeding, as mating system in process of domestic animals breeding, in our country and in the world is unwillingly accepted as a breeding procedure for improvement of certain traits. Nevertheless, inbreeding is necessary for *d i v i s o n* of genes and possibility to get steady combinations. *Wright (1921)* holds that through selection inbreeding method enables appearance of rare, plausible, recessive traits or to eliminates extremely unfavourable recessive traits.

There are many texts in literature describing impact of inbreeding, including not only cattle, pigs and other bovine or small domestic animals, but also lab animals. Some authors have established a reduction of productive traits for each percentage of increase in inbreeding, and determined certain regression equation. Some other authors, on the other hand, praise implementation of inbreeding system and take that genetic share in regression of productive and other traits can be prevented through application of inbreeding, since this process increases homozygous state or genetic purity. These authors regard this method as the one which allows a breeder to select better genetic material from poorer one. *Rice et al. (1957)* believe that inbreeding has to find right place in a process of parenting pairs production selection, as supporting instrument. Such parenting pairs could be used for production of usable or commercial cross breeds, when cross breeding representatives of two breeds or two lines within a single breed. This method is particularly implemented in poultry farming and to certain extent in pig breeding.

Animals that have good reaction on inbreeding should be homozygote for wanted genes and to have superior value as sires for the following reasons:

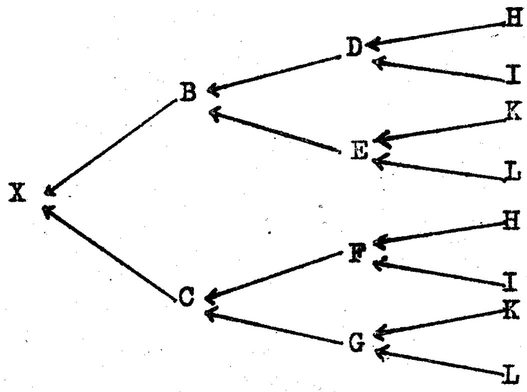
1. Their homozygous state means increased possibility for their germinal cells to be more uniform in comparison to the animals that are unrelated. Therefore their descendants will be more standardized.
2. As wanted genes are usually predominant, the good inbred sire are over-sexed, have great individual virility and they can transmit their main characteristics onto descendants. Inbreeding is the only known

method for increase of the virility. This means that inbreeding, as system, only allows for common preservation of wanted genetic combinations, which are otherwise rapidly scattered at animals that are not inbred.

When implementing the inbreeding one of the inbreeding systems can be applied – mating of brothers and sisters, half-brothers with half-sisters (if implemented through generations then it is called ***regular*** *mating system)*, mating of parents with children, grandparents with grandchildren (***irregular*** *system)*, etc. It has not been established yet which is the best inbreeding method. In practice quality of available mating animals defines type of mating. This is much better than to implement a plan that is developed in advance not taking the quality of animals into consideration. In this way optimum level of inbreeding can be modified and be more flexible system. In this fashion inbreeding can be accelerated, if it is implemented on the animals whose genetic value has been tested, or slowed down if animals are untested W*inters* (1961).

«*Linear breeding*« according to *Rice et al. (1957)*, is the most frequently used breeding method in cattle breeding. The aim of this breeding is to direct relationship towards preferred ascendant within a single breed, usually male animal. This is because the sire gives more descendants than dams, and there is possibility to be better assessed based on their descendants, which furthermore leads to establishment of the high breeding quality. Application of inbreeding is based on the fact that good and eminent fathers are rarity. Within average, slowly reproducing species, such as cattle, where usually one, two or more sires are used for propagation, coming across just one such sire during our life and work can be considered satisfactory. Therefore, when such good quality sire is found, then every effort should be made to preserve his influence, and the only way to do that is linear breeding. Otherwise, daughters and granddaughters of this sire will have in their genealogy not related sires, meaning that grandchildren will have only **25%** of this sire genes, great-grandchildren **12,5%** etc.

