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OLEKSANDR KODAK

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Hungarian University of Agriculture and Life Sciences
Institute of Animal Sciences

Head of Doctoral School
Dr. ANDRÁS SZABÓ DSc

Supervisors
Dr. ISTVÁN NAGY DSc
Full Professor
Dr. KÖVÉR GYÖRGY
Associate Professor

DEVELOPMENT OF SELECTION INDICES IN THE HUNGARIAN PIG BREEDS

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Written by
OLEKSANDR KODAK

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2. Introduction

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 2.558 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, I 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).

3. Literature Review

3.1 Conventional selection index

The index is a numerical expression of the genetic merit of a plant or animal for its further use as a parent for the production of a new generation. Index selection is a method where values of all traits of the selection criteria are combined into a single index value (Sangsuriya et al., 2002). Throughout many generations and centuries selective breeding of domestic animals and plants were based on the phenotypic evaluation of the individuals. First official developing and publication related to index selection was done by Smith (1936). He presented an index in the next form:

$$I = b1x1 + b2x2 + \ldots bmxm$$

Where: I is an index of merit of an individual and b1…bm are weights assigned to phenotypic trait measurements represented as x1…xm.. The selection index was first used for selection among inbred lines of a self-pollinated plant species (Smith, 1936).

Adaptation and application the theory of index selection to the animal breeding was done a bit later just in 1943. Officially Hazel is the father of modern animal index selection originally adapted methods from plant production (Hazel, 1943; Graser et al., 2006). The main problem of Hazel which he met with constructing an index was how to combine information in an optimal way on different individuals Y into a single number I on which selection can be based. Hazel had chosen a linear approach (Hazel, 1943; Weaber, 2005):

$$I=b' (y-\hat{y})$$

Where: b' is a column vector of weightings which need to be calculated and y a row vector of observations. Note that in this very general form the vector y can include single observations on one trait from different animals, or single observations on different traits of one or more animals, as well as means of groups, e.g. mean of all progeny (Weaber, 2005). The Hazel selection index (De Vries, 1989) defines economic merit as:

$$Hi = a1\ BVi1 + a2\ BVi2 +\ldots+ an\ BVin$$

Where: Hi = the aggregate economic merit of an animal, i, as a parent; aj= the relative economic weight of trait j, j = 1…n, where n = the total number of traits BVij = the breeding value of animal i for trait j.

During last 80 years since it has been introduced the theory of index selection has been improved. In general, before constructing a selection index, its purpose needs to be determined. The next step is to identify the traits involved in the breeding goal, and then economic importance of every trait has to be calculated. The problem with conventional selection index is that unless the phenotypic measurements are pre-corrected by the influential environmental factors, these factors can highly modify the results. Unfortunately apart from conventional selection of body weight indices do not use data correction (Csató et al., 2002). Besides, conventional index methodology is based on the phenotype rather than the genetic merit of the animals in the different traits.

3.2 BLUP methodology

Best Linear Unbiased Prediction, or BLUP, is a technique for estimating genetic merits. In general, it is a method of estimating random effects. This is a method of selection and genetic evaluation of animals. It was created and development by scientist Henderson in the 1950s but because of complexity of mathematical calculations and the computer power was too limited to be able to calculate the breeding values using the animal model, the practical implementation thus had to wait until the later 1980's. As we mentioned previously the so called estimated breeding value was developed also by Henderson (1975), it has given possibilities to breeders to rank the animals according to their estimated genetic potential, which resulted in more accurate selection results and thus a faster genetic improvement through generations (Robinson, 1991). The Estimated Breeding Value (EBV) provides an estimate of the genetic potential of the animal which is expressed relative to the population average. The true breeding value (TBV) is the real value of the animal for breeding. The perfect EBV would be equal the TBV. The EBV provides the BEST estimate of the breeding value of an animal. The accuracy indicates the risk of a difference between EBV and TBV, where the TBV may be higher or lower with equal probability (Oldenbroek and van der Waaij, 2014). The correlation between the true breeding value and the predicted breeding value is maximized and estimates realized values for a random variable using unbiased statistical methods (Stas, 2017).

If we compare effectiveness of both methods in practice based on done research, it is possible to make a conclusion that BLUP methodology more appropriate than conventional selection index based exclusively on phenotype. Response would be greater from selection using BLUP than from selection using conventional index (Keele et al., 1988). The BLUP evaluation officially was introduced in Hungary in 2007 and quickly replaced the conventional indices, and pig breeding companies conducting breeding also started to pay more attention to progeny tests based on slaughter-house data than they had done previously (Houška et al., 2010). In literature review of thesis work of Stas (2017) was reviewed experiment of comparison selection based on phenotype performance (conventional index) with selection based on best linear unbiased prediction (BLUP) of breeding value selection for one trait of interest at varying levels of heritability. Genetic improvement was greater for BLUP selection compared to conventional index selection. But with increasing of heritability, the difference between the two methods decreased. Selection based on BLUP had a relative advantage compared to conventional selection index by 55% for traits of low heritability and by 10% for traits of moderate heritability. The level of inbreeding increased faster with selection based on BLUP. Nevertheless, selection based on BLUP will help to improve selection accuracy and efficiency (Stas, 2017).

BLUP advantages are as follows (Csató et al., 2002):

- the most accurate division of criteria that determine the productivity of the animal: the impact of the environment; genetics (heredity)
- the possibility of simultaneous comparison of parameters that were obtained in different environmental conditions from different genotypes, as well as from animals of different generations;

- mathematically accurate records of all documented family ties
- Adjustment of all values of breeding value in relation to each other (for example accounting for genetic competition and the level of mating)
- very high accuracy of tribal assessment, which allows achieving high selection efficiency
- More accurate prediction of breeding values through the use of information on all the relationships
- More accurate comparison of animals at different times or under different management systems by correcting environmental factors
- More direct comparison among animals by using different levels of relevant information and/or by allowing comparisons across different generations.

However, it is also necessary to mention the limits of using BLUP in the Hungarian pig breeding sector. There is no doubt that BLUP simultaneously corrects the phenotypes for systematic effects, and it estimates breeding values while making use of the additive genetic relationships between the animals with the help of matrix algebra. But there is a critical issue in correcting for systematic effects. It only works well if genotypes are sufficiently spread across systematic environmental influences (Oldenbroek and van der Waaij, 2014). There are no sufficient genetic links between Hungarian breeding farms, because of the lack of AI with the semen of the same sires used in many farms. Also breeding animals are rarely brought to various breeding farm, they are mainly sold to commercial farms. So the lack of exchange of animals between farms results in poor genetic links between farms and often it is not possible to estimate systematic farm effects accurately. As mentioned above one of the main goal which is possible to achieve with BLUP is to quantify and eliminate the influence of the environmental factors. Because different genotype in different environment can give different feedback of productivity, this is called genotype environment interaction. In different literature sources different classifications of genotype x environment interaction exist. For example Merks (1986) defines interaction as a change in relative performance of two or more genotypes measured in two or more environments. James (2009) classified interactions as being either of rank-type or of scale-type. He defined rank-type interactions as those in which genotype 1 may be superior over genotype 2 in the first environment, however, the reverse may be true when tested in the second environment. Merks (1986) made a similar classification for rank-type interactions. In addition to the rank-type classification, James (2009) defined scale-type interactions as those in which the differences between genotypes change in magnitude, but not in sign, with changes in environment. The implications of these interactions have to be considered when developing a breeding program. Although the magnitude of the performance differences may change with a scale-type interaction, the ranking of the genotypes for performance will stay the same. However, with rank-type interactions the ranking of the genotypes for performance will change with a change in environment. Therefore, rank-type interactions potentially have more practical importance.

