## 5. Breeding value - the genetic foundation of an individual

Hello everyone. I welcome you to another lecture from the Animal Breeding module. Today we will talk about breeding value. The breeding value represents an estimate of the genetic merit of an individual and represents one of the basic genetic parameters used in livestock breeding. As was already said in previous lectures, the breeding of farm animals is based on the estimation of the genetic merit of the individual, which we obtain using the breeding value.

The aim of breeding process is the breeder's profit, which is obtained through the animal's performance. The performance is affected by many factors, both environmental - which includes, for example, the external and internal environment, nutrition, and the breeder, but mainly by the individual's genetic, which, depending on the monitored trait, affects the given performance from 5 - 10%.

The individual factors contribute to the overall performance in the following proportion: The influence of the breeder represents approximately 60% of the total variance of performance, random environmental influences from 30% and the genetic merit of the individual on average about 10%. Although the genetic merit represents a relatively small part of the total variance, it results in significant genetic progress and, consequently, better economics for the breeder.

Breeding value has several definitions. The breeding value is always presented as an individual's deviation from the population mean. The definitions are based on the time concept of the possibility of determining the genetic merit of an individual. The first definition is based on testing of heredity, when the genetic value of an individual, mainly a sire, was determined based on the progeny performance. Another concept is based on understanding breeding value as the average effect of all genes that the progeny received from the sire or dam. The last definition is already based on a modern view of breeding value, when thanks to advanced computational and molecular genetic procedures, we can determine an individual's genetic merit based on its own performance. As mentioned in the previous slide, the Breeding Value always represents the additive genetic value of an individual expressed as a deviation from the population mean.

Now, we will imagine the essence of breeding value. Here we will start from classical genetic theory, where we consider that the phenotypic value can be expressed as a function of genotype and environment. Further, genetic and environmental effects are expressed as a deviation from the population mean. The total genetic value can be divided into the additive genetic effect, the effect of dominance and effect of interaction, or epistasis. And since minor effects of dominance and epistasis are expected in purebred breeding, it is possible to express the genetic value of an individual only by the additive effect of genes. Breeding values, which represent an estimate of an individual's genetic merit, are therefore based on an estimation of the average additive effect of genes.

We will explain why the breeding value is twice the deviation of the progeny performance from the population mean during random mating. Let's have a sire with the homozygous dominant genotype. This sire will be mated to a group of randomly selected dams in which we expect all genotypes to be represented. As we know, this sire can produce only one type of gametes, and that only with a dominant allele; on the contrary, a group of dams produces all kinds of gametes, in this case, gametes with a dominant and a recessive allele. If the gametes fuse, all genotypes will be represent in the offspring population. Because the mothers were selected randomly, we expect the effect of the mother on offspring performance to be zero. The effect of offspring deviation from the population mean is attributed to the sire. But as it is clear from the picture, the sire contributes only half of its genotype to the offspring - only one allele. To get the whole genetic effect of the sire, we must multiply the deviation by two. Hence, double the progeny performance deviation from the population mean during random mating.

As mentioned, breeding value is defined as the average additive effect of an individual's genes. Since the breeding value includes only the additive effect of genes, it is possible to use it to estimate the genetic merit of the offspring of selected parents and vice versa. It is because the average genetic value of the parents corresponds to the average genetic value of their offspring. Conversely, we can also estimate the parent's average genetic value from the offspring's average genetic value: each offspring receives 50% of its genes from each parent.

The conclusions from the previous slide can also be used to estimation the average progeny performance., with adding the average breeding values of the sire and dam to the population mean. But this formula is only valid for a large group of offspring, not for a single offspring.

And this is because, in the case of one offspring, it is also necessary to put the so-called "Mendelian sampling" in the formula.

The effect of Mendelian sampling will be introduced here. Consider two mating individuals. Both individuals produce two types of gametes.

Suppose four full-sibs are born, for example, in one litter. According to the classical approach, we expect the average relatedness of these offspring to be equal to the value 0.5. However, if we look at the picture, we will find that offspring 1 and 2 have identical genetic merit, while individuals 1 and 4, on the other hand, are genetically unrelated. If we averaged the relatedness across all full-sibs, we would get an expected value of 0.5, as noted. Mendelian sampling, therefore, represents the randomness of which type of gametes will receive a new offspring.

Therefore, we cannot determine one offspring's expected performance thanks to Mendelian sampling. But for a large group of offspring, the effect of Mendelian sampling cancels out because, on average, the offspring match the expected values. Therefore, we can predict the performance with relatively high reliability for a large progeny group.

Breeding value is always only an estimate or a prediction. it is because we are not yet able to determine the exact genetic merit of an individual and the effect of all genes of an individual. And this estimate is expressed as the individual's deviation from the population average - directly as the individual's deviation by own performance or as twice the deviation of the average progeny performance during random mating, the so-called test mating. This test mating was mainly used for performance that we cannot directly measure for individuals - for example, the prediction of the genetic merit for the milk yield of sires in dairy cattle. The only way to obtain exact values of an individual's genetic merit would be if the monitored trait has a coefficient of heritability equal to 1 or if the individual testing was based on an infinitely large group of progeny. Unfortunately, both conditions for quantitative traits are unrealistic in practical breeding.

Estimation of breeding value is possible based on these sources of information and their mutual combination: performance of the ancestor, own performance, performance of full-sibs or half-sibs, and progeny performance.

An estimate of breeding value is obtained using the following formula. The breeding value is expressed as an individual's deviation from the population mean. It is a regressed relationship, represented by the value of the regression coefficient „b“. This regression coefficient takes on a value based on the performance source, with which we estimate the individual's genetic merit. The table also shows the relationships for obtaining individual values of the regression coefficient „b“.

Since the breeding value is an estimate, it is necessary to quantify the accuracy or reliability of this breeding value. The accuracy of the breeding value, is presented by "r", represents the relationship (correlation) between the estimated breeding value and the true genetic value of the individual. The reliability of the breeding value, which is presented as "r2", is expressed by the coefficient of determination. The reliability describes how many per cent of the true genetic value of the individual is explained by the estimated breeding value.

We will show the explanation of the term accuracy in the following figures. Let's have a group of, for example, 1000 individuals. Every individual is presented as a point in the graph. On the y-axis, we plotted the true genetic merit of the individual. On the x-axis we have the predicted breeding value. Let's assume the accuracy of the estimation of the breeding value for the given population is one per cent, which is a value of 0.01. If we were to select the top 10% of individuals based on breeding value, we would choose only the four individuals with the best genetic merit. In this graph, these individuals are marked in green. Individuals marked in black are individuals that have been estimated to have a high breeding value, but their actual genetic merit is average or low. On the contrary, individuals marked in red are individuals with the best genetic merit but with an estimated average or low breeding value. The graph shows that if the accuracy value of the breeding value is low, the predicted breeding value does not correspond very well to the genetic merit of the individual.

If the accuracy of the breeding value is equal to 0.5, we would already have selected a more significant proportion of individuals with the best genetic merit.

And with an accuracy value equal of 0.8, we are already selecting most of the correct individuals based on the breeding value prediction. These graphs, therefore, show a significant influence of the breeding value accuracy parameter on the selection response or genetic gain. If, based on breeding value, we wrongly select individuals with below-average genetic makeup, the response to selection cannot reach high values.

This lecture presented the concept of breeding value and its influence on breeding programs. Thank you for your attention, and I look forward to seeing you in the following video.