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DEVELOPMENT OF SELECTION INDICES IN THE HUNGARIAN PIG BREEDS

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1. Research backgrounds and objective

Different methods of selection have been used in the pig industry throughout the history. The general methods of selection are: random selection, tandem selection, independent culling levels, total score method (index selection), selection index, estimated breeding value (EBV), expected progeny difference (EPD), best linear unbiased prediction (BLUP). Selection based on a selection index is the most commonly used method in genetic improvement programs for pigs (Stas, 2017). In pig industry measuring the important traits are accomplished through two types of performance tests which are station test and field test, respectively (Csató et al., 2002). Station test is more precise and accurate but currently field test have been becoming more and more frequent. The advantage of such an assessment, compared with the use of stations test, is that the assessment is a significantly cheaper. After collecting all required information measurements of different traits are combined to one score called selection index. Thus breeders can perform selection simultaneously for several traits. Structure and form of indices can differ among countries (McPhee, 1981; Morris et al., 1982; Visser, 2004; Nagy et al., 2008; Csató et al., 2002) based on the varying interest in the breeding objective.

In the Hungarian pig breeding sector performance test of pigs is mainly based on field tests. Kaposvár campus has been close partner of Hungarian Pig Breeders Association for many years, together they are responsible for collecting information and developing breeding programme for many different farms across Hungary. Based on the measurements collected in the course of the field tests the future generations' performance can be predicted. The nucleus pig farms in Hungary perform their selection process based on BLUP methodology (Best Linear Unbiased Prediction) where the prediction of breeding values is taking into account environmental factors and performances of relatives. It has to be noted that at present breeding value prediction for reproduction traits is limited to the Hungarian: Duroc, Hampshire, Pietrain, Large White and Landrace breeds. Because for instance breeds as Pietrain, Duroc and Hampshire targeting mainly only average daily gain and lean meat percentage. Besides all pig breeds are selected based on progeny test for feed conversion ratio and for the weight of the valuable cuts (Hungarian Pig Breeders Association).

Special selected breeds or lines for different species are responsible for specific productivity traits. In such way breeds conditionally divided into two types or groups: parental and maternal forms. First one are responsible for carrying production traits such as: lean meat content; backfat thickness; dressing percentage; average metabolic weight; lightness of the meat of the gluteus superficialis muscle; ultimate pH measurement of the semimembranosus muscle; water holding capacity of the gluteus superficialis muscle and so on (Saintilan, et al., 2013; Evans, et al., 2003). Second one are responsible for so call reproduction traits - farrowing after first insemination; number of still born piglets; number of piglets born in total or alive; interval from weaning to first insemination; high for gestation length and age at first insemination; semen quality; age at puberty and so on (Hanenberg, et al., 2001; Zak, et al., 2017).

The economic importance of the international and Hungarian pig breeding sectors is both high. The Hungarian pig population size was 2558 million (148.000 sows) in 2022 year (KSH, 2023). We began our research and

data collecting in 2017 year and in that time based on our investigation population size of pigs was 3.136 million 2015 year (200.000 sows) (KSH, 2023). For this period of time pig population dramatically decrease in Hungary. The most important pig breeds and breed constructions are Hungarian Large White, Hungarian Landrace and their first cross, respectively.

The various methods of quantitative genetics have been applied by breeders for decades in order to improve the performance of domesticated animals in some pre-defined traits. In the pig breeding sector, similarly to other multiparous species, the crossing is widely used in order to increase performance, where generally separate breeds are used to increase reproductive (e.g., number of piglets born alive, number of piglets born dead, number of piglets weaned, litter weight at weaning) and growth and carcass (e.g., average daily gain, feed conversion ratio, lean meat percentage, the proportion of valuable cuts) performances (Bidanel, et al., 2011). Looking at the various traits used in pig breeding number of piglets born alive is among the most important trait from the economic viewpoint, as this trait has the largest economic weight besides the feed conversion ratio (Houska, et al., 2010; Krupa, et al., 2017). Monitoring the actual genetic parameters of the economically important traits and evaluating the genetic progress of the populations is always an important task that helps us to determine the expected efficiency of the breeding program.

