IMPORTANT FACTORS IN THE SUCCESSFUL SHEEP BREEDING

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Abstract: Qualitative traits are determined by one or more hereditary factors, and the influence of the environment on their variability is very small. In the case of traits whose hereditary basis is the result of the action of several genes, a qualitative form of inheritance also occurs. On that occasion, one or several genes appear with very clear effects, while the influence of other genes is insignificant. Breeding and selection of sheep depending on the nature of gene interaction, quantitative traits are inherited according to the type of additive, dominant and epistatic principles. Traditional methods of sheep breeding are increasingly complemented by modern selection methods-DNA analyses, in order to detect genes that influence the expression of certain production traits, or are located in the genome near the place responsible for a given trait. We will briefly discuss these problems.

Key words: sheep, breeding, traits, gene

Introduction

In sheep breeding, important traits such as: body weight, growth, fertility, milk yield, fleece mass, and others, which we call quantitative or polymer traits, can be accurately measured and expressed in kilograms or some other absolute or relative indicators. However, there are also traits that are not of immediate economic importance and cannot all be accurately represented by a measuring scale (color, horniness, form, etc.), so we call them qualitative traits.

Quantitative properties are characterized by high variability, forming a continuous variation curve. The reason for this phenomenon lies in the fact that the trait is the result of the action of not only one, but several or more pairs of genes, where intermediate inheritance occurs. This means that the magnitude of the trait in the offspring will be close to the average of that trait in the parents. In addition, all quantitative traits are strongly influenced by external factors (Moroz, 1992, Erohin, 2004, Petrović and Pantelić, 2015). Under the influence of many non-allelic genes, quantitative traits in the F1 generation have an intermediate manifestation, after which there is a complex separation in the F2 and subsequent generations.

Sheep productive traits are determined by hereditary factors, and the influence of the environment.

In the case of traits whose hereditary basis is the result of the action of several genes, a qualitative form of inheritance also occurs. On that occasion, one or several genes appear with very clear effects, while the influence of other genes is insignificant. Breeding sheep depends on many factors that need to be taken into consideration.

Factors affecting sheep farming

Traditional methods of sheep breeding rely on selection. Modern times bring new knowledge and selection are increasingly complemented by modern DNA analyses, in order to detect genes that influence the expression of certain production traits, or are located in the genome near the place responsible for a given trait (Carillier et al., 2013, 2015).

Starting from the reality that quantitative traits are determined by many genes and that various systems of the organism participate in their definitive formation, such as in milk production (digestive system, cardiovascular system, endocrine system), it is very difficult, or rather impossible, to distinguish the influence of individual genes on this or that system. Therefore, the inheritance of quantitative traits is determined by statistical methods of population genetics, based on a comparative analysis of the variability of a certain trait in the population (Petrović, 2000). We will consider, on one example, the complexity of the formation of the body mass of a young animal up to the age of three months.
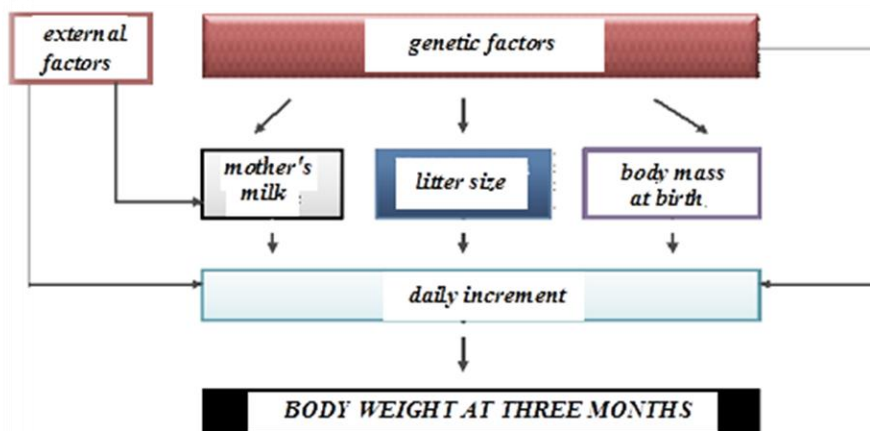

Figure 1. Influence of various factors on the formation of body weight

Depending on the nature of gene interaction, quantitative traits are inherited according to the type of additive, dominant and epistatic principles. According to Petrović (2000), in practical selection work we are mostly dealing with additive inheritance of traits, more precisely with additive genotype, which means the totality of genes of cumulative effect. If the presence of such genes in the individual's genotype is greater, then, provided that they increase productivity, the value of that head will also be greater.

