

METHODS OF IMPROVEMENT OF QUANTITATIVE TRAITS IN PIG BREEDING AND THEIR EFFICACY IN POLISH CONDITIONS

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Improvement of animals based on breeding work is a set of activities aiming to obtain individuals with fixed and desired traits. It is not possible to explicitly define the best traits even in commercial pig breeding because there are different priorities in the expected levels of performance for different traits. Improvement trends differ between breeders and often change depending on consumers preferences.

In pig breeding work we often deal with improvement of polygenic traits determined by many genes. The possibilities of selection based on simply-inherited traits determined by single or a few genes were long and almost completely depleted. These are so called quality traits and are very often connected with color. These traits are slightly or not at all influenced by environment. Traits determined by many genes with constant genetic variability, phenotypically regarded as quality (zero-one) traits, are also economically important. These are so called threshold traits. In pig breeding the example of threshold trait is disease resistance to acute diseases ending with death or survival without middle stages. It is usually a special body feature that makes it impossible for the disease to develop although pathogen entered the body. These traits are considered as threshold traits because when exceeding the threshold of own genes they cause fundamental changes in phenotype. In case of pigs the example of the threshold trait is piglets resistance to oedema disease which is determined by a single gene – mutation in gene FUT1. Usually these types of traits are polygenic.

However the most important pig performance traits belong to the group of quality traits and their improvement is the most important part of almost all breeding programs. The easiest and most effective is the improvement of traits that are determined by genes in a simple way. Then the breeder concentrates on identifying individuals with desired genotypes and after selection keeps them for further breeding. Such situation is unusual because straight majority of traits are determined by many genes. In such case selection of the best genotypes is impossible and breeding decisions are taken based on animals performance value or even better if it is based on animal breeding value.

Genetics of quantitative traits is based on the basic genetic model presented in the following equation: $P = \mu + G + E$

P – phenotypic or performance value of given trait in individual animal

μ - average phenotypic value of all animals in the population

G – genetic value of given trait in individual animal

E - influence of environmental factors on performance of individual animal

The average phenotypic value in the population is the most important value while G and E are deviations from the population average and are relative values. When selecting the best individuals for parents of the next generation we should above all take under consideration their genetic value. However breeders in practice are dealing with performance traits which level depends on combination between genotype and environment. Improvement of animals traits is possible only when there is trait variability. Breeding work is effective under condition that not only phenotypic value of important traits has been improved but also their genotype improved. Breeders are not able to directly evaluate genotype of the individual animal so they are evaluating genotype based on phenotype of the animal and phenotype of its relatives. Interdependence between genotypes of evaluated animals is equal to their coefficient of relationship. Correlation between phenotype and genotype of individual animal is equal to h , that is a square root of heritability of given trait h^2 ($\sqrt{h^2}$).

When analyzing relations between phenotype and genotype we should remember that regression between genotype and phenotype (b_{gp}) is equal to coefficient of heritability of given trait – h^2 . We are able to define what profits we can get when using different types of evaluation i.e. we can find out whether information about higher number of relatives will improve accuracy of individual animal evaluation. For example regression between breeding value of individual

animal and phenotypic value of its father equals $0,5 h^2$ and correlation $- 0,5 h$. In order to evaluate breeding value of individual animal based on phenotypic values of its relatives we are using product of coefficient of correlation, between genotype of evaluated animal and a single relative, and a value obtained from the following equation : $\sqrt{(n/(1+(n-1)R_g h^2))}$, R_g is a coefficient of relationship between evaluated animal and its relatives contributing to animals' evaluation.

Coefficient of regression between breeding value of individual animal and average value of phenotypic values of its relatives is expressed with the following equation: $\frac{nr_g h^2}{1+(n-1)r_g h^2}$. Based on the presented equations we can estimate correlation and regression between breeding value of individual animal and phenotypic value of its relatives. The values of estimated coefficients of correlation and regression are highly influenced by heritability coefficient of given trait – h^2 and number of evaluated relatives.

Taking under consideration above information we can claim that in case of highly heritable traits the most accurate evaluation is based on animal own phenotypic value and in case of low heritable traits the accuracy of evaluation increases when based on relatives performance (progeny is the best).