3.3 Economic methodology

Economic methodology was developed a bit later with purpose to weights and rank traits. After choosing all of appropriate traits and performing the procedures related to construction of selection index, breeders had another problem how to rank traits based of the economic values that will be more beneficial for certain traits. Besides, when constructing an index based on economic values, only one of the traits may be included in the index in order to avoid double counting and recovering one by another. As example such traits are lean meat content and backfat thickness (Houška et al., 2010). With these purposes for ranking traits was developed the so called economic weights.

Different approaches are available for construction and calculation economic weights, it depends on many factors. First citation that we found in literature describing methodology of calculating economic weights dates back to 1966. Authors Moav and Moav (1966) proposed idea about using profit equations to integrate the cost and return of a production system to compare the profitability of lines and crosses. Main idea was that equations could be non-linear and outcome then depends on the levels of performance for the different traits. In 1973 Moav used the profit equation, and the economic weights derived from the interests on national level or producers (Brascamp et al., 1985., Moav and Moav, 1966., Moav, 1973).

The economic value of an individual in animal husbandry is expressed by the profit nowadays (Michaličková, et al., 2016). Breeder is a main person who makes strategy of development for future selection programs. Usually such activity is carried out in four stages (van der Werf, 2006):

- monitoring of production conditions and situation in the product market;
- analysis of profit and production costs;
- definition of important features;

- calculation of economic weight coefficients.

But of course in the end this is main task for breeders decide which traits choose from numerous of them based on their economic importance. Trait or traits must be improved in accordance with the objective of market demand. Because increasing specific productivity of interest will bring together with this increase financial welfare of industry. In general, a selection index as a function of the predicted breeding values of economically relevant traits and marginal economic values is used for example in such countries like Czech Republic and Hungary. The marginal economic values of the traits are calculated as change in predicted profit, holding all other traits constant. As was mentioned by reviewing literature it is possible to make a conclusion that huge differences can be observed between countries, but also between different farms with different environment. Also can be observed a small effect of specific selection methods on reduction in production costs in different markets. Therefore, diversity in genetic lines of pigs is not directly needed maybe just adaptation of lines to specific environments or farming systems. This finding is in accordance with Hanenberg et al. (2010), Stewart and Neal (1999). Pig breeding programs generally focusing on improving traits that are responsible for production and reproduction goals because they are more clear and important. Of course they are short term objectives because always must be focusing on market and customer demand. But breeders and associations also pay attention to other important traits except economic importance such as animal welfare (Kanis et al., 2005).

Breeders generally are applying two approaches for calculating economic weights for pigs, based on the models of De Vries (1989) or Stewart et al. (1990). The first approach is applies to an integrated commercial production system buying their female replacements from the superior production tier. The second approach relates to a commercial sow herd by producing their own replacement gilts and selling weaned piglets to the growing - finishing enterprises (Houška et al., 2004).

On reviewing of two countries Hungary and Czech Republic we will show some examples of approaches to calculating marginal economic values, economic weights and traits that are used for these purposes. In Hungary first estimation of economic values and marginal economic values for traits was done in 2010 (Houška et al., 2010). The final results of the calculation for specific traits in the table 1 we can see.

Basis of constant number of sows was used for the calculation of economic values for Hungary and therefore expressions of economic values were done per sow per year. Model describing by De Vries (1989) was used as approaches for calculating. Based on the data which we can observe (table 1) best marginal economic values were the number of piglets born alive but based on standardized economic values the percentage of valuable cuts in the carcass was most economically important trait (Houška et al., 2010). As authors mentioned in their conclusions for calculating economic weight we just simply need multiplied breeding values by the marginal economic values and we can build economic selection index (Houška et al., 2010). In the research of Houska et al. (2004) it was showed that the production system in Czech Republic is similar to the Hungarian and therefore the model of De Vries

(1989) was used for calculating. Marginal economic value and economic value were also calculated. But for calculating economic weights the so called discounted expressions which were multiplied by marginal economic values were used. Discounted expressions (cumulative - CDE) are expressed of discounted gene flow as a consequence of one mating. “Cumulative” refers to an accumulation of expressions over generations or years. And “discounted” implies to the fact that future return is discounted to today’s values by a discounting factor (Brascamp, 1978; Jiang et al., 1999)

Table 1. Marginal economic values (MEW, in EUR per unit of trait, per sow and year when improving the trait level), genetic standard deviation (GSD), standardized economic values (SEW, in EUR/GSD)

Trait (unit)	**MEW**	**GSD**	**SEW**
Number of piglets born alive (piglets)	54.22	0.61	33.07
Age at slaughter (days)	2.71	15.02	40.70
Days in fattening	2.84	9.91	28.14
Lean meat content in the carcass (%)	22.45	1.62	36.37
Percentage of valuable cuts in carcass (%)	28.81	2.55	73.46

3.4 Genetic parameters

Between breeds exist huge range of traits that deeply examined every year as in laboratory as in field tests. Parameters can be different not just inside one country or breed but as well in one population. Pigs in general are characterized by 3 main parameters it are heritability, permanent environmental effect and genetic or simply trends which show tendency in past and future for specific trait or population.

3.4.1 Parameters for paternal and maternal breeds of pigs

Heritability and permanent environmental effect are two important parameters which quite high related to each other. Heritability is the size with which traits reproduce yourself between generations and environmental effect is size with which heritability can be influenced by specific factors. It can be different factors such as different veterinary manipulations, some changing in diet or some specific habits of sow or boar. Backfat thickness is quite well identified trait between huge number of them first of all that this trait has direct influence on meat quality characterization. And second that this trait has huge size of heritability in general this is around 0,30 - 0,56 units (Bryner, et al., 1992; Kim, et al., 2004). Exactly backfat thickness is good example of well identified and well known trait in world.

Table 2 gives size characteristics for traits which more closed to our research. Size of heritability for the same feature can be differing as was mentioned above. The same is for permanent environmental effect as we found in research of Schneider, et al., (2012) have highest Pe for 4 reproductive traits number piglets born alive, number born dead, number stillborn and litter birth weight of piglets with units 8.2, 2.1, 1.5 and 12.7 respectively. This can be consequence of small population sample size and many other factors. As example Pe was lowest in research of Hamann, et al., (2004) for trait number of pigs born alive but with quite huge number of samples in experiment. Lowest heritability based on analyzed literature was found in experiment of Ferraz, et al., (1993), Schneider, et al., (2012) and Alves, et al., (2018): 0.01 – 0.14 (range), 0,01 ± 0,03 and 0,01 ± 0,01 respectively.

Table 2. Genetic trends of the different pig breeds

№	References	Breed	№ of records	Traits	h²	Pe
1	Hamann, H., et al., 2004	German Landrace	48.577	Number of pigs born alive	0.13 ± 0.013	0.063 ± 0.007
		Pietrain	23.003	Number of pigs born alive	0.12 ± 0.019	0.046 ± 0.012
2	Ferraz, J. B. S., et al., 1993.	Landrace - Large White	2.495 – 14.605	Number of pigs born alive	0.01 – 0.14	
				Litter weight at 21 day	0.18 – 0.22	
3	Schneider, J. F., et al., 2012.	Complex MIX between Duroc x Landrace and Yorkshire	1.152	No. born alive	0.09 ± 0.05	8.185
				No. born dead	0.01 ± 0.03	2.077
				No. stillborn	0.03 ± 0.03	1.480
				Litter birth weight	0.20 ± 0.06	12.679
4	Alves, K., et al., 2018.	Canadian-Yorkshire	24.460	Birth Weight	0.15 ± 0.03	0.17 – 0.01
				Weaning Weight	0.04 ± 0.01	0.17 – 0.01
		Canadian-Landrace	24.884	Birth Weight	0.05 ± 0.01	0.17 – 0.01
				Weaning Weight	0.01 ± 0.01	0.19 – 0.01
5	Gäde, S., et al., 2008.	20% - Large White, 7%-Landrace and 73% from their	31.000	Maternal ability	0.05 ± 0.01	0.11 – 0.02

