2. Quantitative traits and path way coefficients

Hello everyone, I welcome you to another lecture from the Animal Breeding module, the topic of which is:Quantitative traits and path way coefficients. In the lecture, we will introduce quantitative traits and the descriptions of path way coefficients.

If we are talking about the performance of an individual, we are talking about the so-called phenotype. The phenotype is a set of traits observed on individual and is a function of genotype and environment.It is therefore a set of all the traits of an individual that are of interest to us from the point of view of animal genetics.

If we use the basic definition of the phenotype. The phenotype is always defined as a function of the genotype and the environment. We can define the phenotype as the sum of the level of the genotype, the environment and the relationship or interaction between the genotype and the environment.

If we convert this relationship into phenotypic variance, then phenotypic variance is influenced by genetic variance, environmental variance and covariance between genotype and environment. Genetic variance can be divided into variability influenced by the additive component of the genotype, variance influenced by the dominance component and variance influenced by the component of gene interactions or epistasis. Environmental variance can be divided into variance influenced by the permanent or temporary environment.

This slide will explain the terms additivity, dominance and interaction. The concept of additivity can be explained as follows. Each gene has some effect.It is generally assumed that the dominant allele shows a higher performance value (e.g. 5 kg on average) than the recessive allele (e.g. 2 kg on average). The genetic value of the given individual for which we are considering the given genotype, affected only by the additivity effect, is 38 Kg. We obtained this value by summing the individual effects of individual genes. Conversely, dominance represents the relationship of two genes or two allels at one locus. For example: If it exists, let's call it over-dominance. That is, if the alleles at one locus are heterozygous, then is an increase in productivity by, for example, 10 kg. The genetic value of the given genotype affected only by the dominance effect (D) is, therefore, 20 kg since it contains only two gene pairs in the heterozygous state. And interaction, or epistasis, represents the relationship between two genes at different loci. Suppose there is a relationship between the dominant allele A and the dominant allele B, and this relationship increases performance by 10 kg. Therefore, in the genotype we are considering, the interaction effect will increase productivity or performance by 20 kg because the genotype contains one dominant allele A and two dominant alleles B. By summing the effects of additivity, and dominance and the interaction, we get the total genetic value, which is 78 kg for the genotype we are considering.

From the point of view of animal breeding, the transfer of genetic information from individuals to subsequent generations is important. This transmission takes place using sex cells or gametes. As we already know, gametes carry half the number of chromosomes and there are so-called "haploid". An individual with the genotype listed here has these four types of gametes. For each gamete, there is an additive effect of genes because each gamete contains that individual's genes. The effect of dominance and interaction by forming gametes disappears because the gametes are haploid; therefore, there can be no interactions at the locus level. In some gametes, the interaction effect also does not occur due to random segregation of alleles or chromosomes. Only half of the additive genetic effect is transfers through the gametes.

Thanks to the formation of gametes and the transmission of a genetics or rather additive genetic effect between parents and offspring, it is possible to observe the genetic similarity between related individuals, such as the already mentioned parents and offspring, but also siblings full of half, distant relatives and distant siblings. This genetic similarity can be studied thanks to the so-called path way coefficients.

The pathway coefficients define a relationship or dependence from one variable to other variable, i.e., a relationship between at least two variables. In general, we distinguish two types of patway coefficients - the first type, where another variable fully determines one variable. We professionally call this type the statistical term "regression". The second type is regarding the equal status of both variables. We professionally call this type of statistical term "correlation."

Only the following two rules are sufficient for working with pathway coefficients. Rule one: If another variable (E) lies between variables X and variable Y, the connection from variable X to variable Y consists of two sub-connections (X-E, E-Y). The pathway coefficient from variable X to variable Y is obtained as a product of partial connections. The second rule: If it is possible to find a more significant number of possible connections between two variables, the total connections - the total pathway coefficient, is equal to the sum of the single connections.

We will present the given rules here in the following case of two full-sibs. There is no relationship between the phenotype of individual X and individual Y. The only possible relationship is through the genetic merit of individuals. And that through the genetic equipment of the father and the genetic equipment of the mother. Through meiosis, everyone receives half of their parents' genetic merit. Here, we will use rule 1 of pathway coefficients: If another variable (E) lies between the variables X and Y, the connection from X to Y consists of the product of partial connections. In this case, 0.5 x 0.5. The same rule applies to the mother. And since these two individuals are full-sibs who have the same parents, we can use rule 2 of pathway coefficients: If a more possible connections can be found between two variables, X and Y, the total pathway coefficient is equal to the sum of the single connections. In this case, through the father and the mother. The genetic relationship between individuals X and Y equals the value 0.5. It is necessary to realize that single connections can be the product of partial connections.

The same is true for the following case. We will again use both pathway coefficient rules. The genetic relationship between individual X and Y is equal to 0.3125. There are two so-called genetic "paths" between individuals X and Y. One is expressed as red and the other as blue. The red "path" reaches a value of 0.5 quoters, again assuming that each offspring receives 50% of its genes from its parent, and the sub-sections path are multiplied, and the blue "path" reaches a value of 0.5 squered, according to the same rules. At the end, we add up both paths (blue and red). Thus, the genetic value between individual X and Y is equal to the value 0.3125, as already mentioned.

We proceed similarly when defining the genetic relationship between the offspring and own parents when the genetic similarity is equal to the value of one and the genetic similarity between the offspring and only one parent when the genetic similarity is similar to the value of 0.5.

We can continue with half-sibs, when the genetic similarity is equal to 0.25. Own siblings, when the genetic similarity is similar to the value 0.5 and, for example, a cousin and cousin, when the genetic similarity is equal to the value 0.125.

From the principles of pathway coefficients mentioned above, we can derive rules that are mainly used in the estimation of genetic parameters, which include, for example, coefficient of heritability. The group of animals related to each other have similar genotypes. Therefore, differences within groups of related animals are primarily conditioned by the influence of the environment. And further that different groups of related animals have different genotypes. Therefore, differences in the performance of related animals in different groups are mainly caused by differences in the additive genetic part of their gene pool.

In this lecture, the quantitative traits and the concept of pathway coefficients for determining the genetic relationships between two individuals were presented. Thank you for your attention and I look forward to seeing you in the next lecture.