ESTIMATION OF (CO)VARIANCE COMPONENTS FOR AGE AT FIRST FARROWING AND FARROWING INTERVAL IN CZECH LARGE WHITE [1]

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ABSTRACT

We aimed to estimate the variance and covariance components for the original and transformed age at the first farrowing (AFF) and farrowing interval in this study. The data from 25,094 sows (77,544 observations) of the Czech Large White pig breed between January 2000 and December 2015 provided by Czech Pig Breeders Association were used for the analyses. Data higher than the median were only transformed. The farrowing interval was evaluated separately from the first to the fourth parity (FI1–FI4). The heritabilities for the original traits were very low: 0.17, 0.11, 0.07, 0.06, and 0.06 for AFF and FI1–FI4, whereas those for the transformed traits were higher: 0.19, 0.14, 0.11, 0.11, and 0.12 for AFF and FI1–FI4, respectively. The phenotypic correlations between the traits were low, but significant. The estimated genetic correlations between all the farrowing intervals were clearly lower than one, indicating that all the farrowing intervals should be treated as different traits. Using the transformation procedure decreased the skewness and kurtosis of the original data in our study. The heritabilities of the analysed farrowing intervals were only increased owing to the transformation.

Key words: pigs, breeds, Czech Large White, reproduction, farrowing interval, parity, genetic parameters

1 INTRODUCTION

One of the main objectives in pig breeding is shortening farrowing intervals, which makes it possible to increase the number of piglets per sow per year with a significant economic impact. Age at first farrowing, which includes age at first service, conception rate, and gestation length, also has been used as a measure of the reproductive efficiency for gilts (Holm *et al.*, 2005). Low heritability of the farrowing interval (usually ranging from 0.01 to 0.05; Hanenberg *et al.*, 2001; Serenius *et al.*, 2003) is the main problem, as it provides only a small selection progress. Besides, conventional methods routinely applied to estimate breeding values and genetic parameters are based on the assumption of normal distribution of measurements. However, an extremely skewed (unbal-

anced) distribution was found for farrowing interval. Wolf (2012) presented a general transformation formula for interval traits connected with reproduction in pigs, which was an adaptation of the transformation suggested by Ten Napel *et al.* (1995) and was applied on the weaning-to-first-service interval in pigs by Hanenberg *et al.* (2001), Holm *et al.* (2005), and Lundgren *et al.* (2010). The frequently asked question in this regard is whether the trait should be taken as a single or repeated trait if measured more than once per animal. Traits should be considered as repeated if the variances between repeated measurements are the same and if genetic correlations are equal to one (Falconer and MacKay, 1996). The objective of this study was to estimate the variance and covariance components for original and transformed data

of age at first farrowing and from the first to the fourth farrowing interval.

2   MATERIALS AND METHODS

The analyses were based on performance test data for the Czech Large White (CLW) breed. Data collected between January 2000 and December 2015 were analysed. All data were provided by the Pig Breeders Association of the Czech Republic. Detailed information on the pedigree and populations of the analysed breed has been reported by Krupa *et al.* (2015, 2016). A flexible allocation of the records to herd-year-season (HYS) classes as first described by Wolf *et al.* (2005) was applied separately for each trait and was based on the season in which the farrowing date fell: March through May (spring), June through August (summer), September through November (autumn), and December through February (winter) of the next year. The minimum records per class were 20. Data from 78 herds (average number of observations was 308.7 per herd) were used (eight herds were excluded due to low number of observations). The total number of HYS effect classes was 999 for age at first farrowing. The average number of observations per HYS class was 24 for age at first farrowing.

Two reproductive interval traits, age at first farrowing (AFF) and farrowing interval, were analysed. The formula below presented by Wolf (2012) was used for data transformation, where only part of the data needed to be transformed (observations greater than the median) to overcome the skewness and to increase the heritability of the interval traits. This approach ensured that the difference between the maximum and median of the transformed data was equal to the difference between the median and the minimum. The equation for this method then is

$$z = \begin{cases} y & \text{for } y \leq y_{med} \\ y_{med} + (y_{med} - y_{min}) \times \dfrac{\ln(y - y_{med} + 1)}{\ln(y_{max} - y_{med} + 1)} & \text{for } y > y_{med} \end{cases}$$

$$z = \begin{cases} y & \text{for } y \leq y_{med} \\ y_{med} + (y_{med} - y_{min}) \times \dfrac{\ln(y - y_{med} + 1)}{\ln(y_{max} - y_{med} + 1)} & \text{for } y > y_{med} \end{cases}$$