		crosses				
				Savaging of piglets	0.02 ± 0.02	0.68 – 0.20
6	Noguera, J. L., et al., 2019.	Experiment among three varieties of the Iberian pig breeds	18.193	Number born alive	0.078 ± 0.021	0.361 – 0.051
				Total number born	0,086 ± 0,022	0,371 – 0,053
7	Roehe, R., et al., 1995.	Yorkshire - Landrace	30.357 – 42.041 (univariate analyses)	Number of pigs born in total	0.10 – 0.15	
				Number of pigs born alive	0.09 – 0.14	
				Number of weaned pigs	0.06 – 0.08	
8	Kaufmann., 2000.	Large White	18.151	Birth weight of piglets	0.02	
			15.360	Weaning weight of piglets	0.08	
9	Lee, J. H., 2015.	Berkshire	2.457	Total number of piglets born	0.07 ± 0.03	0.75
				Number of piglets born alive	0.06 ± 0.03	0.70

h^2 - heritability; Pe – permanent environmental effect

3.5 Conclusions from the literature

Conventional selection index resulted huge benefit in past, animals were selected based on phenotypic variation. However after some period of time when the methodology reached its maximum potential new procedures became widespread. Best linear unbiased prediction (BLUP) is a method that substitutes conventional phenotypic measurements in the selection theory. It is more precise and accurate in prediction genetic potential of animals, taking into consideration the relationships among the animal and environmental factors. BLUP allows comparing animals merit within different farm with different environment, which is impossible to do with conventional methods.

Economic methodology for constructing selection index is the method by which we evaluate the economic importance of each trait for getting so called economic weights. This coefficient can be used to calculate aggregated breeding value thus profit can be maximized in the procedure of selection.

4. Objectives of the dissertation

The main objective of this PhD study was to construct different BLUP indices for two separate breeds' types from applying the so-called desired gain index methodology. And choose bests models which fit data with best precise based on log-likelihood values. Breeding value estimation of various traits and individuals was realised by the aggregate genotype. Weighted traits relating to economic weights (index weighting factors) avoid the needs of the accurate calculation of economic weights.

The next objectives were targeted in my dissertation:

- Build different models for two separate breeds' types.
- Evaluate genetic parameters for:
  - paternal breeds of pigs (Hungarian: Duroc, Hampshire and Pietrain)
  - maternal breeds of pigs (Hungarian: Large White and Landrace)
- Evaluate genetic trends
- Construct different BLUP indices with the aim to improve all traits with one additive genetic standard deviation. In the end, index value convert to get mean of index 100 and standard deviation 20. The reason for this conversion to make sure that the constructed index of this study comparable with that of those indexes used by the Hungarian Pig Breeders Association.
- Chose best models for indices construction for two separate breed types with using log-likelihood values evaluation.

5. Materials and methods

5.1 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 and Hungarian: Large White, Landrace and one cross Hungarian: Large White x Landrace and Landrace x Large White).

Data used in our research were collected by Hungarian Pig Breeders' Association from 21 herds for (paternal) breeds Hungarian Duroc (HD), Hungarian Hampshire (HH) and Hungarian Pietrain (HP). And from 56 herds for (maternal) 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 4.

Table 3. Farrowing records

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

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.

5.2 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 5. 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.

Table 4. The structure of the applied animal models

Model	**Traits**			**Factors (Type)**								
				Animal	**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	x	x	x	x	x			x	x	x	x	x
2	x	x		x	x			x	x	x	x	x
3	x	x		x	x	X	x	x	x	x	x	
4	x	x	x	x	x	X	x	x	x	x	x	
5	x		x	x	x			x	x	x	x	x
6	x		x	x	x	X	x	x	x	x	x	
7		x	x	x	x				x	x	x	x
/Breeds	**Hungarian - Large White, Landrace and F1 generation**											
8	x	x		x	x			x	x	x	x	x
9	x	x		x	x	X	x	x	x	x	x	
10	x	x	x	x	x			x	x	x	x	x
11	x	x	x	x	x	X	x	x	x	x	x	
12	x		x	x	x			x	x	x	x	x
13	x		x	x	x	X	x	x	x	x	x	
14		x	x	x	x				x	x	x	x

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) = I2e and 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 log-likelihood 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, which is summarized in Table 6. 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.

6. Results and Discussion

6.1 Descriptive statistics of the measured traits

In the table 6 descriptive statistics of the measured traits are summarized. The highest value of mean for number of piglets born alive (NBA) observed in HLW breed and smallest in HH breed. The highest value of number of weaned piglets (NWE) was in HL breed and smallest for HD breed. And litter weight at weaning (LWWE) was highest of corse in F1 cross and smallest in HD breed.

Table 5. Descriptive statistics of the measured traits

Group	Trait	Mean	SD	Maximum	Minimum
Duroc	NBA	9.27	2.45	16	1
	NWE	8.35	1.83	14	2
	LWWE	54.14	16	110	14
Hampshire	NBA	9.15	2.38	16	2
	NWE	8.76	2.23	14	2
	LWWE	61.45	17.17	103	15
Pietrain	NBA	9.19	2.43	16	1
	NWE	8.79	2.1	14	2
	LWWE	54.81	15.58	110	14
Large White	NBA	11.23	2.81	19	1
	NWE	10.28	1.94	16	1
	LWWE	75.50	19.27	130	5
Landrace	NBA	11.03	2.59	19	1
	NWE	10.34	1.71	16	1
	LWWE	69.76	15.38	130	6
F1	NBA	11.16	2.80	19	1
	NWE	10.23	1.58	16	1
	LWWE	78.98	18.28	130	6

F1—cross of Hungarian Large White and Hungarian Landrace; NBA: number of piglets born alive; NWE: number of weaned piglets; LWWE: litter weight at weaning; SD: standard variation.

6.2 Heritability and permanent environmental impact (maternal)

In table 7 the estimated heritability and their standard errors are presented for all 5 breeds and F1 cross. As we mentioned previously that breed was as fixed factor in our models therefore we got heritability values as average for all breeds. The results for breeds HD, HH and HP of the models analyses show that NBA of models 1, 2, 3, 4, 5 and 6 was low and was estimated to be 0.10, 0.11, 0.11, 0.10, 0.10 and 0.10, respectively. There was also a slight tendency for NWE of models 1, 2, 3, 4 and 7 to be evaluated with 0.08, 0.09, 0.08, 0.08 and 0.09 respectively. Measuring heritability from LWWE of models 1, 4, 5, 6 and 7 had a same low tendency by 0.12, 0.11, 0.13, 0.12 and 0.12, respectively. Standard errors for estimated parameters were less than 0.03 in all models.

Irgang et al. (1994) reported higher heritability for Duroc breed for NBA like in case of Skorupski et al. (1996) with value 0.16. Hamann et al. (2004) and Chen et al. (2003) reported a heritability of 0.08-0.09 for NBA of Hampshire and Duroc. Concerning NWE it was 0.05 for Hampshire and 0.07 for Duroc. LWWE in study of Chen et al. (2003) showed smaller result for Duroc and Hampshire with values 0.07 – 0.08 respectively.