To characterize and possibly predict the response, we built and used linear regressions based on available genetic parameters for attaining the genetic trends for five pure breeds and their cross (Tinh, et al., 2021). Additionally, based on these predictions, the overall genetic merit was also determined as an inevitable condition of carrying out efficient selection using the procedure of desired gain (Brascamp, et al., 1984; Suzuki, et al., 2005). Coefficients of the index for breeding value estimation were realized for targeted traits by applying aggregate genotype where estimated index-weighted factors were taken into account (Brascamp, 1984). The advantage of this is avoiding the necessity of calculating economic weights while estimating index-weighing factors (Gjedrem, 1972; Pešek and Baker, 1969).

2. Materials and methods

1. Data collection

Our research was extended and divided on two parts. First one was related to examine paternal and second maternal breeds of pigs. Testing was based on totally 5 pure breeds (Hungarian: Duroc, Hampshire, Pietrain, Large White and Landrace and one cross Hungarian: Large White x Landrace and Landrace x Large White).

In Hungary, the selection process and prediction of genetic merit for reproduction traits for maternal breeds are focused mainly on the number of piglets born alive and litter weight at weaning. Data used in our research were collected by Hungarian Pig Breeders' Association from 21 herds for breeds Hungarian Duroc (HD), Hungarian Hampshire (HH) and Hungarian Pietrain (HP). And from 56 herds for breeds Hungarian Large White (HLW), Hungarian Landrace (HL), and F1 generation (Large White boars mated with Landrace sows and Landrace boars mated with Large White sows) were collected between 2001 and 2018 in the course of the field test. Number of herds, sows and the number of farrowing records were summarized in table 1.

Breed/Name	Herds	Sows	Number of Farrowings		
Total	21	2843	8806		
HD	10	1294	3796		
HH	7	381	1246		
HP	16	1168	3764		
Total	56	27561	73871		
HLW	42	16749	50147		
HL	23	4372	12645		
F1	34	6440	11079		

Table 1. Farrowing records

HD: Hungarian Duroc; HH: Hungarian Hampshire; HP: Hungarian Pietrain; HLW: Hungarian Large White; HL: Hungarian Landrace and F1 generation (Large White boars mated with Landrace sows and Landrace boars mated with Large White sows).

The recorded traits were number of piglets born alive (NBA), number of weaned piglets (NWE), and litter weight at weaning (LWWE), which directly affect future genetic diversity for any species.

2. Animal Model

The farrowing data set was used for testing 14 repeatability animal models to select the most appropriate model for estimating genetic parameters, and the structures of these models are presented in table 2. The breeds (HD, HH, HP and HLW, HL and cross F1) were analyzed together (was built 7 models for paternal and maternal forms, totally 14) as one population constructing their common pedigree. In this way, the

heterosis effect could also be accounted for including the breed construction of the animals in every model.

Model		Traits	5	Factors (Type)									
					Rep	FSA	SWA	FYM	WYM	Breed	Herd	Parity	
	NBA	NWE	LWWE	(A)	(R)	(C)	(C)	(F)	(F)	(F)	(F)	(F)	
/Breeds	Hungarian - Duroc, Hampshire and Pietrain												
1	Х	Х	Х	Х	X			Х	Х	Х	X	Х	
2	х	Х		Х	х			Х	Х	Х	Х	Х	
3	Х	Х		Х	Х	Х	Х	Х	Х	Х	Х		
4	Х	Х	х	Х	х	Х	Х	Х	Х	Х	Х		
5	х		Х	Х	X			Х	Х	Х	X	Х	
6	х		Х	Х	X	Х	Х	Х	Х	Х	X		
7		Х	Х	Х	х				Х	Х	х	Х	
/Breeds	Hungarian - Large White, Landrace and F1 generation												
8	Х	Х		Х	Х			Х	Х	Х	X	Х	
9	Х	Х		Х	Х	Х	Х	Х	Х	Х	X		
10	Х	Х	х	Х	Х			Х	Х	Х	X	Х	
11	Х	Х	Х	Х	Х	Х	Х	Х	Х	Х	X		
12	х		х	Х	X			х	Х	х	x	Х	
13	X		Х	Х	X	X	X	X	Х	Х	X		
14		Х	x	Х	х				х	Х	X	Х	