Quantitative traits of sheep are characterized by high variability. There are practically no two identical individuals, and even identical twins do not have the same phenotypic values (Petrović, 2000, Caro Petrović, 2014). It is, therefore, a phenotypic manifestation of a trait, the variation of which is largely influenced by environmental factors (Petrović et al., 2013,

2015). According to the mentioned factors, it follows that the phenotypic variability, which we can practically measure, consists of:
- variability caused by the genetic characteristics of the animal (genetic component)
- variability caused by the conditions of the external environment (middle component).
So, for example, if we present a certain trait, such as, say, milk yield, graphically, by including a larger number of individuals (1000 heads), we get a bell-shaped line, the so-called normal distribution or Gaussian curve (Figure 2).
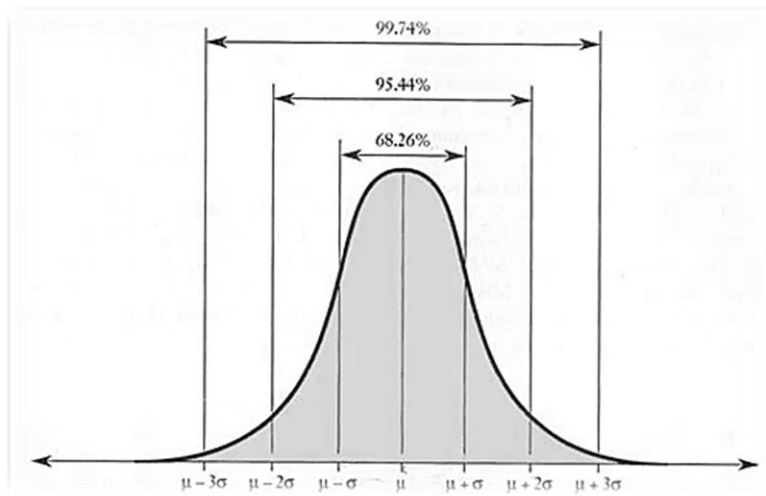

Figure 2. Distribution of milk yield of lactating sheep

The normal distribution, as seen in Figure 13, has a symmetrical bell shape and about 2/3 or 68% of the measurements are within one standard deviation from the mean . Close to 95% of the measurement, ie milk yield in this case, is within two standard deviations, while 99% of the value of the observed trait will be concentrated within three standard deviations.

In the selection, the fact that the largest number of individuals is around the mean value for quantitative traits, while only a smaller number are below (minus variants) and above the mean value (plus variants) is significant. In the given example of milk yield of cows, we see that the superior heads are located to the right of the average value, but that their frequency, i.e. their number, decreases with increasing milk yield. This shows that the highest concentration of genes responsible for high production is in a small number of superior sheep, which is of great importance when designing practical breeding programs and determining selection criteria.

Qualitative traits are determined by one or more hereditary factors, and the influence of the environment on their variability is very small.

In the case of traits whose hereditary basis is the result of the action of several genes, a qualitative form of inheritance also occurs. On that occasion, one or several genes appear with very clear effects, while the influence of other genes is insignificant. The most important characteristics from this group are the color of the skin, wool, horniness and silence, size and shape of the auricle, etc.) Also, degenerative phenomena caused by lethal and semi-lethal genes are also inherited by this mechanism. Phenotypes of qualitative traits are clearly different from each other and can be grouped by classes. Their variability is intermittent or discontinuous.

Progress in sheep selection

In the last few decades, progress has been made in the selection of sheep, and the use of genetic markers has made it possible to discover the genes responsible for the manifestation of significant properties or to determine their approximate location in the genome. So, genetic markers are not genes that determine production or other properties, but indicate a specific location in the genome where those genes are potentially located. In addition, genes responsible for some of the economically important traits of sheep and goats have been identified in recent years (Kijas et al., 2012, Zhang et al., 2013). Since the eighth decade of the 20th century, with the development of molecular genetics methods, sheep breeding has been one of the first to meet modern selection procedures. All genetic markers known at the time were used experimentally and in practice. The use of microsatellites in the selection of sheep and goats had a special effect, with the aim of characterizing certain breeds and determining their genetic distance and diversity. These researches are still relevant today (Arora et al., 2011; Zinoveva et al., 2015; Caro Petrovic et al.,2021).

