ISAGREED

Genetic value of animal

Modul no. 3: Animal Breeding

Juraj Candrák
Slovak University of Agriculture in Nitra,
Faculty of Agrobiology and Food Resources

Erasmus+ project 2021-1-SK01-KA220-HED-000032068

Co-funded by
the European Union

The importance and place of knowledge of the genetic value of animal in the process of animal breeding

- Breeding goals
- Animal pedigrees (DNA tests, genotyping)
- **Genetic Value - Estimation of Breeding Values**
- Selection and mating
- Creating a new generation
- Genetic gain

Erasmus+ project 2021-1-SK01-KA220-HED-000032068

Co-funded by the European Union

Genetic value of animal - concept

Genetic value - estimation of breeding values

When estimating breeding values, we start from the knowledge that the overall phenotypic expression of any trait can be expressed according to the basic biological equation:

$$\mathbf{P = G + E}$$

P - phenotype, G - genotype, E - environment

ISAGREED

Co-funded by the European Union

Genetic value of animal - concept

Breeding value.

It represents an estimate of the genetic makeup (genetic value) of an individual for a specific trait .

It is most often expressed in the form of a deviation from the average of the population (group) of animals (absolute breeding values, relative breeding values).

The term breeding value is generally used to estimate genetic value for traits of a quantitative nature.

Individual breeding values form part of the simple or complex selection indices.

ISAGREED
Co-funded by the European Union

Estimation of breeding values - history - future

Significant methods of estimating breeding values

Mother-daughter method

CC (Contemporary Comparison) test

The BLUP method

Genomic approaches in estimating breeding values

Co-funded by the European Union

Estimation of breeding values - BLUP method

Best **L**inear **U**nbiased **P**rediction

Linear model with mixed effects.

Simultaneous use of fixed and random effects.

Practical use even for unbalanced data sets.

Any number of environmental effects.

The method is based on mixed model theory for the simultaneous estimation of genetic and environmental effects, and is closely related to the method of estimating the components of variance in these models (Henderson, 1953, 1954).

Co-funded by the European Union

Estimation of breeding values - BLUP method

BLUP - sire model (Paternal model)

Estimation of breeding values of only some individuals in the population (usually males).

BLUP - animal model (Individual model)

Estimation of the breeding values of all individuals in the population.

Use of all available information in the estimation: pedigree, own performance, descendants, other relatives in the colateral line.