In pig breeding traits that are being improved belong to the 3 main groups: reproduction performance, fattening and slaughtering performance. The main goal of breeding work is improvement of pure breeds. The next step after obtaining positive results from the first phase is selection of proper animals for mating. This goal has to be taken under consideration already in the first phase of breeding work when selection directions for different breeds and their genetic identity are diversified. The basic tool in reproduction works and pig production is commercial crossing.

Commercial crossing is successful in Poland thanks to having sire and dam lines and breeds that have the following features:

Dam component:

- High reproduction performance,
- High daily gain,
- The best feed conversion possible to obtain,
- Good musculature,
- stress resistant.

Sire component:

- High daily gain,
- High lean meat and good quality meat
- The best feed conversion possible to obtain
- Stress resistant (not for all breeds);

Market demands contributed to defining general breeding goal that includes goals for all breeds: the aim is to produce as much meat as possible at the lowest possible cost. This goal includes lowering of fatteners production costs, improving sows' prolificacy, improving daily gain and lean meat content up to 55% and preserve good quality meat at the same time.

Here are the target performance values of the most important maternal traits:

1.	Number of alive born piglets	12
2.	Number of piglets at 21 days	11
3.	Age at first farrowing	340 days
4.	Prolificacy	23
5.	Number of teats	14
6.	Period between litters	160 days
7.	Daily gain	680 g
8.	Lean meat percentage	57 % for gilts 60 % for boars
9.	Free from gene RYR1 ^T mutation	genotype RYR1 ^{NN}

Here are the target performance values of the most important paternal traits:

- | | | | |
|----|---|--------|--|
| 1. | Lean meat percentage | | duroc, hampshire 61%,
pietrain, Belgian landrace 63%. |
| 2. | daily gain | 850 g | |
| 3. | Feed conversion | 2,5 kg | |
| 4. | Free from gene RYR1 ^T mutation | | genotype RYR1 ^{NN} |
| 5. | Number of teats | 14 | |

In order to obtain the target performance values and to confirm them with animals breeding value it is necessary to go through all stages of breeding work. Below there is a scheme of basic elements of breeding work, obtained phenotypic progress and degree of completion of the breeding goal.

