Simultaneous estimation of genetic parameters for production and litter size traits in Czech Large White and Czech Landrace pigs

E. Krupa, J. Wolf

Institute of Animal Science, Prague-Uhříněves, Czech Republic

ABSTRACT: Genetic parameters for total number of piglets born per litter, number of piglets weaned per litter, lean meat content, and average daily gain from birth till the end of the field test were estimated for Czech Large White (445 589 records) and Czech Landrace (149 057 records) pigs using a four-trait animal model. The following heritabilities were estimated (first number: Large White, second number: Landrace): 0.10 ± 0.004 and 0.09 ± 0.007 for total number born; 0.09 ± 0.005 and 0.07 ± 0.008 for number weaned; 0.39 ± 0.004 and 0.36 ± 0.009 for lean meat content; 0.21 ± 0.004 and 0.18 ± 0.006 for daily gain. The highest genetic correlation (approximately 0.85 in both breeds) was estimated between both litter size traits. In Czech Landrace, all remaining genetic correlations were < 0.20 in their absolute value. Negative correlations of approximately -0.25 were estimated in Czech Large White between daily gain and both reproduction traits. All remaining correlations in Czech Large White were also < 0.20 in their absolute value. The estimated non-zero correlations between production and reproduction traits are, besides of other arguments, one reason to recommend a joint genetic evaluation of production and reproduction traits. If more than one litter trait is included in the genetic evaluation, repeatability models should be used instead of separate treating the first and the second and subsequent litters; this is because of the high correlations among litter size traits which are expected to cause numerical problems if multi-parity models are used.

Keywords: total number of piglets born; number of piglets weaned; lean meat content; average daily gain; heritability; genetic correlation; REML

Since 2005, the genetic evaluation of Czech pig dam breeds has been based on a four-trait model with lean meat content, average daily gain from birth till the end of the field test, number of piglets born alive in the first litter, and number born alive in the second and subsequent litters (Wolf et al., 2005). This procedure ensured a continuous increase in the number of piglets born alive over years.

The number of piglets born alive has positive genetic correlations with the total number of piglets born and the number of piglets weaned (Wolf et al., 2002; Huby et al., 2003; Serenius et al., 2004) so that also the latter two traits have shown a positive trend over years. However, the higher number of piglets born alive has also increased the losses until

weaning (Serenius et al., 2004; Su et al., 2007) so that the number of piglets weaned has risen more slowly than the number of piglets born.

From the economical point of view, the number of piglets weaned is the most important litter trait. Furthermore, the total number of piglets born is a measure for the biological potential of the sow and is also connected with the feeding costs for the sow. Thus, the Czech pig breeders would like to replace number of piglets born alive by the total number of piglets born and the number of piglets weaned.

The objective of the present paper is therefore to estimate genetic parameters for the total number of piglets born, number of piglets weaned, lean meat content, and average daily gain from birth

until the end of the field test from large data sets of the breeds Czech Large White and Czech Landrace using a multiple-trait animal model. These genetic parameters will be the basis for the new genetic evaluation of production and reproduction traits in Czech pig dam breeds.

MATERIAL AND METHODS

Animals and traits

The analyses were based on performance test data (production and reproduction traits) for the breeds Czech Large White (CLW) and Czech Landrace (CLA) from 1995 to 2011. The traits considered were lean meat content (in %) at the end of the performance test estimated from ultrasonic measurements unadjusted for live weight, average daily gain from birth till the end of the field test (in g/day) calculated as weight at the end of the test divided by age at the end of the test, total number of piglets born per litter, and number of piglets weaned per litter.

The field test for production traits started at an age of 80–88 days and lasted till 56–70 days (from January 1, 2003; this interval was changed to 49–63 days for gilts; the duration of the test for

young boars was not affected). The weight at the beginning of the test was approximately 30 kg. The number of piglets weaned was recorded 21 days after birth. There was no cross-fostering.