Heritability and its standard errors for maternal breeds of pigs are presented in table 7. Heritability for NBA and NWE was low for all models ranging between 0.07 and 0.08 and between 0.06 and 0.07, respectively. On the contrary, the heritability of LWWE was higher in comparison with NBA, showing heritability estimates between 0.12 and 0.14. Wolf et al., (2005) found in their experiment higher heritability for

Large White and Landrace breeds for the number of piglets born alive in parity one, which ranged between 0.09 - 0.13 and between 0.09 - 0.12, respectively. For subsequent parities higher values (0.10–0.13 and 0.11–0.14) were reported. Kasprzyk (2007) found lower values for Landrace breed h2 = 0.023; NBA, h2 = 0.027; the number of piglets on the 21st day and h2 = 0.03 for the litter weight at 21 days. Suárez et al., (2005) estimated higher heritability compared to the current experiment for the Large White breed in the frame of 3 parities where estimates were 0.18, 0.17 and 0.19 for NBA. They also obtained the same result for NWE (0.05, 0.07, and 0.05). In the study of Dube et al., (2013) for the Large White breed, approximately the same results for heritability traits were found for NBA and NWE with 0.07 and 0.03, respectively. On the other hand, h2 for LWWE was lower compared to that in our research (0.06). Suarez et al., (2004) observed two times higher heritability in the Large White breed in the range of 0.15–0.20 for NBA compared to our study, depending on number of parities, but obtained a similar result for NWE (0.03–0.08), depending on parities. Similarly, higher results of heritability were obtained for the Landrace breed for NBA in the range of 0.16–0.27, but NWE had lower heritability, as found in our experiment (0.04–0.09). Nagyné-Kiszlinger et al., (2013) got the same result of heritability for NBA as found in our experiment for Large White (0.09), Landrace (0.06), and F1 (0.06–0.07). Krupová et al., (2017) found in their study slightly higher results for Large White and Landrace breeds for trait NBA and NWE with values of 0.099, 0.102 and 0.091, 0.076, respectively. Size of heritability is the main factor which affects the future selection process in terms of genetic information as it flows from one generation to the next and directly impacts the diversity in the population of our case pigs. Lower or higher heritability that we observed in different investigations depends on many factors. Firstly, it is nature's limitation for how specific traits contribute to their genetic flow. Secondly, between different herds or the same breeds, genetics can be observed at different stages of the selection process. Thirdly, and maybe the most important factor, it is maintaining proper and precise data collection and future processing of information.

Permanent environmental effects for paternal breeds (table 7) in our results were also the average value for all breeds. NBA had low impact on models 1, 2, 3, 4, 5 and 6 ranged from 0.07 to 0.08. Likewise, NWE showed low magnitude to be 0.05, 0.05, 0.04, 0.04 and 0.05 for all models 1, 2, 3, 4 and 7, respectively. Similarly, LWWE had lowest values of environmental impact in comparison with NBA and NWE and was assessed at 0.03, 0.03, 0.03, 0.02 and 0.03 for models 1, 4, 5, 6 and 7 respectively. Standard errors for estimated parameters were less than 0.03 in all models.

Skorupski et al. (1996) reviewed smaller PE for Duroc breed for NBA with value 0.05. Chen et al. (2003) reported about same PE for NBA for Hampshire and Duroc 0.06 – 0.08 respectively. The same results were for NWE for both breeds with value 0.04. However in case of LWWE Chen et al. (2003) had higher values for both breeds Duroc – 0.07 and Hampshire – 0.06.

Permanent effects also are presented in table 7 for maternal breeds and the values are low for all traits. For NBA, NWE, and LWWE, it ranged between 0.06 and 0.08, between 0.01 and 0.05, and between 0.01 and 0.03 respectively.

Nagyné-Kiszlinger et al., (2013) obtained similar results for permanent environmental effects in NBA with a value of 0.06 for 2 breeds and F1 cross. Skorupski et al., (1996) got the same results for permanent environmental variance ratios of NBA, 0.06 and 0.05 for Large White and Landrace, respectively. Krupa and Wolf (2013) found higher results than in our case of permanent environmental effects for NWE, with values of 0.05 and 0.06 for Large White and Landrace, respectively.

Table 6. Estimated heritabilities and maternal permanent effect of the examined traits

Model	**h^2**			**Pe**		
	NBA	**NWE**	**LWWE**	**NBA**	**NWE**	**LWWE**
	Breeds: Hungarian - Duroc, Hampshire and Pietrain					
1	0.10 ± 0.01	0.08 ± 0.01	0.12 ± 0.01	0.08 ± 0.01	0.05 ± 0.01	0.03 ± 0.01
2	0.11 ± 0.02	0.09 ± 0.02	-	0.08 ± 0.02	0.05 ± 0.01	-
3	0.11 ± 0.02	0.08 ± 0.02	-	0.07 ± 0.01	0.04 ± 0.01	-
4	0.10 ± 0.02	0.08 ± 0.01	0.11 ± 0.01	0.07 ± 0.01	0.04 ± 0.01	0.03 ± 0.01
5	0.10 ± 0.02	-	0.13 ± 0.01	0.08 ± 0.02	-	0.03 ± 0.01
6	0.10 ± 0.02	-	0.12 ± 0.01	0.08 ± 0.02	-	0.02 ± 0.01
7	-	0.09 ± 0.02	0.12 ± 0.02	-	0.05 ± 0.01	0.03 ± 0.01
Breeds: Hungarian - Large White, Landrace and F1 generation						
8	0.08 ± 0.004	0.07 ± 0.004	-	0.07 ± 0.004	0.02 ± 0.003	-
9	0.08 ± 0.004	0.07 ± 0.005	-	0.06 ± 0.004	0.01 ± 0.004	-
10	0.07 ±	0.07 ±	0.13 ±	0.07 ±	0.02 ±	0.02 ±

	0.003	0.003	0.004	0.003	0.003	0.003
11	0.08 ± 0.002	0.06 ± 0.003	0.12 ± 0.004	0.06 ± 0.002	0.02 ± 0.004	0.02 ± 0.003
12	0.08 ± 0.005	-	0.14 ± 0.005	0.07 ± 0.005	-	0.02 ± 0.005
13	0.08 ± 0.005	-	0.14 ± 0.005	0.06 ± 0.005	-	0.01± 0.004
14	-	0.07 ± 0.004	0.13 ± 0.005	-	0.02 ± 0.004	0.02 ± 0.005

NBA: number piglets born alive; NWE: number weaned piglets; LWWE: litter weight at weaning; h^2: heritability; Pe: maternal permanent effect

Differences obtained in results for permanent environmental effect can be explained only from one side in that some farms could have been equipped differently in terms of the artificial controlling environment. Therefore, this could be one of the main reasons why the difference is higher or lower. This is also one indicator that should include additional information collected in the classical approach of BLUP methodology. This would allow for a deeper analysis of how different farms are equipped, such as barn temperature fluctuating over the years and how farms were being modernized over a period of time or possibly years.