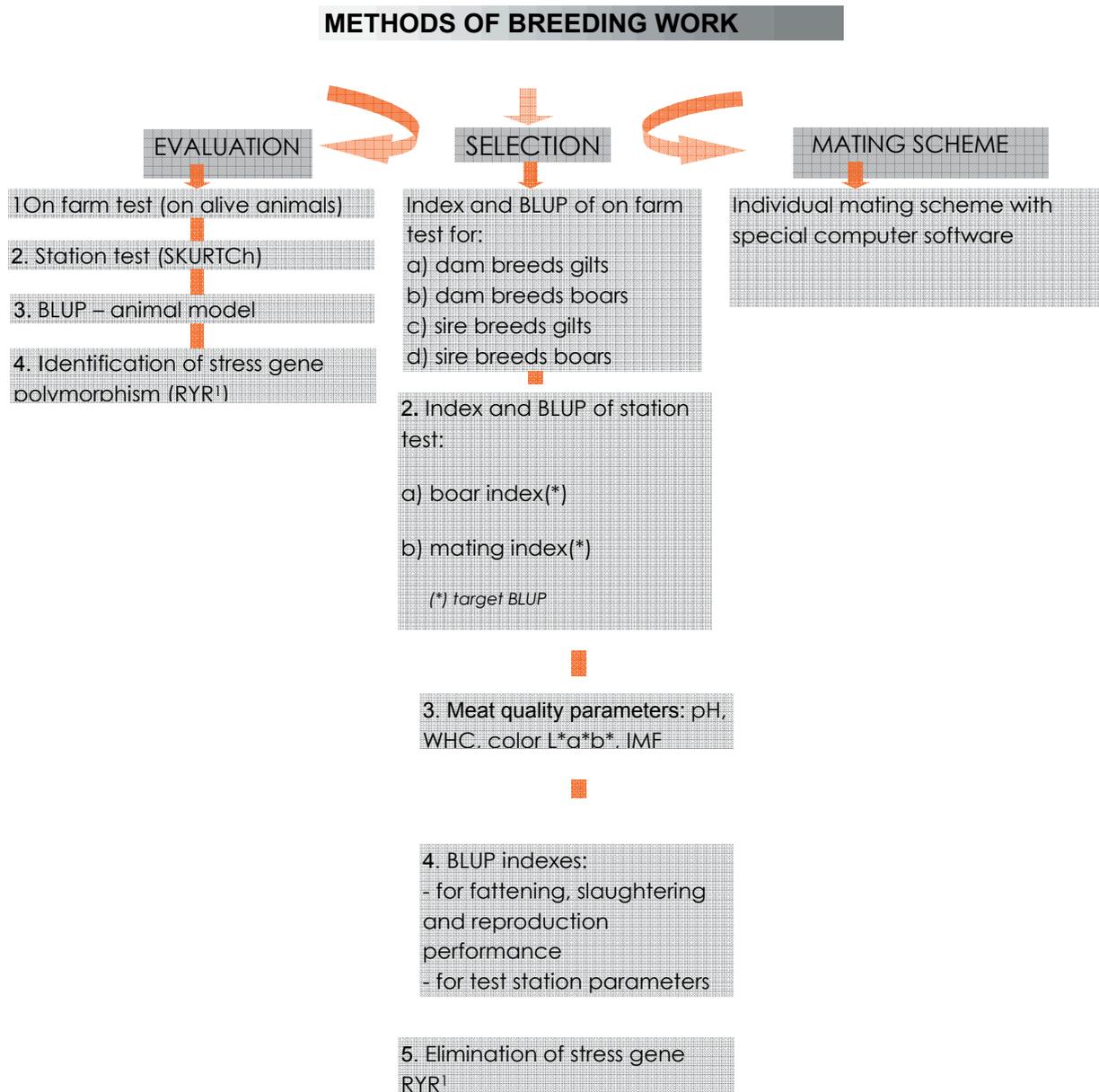


Table 1. Phenotypic progress in reproduction performance traits obtained in the period 1996 – 2007 for dam and sire* breeds

	Productivity	Number of piglets at 21 days	Prolificacy	Period between litters, days	Age at first farrowing, days
Polish Large White (plw)	+ 0,29	+ 0,15	+ 1,75	- 13,0	- 6,0
Polish Landrace (pl) pulawska	+ 0,26	+ 0,35	+ 1,9	- 14,0	- 1,0
duroc	- 0,43	- 0,43	+ 0,25	- 11,0	- 2,0
hampshire	+ 0,75	+ 0,77	+ 2,25	- 7,0	- 10,0
pietrain*	+ 1,35	+ 1,39	+ 3,26	- 6,0	- 33,0
	+ 0,07	+ 0,2	+ 1,42	- 11,0	+ 1,0

* for pietrain since 1997

Table 2. Phenotypic progress in fattening and slaughtering performance obtained in the period 1996 – 2007 for boars and gilts of dam and sire* breeds

		Daily gain, g	Backfat thickness, mm	Height of the loin eye, mm	Lean meat, %
plw	♂	+ 84	- 3,66	+ 8,28	+ 5,96
	♀	+ 80	- 3,0	+ 6,39	+ 5,95
pl	♂	+ 73	- 3,22	+ 8,29	+ 5,51
	♀	+ 62	- 3,84	+ 6,95	+ 6,13
pulawska	♂	+ 28,5	- 1,7	+10,09	+ 3,84
	♀	+ 1,6	- 1,52	+ 7,96	+ 4,06
duroc	♂	+ 98,4	- 3,7	+ 9,59	+ 6,28
	♀	+ 104,5	- 4,3	+ 6,78	+ 6,46
hampshire	♂	+ 130,9	- 3,8	+ 6,81	+ 6,0
	♀	+ 175,1	- 3,8	+ 7,46	+ 5,3
pietrain*	♂	+ 91,3	- 1,35	+ 4,92	+ 1,17
	♀	+ 104,4	- 2,05	+ 3,85	+ 1,50

* for pietrain since 1997

Table 3. Degree of completion of breeding goal for sire breeds

TRAIT	TARGET VALUE	EVALUATION RESULTS		DEGREE OF COMPLETION OF BREEDING GOAL	OF OF
		2007			
Lean meat, %	61 duroc	60,1		98,5%	
	61 hampshire	61,5		100,8%	
	63 pietrain	63,3		100,5%	
Daily gain, g	850 duroc	706		83,1%	
	850 hampshire	717		84,4%	
	850 pietrain	676		79,5%	