No editing of production data was required as all records were in the required range. For litter size data to be retained for analysis, the following conditions had to be met: litters were purebred CLW or CLA and had complete information for all litter size traits. Gestation length was in the interval of 105–125 days. The minimum sow age at first farrowing was 300 days. Parities greater than 10 were not considered. The age of the sow for parities 1–10 had to be in the following intervals: 300–500, 450–750, 600–950, 750–1150, 900–1350, 1050–1550, 1200–1750, 1350–1950, 1500–2150, and 1650–2350 days. The total number of piglets born was at least 4. The number of piglets that died from 24 h after birth until weaning was not greater than 4. The farrowing interval was 130–300 days. Reproduction records from sows with only one litter were omitted for problems with the estimation of the permanent environmental effect of the sow.

A flexible allocation of records to herd-year-season classes was applied according to Wolf et al. (2005). Herd-year-season classes preferably were formed according to natural seasons (spring,

Table 1. Number of observations, means, and standard deviations (SD) for all traits and covariates used in the models for both Czech dam breeds

Trait or covariate	Number	Mean	SD
Czech Large White			
Lean meat content (%)	357 100	61.3	2.69
Average daily gain from birth until end of test (g/day)	357 100	586	77.2
Total number of piglets born	88 489	12.2	2.75
Number of piglets weaned	88 489	10.2	2.16
End weight in the field test (kg)	357 100	92.0	11.00
Age at first farrowing (days)	19 815	371	36.6
Farrowing interval (days)	68 674	164	27.2
Czech Landrace			
Lean meat content (%)	119 231	61.5	2.53
Average daily gain from birth until end of test (g/day)	119 231	621	87.1
Total number of piglets born	29 826	12.3	2.77
Number of piglets weaned	29 826	10.3	2.15
End weight in the field test (kg)	119 231	95.5	12.17
Age at first farrowing (days)	7 070	366	35.2
Farrowing interval (days)	22 756	166	28.2

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summer, autumn, winter) and normally had a length of three months: March through May, June through August, September through November, and December through February of the following year. The minimum total number of records for each herd-year-season class was 30 where at least 5 of them were on production traits and at least 5 were on reproduction traits. If the number of observations in a three-month-interval was less than 30 or the minimal number of observations for production and reproduction traits was not fulfilled, the time interval was extended until those numbers were reached. After applying all restrictions when editing reproduction data and after forming the herd-year-season effects, 12.5 or 13.7% of records for CLW or CLA, respectively, were excluded from the further analyses. The number of herd-year-season classes was 3139 for CLW and 1319 for CLA. The average number of observations for production and reproduction traits per herd-year-season class was 113 and 29 for CLW and 90 and 23 for CLA.

Summary statistics for all traits and covariates used in the models are given in Table 1 for the edited data sets for both breeds. The trait means were very similar in the two breeds; only in average daily gain an appreciable difference of 35 g/day in favour of CLA was observed. The average number of litters per sow was 4.18 or 3.95 for CLW and CLA, respectively. These numbers are relatively high because sows with only one litter size record

were excluded from the analysis. The animals in the final data set for CLW were from 98 herds with a total of 3139 herd-year-season effects; the number of herds was 44 with 1326 herd-year-season effects in CLA.

Statistical methods

First, the General Linear Models (GLM) procedure as implemented in the statistical package SAS (Statistical Analysis System, Version 9.2, 2008) was applied to data for studying the influence of factors affecting the four investigated traits. Then four-trait animal models were used for the estimation of genetic parameters. The statistical model in matrix notation can be written as follows:

$$y = \mathbf{X}b + \mathbf{Z}a + \mathbf{W}z + e$$

where:

y = vector of observations of traits under investigation

$\mathbf{X}$, $\mathbf{Z}$, $\mathbf{W}$ = known incidence matrices for the fixed effects, the random additive genetic animal effects, and the remaining random effects, respectively

b = vector of fixed effects

a = vector of additive genetic animal effects

z = vector of further random effects

e = vector of residuals

Table 2. Factors included (×) in the four-trait animal model for the estimation of genetic parameters