Very interesting research in Tuvan sheep was carried out by Beketov et al (2022) using 11 microsatellite markers (Figure 3).
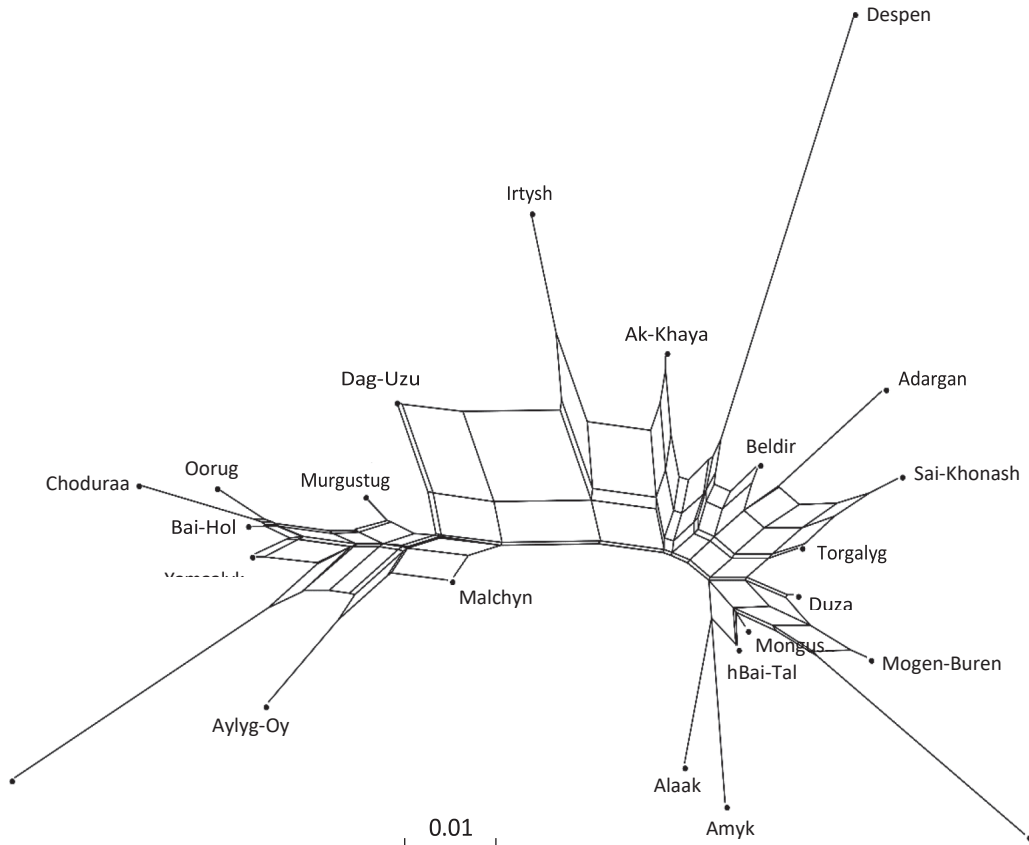

Figure 3. Neighbor-net dendrogram of relationships between the studied populations of Tuvan short fat-tailed breed sheep con- structed on the basis of the F_{ST} pairwise genetic distance matrix (Beketov et al., 2022).

The data obtained by the authors show that this autochthonous race is currently represented by two main types (mountain and steppe), as well as numerous local intermediate populations. Regardless of the fact that the diversity of alleles was determined, a significant lack of heterozygotes (from 15.3 to 35.6%) was detected in all the studied populations. It was also established that interpopulation differences in the group of Tuvan sheep of the steppe type (F_{ST} = 0.013–0.153, Jostov D = 0.029–0.461) were more pronounced than in the group of Tuvan sheep of the mountain type (F_{ST} = 0.01– 0.071, Jostov D = 0.029– 0.247). The authors believe that adaptation to different natural and climatic conditions, including the typological composition and productivity of pastures on the territory of Tuva, is one of the possible reasons for the heterogeneous differentiation of the Tuvan short-tailed sheep population structure.

The last decade, thousands of SNPs have been discovered for which the exact position in the genome is known, as well as the consequence of the nucleotide base change. For example, some research has shown (Figure 31) that sheep with a heavier fleece in a certain SNP have adenine (A) base, while animals with lighter fleece in the same SNP have a guanine (G) base.

The application of genomic selection in sheep breeding is gaining momentum. Among the leading countries are Australia, New Zealand, Russia, China, more precisely the countries with the most developed sheep farming. When it comes to European countries, France stands out the most, especially with the Lacon dairy breed.

Various researches were applied and interesting ones were obtained. Factor-2 (MEF2B) which has a major impact on meat quality (Zhang et al., 2013). The MEF2B gene encodes a MEF2 family protein. In order to improve meat production, it was determined that the interaction of proteins from the MEF2 family with the promoter of the sheep myostatin gene has a stimulating effect on the expression of myostatin. Myostatin is a protein that limits muscle growth, and if its mutation occurs, the effect on sheep meat production changes. (Chen et al., 2015).

Conclusion

In addition to traditional selection methods, modern genome detection techniques have been increasingly developed in recent decades. Thus, the essence of the genotype is delved deeper and deeper, which enables the study of all parameters necessary for determining the value of individuals and groups of sheep populations. This will increase the selection effect and contribute to faster genetic progress, which is the goal of sheep breeding.

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