6.3 Genetic trends

In the table 8 are summarized the estimated genetic trends for all 14 models for all 5 breeds and one F1 cross. Genetic trends were not significant for NBA and NWE traits in case of Duroc breed but tendency of different models was the same. Significant difference observed for LWWE trait with Pr>|t| 0.01, 0.02, 0.01,0.02 and 0.01 with trend 0.17, 0.20, 0.15, 0.14 and 0.16 kilogram per year for models 1, 4, 5, 6 and 7 respectively. Genetic trends of Hampshire breed were not significant for

NBA and NWE but showed same tendency for all models. LWWE was significant for models 1, 4 and 7 with Pr>|t| 0.04, 0.03 and 0.04, with negative trends -0.24, -0.25 and -0.24 kilogram per year, respectively. Estimated genetic trends of Pietrain breed were significant for NBA and NWE traits. NBA had positive trends with Pr>|t| 0.008, 0.009, 0.005, 0.004, 0.01 and 0.006 with a ranged value 0.01 – 0.02 piglets per year for all models (1 – 6) respectively. NWE had Pr>|t| 0.001, 0.002, 0.001, 0.0008 and 0.002 with same genetic trends 0.02 piglets per year for models 1, 2, 3, 4 and 7 respectively. LWWE was not significant but showed the same trend in all models, which ranged 0.08 – 0.11 piglets per year. Chen et al. (2003) got smaller result in Duroc breed for LWWE 0.087 kilogram per year but showed positive value in case of Hampshire 0.007 kilogram per year. The positive and significant genetic trend in case of LWWE for breed Duroc can be explained due increase average daily gain during the suckling period. LWWE for breed Hampshire was negative, it can happen because of constant non-significant decrease in piglets amount during birth and weaning. Concerning the Hungarian Large White, Hungarian Landrace and their cross (F1) Nagy (2017) reported a very small positive annual genetic trend (0.01) for NBA and a small negative genetic trend (-0.04) for NWE. These results were not favorable but it has to be noted that these pig breeds are simultaneously selected for growth and carcass traits (Hungarian Pig Breeders Association, 2017) where they showed higher efficiency. It has to be emphasised that at present the Duroc, Hampshire and Pietrain breeds are not selected for reproductive traits thus the lack of positive trends are not surprising.

The HLW had positive and significant trends for all seven models and for all three traits. Thus, NBA had a prediction ranging between 0.04 and 0.05 piglets per year, NWE had a lower value contrary to NBA ranging between 0.01 and 0.02 piglets per year, and the LWWE trend was between 0.08 and 0.1 kg per year. The HL (Table 8) had significant genetic trends for NBA, showing -0.01–-0.02 piglets per year and for NWE ranging between 0.003 and 0.006 piglets per year. Genetic trends of LWWE in the case of Landrace were not significant. The F1 (Table 8) had significant genetic trends for all three traits but with negative tendencies. NBA and NWE showed similar tendencies with -0.01–-0.02 and -0.01–-0.02 piglets per year, respectively. The genetic trend for LWWE was not significant in model number 11, but for all other models, we observed negative trends of -0.02–-0.08 kg per year. The estimated genetic trends for all models related to the maternal breeds generally showed the same tendency and varied in a small range. Models 8–9, 10–11, and 12–13 characterized the same traits but partly contained different factors. Chen et al., (2003) estimated different results in contrast to that in the current study for all traits and average values (Large White and Landrace breeds) of genetic trends were 0.018 piglets per year for NBA, 0.114 kg per year for LWWE, and 0.004 piglets per year for NWE. Chansomboon et al., (2010) reported negative and significant genetic trends as average for Large White, Landrace, and F1 (cross of Large White and Landrace) for reproduction traits. Genetic trends had the values of -0.017 piglets per year for NBA, -0.019 piglets per year for NWE, and -0.022 kg per year for LWWE. Similarly, we obtained in our research negative trends but for Landrace breed just for NBA and F1cross for all three traits. Genetic gain for the Landrace breed in the experiment of Kasprzyk (2007) exhibited the same negative tendency as in the current experiment with a value of -0.05 piglets per year for NBA, but in the case of NWE result was different and negative (-0.04 piglets per year) and LWWE had a negative trend of -0.48 kg per year. It should be noted that a breed such as Landrace is selected mainly for growth and carcass traits, which may have contributed to the reported selection inefficiency observed for the analyzed populations. Based on our findings, no substantial genetic improvement can be expected in the near future for Hungarian and Landrace breeds in our herds.

Table 7. Estimated trends for paternal and maternal breeds of pigs

Breeds	**Models**	**NBA**		**NWE**		**LWWE**	
		Pr > |t|	**B**	**Pr > |t|**	**B**	**Pr > |t|**	**B**
Duroc	1	0.61	0.003	0.6	-0.002	0.01	0.17
	2	0.39	0.005	1.0	-0.000005	-	-
	3	0.4	0.005	0.9	-0.0004	-	-
	4	0.6	0.003	0.5	-0.003	0.02	0.2
	5	0.63	0.003	-	-	0.01	0.15
	6	0.61	0.003	-	-	0.02	0.14
	7	-	-	0.40	-0.003	0.01	0.16
Hampshire	1	0.24	-0.01	0.33	-0.005	0.04	-0.24
	2	0.17	-0.014	0.18	-0.008	-	-
	3	0.1	-0.02	0.1	-0.009	-	-
	4	0.2	-0.01	0.22	-0.006	0.03	-0.25
	5	0.19	-0.01	-	-	0.07	-0.21
	6	0.13	-0.02	-	-	0.06	-0.21
	7	-	-	0.42	-0.004	0.04	-0.24
Pietrain	1	0.008	0.02	0.001	0.02	0.22	0.09
	2	0.009	0.02	0.002	0.02	-	-
	3	0.005	0.02	0.001	0.02	-	-
	4	0.004	0.02	0.0008	0.02	0.23	0.08

	5	0.01	0.01	-	-	0.15	0.11
	6	0.006	0.01	-	-	0.17	0.10
	7	-	-	0.002	0.02	0.21	0.09
Large White	8	<0.0001	0.04	<0.0001	0.02	-	-
	9	<0.0001	0.04	<0.0001	0.02	-	-
	10	<0.0001	0.04	<0.0001	0.01	<0.0001	0.09
	11	<0.0001	0.05	<0.0001	0.02	<0.0001	0.1
	12	<0.0001	0.04	-	-	<0.0001	0.1
	13	<0.0001	0.05	-	-	<0.0001	0.1
	14	-	-	<0.0001	0.01	<0.0001	0.08
Landrace	8	<0.0001	-0.02	0.04	0.003	-	-
	9	<0.0001	-0.01	0.0007	0.005	-	-
	10	<0.0001	-0.02	0.005	0.004	0.5	-0.02
	11	<0.0001	-0.02	<0.0001	0.006	0.3	0.02
	12	<0.0001	-0.02	-	-	0.7	-0.009
	13	<0.0001	-0.01	-	-	0.1	0.03
	14	-	-	0.001	0.005	0.6	-0.01
F1	8	<0.0001	-0.02	<0.0001	-0.02	-	-
	9	<0.0001	-0.02	<0.0001	-0.02	-	-
	10	<0.0001	-0.02	<0.0001	-0.02	0.004	-0.06
	11	<0.0001	-0.01	<0.0001	-0.01	0.2	-0.02
	12	<0.0001	-0.02	-	-	<0.0001	-0.08
	13	<0.0001	-0.01	-	-	0.007	-0.05
	14	-	-	<0.0001	-0.02	0.002	-0.06

NBA: number of piglets born alive; NWE: number of weaned piglets; LWWE: litter weight at weaning; F1: Hungarian - Large White x Landrace and Landrace x Large White

6.4 Index weighting factors, genetic correlation and index by breeds

The calculated index coefficients satisfying the desired gain of one additive standard deviation for traits in frame of my investigations (index are presented in table 9). As mentioned above the calculated index scores were further modified in order to get index mean equal to 100 and standard deviation equal to 20. The reason for this conversion was to make the constructed index of this study comparable with that of those indexes used by the Hungarian Pig Breeders Association (2017). At present the BLUP index of the HD, HH, HP and HLW, HL breeds consists of number of piglets born alive (NBA), number of weaned piglets (NWE) and litter weight weaning (LWWE). The main difference between the index of the present study and that of the Hungarian Pig Breeders Association (2017) is that the latter is based on the calculation of the economic values.