Factor in the model	Type of factor	TNB	NW	LM	ADG
Weight at the end of the test	C	–	–	×	–
Quadratic regression on a covariate[a] within parity	C	×	×	–	–
Parity class	F	×	×	–	–
Device for ultrasonic measurement of lean meat content	F	–	–	×	–
Type of test	F	–	–	×	×
Breed of service sire	F	×	×	–	–
Herd-year-season	F	×	×	×	×
Mating type	F	×	×	–	–
Sex	F	–	–	×	×
Animal	A	×	×	×	×
Litter the animal is from	R	–	–	×	×
Permanent effect of the sow	R	×	×	–	–
Residual effect	R	×	×	×	×

C = covariate, F = fixed, A = random animal additive genetic effect, R = random, TNB = total number of piglets born, NW = number of piglets weaned, LM = lean meat content, ADG = average daily gain from birth till the end of the field test
[a]covariate is age at the first farrowing in the first parity and farrowing interval in the second and subsequent parities

Vector *b* contained the fixed factors and covariates summarized in Table 2 and vector *z* contained two random factors (litter the animal is from and permanent environmental effect of the sow).

For the factor "parity class", codes 1–4 were used for parities 1–4, code 5 summarized parities 5 and 6, and code 6 summarized parities greater than 6. This was done to keep the number of records for the parity orders reasonably high. Two devices have been used for measuring the lean meat content at the end of the field test so that the factor "Device for ultrasonic measurement" had to be included in the model for lean meat content. The factor "Type of field test" had to be included in the models for production traits as the methodology of the field test has been several times modified since 1995. Mating type was either artificial insemination or natural mating.

The pedigree was traced back to 1985. Variance and covariance components were estimated by restricted maximum likelihood (REML) and optimization using a quasi Newton algorithm with analytical gradients (Neumaier and Groeneveld, 1998) as implemented in VCE 6.0 program (Groeneveld et al., 2008). The calculations were carried out separately for each breed.

RESULTS

The estimated proportions of variance for the individual random factors included in the four-trait animal model are presented in Table 3 for both breeds. The results were similar for both breeds. Production traits showed clearly higher heritability estimates than reproduction traits. The heritability of lean meat content was nearly twice the value of the heritability of daily gain. The heritabilities for reproduction traits were low and did not exceed a value of 0.10. Other than the additive genetic effect of the animal expressed by the heritability, the proportion of variance caused by the litter of origin was larger for daily gain than for lean meat content. The proportion of variance for the permanent environmental effect of the sow on both reproduction traits amounted to about 5% of the total variance. This proportion of variance was in its value closer to the heritability estimates in CLA than in CLW. The estimated proportions of variance for the residual effect indicated that a great part of the total variability is caused by unknown factors (50–60% in production traits and approximately 85% in reproduction traits).

Correlation estimates for all pairs of traits and all random factors in the model are listed in Table 4. Again, the results for both breeds were similar. Additive genetic correlations were the only correlations which could be estimated for all pairs of traits. Most of the genetic correlations were relatively low in their absolute value; a very tight correlation of approximately 0.85 was estimated between the total number born and number weaned. Low negative, but mostly significant genetic correlations were found between daily gain and both reproduction traits, whereby higher negative values were estimated for CLW than for CLA. A negative

Table 3. Estimated proportions of variance (± standard errors) for all random factors in the model and for both breeds

Proportion of variance	TNB	NW	LM	ADG
Czech Large White				
Additive genetic effect (heritability)	0.10 ± 0.004	0.09 ± 0.005	0.39 ± 0.004	0.21 ± 0.004
Litter of origin	–	–	0.10 ± 0.001	0.22 ± 0.002
Permanent effect of the sow	0.05 ± 0.004	0.05 ± 0.004	–	–
Residual effect	0.85 ± 0.004	0.87 ± 0.005	0.51 ± 0.005	0.57 ± 0.004
Czech Landrace				
Additive genetic effect (heritability)	0.09 ± 0.007	0.07 ± 0.008	0.36 ± 0.009	0.18 ± 0.006
Litter of origin	–	–	0.11 ± 0.003	0.24 ± 0.005
Permanent effect of the sow	0.06 ± 0.007	0.06 ± 0.007	–	–
Residual effect	0.85 ± 0.007	0.87 ± 0.007	0.53 ± 0.009	0.59 ± 0.009