Table 4. Degree of completion of breeding goal for dam breeds

TRAIT	TARGET VALUE	RESULTS 2007		DEGREE OF COMPLETION OF BREEDING GOAL		OF OF
		PLW	PL	PLW	PL	
		Number of alive born piglets	12	11,37	11,43	
Number of piglets at 21 days	11	10,58	10,64	96%	97%	
Age at first farrowing, days	340	356	346	95%	98%	
Perid between litters, days	160	179	180	88%	88%	
Daily gain, g	♂ 680	702	696	103,2%	102,4%	
Lean meat,%	♀ 57	58,1	57,7	101,9%	99,8%	101,2%
		59,9	59,3			
	♂ 60					

In the National Breeding Program in the recent years there was a great pressure put on improving fattening and slaughtering performance. Improvement of fertility and prolificacy was not the priority lately. Changes in the program were necessary in order to improve traits, which values were far behind results obtained in other EU countries. Such situation made Polish pigs less competitive on the common market. The level of fertility and prolificacy performance was satisfying and improvement of their genetic background would not be successful without improvement of environmental conditions at the same time, which was limited due to breeders poor investment capabilities. After obtaining high level of fattening and slaughtering performance we can finally treat reproduction performance as a priority.

In the last ten years the progress in the most numerous breeds, plw and pl, in number of alive born piglets was 0,14 and in number of reared piglets was 0,15 per generation. Obtained progress was the highest in the color breeds (duroc, hampshire i pietrain). The great role in obtained progress played the improvement of environmental conditions. Reproduction performance traits are low heritability traits and it is difficult to expect effective selection if it is based on results of phenotypic evaluation. There is a simple conclusion that the most effective would be introduction of a method strictly connected with breeding value estimated based on performance of great number of relatives.

For a very long time there was only one common index for all breeds used in breeding practice. This index was calculated for fattening and slaughtering performance. Selecting animals according to above index favors individuals

with high daily gain and lean meat percentage. In case of sire breeds it is legitimate. But in case of dam breeds it is not the best solution because it favors pigs from less numerous litters that grow the fastest. This error is partially eliminated by the fact that there are more pigs from more numerous litters. What is more, in breeding practice there is a threshold selection that puts up minimum performance standards, including reproduction performance, for individuals of each breed.

In case of improvement of fattening and slaughtering traits the simple selection index has been used for a very long time. High heritability of these traits and high estimation accuracy created the possibility to obtain phenotypic and genetic progress. Taking under consideration the importance of fattening and slaughtering traits and the necessity to improve them as fast as possible the BLUP method was introduced into breeding practice in Poland in 1998. A few years before introduction of BLUP method the system of data processing was developed and tested. Thanks to the system it was possible to collect all the data and information essential for BLUP calculations. Breeding value for fattening and slaughtering performance has been estimated based on the results obtained from on the farm test.

The background for fattening and slaughtering performance calculations is a period of 6 months. That means that breeding value of individual animals is related to the average estimated based on results of all animals evaluated in the last 6 months. Calculations take place in National Research Institute of Animal Production on monthly basis for each breed.

Described model enables to calculate breeding values for animals from all over the country. The influence of permanent factors like: gender, piggery, circle and random factors such as litter and individual effect have been included in the model.

$$y = X_{sas} + X_{pap} + X_{hah} + Z_{mm} + Z_{aa} + e$$

where:

y – is an observation vector

as – vector of circle effects

ap – vector of gender effects

ah – vector of breeding effects, m – vector of litters effect

a – vector of individuals effects e – error vector

XS – incidence matrix for the circle

Xp – incidence matrix for gender

Xh – incidence matrix for breeding

Zm – incidence matrix for litters

Za – incidence matrix for individuals

Each month calculations give us estimated breeding values for daily gain H(PD), carcass lean meat H(PM) and selection index H(IN) for boars and gilts of all breeds tested on farms and boars for mating and sows that progeny was tested on the farm. Obtained results are shown in the way that enable us to know what is the breeding value of the boar now and how it has changed on the background of every month calculations. It is a very important information based on which we can make a decision about the future of the boar that is if we want to keep it or eliminate from breeding.