Table 8. Selection indexes weighting factors for the examined traits

Models	**Index**
/Breeds	**Hungarian - Duroc, Hampshire and Pietrain**
1	12.9199*ebv1 + 5.2524*ebv2 + 2.4661*ebv3
2	13.9283*ebv1 + 18.882*ebv2
3	13.8091*ebv1 + 18.9603*ebv2
4	12.3868*ebv1 + 5.9788*ebv2 + 2.4762*ebv3
5	16.0511*ebv1 + 2.5533*ebv3
6	15.8871*ebv1 + 2.5689*ebv3
7	20.516*ebv2 + 2.517*ebv3
/Breeds	**Hungarian - Large White, Landrace and F1 generation**
8	15.6805*ebv1 + 26.3388*ebv2
9	15.1689*ebv1 + 25.9797*ebv2
10	14.4687*ebv1 + 11.2599*ebv2 + 1.7521*ebv3
11	13.8544*ebv1 + 12.3412*ebv2 + 1.8160*ebv3
12	16.8858*ebv1 + 2.1646*ebv3
13	16.2625*ebv1 + 2.1174*ebv3
14	25.2420*ebv2 + 2.0141*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.

In the tables 10 – 12 are presented results of the genetic correlation (Pearson's correlation) for paternal breeds. The analysis resulted at moderate to high correlation coefficients between indexes (aggregate genotype) and traits for all three breeds. In all models, it ranged 0.66 - 0.97 for Duroc breed, 0.84 - 0.98 for Hampshire breed and

0.77 - 0.97 for Pietrain breed. Genetic correlation among trait values in models was also different for all breeds. In case of Duroc breed, NWE had a high and same correlation with NBA 0.87 for models 2, 3 and 4 but LWWE had the lowest correlation with NBA 0.14, 0.10 and 0.12 for models 4, 5 and 6 respectively. LWWE also had a low correlation with NWE 0.12 and 0.10 for models 4 and 7 respectively. Hampshire had a high correlation between traits NWE and NBA 0.91, 0.91 and 0.90 for models 2, 3 and 4 respectively. LWWE for Hampshire breed had a moderate correlation with NBA 0.51, 0.54 and 0.54 for models 4, 5 and 6 respectively. LWWE also had a moderate correlation with NWE 0.57 and 0.60 for models 4 and 7 respectively. Pietrain breed had a high and the same correlation between values of NWE and NBA traits 0.88 for models 2, 3 and 4. LWWE had a low correlation value with NBA 0.37, 0.38 and 0.38 for models 4, 5 and 6 respectively. LWWE also had a low correlation with NWE trait 0.35 and 0.36 for models 4 and 7 respectively.

Table 9. Genetic correlation coefficient (Pearson's correlation) between examined traits and the selection index scores Duroc breed

Models	**Traits**			
	Traits	**NWE**	**LWWE**	**Index**
1	NBA	0.87	0.13	0.71
	NWE	-	0.13	0.67
	LWWE	-	-	0.78
2	NBA	0.87	-	0.97
	NWE	1	-	0.96
3	NBA	0.87	-	0.97
	NWE	1	-	0.96
4	NBA	0.87	0.14	0.73
	NWE	1	0.12	0.67
	LWWE	-	1	0.78
5	NBA	-	0.10	0.70
	LWWE	-	1	0.78
6	NBA	-	0.12	0.72
	LWWE	-	1	0.78
7	NWE	1	0.10	0.66
	LWWE	-	1	0.81

NBA: number born alive; NWE: number weaned; LWWE: litter weight at weaning

Table 10. Correlation coefficient between examined traits and the selection index for Hampshire breed

Models	**Traits**			
	Traits	**NWE**	**LWWE**	**Index**
1	NBA	0.91	0.52	0.84
	NWE	-	0.59	0.86
	LWWE	-	-	0.89
2	NBA	0.91	-	0.97
	NWE	1	-	0.98
3	NBA	0.91	-	0.97
	NWE	1	-	0.98
4	NBA	0.90	0.51	0.84
	NWE	1	0.57	0.86
	LWWE	-	1	0.89
5	NBA	-	0.54	0.84
	LWWE	-	1	0.91
6	NBA	-	0.54	0.84
	LWWE	-	1	0.91
7	NWE	1	0.60	0.89
	LWWE	-	1	0.90

NBA: number born alive; NWE: number weaned; LWWE: litter weight at weaning

Table 11. Correlation coefficient between examined traits and the selection index for Pietrain breed

Models	**Traits**			
	Traits	**NWE**	**LWWE**	**Index**
1	NBA	0.88	0.37	0.82
	NWE	-	0.37	0.78
	LWWE	-	-	0.83
2	NBA	0.88	-	0.97
	NWE	1	-	0.97
3	NBA	0.88	-	0.97
	NWE	1	-	0.97
4	NBA	0.88	0.37	0.82
	NWE	1	0.35	0.77
	LWWE	-	1	0.83
5	NBA	-	0.38	0.81
	LWWE	-	1	0.85
6	NBA	-	0.38	0.81
	LWWE	-	1	0.85
7	NWE	1	0.36	0.81
	LWWE	-	1	0.84

NBA: number born alive; NWE: number weaned; LWWE: litter weight at weaning

Tables 13 – 15 are presented results of the genetic correlation (Pearson's correlation) for maternal breeds. The index for HLW had a high correlation with traits (from 0.74 to 0.91). NWE had a moderate correlation with NBA (ranging from 0.48 to 0.50). On the contrary, LWWE had a low to moderate correlation with NBA and NWE (ranging from 0.32 to 0.37) and (ranging from 0.56 to 0.58), respectively. HL index had a moderate to high correlation with traits (0.67–0.91). NBA and NWE had a moderate correlation (0.56–0.60), but LWWE had a low to moderate correlation with NBA and NWE (0.33–0.39 and 0.28–0.31, respectively). F1 index had a moderate to high correlation with traits (0.66–0.89). NBA and NWE had a moderate correlation (0.38–0.44); in contrast, LWWE had a low to moderate correlation with NBA and NWE (0.20–0.24 and 0.38–0.43, respectively).

In the work of Suárez et al. (2005), negative genetic correlations were found between NBA and NWE in frame of 3 parities respectively (-0.23, -0.96, and 0.01) for the Large White breed in contrast to our findings. However, Dube et al. (2013) found positive genetic correlations with values for NBA with NWE and LWWE of 0.88 and 0.32, respectively. NWE and LWWE correlated on level 0.78. Suarez et al. (2004) estimated in their study contradictory results for genetic correlation between NWE and NBA depending on the number of parities of the Large White breed (0, -0.66, and -0.67 for parities 1–3, respectively). They obtained similar results for Landrace breed (0.07 and -0.45 for parities 1–2, respectively). On the contrary, Krupová et al. (2017) found in their study high correlations between the traits NBA and NWE for Large White and Landrace breeds of 0.954 and 0.979, respectively. The NBA showed a correlation of 0.99 with the NWE and 0.78 with the LWWE in experiment of Kasprzyk (2007). The correlation between NWE and LWWE was 0.82, which was higher compared to that in our study.

Table 12. Genetic correlation coefficient (Pearson's correlation) between examined traits and the selection index for the Large White breed.

Models	**Traits**			
	Traits	**NWE**	**LWWE**	**Index**
8	NBA	0.48	-	0.85
	NWE	-	-	0.88
9	NBA	0.50	-	0.86
	NWE	-	-	0.88
10	NBA	0.48	0.32	0.74
	NWE	-	0.58	0.78
	LWWE	-	-	0.85
11	NBA	0.48	0.33	0.74
	NWE	-	0.57	0.77
	LWWE	-	-	0.86
12	NBA	-	0.32	0.74
	LWWE	-	-	0.87
13	NBA	-	0.37	0.77
	LWWE	-	-	0.88
14	NWE	-	0.56	0.86
	LWWE	-	-	0.91

NBA: number born alive; NWE: number weaned; LWWE: litter weight at weaning

Table 13. Genetic correlation coefficient (Pearson's correlation) between examined traits and the selection index for the Landrace breed.

