10. Genetic and environmental variation of quantitative traits in poultry

Hello. The topic of this lecture is genetic and environmental variability in quantitative traits of poultry. The lecture is part of Module 4, Precision Livestock Farming. The creation of this presentation was supported by the ERASMUS+ KA2 grant as part of the ISAGREED project, Innovation of content and structure of study programs in the field of management of animal genetic and food resources using digitization.

The difference between qualitative and quantitative traits lies in the number of genes that determine them and the influence of the environment on the development of the trait. Quantitative traits are influenced by a large number of genes with small effects (polygenes), often additive, and the expression of the trait is also influenced by the environment. The phenotypic value of a trait in an individual is therefore equal to the effect of genotypes and environmental factors. The result of this multifactorial action is the occurrence of continuous, gradual phenotypic variability in the population. All productive traits are of this type, including some polygenic diseases such as mastitis in cattle.

The phenotypic value of an individual for a specific trait is therefore equal to the sum of the effects of genotype and environmental influence, including random environments that we are not able to detect, analyze, and consider. This applies, for example, to body weight, abdominal fat, egg size, egg weight, shell thickness, fertility, hatchability, feed consumption, and others.

The relationship between genotype and phenotype, or the path from genotype to phenotype, is very complicated. In particular, the cascade of genes influencing various metabolic pathways involved in trait development, gene expression, and interactions at different levels are further influenced by developmental factors and effects of external and internal environments.

This also affects the nature of genetic variability. Genetic variability is determined by the proportions of different genotypes in the population. In the case of qualitative traits, genetic variability can be directly identified based on phenotypic variability (for Mendelian traits). For quantitative traits, statistical methods are needed to quantify genetic variability and obtain estimates of population parameters (such as mean, variance, etc.) due to the continuous variability caused by a large number of genes with additive effects and the influence of environmental differences.

Genetic variability is caused by differences in DNA sequences among individuals. Genetic differences can be caused by mutations, recombination, or other genetic processes. Genetic variability is a source of evolution and allows populations to adapt to a changing environment.
Genetic variability is important in animal breeding programs because it provides a source for selection. By selecting animals with desired traits and breeding them together, breeders can increase the frequency of desirable traits in the population. This can lead to improvements in productivity, health, and other traits that are important for animal production.

Environmental variability is divided into systematic and nonsystematic effects. Nonsystematic effects vary in direction and magnitude for each individual in an unknown manner, they cannot be corrected, they introduce "noise" (inaccuracy) into genetic estimates and predictions and increase residual error. Systematic effects act on a group of animals in the same direction and

magnitude, they can be eliminated computationally or through standardization, and they are divided into: internal effects (age, litter frequency, litter order, lactation order, sex, etc.) and external effects (management, region, barn, year, season, etc.).

Environmental variability. Environmental variability refers to differences in environmental conditions that can affect the performance of animals.

Environmental variability can have a significant impact on quantitative traits in poultry, for example, temperature and humidity can affect growth rate and feed efficiency, and other environmental factors such as lighting and stocking density can also affect poultry performance. Farmers can manage environmental variability in their flocks through appropriate housing and management practices. For example, farmers can use ventilation systems to regulate temperature and humidity, provide appropriate lighting conditions, and control stocking density to reduce stress in birds.

Most production traits in poultry are of a quantitative nature (polygenic inheritance, additive gene action, environmental influence, continuous phenotypic variability). Estimating genetic and environmental variability can be used to calculate other genetic parameters. Genetic parameters are statistical parameters such as heritability, repeatability, genetic correlation, and phenotypic correlation. Estimating genetic parameters is a statistical method used to estimate genetic parameters of traits in animals. Estimating genetic parameters is an important issue in animal breeding. Estimating additive genetic and possible non-additive genetic variations contributes to a better understanding of genetic mechanisms. Genetic parameters play a significant role in designing breeding programs and are necessary for evaluating economically important traits.

Central genetic parameter - heritability. Heritability is the proportion of phenotypic variability that is caused by genetic variability. It is a measure of how much of the trait's variability is due to genetic factors and is essentially an estimate of the genetic structure (variability) in the population. Heritability ranges from 0 to 1, with 0 meaning all variability is due to environmental factors and 1 meaning all variability is due to genetic factors (both values are unrealistic extremes!). The data source is measured trait values of individuals in the population. Heritability is estimated by comparing the phenotypic variability of a trait with the genetic variability of that trait, which is done by comparing the phenotypic variability in the population with the expected phenotypic variability based on the genetic and kinship relationships among individuals in the population.

In the table, we can see the typical range of heritability values estimated in different chicken populations. Higher values are associated with body weight or its parts, while lower values are associated with reproductive traits.

Currently, molecular data obtained from whole-genome sequencing also contribute to the estimation of genetic parameters. QTL mapping methods are actively used in chickens to identify chromosomal regions that contribute to the variability of traits related to growth, disease resistance, egg production, behavior, and metabolic parameters. However, for successful utilization of this information in breeding programs, mapping with higher resolution and better knowledge of the genetic architecture, which is the basis of QTL, is necessary.

There is a QTL database for animals called QTLdb. As of April 25, 2023, Chicken QTLdb has published 18,411 QTL/eQTL/associations. These data were obtained from 386 publications and represent 372 basic traits, 115 trait variants, and describe 39 eQTL genes.

An example of QTL region identification and candidate gene identification using whole-genome SNP for growth and feed efficiency in broilers is shown in this image. Estimation of genetic parameters and identification of QTL for feed efficiency in purebred broilers was conducted using a whole-genome association study. Broilers were genotyped using a 55 K chip SNP; Genomic heritability estimates for seven growth traits and feed efficiency traits ranged from 0.12 to 0.26; The region on chromosome 16 (2.34-2.66 Mb) was associated with BW28 and BW42 traits, and the most significant SNP in this region accounted for 7.6% of genetic variance for BW28; Chromosome 1 (91.27-92.43 Mb) was associated with feed intake, and the genes NSUN3 and EPHA6 were found in this QTL region; The most significant SNP in this region accounted for 4.4% of the genetic variance for feed intake. The most likely candidate genes for these QTL were identified as NSUN3, EPHA6, and AGK. These genes are involved in mitochondrial function and behavior regulation. The results of this case study contribute to the identification of candidate genes and variants for growth and feed efficiency in chickens.

And thank you for your attention.