Sows results are presented in the same way as boars results. In case of sows we are able to trace how the breeding value of individual animals estimated based on tested progeny has been changing in time.

Works over introduction of BLUP method for estimating reproduction traits were initialized in 2004. The first step was a development of methodological principles to change evaluation rules. Methodology of data flow, data base and its manual, were created. It was necessary to introduce changes in the methodology of data base in order to make it easier accessible and easier to update more frequently. We had to develop and install data filter system to minimize the risk of errors and mistakes.

In 2005 BLUP method started being used for reproduction traits – number of alive born piglets and number of piglets at 21 days of age. Data base for estimating breeding value of reproduction traits has a growing trend. Breeding value is standardized for the next litter and calculations are done on 2-weeks basis. Breeding value for 2 traits has been estimated according to the following equation:

$$Y = X_1b_1 + X_2b_2 + X_3b_3 + Z_a + e$$

where:

Y – observation vector for given trait

X1, X2, X3 – incidence matrixes for permanent factors

b1 – vector of permanent effects in the year

b2 – vector of permanent effects for litters

b3 – vector of permanent effects for a piggery (number of area is included in the piggery number)

Z – incidence matrix for an individual effects

a – vector of breeding values of estimated individuals

e – vector of random errors

Breeding values for reproduction traits have been estimated since 2007 but the results were not universally available. They were used to development of data base and methodology for data processing before introducing more advanced BLUP system for estimating overall BLUP breeding value. It is the best solution for the effective breeding work.

In 2007 National Research Institute of Animal Production a team ran by professor Marian Różycki developed overall BLUP models for selection of different breeds. Overall BLUP models were introduced into practice at the beginning of 2008 in cooperation between Institute and POLSUS specialists.

Radical diversification of selection in dam and sire breeds has been introduced. Dam breeds are selected in the direction of improvement of reproduction performance. The highest pressure has been put on number of piglets at 21 days of age. This trait is highly correlated with prolificacy and carries lower error risk. Improvement of other traits in this model will be less intensive. It was recognized that lean meat in dam breeds has reached the level high enough and the rate of improving that trait might be lowered. Growth rate has been declared as more important trait for pig producers and highest pressure on selection of this trait has been put in the selection process.

Selection criteria for sire breeds are more balanced and 70% of selection pressure is put on fattening and slaughtering traits while still improving reproduction traits at the same time.

Efficacy of reproduction performance estimation

Reproduction performance estimation is ran on the farm and has no other alternative. Breeding work aiming toward improvement of reproduction performance for many years was based only on herd management without using selection and evaluation methods. That was the main reason why it did not result in proper breeding progress, especially when we keep in mind that reproduction traits are of low heritability. It was necessary to develop methodology of reproduction performance estimation. Genetic parameters were estimated and their values were on a proper level for these traits. The lowest value of heritability coefficient was obtained in all breeds in the number of alive born piglets. For plw h^2 for this trait was = 0,115, for Polish landrace it was similar. Obtained value is similar to results obtained in other breeding programs and scientific publications and enables implementation of breeding value estimation of this group of traits with BLUP method.

Efficacy of fattening and slaughtering performance estimation

Fattening performance is estimated based on weighing boars and gilts once and then calculating their average daily gain since the day of birth till the day of estimation. Genetic parameters of this trait in the population and especially its heritability coefficient (h^2) show how accurate our estimation is and whether it is useful in the breeding work.

To analyze this parameter plw breed was used. Sire breeds have relatively low number of animals and not a lot of pure breed animals are estimated. In case of Polish landrace imported boars have the great influence on the population. Lack

Table 5. Fattening and slaughtering performance values of boars and gilts in 2005 („POLSUS” data).