Models	**Traits**			
	Traits	**NWE**	**LWWE**	**Index**
8	NBA	0.59	-	0.90
	NWE	-	-	0.88
9	NBA	0.60	-	0.91
	NWE	-	-	0.88
10	NBA	0.56	0.34	0.83
	NWE	-	0.31	0.68
	LWWE	-	-	0.77
11	NBA	0.56	0.33	0.83
	NWE	-	0.28	0.67
	LWWE	-	-	0.77
12	NBA	-	0.36	0.83
	LWWE	-	-	0.82
13	NBA	-	0.39	0.83
	LWWE	-	-	0.83
14	NWE	-	0.28	0.76
	LWWE	-	-	0.84

NBA: number born alive; NWE: number weaned; LWWE: litter weight at weaning

Table 14. Genetic correlation coefficient (Pearson's correlation) between examined traits and the selection index for F1.

Models	**Traits**			
	Traits	**NWE**	**LWWE**	**Index**
8	NBA	0.40		0.85
	NWE			0.82
9	NBA	0.44		0.87
	NWE			0.83
10	NBA	0.38	0.23	0.73
	NWE		0.43	0.66
	LWWE			0.81
11	NBA	0.41	0.23	0.75
	NWE		0.38	0.66
	LWWE			0.79
12	NBA		0.20	0.73
	LWWE			0.81
13	NBA		0.24	0.76
	LWWE			0.81
14	NWE		0.41	0.78
	LWWE			0.89

NBA: number born alive; NWE: number weaned; LWWE: litter weight at weaning

In the table 16 and 17 are present results of ranging the estimated index scores for paternal and maternal breeds of pigs. Which are presented for seven models and every genotype separately. Calculated aggregate genotypes for paternal breeds showed the highest index values for HD ranging from 49.77 to 186.56. Compared to Duroc the index scores were somewhat lower for the HH and HP breeds where the minimum and maximum index scores were 30.92 and 165.97, respectively.

The results of index scores for maternal breeds as we can see have wider range of index scores for HLW in all seven models compare to HL and F1. Lowest value and ranging observed for F1 generation.

Table 15. Range of the estimated index scores for paternal breeds

Models	**Breed**	**Scores**
1	Duroc	49.77 - 186.56
	Hampshire	44.66 - 163.97
	Pietrain	30.92 - 165.97
2	Duroc	44.07 - 179.91
	Hampshire	19.35 - 162.10
	Pietrain	35.55 - 180.96
3	Duroc	45.89 - 181.03
	Hampshire	19.26 - 158.56
	Pietrain	37.04 - 179.70
4	Duroc	46.41 - 186.88
	Hampshire	43.94 - 163.64
	Pietrain	29.95 - 166.75
5	Duroc	48.91 - 184.03
	Hampshire	41.84 - 165.73
	Pietrain	28.45 - 167.53
6	Duroc	49.11 - 184.23
	Hampshire	41.06 - 165.55
	Pietrain	27.22 - 165.58
7	Duroc	46.43 - 179.38
	Hampshire	46.11 - 172.07
	Pietrain	35.56 - 163.53

Table 16. Range of the estimated index scores for maternal breeds

Models	**Breed**	**Scores**
8	Large White	-3.97 – 190.79
	Landrace	13.37 – 173.78
	F1	27.74 – 171.60
9	Large White	-0.93 – 188.99
	Landrace	17.25 – 175.70
	F1	24.88 – 175.98
10	Large White	-4.15 – 175.12
	Landrace	18.79 – 181.15
	F1	14.63 – 161.33
11	Large White	-1.81 – 178.63
	Landrace	23.49 – 178.71
	F1	14.66 – 160.63
12	Large White	-2.30 – 179.89
	Landrace	18.00 – 182.61
	F1	5.22 – 163.98
13	Large White	-1.03 – 187.16
	Landrace	22.74 – 180.79
	F1	6.51 – 164.31
14	Large White	-23.77 – 172.39
	Landrace	37.18 – 168.76
	F1	13.14 – 159.12

6.5 Models' fit, estimated genetic parameters of the best fitting model

In Table 5, it can be seen that the models differed in one fixed factor, including either parity or the age of the sow at farrowing and/or at weaning. Based on the estimated log likelihood-value models (Table 18), including parity were inferior compared to those models containing age for both type of breeds paternal: the two-traits (15 216 vs. 15 361; 15 605 vs. 15 808) and for three-traits (15 046 vs. 15 229) respectively. And for maternal: the two-traits (154 325 vs. 156 095; 145 979 vs. 148 224) and for the three-trait (167 132 vs. 169 370) models respectively.

The worst-fitting model for breeds HD, HH and HP was model number 7 with value 10 335. Best fitting model that better describe data was model number 6 (15 808 – table 18). Estimated variance–covariance components of the best-fitting model (model 6) for this breeds presented in table 18.

Altogether the worst-fitting model (HLW, HL and F1) was model 14, with the lowest log-likelihood value of 95 842. On the contrary, model 11 gave the best fits of log-likelihood value of 169 370 with data (Table 18). Estimated variance–covariance components of the best-fitting model (model 11) also presented in Table 18.

Table 17. Log-likelihood values of the used 14 models and estimated variances (diagonals) and covariance (off-diagonals) of the best fitting model

Trait		**Factors**	**NBA**	**NWE**	**LWWE**
Hungarian - Duroc, Hampshire and Pietrain					
Type		**A**	0.57		1.39
Models	**Log likelihood**				21.71
1	15 046				
2	15 216	**Pe**	0.41		1.25
3	15 361				3.79
4	15 229				
5	15 605	**Res**	4.48		13.91
6	15 808				148.45
7	10 335				
Hungarian - Large White, Landrace and F1 generation					
8	154 325	**A**	0.56	0.15	1.18
9	156 095			0.17	1.27
10	167 132				29.46
11	169 370	**Pe**	0.45	0.12	0.51
12	145 979			0.07	0.53
13	148 224				5.20
14	95 842	**Res**	6.16	1.76	10.32
				2.62	17.29
					209.36

A: additive genetic; Pe: maternal permanent; Res: residual; NBA: number of piglets born alive; NWE: number of weaned piglets; LWWE: litter weight at weaning.

Figures 1 – 5 below give graphical descriptions for 2 best fitting models. First for HD, HH, HP (1 – 2) and second for HLW, HL and F1 generation (3 – 5).

Figures 1 – 2 (paternal breeds) show changing for traits NBA and LWWE. In case of HD trait NBA have positive trend but LWWE positive changing possible observe just in last years. Simply indicate that breeders hardly worked on this trait. HH and HP in case of NBA and LWWE have constant positive trend. There are two negative outliers in 2013 year for HH breed. I do not know obvious reasons of this.

