## 11. Management of economic and genetic progress in a population

Today's topic will focus on the area of managing genetic and economic progress in a population. 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 Collaborative Partnership Grant - Innovating the structure and content of the curricula in the management of animal genetic and food resources using digitalization.
Genetic progress - selection response - selection efficiency - Genetic gain can be defined as the achievement of a positive outcome of a particular trait or characteristic in livestock by selection over a period of time. A positive result is understood as a genetic improvement of a given trait, its stabilisation or the creation of a new expression of the trait.
Examples of trait improvement may be an increase in milk yield (milk production) of dairy cows, or an improvement in quality traits within meat performance. An example of trait stabilisation is the stabilisation of certain external characteristics of livestock (maintenance of established breed standard parameters). An example of a new manifestation of a trait may be a new (specific) colouring of the coat of the animals (furanimals, domestic animals).
Economic progress is the expression of genetic progress (genetic gain) of one or more traits, or groups of traits, in economic (financial, monetary) form.
The achievement of genetic progress is directly dependent on the definition of breeding objectives within a given population of a particular breed of livestock. Breeding objectives comprise a set of multiple traits, characteristics and parameters that we want to achieve for a given breed over a period of time. These traits include major production traits, reproductive traits, exterior traits, longevity of the animals and other often new traits that are beginning to be evaluated for a given breed.
A prerequisite for making progress in animal breeding is knowledge of basic pedigree information and its possible verification by DNA analysis. Knowledge of the genetic quality of individual animals (estimated breeding values of individual traits) is also considered to be a very important element. On the basis of the estimated genetic quality, specific selection is made and mating of the animals takes place (mating plans), which is the basis for the creation of a new generation of offspring. The achievement of genetic progress is confirmed by the higher average genetic quality of the offspring compared to the average genetic quality of the parents.
We characterized the genetic gain at the beginning of the presentation. The selection difference is the difference in the average value of the trait of selected part of the population (group of animals) to reproduction compared to the total baseline population (group of animals). The selection criterion represents the absolute value of the trait of interest or the value of the deviation of the trait of an individual or group of animals from the mean value.
The selection intensity represents the proportion of animals culled relative to all animals in the sampling frame. Generation interval represents the average age of the parents at the birth of the offspring or progeny. Selection pressure
is, in genetic terms, the effect of selection on the frequency of a particular allele or alleles in populations of animals. Accuracy (reliability of selection) is actually the reliability of

selection, which expresses how the estimated genetic value (breeding value) of an individual resembles the actual so-called true value.
Estimation of genetic gain is a very important evaluation tool in terms of livestock breeding options. Its knowledge is important in the design, modification and control of the breeding programmes themselves. The basic (initial) equation for estimating genetic gain is very simple.
For a particular trait, it represents the heritability of the trait multiplied by the selection difference of the trait. A simple expression of the selection difference can be expressed more accurately on the basis of a normal distribution curve at a defined selection intensity and a known phenotypic standard deviation. It is in fact the standardised selection difference (the proportion of variability expressed by the standard deviation) that is an accurate representation of real selection at a particular time, in a particular group or population of animals.
In this way, we estimate the genetic gain per generation, or if we divide this genetic gain by the average generation interval, we obtain the estimated genetic gain per 1 year.
The most accurate estimate of genetic gain is to simultaneously consider all four gene transfer pathways (mother-daughter, mother-son, father-daughter, father-son) under their different intensities of selection and their different average generation intervals.
In estimation the genetic quality of animals, the accuracy of this estimation plays an important role and hence the correct consideration of important environmental factors in the estimation of breeding values.
The most important environmental factors are: the herd - the level of nutrition - the housing - the breeding technology itself. Then there are the temporal factors: generation - year - season - month - day. Age - stage - season - sex of the individual - human are also important factors. But we must not forget the very complex relationships of the interaction of a particular genotype and environment. Estimation of these influences is considered to be the most complex. Only a comprehensive assessment of all the influences will give us highly reliable estimates of the genetic quality of the animals and thus the possibility, within the framework of selection intensity, to select the most suitable animals for reproduction.
Genomic selection brings a significant (positive) change in the amount of genetic gain values achieved for individual traits in livestock (cattle). The use of advanced genomic technologies and techniques to identify and select animals with desired genetic traits can significantly accelerate genetic progress. Genomic selection allows the identification of genetic markers associated with many traits, enabling more accurate and efficient selection of breeding animals. As an example, in dairy cattle, we are seeing a huge increase in the use of young genomic bulls without the existence of their progeny. In general, genomic evaluations of young animals provide much higher confidence in knowing their genetic quality than is the case with traditional systems. However, traditional systems still have their justification as they represent a reliable verification of new systems and, together with genomic information (combined, extended breeding values), clarify the decision-making system in animal breeding itself.
In the presented figure (slaid 7) we show a real example of the impact of genomic selection on the increase of genetic progress (gain) in the Holstein population in Canada. The advance of

genomics in animal selection (expressed by the green line, 2009) clearly confirms the higher real values of genetic progress compared to traditional approaches (dashed line).

The introduction of genomic selection has literally revolutionized animal breeding (especially dairy cattle) by allowing breeders to accelerate genetic progress and increase overall performance and economic efficiency in animal populations and breeding operations. Genomic data analysis facilitates the identification of genetic markers, the study of genetic variability and the prediction of complex traits within animal populations.

The next figure (slaid 8) compares the total realized genetic gain of specific traits in Canada before and after the introduction of genomic selection. For milk production, there is an approximate doubling of genetic gain, similarly for other milk performance traits (fat, protein). For traits such as: herd life, somatic cells and some other secondary traits, the increase is more than double.

A similar comparison was made in the Slovak Republic in the Holstein population. In the genetic evaluation of milk performance traits (kilograms of milk), a very similar trend of increase in genetic gain was observed as in the much larger population in Canada. The only difference was a slight time delay in the use of genomics, which was reflected with a later increase in significantly higher genetic gain (but only a 1 year delay). The above shows the strong interconnectedness of the worldwide Holstein population and the resulting similar genetic trends in the evolution of genetic quality of individual cattle populations.

Genetic progress in the form of achieving higher increases in the genetic quality of animals concerns all the traits evaluated: production traits, exterior traits, longevity, somatic cells, calving easy, fertility, health, temperament. The above are combined in a number of complex indexes, where the basis becomes a variety of selection indexes with emphasis on the economic value of individual traits in a given livestock population (breed).

Genetic advances also apply to novel traits in animal selection and breeding (methane production, feed intake and utilization, immune response, animal temperament and many others).

Sophisticated statistical and computer models are used to analyse the relationship between genetic markers and the new phenotypic data observed. From a research perspective, but also for practical applications, genome-wide association studies (GWAS) are fundamental (crucial). GWAS is a research approach that is used to identify genomic variants that are statistically associated with a particular trait or characteristic . The models also help in estimating breeding values for new specific traits based on their genomic information. Prediction models take into account relationships (correlations) genetic markers and target traits in order to accurately estimate the genetic potential of individuals.

An important element of genetic progress is the continuous development of new biotechnological methods and approaches, together with the sustainability and economic efficiency of animal breeding.

New genomic approaches can help to assess more objectively the structure and genetic diversity within animal populations. By studying the genetic relationships and origins of individuals, distinct genetic relationships can be identified, refining direct measurement of genetic diversity and a true understanding of the evolutionary history of individual animal populations and species.

From a human perspective, however, all practices should be directed towards the production of healthy food of animal origin and the breeding of healthy animals.