	Number of animals	Age at the day of evaluation	Weight at the day of evaluation	Standardized daily gain	Average backfat thickness	Height of loin eye	Lean meat %	Index
boars	X 5 934	174	114	674	9,6	53,6	58,3	106
	Sd	14	13	87	1,8	5,1	2,5	16
	V%	8,1	11,7	12,8	18,8	9,5	4,4	15,2
gilts	X 24 720	172	103	620	11,0	52,8	56,5	104
	Sd	15	12	75	1,9	5,3	2,6	14
	V%	8,6	11,9	12,1	17,1	10,1	4,6	13,5

of results of own performance calculated using Polish methodology is the main reason why reproduction performance calculation is biased with errors. Daily gain and fattening and slaughtering parameters for plw boars and gilts obtained in 2005 are presented in the table below.

In order to analyze what are the possibilities of success in breeding work it is necessary to know all genetic parameters of given population. Below you can find basic genetic parameters estimated for results of plw boars on alive animals in the period 1996 – 2004. In this period the methodology of estimation was stable. Changes introduced into estimation methodology in 2005 make it hard to compare obtained results.

Table 6. Results and values of heritability of fattening and slaughtering performance of plw boars obtained in the on farm test in the period 1996-2004 (National Research Institute of Animal Production)

	Number	Age at the day of evaluation	Weight at the day of evaluation	Standardized daily gain	Average backfat thickness	Height of loin eye	Lean meat %	Index	
boars	X	35	179	113	636	11,0	49,7	57,6	122
	223		13	12	65	2,2	5,4	2,3	15
	Sd		7,1	11,6	10,2	19,9	10,8	4,0	14,6
	V%		0,31	0,18	0,18	0,20	0,09	0,18	0,18
	h^2								

Presented parameters are lower than those that can be found in the literature. But we should remember that data was collected in a very long time by a lot of people measuring animals which had a negative influence on the accuracy. To sum up we should state that trait heritability coefficient $h^2 = 0,2$ gives a possibility to conduct successful selection. As an example we can use dairy cattle and huge progress, obtained through indirect selection of bulls, in its milk yield with heritability coefficient $h^2 = 0,18$.

Estimation of breeding values should give us as much information as possible about animals genetic value of given trait. Different sources of information about performance value like: own performance, ancestors performance, full siblings performance, other relatives performance and progeny performance give us a chance to improve accuracy of estimated performance value.

Table 7. Examples of evaluation accuracy according to the information source (Strabel 2005)

Source of information	Evaluation accuracy			
	$h^2 = 0,10$	$h^2 = 0,3$	$h^2 = 0,5$	
1. Parents			0,39	n.n.
2. Own phenotype	0,32		0,55	
3. Average of 5 full siblings	0,32		0,48	
4. Average of 10 half siblings	0,23		0,33	
5. Average of 5 progeny	0,34		0,54	
6. average of 10 progeny	0,45		0,67	
7. Average of 100 progeny	0,85		0,94	
8. Average of 3 observations of the individual animal			0,67	

Heritability coefficient has a direct influence on estimation accuracy. E.g. estimation of a trait with low h^2 (0,10) based on 10 progeny is less accurate than estimation of a trait with higher h^2 (0,3) based on animals' own performance. So heritability coefficient determines the method of estimation and selection.

In general selection based on parents and siblings performance has rather low opinion. The highest selection accuracy belongs to estimation based on progeny performance because breeding value is a capability to pass genetic assumptions to the progeny.

Knowing genetic parameters it is possible to set an equivalent of number of progeny based on which the individual will be estimated in order to obtain the same results as based on individual own performance.

Evaluation accuracy based on own phenotype	Evaluation accuracy based on progeny
H	$\sqrt{n/n+a}$ where $a = 4-h^2/h^2$

$$H = \sqrt{n/n + a} \quad \text{that gives } n = 4 - h^2/1-h^2$$

For traits with heritability coefficient $h^2 = 0,30$ progeny testing is sensible when done on at least 5 animals. If we do not have at least 5 progeny then estimation based on own performance is more important. If trait heritability coefficient $h^2 = 0,1$ progeny testing is sensible when done on at least 4 animals. In the national breeding practice we assumed that minimal number of 8 progeny tested in test stations gives proper estimation accuracy.