Table 2. The structure of the applied animal models

NBA: number of piglets born alive; NWE: number of weaned piglets; LWWE: litter weight at weaning; REP: repeatability measurements; FSA: age of farrowing sows; SWA: sows age at weaning; FYM: farrowing year-month; WYM: weaning year-month; A: additive genetic effect; R: random effect; F: fixed effect.

Traits that were analyzed in models are the number of piglets born alive (NBA), number of weaned piglets (NWE), and litter weight at weaning (LWWE). Best Linear Unbiased Prediction (BLUP) and Restricted maximum likelihood methodology (REML) were used for the estimation of breeding values and variance–covariance components. PEST (Groeneveld, E., 1990) and VCE 6 (Groeneveld, E., et al., 2008) software were used (for data coding) for the estimation of breeding values and variance components.

The basic repeatability model was:

$$y = Xb + Za + Wpe + e$$

Where: y is the vector of observations; b is the vector of fixed effects; a is the vector of random animal effects; pe is the random vector of permanent environmental effects (dam identity); e is the vector of random residual effects; and X, Z, and W are the incidence matrices relating records to fixed, animal, and random maternal permanent effects, respectively.

Expected values of a, c and e were E(a) = E(c) = E(e) = 0. The variance– covariance structure was assumed to be V(a) = A2a, V(c) = I2c V(e) = I2eand V(a) = A2a, V(e) = I2e Cov(a,e) = Cov(e,a) = Cov(c,e) = Cov(e,c) = 0 and Cov(a,e) =Cov(e,a) = 0, where A is the numerator relationship matrix. Additionally, cov(y,a) = ZAI2a.

The suitability of the different models was compared using the loglikelihood values calculated by the VCE software. The model with the largest log-likelihood value provides the best fit. SAS 9.4 (SAS., 2013) was used for descriptive statistical analysis. In addition, SAS 9.4 was also applied to calculating the genetic trend for every trait, which is the linear regression coefficient of the average breeding value of animals born in the same year (regressed on the successive years of birth). Additionally, Mix software was used (Nath, M., et al., 2002) for the calculation of the maternal desired index with the purpose of improving all traits by one additive standard deviation where the assignment of relative economic values of the examined traits is not necessary. The breeding goals are defined as the ultimate levels of the traits of interest. The desired gain index is constructed to attain the predetermined breeding goals in minimum number of generations of selection. A detailed description of the index weighing factors' calculation was given by Yamada et al. (1975). The calculated index scores were transformed in order to obtain index mean and standard deviation equal to 100 and 20, respectively, as it is used in Hungarian pig breeding (Hungarian Pig Breeders Association. Pig Performanc., 2017). When constructing the index the objective was to improve all traits with one additive standard deviation.

3. Results

1. The results of heritability (HD, HH and HP) of the models analyses show that NBA for all models was low and range in diapason 0.10 - 0.11. There was also a slight tendency for NWE in all models too and evaluated with values between 0.08 - 0.09. Measuring heritability of LWWE for all models had a same low tendency and range 0.11 - 0.13. Standard errors for estimated parameters were less than 0.03 in all models.