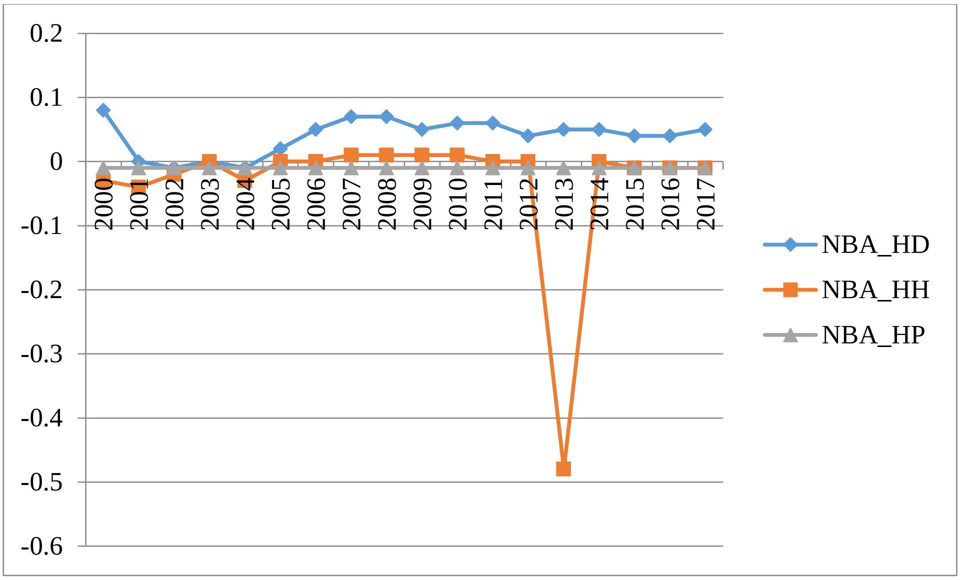

Figure 1. Estimated trends of best fitting model for number piglets born alive by years

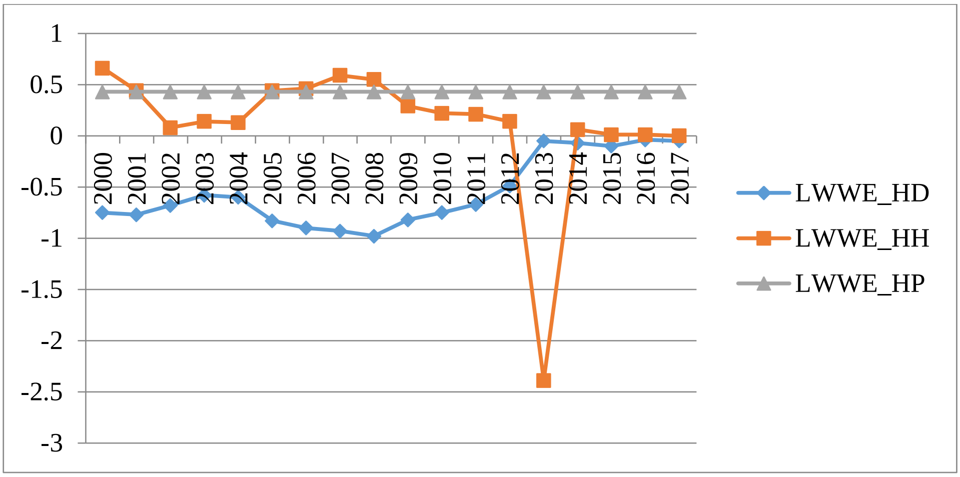

Figure 2. Estimated trends of best fitting model for litter weight at weaning by years

From figures 3 – 5 (maternal breeds) possible make conclusion that selection for traits NBA, NWE and LWWE are negative constant. Possible to see any positive change just for F1 generation that is the reason of heterosis effect. But F1 has also negative trend for NWE trait (figure 4) because I think this is question just of survival of piglets before weaning.

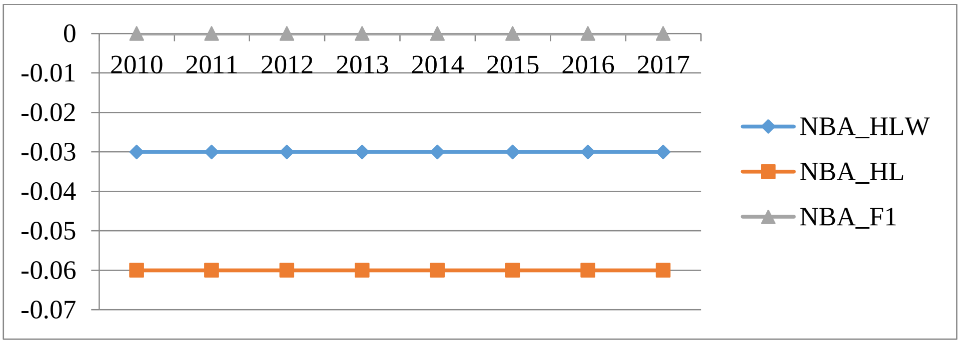

Figure 3. Estimated trends of best fitting model for number piglets born alive by years

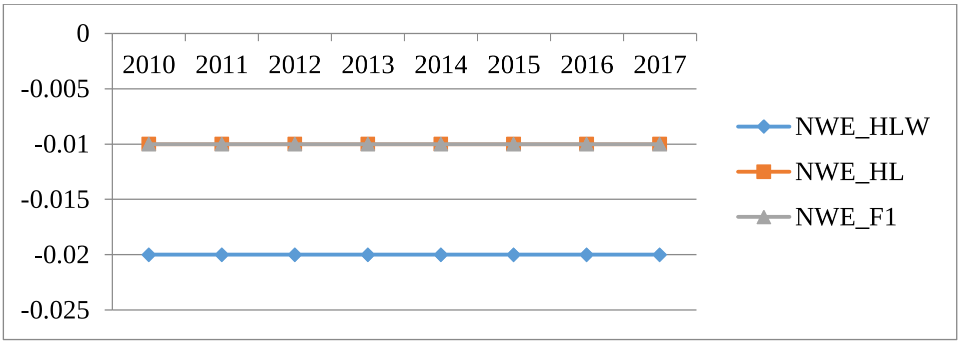

Figure 4. Estimated trends of best fitting model for number of weaned piglets by years

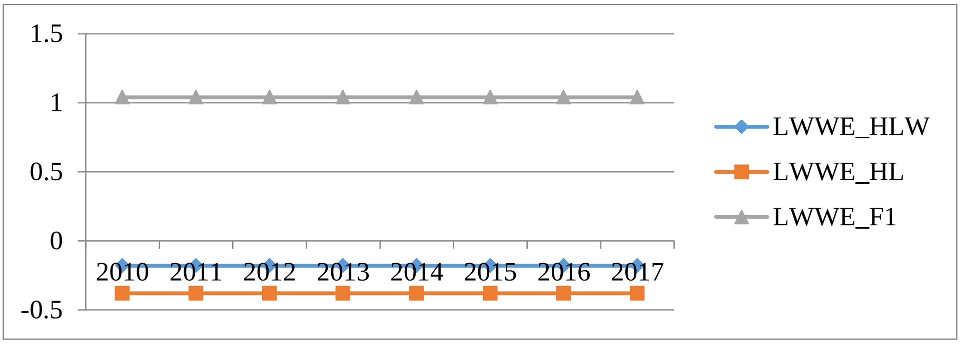

Figure 5. Estimated trends of best fitting model for litter weight at weaning by years

7. 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.

8. 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).

9. Summary

Farrowing records of 5 Hungarian breeds of pigs were reported: Duroc (HD), Hampshire (HH) and Pietrain (HP) and maternal: Large White (HLW), Landrace (HL). Also were reported results for F1 cross generation of Large White and Landrace.

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.

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.

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.

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.

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.

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).

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13. Curriculum vitae

Oleksandr Kodak was born on 28th of March in 1984 in Poltava, Ukraine. He graduated from high education in 2006 in Poltava State Agrarian Academy (M.Sc.) his first high education. Second he got from Kaposvar University (M.Sc.) in 2013 year. From 2017 up to august 2022 year, he was a PhD student first Kaposvar University and because of merging many universities in the end Kaposvár Campus, Hungarian University of Agriculture and Life Sciences.

Since 2006 when he began his career, he worked in couples of scientific institutions (Poltava State Agrarian Academy and Kvasnytskyy Pig Breeding Institute of the National Academy of Agricultural Sciences of Ukraine). Also he has relations to the FAO UN where had his first the contract in 2015 year. Also he worked in Ministry of Agricultural Policy and Food of Ukraine as independent consultant.