Young animals are estimated based on own performance in range of fattening and slaughtering traits. In the table above you can find heritability coefficients for on farm performance test. Estimation based on the results of on farm test is more accurate when introducing results standardization for age and body weight. Apart from results of growth rate estimation the highest accuracy is also presented by PIGLOG 105 backfat thickness measurements. Backfat thickness measurements have pretty high accuracy. In national research on backfat thickness measured with ultrasound on breeding animals obtained results were very diverse. Dawidek (1991) stated that for plw and Polish landrace heritability coefficients for backfat thickness were $h^2 = 0,221$ and $h^2 = 0,085$, and Eckert (1995) stated that it was $h^2 = 0,320$ and $h^2 = 0,277$ respectively. Presented results prove high usefulness of ultrasound measurements in breeding work.

Below you can find genotypic correlation coefficients between results of tissues thickness PIGLOG 105 measurements and results of caliper measurements taken after slaughtering and lean meat percentage determined based on dissection.

Table 8. Genotypic correlations between tissues thickness measured with PIGLOG 105 and with caliper after slaughtering and lean meat percentage.

Parameters	Coefficients of correlation
PIGLOG 105 – backfat thickness over the last rib	- 0,72
PIGLOG 105 – backfat thickness over 13/14 rib	- 0,71
PIGLOG 105- loin thickness	0,36
Caliper – backfat thickness over the last rib	- 0,90
Caliper – backfat thickness over 13/14 rib	- 0,90
Caliper – loin thickness	- 0,83

Evaluation of completed and expected breeding progress

Breeding progress is breeders success in each generation of breeding animals if their performance is higher than performance of their parents. It is a difference between values of the same trait in two consecutive generations. Breeding progress is the effect of selection causing positive changes in progeny genes frequency comparing to their parents. Boar and sow have their progeny in a few following years. Genotype of their progeny might not significantly change in the following litters and that it is why we should use the model of estimation according to following years in the analysis of pig breeding progress. So in Polish pig breeding it is the best to calculate breeding progress based on the time unit – generation gap or the year. Nucleus boars give progeny in a few following years that is why selection differential is regarded as a performance differential of the most important boars traits in following years. In a result the influence of sows and boars replacement is compensated.

Breeding work over plw breed was used as a model example. In the table below you can find boars replacement percentage in nucleus herds.

Replacement percentage of plw nucleus sows is lower and stays on approximately 30%.

In previous years in plw breed certain progress in phenotypic values of fattening and slaughtering performance has been obtained (analysis in results discussion). Methodology which did not include traits standardization was the reason of decreasing the growth rate. It is clearly visible in table 10 where presented lean meat % was estimated based on phenotypic selection differential.

$$\text{Trend} = 59,1 - 56,7 = 2,4$$

$$\text{Average yearly trend} = 2,4/8 = 0,3$$

$$\text{Trend of replacement boars} = 59,5 - 56,6 = 2,9$$

$$\text{Average yearly trend of replacement boars} = 2,9/8 = 0,4$$

Completed breeding progress

Table 9. Number of estimated boars.

Year of estimation	Number of boars	Number of estimated boars	Number of nucleus boars	Number of new boars	Replacement %
1996	8401	434	–	–	–
1997	8448	398	197	49,5	
1998	8923	389	189	48,6	
1999	6182	377	173	45,9	
2000	5429	333	147	44,1	
2001	5150	329	162	49,2	
2002	5478	329	158	48,0	
2003	4841	306	159	52,0	
2004	3951	293	137	46,8	
Total	56801	354 ^(*)	165 ^(**)	46,7	

^(*) average number of nucleus boars in given year

^(**) average number of new boars introduced in the given year

Table 10. Boars lean meat percentage estimated in the period 1997-2004 and phenotypic selection differential

Year of estimation	Number of estimated boars	Average lean meat, %	Progeny of new boars		Superiority ^(*)
			number	lean meat %	
1997	8448	56,7	2671	56,6	- 0,1
1998	8923	57,1	3178	56,9	- 0,2
1999	6182	57,2	2196	57,1	- 0,1
2000	5429	57,7	1999	57,8	+ 0,1
2001	5150	58,3	2252	58,2	- 0,1
2002	5478	58,5	2113	58,7	+ 0,2
2003	4841	58,9	1915	58,8	- 0,1
2004	3951	59,1	1549	59,5	+ 0,4

^(*) X general in the given year – X New boars introduced into the herd in the given year

The product of difference between trait genotypic values in generations and coefficient of heritability is presented in the table below.

