Topic 1: Genetic Parameters in Animal Breeding Lecture

The topic of this lecturer is Genetic Parameters in Animal Breeding. The lecture is part of Module 3, Animal Breeding. The creation of this presentation was supported by the ERASMUS+ KA2 grant within the project ISAGREED, Innovation of content and structure of study programs in the field of management of animal genetic and food resources using digitization.

We will deal with genetic parameters, especially heritability and the principle of methods for its estimation.

Genetic parameters are statistical values that define the genetic potential and heritability of traits in a population of animals. Heritability is expressed as a population statistical parameter known as the heritability coefficient. This coefficient measures the proportion of total phenotypic variability in a trait that can be attributed to genetic variability. This proportion can range from 0 to 1.

Another genetic parameter is genetic correlations, which quantify the extent to which genes influencing one trait simultaneously affect another trait. The values of genetic correlations range from -1 to +1. Positive genetic correlations indicate that improvement in one trait will lead to improvement in another trait. Negative genetic correlations indicate a trade-off between traits, where improvement in one trait may lead to a decrease in another.

The last genetic parameter is repeatability coefficient, r, which estimates the genetic variability in repeated traits throughout an individual's lifetime.

Methods for estimating genetic parameters require knowledge of phenotypic values, which are measured production traits, and quantification of kinship relationships, which determine shared gene proportions. These relationships can be determined using pedigree data or currently using genomic data. How do we estimate them? We must use statistical methods, particularly linear models such as regression analysis, analysis of variance, covariance analysis, and correlation analysis. The goal is always to estimate the genetic and environmental components of new variance, with genetic variance further divided into 3 main components, where the additive genetic variance is of most interest.

Among the oldest methods for estimating genetic parameters is the analysis of variance using least squares method. Balanced data is advantageous for this method, but for unbalanced data, modified Henderson's methods must be used, which are included in various software packages like SAS, Harvey, etc. In practice, maximum likelihood methods (or its various REML variants) are more commonly used, as they provide the best estimates even for unbalanced data. Bayesian methods are still used in research areas.

We will describe the use of utility values in families to estimate heritability. Phenotypic variances between families and within families are always calculated. If the variance between families is low, then the variance within families is high. In this case, a high heritability value is calculated for these traits. Conversely, if the variance within families is high and the variance between families is low, then a low heritability value is estimated. This is because the variance within families, or among individuals within the family, is more influenced by environmental variance. On the other hand, the variance between families is more influenced by genetic variance. It follows the rule that the total variance of a trait in a population is caused by the variance between families, which is the same as the covariance within families, and the variance within families.

The scheme of such an experiment can be seen in the following picture. We have three families, where each family consists of a father who has many offspring with multiple mothers. Phenotypic values are measured in these offspring. We can assess the variability within offspring along with the variability between groups of related individuals according to fathers

or according to fathers and mothers simultaneously. We can group half-sibs (with 25% common genes). But we can also assess groups of full-sibs (with 50% common genes).

This model is best applied using analysis of variance. ANOVA can detect important sources, effects that contribute to differences between individuals. In our case, those will be the parents. Further, determine their contribution to the total variance. The main ways to determine this variance is to derive the sum of squares of deviations from the mean and degrees of freedom. It is important to have individuals in groups with the same degree of relatedness. For example, groups of half-siblings according to father. Or the parent-child relationship. It holds that covariance, or similarity between family members, or groups, is equal to the variance component between groups.

If we use the model of half-sibs families, then the variance between half-sibs families (paternal) is equal to the covariance between half-sibs, which is equal to a quarter of the additive genetic variance. The variance in half-sibs families is equal to the residual variance, which is generally referred to as environmental variance. The heritability is then equal to the ratio of the additive genetic variance to the total phenotypic variance, which is equal to four times the paternal variance, or the variance between half-sibs families to the total phenotypic variance.

We can see the simplified design of the experiment in this scheme. Each father has one offspring with one mother. Therefore, we evaluate the variability between offspring by groups according to fathers. Then it naturally follows that the additive genetic variance is equal to four times the paternal, sire variance. We can estimate the sire variance using analysis of variance.

This model is called the paternal model or sire model. It is a one-factor analysis of variance, where the only fixed effect in the equation is the effect of fathers. It is assumed that fathers and mothers are unrelated, randomly paired, and not affected by selection. Another assumption is that we have a balanced design. This means that p fathers are paired with n mothers, and they have 1 offspring.

In the resulting table of the new paternal model, we see 3 rows. The last row is the total phenotypic variance. The first and second rows express the estimation of variance between families and within families. The degrees of freedom df, formulas for calculating sum of squares of deviations from the mean according to the source of variability, and the calculation of the mean square, or variance, as the ratio of SS and df are expressed here. Statistics end here, and in the last column, the genetic part begins. The environmental variance is directly equal to the variance within families (residual). In the variance between families (between groups according to fathers), MSa includes genetic variance.

The variance among fathers MSa is equal to the residual variance plus n0 times the genetic variance. N0 is the weighted number of offspring per father. Because the residual variance is directly equal to the within family variance, we can directly calculate the genetic variance as the difference between MSA, i.e. paternal variance minus MSe residual variance, divided by n0.

Furthermore, we calculate the intraclass correlation coefficient rho as the ratio of genetic variance to total phenotypic variance.

The estimate of the heritability coefficient is obtained by multiplying this intraclass correlation coefficient by four. Four because we calculate genetic variance based on half-sib groups. And we know that half-siblings have a quarter genetic resemblance.

For correct interpretation of the heritability estimate results, it is necessary to calculate its standard error. Its value, as we see from the formula, depends mainly on the number of half-sib groups p and the weighted number of offspring per father.

What is the importance of estimating heritability? An estimated high heritability suggests that the phenotypic variance of a trait in the population is largely influenced by genetic variability. Breeding programs can focus on traits with high heritability and thus achieve faster genetic progress (genetic gain).

In conclusion, understanding genetic parameters is crucial for efficient animal breeding. Heritability, genetic correlations, and advancements such as GWAS and genomic selection allow targeted improvement of traits to increase productivity and profitability in animal production.