TNB = total number of piglets born, NW = number of piglets weaned, LM = lean meat content, ADG = average daily gain from birth till the end of the field test

Table 4. Estimated correlations among traits (± standard errors) for all random factors in the model and for both breeds

Type of correlations	Pair of traits	Czech Large White	Czech Landrace
Additive genetic	TNB, NW	0.86 ± 0.013	0.85 ± 0.022
	TNB, LM	0.00 ± 0.007	0.04 ± 0.015
	TNB, ADG	−0.26 ± 0.025	−0.07 ± 0.039
	NW, LM	−0.02 ± 0.007	0.00 ± 0.018
	NW, ADG	−0.22 ± 0.025	−0.17 ± 0.041
	LM, ADG	−0.18 ± 0.012	−0.06 ± 0.024
Litter of origin	LM, ADG	−0.01 ± 0.006	0.09 ± 0.008
Permanent effect of the sow	TNB, NW	0.80 ± 0.024	0.90 ± 0.024
Residual effect	LM, ADG	−0.03 ± 0.004	0.07 ± 0.008
	TNB, NW	0.78 ± 0.002	0.87 ± 0.008

TNB = total number of piglets born, NW = number of piglets weaned, LM = lean meat content, ADG = average daily gain from birth till the end of the field test

genetic correlation was also detected between both production traits; the higher negative value was again observed in CLW.

The correlation caused by the litter of origin between both production traits was very low. In CLW, it did not differ significantly from zero and in CLA the value was less than 0.10. The correlations caused by the permanent environment effect of the sow were very large between both reproduction traits. Whereas the residual correlations between both production traits were close to zero, the residual correlations between the reproduction traits were very high. Phenotypic correlations were also estimated for all pairs of traits (not shown in Table 4). Most of them were near zero, only the phenotypic correlation between the reproduction traits was approximately 0.75 in both breeds.

DISCUSSION

Though production and reproduction traits are often treated separately in genetic evaluation, a joint genetic evaluation of both trait groups has several advantages as stated by Peškovičová et al. (2002). As the heritabilities for reproduction traits are very low, additional information via genetic correlation with production traits will be useful for improving the accuracy of genetic evaluation. A further argument is that not a trait value, but an animal as a whole is selected so that a joint genetic evaluation of all traits is the natural way. Furthermore, each animal gets a breeding value

estimate for all traits; the linear combination of the breeding values multiplied by the economic weights for traits results directly in the aggregate genotype to be used for selection. Therefore, the joint genetic evaluation of all traits should be the method of choice if there are not insurmountable operational problems. Always good reasons need to be given for not doing a joint analysis.

Very low genetic correlations between litter size traits on the one hand and growth rate or lean meat content (backfat thickness) on the other were reported by several authors (Noguera et al., 2002; Arango et al., 2005; Kapell et al., 2009). However, litter size and production and quality traits are probably not independent as shown in a selection experiment by Estany et al. (2002a, b). In this experiment, a line selected for litter size was compared with a control line in the time interval 75−165 days of age. The pigs from the selected line showed higher body weight throughout most of the test period but they were not different from the pigs of the control line at the end of the test. It means that the selected line grew faster at the start of the test and more slowly at the end of the test resulting in similar growth rates for both lines in the test (Estany et al., 2002a). The different growth pattern of both lines will cause a change in the genetic correlation between litter size traits and growth rate if the time interval for the test is changed.

A further consequence of the mentioned selection experiment is that the major consequences of selection for litter size might be expected in

the physiological pathways associated with fat metabolism as correlated effects mainly occurred in the timing and pattern of fat metabolism (Estany et al., 2002b). The authors assume that selected pigs are more mature at the same age. This is in agreement with the findings of Hyánková and Novotná (2007) who concluded from a long-term selection experiment with Japanese quail that the sequence of ontogenetically determined processes during postnatal growth is independent of the selection history of the population. However, selection on growth performance, for example, alters the chronological age at the onset of consecutive developmental events. Such a change of the developmental rate determines the phenotypic manifestation of the genotype and probably plays a role in growth and reproductive efficiency.

