## Topic 2: Genetic value of Animal
## Lecture

Today's topic will focus on the area of estimating the genetic value of various characteristics and features of the quantitative character of livestock. The lecture is part of module number 3 – Animal breeding, which is part of the ISAGREED project. This presentation was supported by the Erasmus plus KA2 Partnership grant for cooperation entitled: Innovation of the structure and content of study programs in the field of management of animal genetic and food resources using digitalization.

The genetic value of an animal represents the genetic potential of a particular trait that the animal can pass on to its offspring (usually associated with quantitative traits). We don't really know the genetic value of an individual. We only estimate it in the form of the breeding value of a particular trait. Estimating the genetic value (breeding value) is a key element in livestock breeding. It allows breeders to identify and select individuals that have the greatest potential to improve certain traits within the entire population. In the breeding process itself, the estimation of the breeding values of livestock occupies a central and irreplaceable place.

Estimation of breeding values (knowledge of the genetic quality of animals) is now carried out on the basis of two basic approaches. The first (classical) approach is an estimate based on several phenotypic manifestations of individual animal characteristics over a longer period of time (usually related to the length of the generation interval of a particular species and breed of livestock). Knowledge of the pedigree information of individual animals also plays an important role in this approach.

The second approach is to estimate the breeding value based on molecular-genetic information obtained during the so-called genotyping of animals. Currently, genomic information is most widely used at the level of its different abundance and density. Both of these approaches can be used separately or combined into a single system for estimating the genetic quality of animals.

The importance of knowing the breeding value of an individual is in the subsequent improvement of several productive but also non-productive characteristics of animals in the next generation (production of milk, meat, eggs, wool, sports performance). An important element is also the current genetic improvement of health, reproductive characteristics, fertility, disease resistance, longevity, viability. The final goal is in fact the economic efficiency of individual livestock farms (reduction of costs, increase of economic revenues from the production or sale of breeding animals). For this reason, individual breed values enter into different types of selection indices (global-aggregate selection indices, or selection indices specific to a given group of traits, exterior, fertility, quality of animal products).

In the past, important methods were based mainly on the knowledge of pedigree information and information about the performance (phenotype) of individual animals in a wider time horizon. In the past, mother-daughter methods and especially the peer method (CC test) played an important role. Gradually, with the advent of computer technology, the BLUP (Best Linear Unbiased Prediction) method began to be used very intensively. It was an advanced statistical method that combines in various forms and depths the pedigree information and information on the performance of animals needed to estimate their breeding value.

Recently, new (modern) genomic approaches have emerged in the estimation of breed values, which are carried out either in the form of so-called direct (pure) genomic breed values, or as part (extension) of existing (traditional) approaches based on the BLUP method in the form of several forms of the GBLUP method (Genomic BLUP).

Best Linear Prediction . Linear model with mixed effects. Simultaneous use of fixed and random effects. Practical use even for unbalanced data sets. Any number of environmental effects. BLUP is the basis of the methods known as the Animal model. In 1999, STN (Slovak

Technical Norm) 466114-1 Estimation of breeding values of cattle milk yield indicators, Part 1: BLUP method, was published in the Slovak Republic.

Linear mixed models in the form of BLUP are the basis of traditional estimation of livestock breeding values (BLUP models). BLUP - sire model (paternal model) - estimation of the breeding values of only some individuals in the population (usually males). BLUP - animal model (individual model) - estimation of the breeding values of all individuals in the population. If we estimate breed values for one trait, these are so-called single-trait models, if for several traits at the same time, these are multi-traits models using correlation relationships between traits.

An important condition for the use of the BLUP method is the initial knowledge of the basic genetic parameters necessary for the estimation of the breeding values themselves. The BLUP method is used in many modifications. Probably the most well-known use of this method is the BLUP-Animal model (additive genetic model of breeding value estimation). The basic principle of using the BLUP Animal model is the knowledge of four basic groups of information about animals: pedigree information, own performance, offspring performance and performance of other relatives in the collateral row. Knowing all groups of information is time-consuming, but it brings an extremely reliable estimate of breeding values. The advantage of this method is that the absence of a certain group of information does not have a limiting effect on the estimate itself (but the reliability of the estimate usually decreases).

The BLUP method (Best Linear Unbiased Prediction) is a solution to a large system of equations where the individual breeding values of animals are unknown, as well as the levels of all effects affecting the evaluated trait. The best prediction means the best of all possible linear unbiased estimates (the correlation between true and estimated breed values is maximized, with this method the smallest residual variance of the trait is achieved). Linear means that the measured phenotypic expression of the trait is distributed in a linear combination of all monitored effects. An unbiased (unbiased) prediction is the fact that the average value of the calculated estimated breeding values is equal to the mean value of the actual (true) genetic values. The prediction is because it is an estimate of random effects (an estimate of breed value is a typical estimate of a random, genetic effect). The BLUP method is very closely related to the method of estimating the main components of variance in these models.

The above model (without taking into account kinship) estimates the individual levels of unknown fixed effects b and unknown random effects (breed values) a. For solving large problems (large numbers of animals, large numbers of equations), it is usually not possible to use the previous procedure using the inversion of the coefficient matrix. Several iterative procedures and methods have been created that solve the problem in practice quite accurately.

When using a kinship model, kinship relationships are expressed using a kinship matrix (A), which is actually a matrix of additive genetic similarity. The correctness and truthfulness of pedigree information plays a very important role in this case of using the Animal model.

There are several methods of taking genomic information into account when estimating breed values. Most of these methods are created on the basis of or modification of the BLUP method. In general, all these methods can be divided into two groups: the first uses multi-step approaches when considering genomic information, and the second group uses one-step approaches. Methods based on a one-step approach, which are intensively verified and applied, are proving to be very promising.

The essence of the one-step approach: the basic principle is the modification of the additive genetic similarity matrix by the genomic similarity matrix (the modification consists of inversion of the additive genetic similarity matrix using the genomic affinity matrix). Apart from taking into account the genomic matrix of similarity, nothing changes in the method of estimating breed values. The advantage is that genomically modified breed values are estimated even for animals that are not genotyped. The one-step procedure is quite computationally demanding in the case of a large number of genotyped animals (however, the current performance of computer technology partially eliminates this problem)

There are features and characteristics of livestock that are significantly affected by the maternal effect. Such models are called models with a maternal effect. This is mainly an estimate of the breed values of traits, where the mother has a relatively significant influence on her offspring during pregnancy, which is typical only for female mammals. Models with maternal effects are typical in estimating breed values, fertility indicators and calving ease traits.

Estimating breed values based on nonlinear models is not so typical, but there are indicators where it is more advantageous to use nonlinear approaches. Most often, nonlinear models evaluate some indirect utility properties. Nonlinear systems for evaluating the growth and development of livestock are known with direct performance properties. The growth of animals generally behaves in a non-linear manner, especially if we observe growth over a longer period of time. In a short period of time, the growth of animals, as a rule, behaves linearly. Within the indirect performance characteristics of livestock, the evaluation of longevity and survivability of animals has recently become increasingly important in modern breeding. In fact, longevity appears to be a summary indicator that, in its essence, expresses all the characteristics of animals. As an example, we can mention the longevity of cows in reproduction and their lifelong performance, which is currently coming to the forefront of selection criteria and has a very close relationship with the economic efficiency of milk and meat production.