$$\Delta_h = DS * h^2$$

DS = difference between trait genotypic values in two consecutive generations.

h^2 = heritability coefficient.

h^2 for daily gain = 0,18, h^2 for lean meat = 0,18

Results presented above clearly show that breeding progress has been obtained. It is considered that 1% of breeding progress for a trait is a good result. In 2005 breeding progress in growth rate was 1,8% and for lean meat -0,3%. It is a result of a new selection index designed for dam breeds. This index consists of 60% for growth rate and 40% for lean meat%. Keeping high rate of breeding progress could lead in 2012 to very high or even too high levels of selected

Table 11. Results of plw boars performance obtained in 2005 and results of plw boars introduced into the herd in 2005 and giving progeny in 2006.

	Number of animals, variability	Daily gain g	Lean meat %
Boars evaluated in 1995	n = 5934	674	58,3
	SD	87	2,5
Selected boars	n = 345	743	59,3
	SD	89	2,2
Estimated completed breeding progress		12,42 g trait 1,8 % progress	0,18 % trait 0,3 % progress

slaughtering and fattening traits for dam breeds. That is why total BLUP model including fattening, slaughtering and reproduction traits, has been introduced into breeding practice. Correlation between slaughtering and reproduction traits is negative so we should expect slower rate of breeding progress in case of lean meat %. It is proper situation for plw breed which is a dam breed with high reproduction performance and fattening and slaughtering performance is on a second place.

Desired breeding progress

Breeding goal is to obtain progeny with higher value of selected trait or traits than the average value in parents' generation.

Estimation of expected progress is important to estimate the accuracy of selection, accuracy of estimation and intensity of herd replacement expressed as a distance between generations.

$$\Delta g = i * r_{ip} * \delta_A * T$$

- i = selection intensity

- r_{ip} = breeding value accuracy

- δ_A = additive genetic variability

- T = distance between generations

Δgp = for plw boars growth rate.

$$\Delta gp = (((743-674)/87) * 0,424 * 36,888) / 2,5$$

Δgm = for plw boars lean meat.

$$\Delta gm = (((59,3-58,3)/2,5) * 0,424 * 0,45) / 2,5$$

$$\Delta gp + \Delta gm / T + T = \Delta g \text{ (total)}$$

$$\Delta g \text{ (total)} = 0,998 \%$$

The average expected breeding progress usually is not higher than 2%. In the process of realization of breeding program there is a negative influence of environmental factors that limit free mating and other complication. That is the main reason why completed breeding progress usually do not exceed 1%. It is low especially when level of population performance is high. In case of National Breeding Program for plw breed (boars) the expected breeding progress based on current information was $\Delta g \text{ (total)} = 0,998 \%$. It is a good result. Breeding Progress might be increased by:

- shortening generation distance

- improving estimation accuracy and as a result improving genetic parameters like heritability.

- conducting more intensive selection. Selection differential for daily gain is $i = 0,793$ and shows that selection in the population is 50%.

In fact selection was even more intensive – $345/5934 * 100\% = 5,81 \%$, and that means standardized selection differential is approximately 2,06. Reaching such high selection intensity is hinder by small number of herds free from diseases which limits genetic flow. Breeding progress might be obtained when using for next generation animals that differ from the population for at least 1 SD. There are at least 16% of such individuals in the herd.

Data analysis clearly show that there are possibilities to increase breeding progress rate by using all estimation results and by better choosing boars for replacement.

Progress can be increased if we use all available breeding tools.

Table 12. The value of selection differential expressed in standard deviation units according to percentage of herd left after selection (L. Lush, 1961)

% left after selection	Selection differential	% of herd left after selection	Selection differential
90	0,20	20	1,40
80	0,35	10	1,75
70	0,50	5	2,06
60	0,64	4	2,15
50	0,80	3	2,27
40	0,97	2	2,42
30	1,16	1	2,67

In order to obtain higher genetic progress selection should be more intensive (artificial insemination), evaluation accuracy should be improved and distance between generations shortened. We should estimate as many animals as possible and then take selection decisions. As a result selection will be more intensive and will have the highest influence on the level of breeding progress. Variability in population does not depend on the breeder and usually diminishes along with genetic progress. It is a negative effect of success obtained in breeding work.