Especially in CLW, low negative genetic correlations were found between both litter size traits and average daily gain in the present investigation. This is in agreement with Hermesch et al. (2000), Chen et al. (2003), and to a certain degree with Holm et al. (2004). The latter authors estimated relatively high correlations of approximately 0.50 between the number of piglets born alive and adjusted age at 100 kg of live weight, which means also negative correlations between litter size and growth rate. The main problem in comparing results referring to growth with literature values is that there is a great diversity in the definition of the trait which characterizes growth so that different results are expected also for the genetic correlations for the reasons explained above.

A general finding from the literature is that genetic correlations in litter size traits between the first and second litters are mostly lower than genetic correlations among the second and subsequent litters (Hermesch et al., 2000; Hanenberg et al., 2001; Wolf et al., 2002; Serenius et al., 2003). Consequently, it is often recommended to treat litter size traits in the first litter and in the second and subsequent litters as different traits (Fischer et al., 1999; Hermesch et al., 2000; Holm et al., 2005). This procedure has been also used in the genetic evaluation of dam pig breeds in the Czech Republic, where numbers of piglets born in the first litter and in the second and subsequent litters were differentiated, whereas a repeatability model was used for the latter trait (Wolf et al., 2005). However, keeping this procedure in the situation where number of piglets born alive is to be replaced by total number of piglets born

and number of piglets weaned in the new animal model for genetic evaluation would mean that the number of litter size traits increased to four. When testing such a model, numerical instabilities occurred because of the high correlations between the four litter size traits. Therefore, we decided to use a repeatability model for both litter size traits including all litters which ensures numerical stability and robustness of the model. Model building is always a compromise which must balance the measure of the attention to detail with the practicality of the model.

Hanenberg et al. (2001) stated that on the basis of their estimates of genetic parameters, there are possibilities for improving reproduction traits by selection on more than litter size at birth. The breeding goal should be increased number of piglets per sow per year. To achieve this breeding goal, the number of weaned piglets per sow per litter must be in the centre of attention complemented by one or more reproductive interval traits. The total number of piglets born may give some additional information on the biological potential of the sow and increase the accuracy of the breeding value for the number of weaned piglets via the high genetic correlation. In addition to the four-trait animal model with two litter size traits and two production traits, genetic evaluation for the transformed farrowing interval will be carried out for the Czech pig dam breeds in a separate run. The transformation was proposed by Wolf (2012), because the original distribution of the farrowing interval showed high values of skewness and kurtosis. The breeding value estimation for the farrowing interval will first be carried out separately because data on lactation length needed as covariate in the model are available only for a relatively low number of sows. Moreover, farrowing interval is used as covariate for litter size traits so that the inclusion of farrowing interval as further dependent variable in the four-trait animal model would cause problems. In the long-term perspective, ways should be found to integrate farrowing interval in the four-trait animal model. The use of recursive models (De Maturana et al., 2010; Ibáñez-Escriche et al., 2010) may be one way to resolve the problem.

CONCLUSION

Similar, but not identical results were achieved for Czech Large White and Czech Landrace so that the

separate genetic evaluation of both breeds should continue. Though the correlations between production and reproduction traits were low, several non-zero correlations were estimated especially with growth rate. This is, besides of other arguments, one reason for a joint genetic evaluation of production and reproduction traits. Because of numerical reasons, a repeatability model should be used for both litter size traits. Genetic correlations may change with selection and should be newly estimated in regular time intervals.

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Corresponding Author

Ing. Emil Krupa, Ph.D., Institute of Animal Science, Přátelství 815, 104 00 Prague 10-Uhříněves, Czech Republic
Tel. +420 267 009 574, e-mail: krupa.emil@vuzv.cz