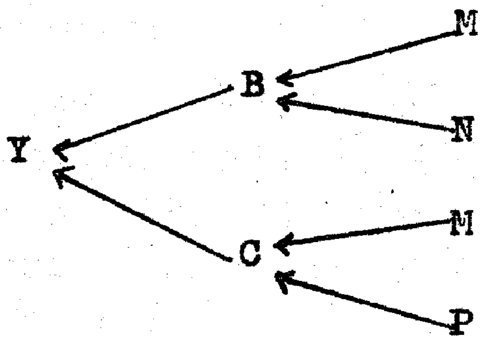
Figures 23, 24, 25 and 26 show what is and what is not a linear breeding.



F_X = 12,5 %

25 % « blood « from H
25 % « blood « from I
25 % « blood « from K
25 % « blood « from L

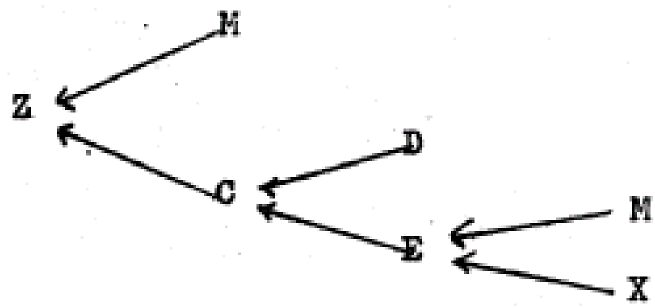
Figure 23. Not linear breeding according to *Rice et al. (1957*)
Slika 23. Ne-linijski odgoj prema *Rice et al. (1957*)



F_Y = 12,5 %

50 % « blood « from M
25 % « blood « from N
25 % « blood « from P

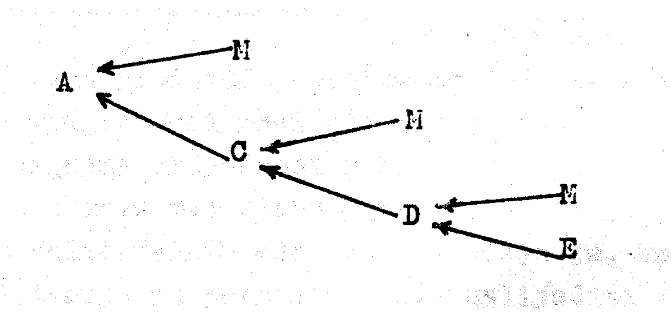
Figure 24. Linear breeding on M according to *Rice et al. (1957*)
Slika 24. Linijski odgoj na M prema *Rice et al. (1957)*



F_Z = 12,5 %

62,5 % « blood « from M
25,0 % « blood « from D
12,5 % « blood « from X

Figure 25. More intense linear breeding on M. according to *Rice et al. (1957*)
Slika 25. Intenzivniji linijski odgoj na M prema *Rice et al. (1957)*



FA = 37,5 %

87,5 % « blood « from M

Figure 26. Extremely intense linear breeding on M according to *Rice et al. (1957*)
Slika 26. Izrazito intenzivni linijski odgoj na M prema *Rice et al. (1957)*

When a sire perishes then level of relationship after him depends on his closest relatives. Mating of these animals relationship and inbreeding on the sire in the following generation can persist, but can never increase.

From the all above said it can be seen that inbreeding, as a method, can be applied, with precise selection of characteristics, followed by performance and pro-gene tests, where the results will be carefully collected, both in terms of the type and production characteristics.

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

R. Telalbašić, M. Baban, A. Rahmanović

Rezime

Cilj ovog rada je predstavljanje naučnoj i stručnoj javnosti oblike odgoja u srodstvu koji su u uobičajeni i koji se sprovode sa različitim vrstama domaćih životinja sa ciljem povećanja populacije sa odličnim proizvodnim kapacitetima. Na taj način praćenje 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 koeficijen odgoja u srodstvu.

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