2. The ratios of the permanent environmental variance to the phenotypic variance (HD, HH and HP) for NBA had low impact in all models and ranged from 0.07 to 0.08. Likewise, NWE showed low magnitude between 0.04 - 0.05 for all models. Similarly, LWWE had lowest values of environmental impact in comparison with NBA and NWE and was assessed at range 0.02 - 0.03 for all models. Standard errors for estimated parameters were less than 0.03.

3. Genetic trends were not significant for NBA and NWE traits in case of HD breed. Significant difference observed for LWWE trait with Pr>|t| ranging 0.01 - 0.02 with trends values 0.14 - 0.20 kilogram per year. Genetic trends of Hampshire breed were not significant for NBA and NWE but showed the same tendency for all models. LWWE was significant with Pr>|t| 0.03 - 0.04, with negative trends -0.25 - -0.24 kilogram per year. Estimated genetic trends of Pietrain breed were significant for NBA and NWE traits. NBA had positive trends with Pr>|t| 0.01 - 0.009 with a ranged value 0.01 - 0.02 piglets per year for all models. NWE had Pr>|t| 0.001 - 0.0008 with the same genetic trends 0.02 piglets per year. LWWE was not significant.

4. Heritability (HLW, HL and F1) for NBA and NWE was the same for all seven models. On the contrary, heritability estimates for LWWE were higher in comparison with NBA and NWE.

5. The permanent environmental variance component (HLW, HL and F1) was small for all traits. The HLW breed had positive and significant genetic trends for all seven models and for all three traits. HL breed had

significant trends for NBA, which was negative and for NWE the results were positive.

6. Using the estimated breeding values a desired index was constructed in order to improve each trait by one additive genetic standard deviation. The constructed indices result in one number (aggregate genetic merit).

4. New scientific results

1. Based on the estimated log likelihood-value models, including parity were inferior compared to those models containing age for both type of breeds paternal as for maternal. Models 6 and 11 had best fits with data with next values 15 808 and 169 370 for paternal and maternal breeds of pigs respectively.

2. Next index was constructed for two types of breeds. Here are description of indexes from models which best fits data. Paternal breeds index - 15.8871*ebv1 + 2.5689*ebv3 and maternal breeds index - 13.8544*ebv1 + 12.3412*ebv2 + 1.8160*ebv3 (ebv are the estimated breeding values for traits: ebv1 - number of piglets born alive, ebv2 - number of weaned piglets, and ebv3 - litter weight at weaning).

5. Conclusions and suggestions

It can be seen that index methodology named an aggregate genotype is an appropriate tool that we can apply for ranking animals.

The desired gains index technique is a good tool for determining the economic importance of traits where the economic values cannot be determined. Animals can be selected based on their overall performance.

Using the desired gain index method for paternal as for maternal breeds of pigs would probably increase the annual genetic trends of the traits involved in the index.

The indexes which were construct in frame of my investigations of course possible to use in practice. But in general these indexes can be applied just inside of this breeds and Hungary. Because out of country will exist new environments and some other traits characteristics. Therefore this methodology can be used for construction new indexes out of Hungary but will require new income data.

6. Publications written in the topic of the dissertation

Kodak, O., & Nagy, I. (2019). Historical overview of the selection indices applied in pig breeding. Acta Agraria Kaposváriensis, 23(1), 22-31.

Oleksandr Kodak, Farkas JánosGyörgy Kövér, István Nagy (2020). Application of selection indices for Hungarian pig breeds. Scientific and Information Bulletin of the Faculty of Biology and Technology. Kherson. Vol. 13. C.10-13.

Kodak, O., Kiszlinger, H. N., János, F., Kövér, G., & István, N. (2020). Index selection as a key in the selection process for pigs. Hampshire, 7(381), 1-246.

Kodak, O., Nagyne-Kiszlinger, H., Farkas, J., Köver, G., & Nagy, I. (2022). Genetic Parameters of Reproductive Performances in Hungarian

Large White, Landrace, and Their Crossbred F1 Pigs from 2010 to 2018. Diversity, 14(12), 1030.