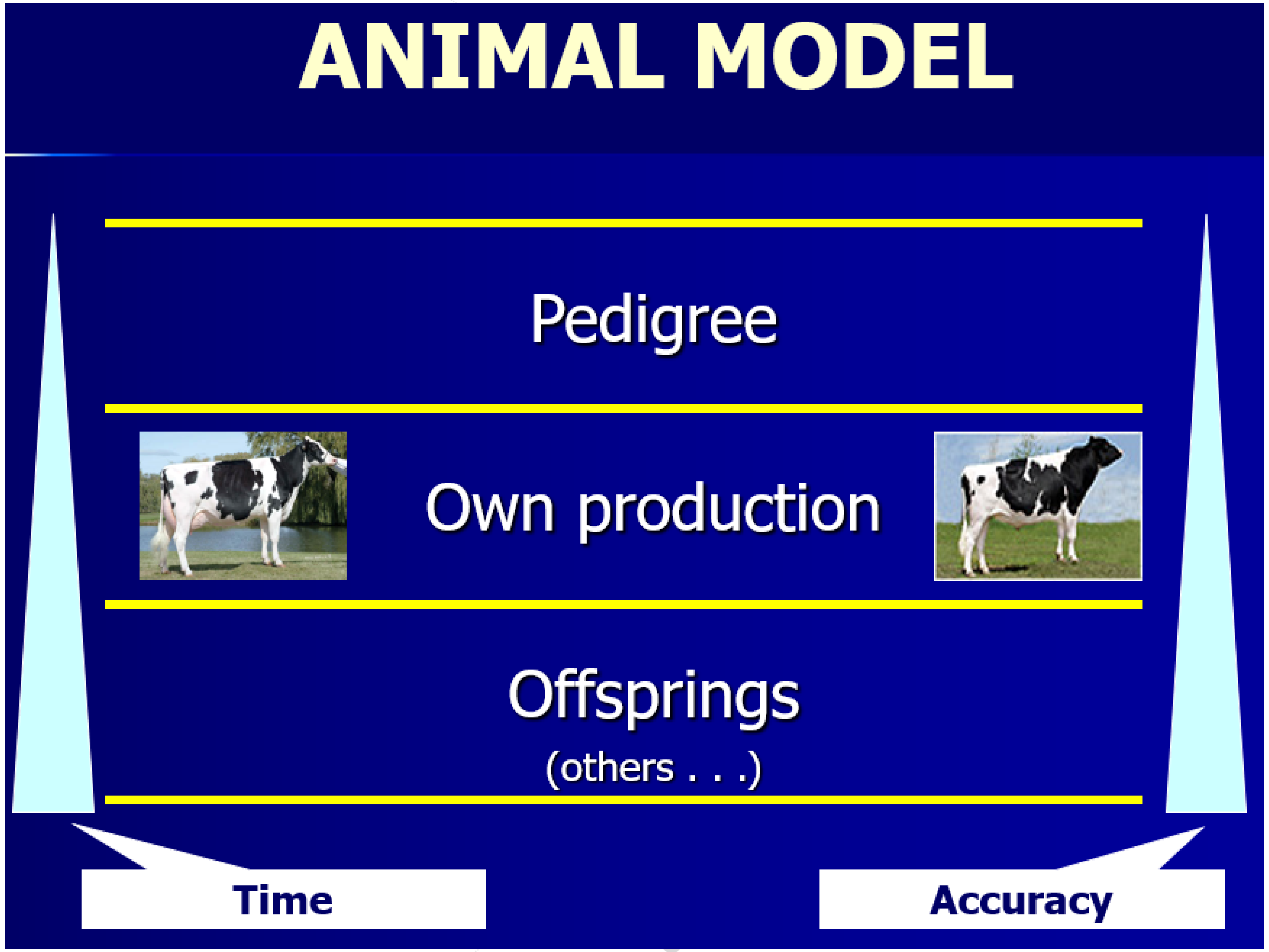
Single-trait models

Multiple-traits models

Erasmus+ project 2021-1-SK01-KA220-HED-000032068

Co-funded by the European Union

Estimation of breeding values – BLUP animal model



ANIMAL MODEL

Pedigree

Own production

Offsprings

(others . . .)

Time

Accuracy

Source: Breeding value estimation, Candrák, 2007

Co-funded by
the European Union

Estimation of breeding values – BLUP animal model

BLUP - Animal model (without taking into account family relationships)

We can simply write the model schematically:

y = average + environmental effects + animal + residue

in matrix notation:

$$y = Xb + Za + e$$

y Column vector of phenotypic observations (measured utility)
b column vector of unknown fixed effects
a column vector of unknown random effects (breed values), N(0,)
X, Z matrix of explanatory variables assigning utility to fixed and random effects
e random error vector (residual), N(0,)

ISAGREED
Co-funded by the European Union

Estimation of breeding values – BLUP animal model

BLUP - Animal model (without taking into account family relationships)

Model solution:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + Ik \end{bmatrix}\begin{bmatrix} b \\ a \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

$$k = (1 - h^2)/h^2$$

BLUP - Animal model (taking into account family relationships)

Model solution:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + A^{-1}k \end{bmatrix}\begin{bmatrix} b \\ a \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

Estimation of breeding values– BLUP animal model

BLUP - Animal model (Consideration of genomic information)

Model solution:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z+H^{-1}k \end{bmatrix} \begin{bmatrix} b \\ a \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

The H^{-1} matrix is calculated according to the following relation:

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} - A^{-1}_{22} \end{bmatrix}$$

G^{-1} is an inverse genomic matrixA^{-1}_{22} is the inverse matrix of the additive affinity of genotyped animals calculated on the basis of pedigree information.

Co-funded by the European Union

Estimation of breeding values – BLUP animal model

BLUP - Animal model (model with maternal effects)

The model can be written as:

$$y = Xb + Z_1a + Z_2m + Z_3p + e,$$

y – the trait evaluated;
a - additive genetic effect,
m - maternal genetic effect,
p - permanent effect of the environment,
e - residue

ISAGREED
Co-funded by the European Union

Estimation of breeding values – nonlinear models

Survival analysis

It is based on nonlinear regression analysis.
It allows you to take into account environmental influences and factors that are time-dependent and also evaluates censored data (it also processes incomplete information).

Survivability models are built on two features:
function and survival function.
The hazard function measures the risk of discarding an animal at a certain time.
The survivability function expresses the probability of survival up to a certain period of time.

ISAGREED
Co-funded by the European Union

ISAGREED

Partners:

SLOVAK UNIVERSITY OF AGRICULTURE NITRA

Mendel University in Brno

Siedlce University of Natural Sciences and Humanities

CZU Czech University of Life Sciences Prague

Thank you for your attention!

This presentation has been supported by the Erasmus+ KA2 Cooperation Partnerships grant no. ***2021-1-SK01-KA220-HED-000032068 "Innovation of the structure and content of study programs in the field of animal genetic and food resources management with the use of digitalisation - Inovácia obsahu a štruktúry študijných programov v oblasti manažmentu živočíšnych genetických a potravinových zdrojov s využitím digitalizácie"****. The European Commission support for the production of this presentation does not constitute an endorsement of the contents which reflects the views only of the authors, and the Commission cannot be held responsible for any use which may be made of the information contained therein.*

Juraj Candrák
juraj.candrak@uniag.sk

ISAGREED

Co-funded by the European Union