where Z is the transformed value and y is the original value of the trait and y_{med}, y_{min}, and y_{max} are the median, minimum, and maximum values. The farrowing intervals in different parities (FI1–FI4) were treated as different traits. Not all sows had data available for each trait; 6,355 sows had complete data structure (values for all traits). The five-trait animal model was used to estimate the vari-

ance and covariance components for the original (AFF$_o$ and FI1$_o$–FI4$_o$) and transformed (AFF$_t$ and FI1$_t$–FI4$_t$) traits. The Pearson's correlations coefficients between the phenotypic values of the evaluated traits were computed using CORR and the general linear model (GLM), both implemented using the statistical package SAS® (SAS Institute Inc., 2008); these coefficients were used to derive the fixed part of the model. After these procedures, the following effect remained in the model equations: fixed effect of the linear and quadratic regression on lactation length (used only for the farrowing interval trait), breed of service sire (four classes), mating type (two classes: artificial insemination and natural mating), random effect of HYS, and random effect of the animal. The average number of sires per herd was 46.37. The average number of sires per class of the HYS effect was 6.71. The following criteria were used for the mentioned effect: breed of service sire is Czech Large White, Czech Landrace, or Duroc, the sire line is the Czech Large White breed, gestation length is 100–130 days, first farrowing was within 260–500 days, and farrowing interval varied from 120 to 350 days; parities greater than four were not considered. The total number of piglets born varied from 4 to 22. After applying all the criteria and forming the HYS classes, the total number of sows was 23,874. The number of observations for age at the first farrowing and the farrowing interval was 76,860. Thus, the average number of litters per sow was 3.22. The pedigree was tracked back to the year 1980. The total number of animals in the pedigree was 37,199. The number of base animals (animals with both parents unknown) was 2,377. The number of inbred animals was 21,803, where 21,245 animals had less than 5 % inbreeding. The average inbreeding was 1.24 %. Variance and covariance components were estimated using the restricted maximum likelihood and were optimised using a quasi-Newton algorithm with analytical gradients (Neumaier and Groeneveld, 1998) as implemented in the VCE 6.0 program (Groeneveld *et al.*, 2008).

3   RESULTS AND DISCUSSION

Descriptive statistics for the original and transformed traits are summarised in Tables 1 and 2, respectively. The average length of the original age at first farrowing was 369.6 days. In previous papers, Serenius and Stalder (2004) and Serenius *et al.* (2004) published slightly lower ages at first farrowing for Finish Large White sows (368.5 days and 362.1 days, respectively). In contrast, Knauer *et al.* (2011) reported higher age at first farrowing (405.0 days) for 801 gilts of Landrace-Large White crosses. The low number of observations, differences in the breeds, and the restriction for data editing

Table 1: Descriptive statistics for the original data

	AFF_o [1]	$FI1_o$ [2]	$FI2_o$ [3]	$FI3_o$ [4]	$FI4_o$ [5]
Total number of sows	24,094	17,910	13,643	10,028	7,142
Minimum	286.00	121.00	120.00	120.00	123.00
Mean	369.57	165.84	159.00	158.09	157.71
Median	362.00	154.00	151.00	150.00	150.00
Maximum	500.00	350.00	346.00	350.00	344.00
Standard deviation	35.71	31.49	25.13	24.56	24.00
Skewness	1.03	2.44	3.14	3.26	3.32
Kurtosis	0.99	6.91	12.33	13.13	14.05

[1] original age at first farrowing, [2] original first farrowing interval, [3] original second farrowing interval, [4] original third farrowing interval, [5] original fourth farrowing interval.

could explain the slight differences in age at first farrowing between the studies. Based on original data, the first farrowing interval was 165.8 days on average. Farrowing intervals in the next parities were slightly shorter and varied from 159.0 days ($FI2_o$) to 157.7 days ($FI4_o$). This was similar to the trend observed by Serenius *et al.* (2003) from the first to the third farrowing interval in Finish Large White sows. With regard to the transformed data, a slight decrease in the average farrowing interval over parities (from 158.6 to 153.1 days for FI1 to FI4, respectively) was observed. For all the traits, skewness as well as kurtosis and the standard deviation decreased after transformation, except for age at first farrowing, where the standard deviation as a parameter of variability remained almost the same. However, farrowing intervals slightly decreased, and the average age at first farrowing slightly increased to 375.7 days when comparing the original and transformed data. Nevertheless, the results indicate that the main objective of data transformation was achieved in our study.

The relative proportion of phenotypic variance explained by the used effects for all the traits is summarised in Table 3. The coefficient of determinations for the original data reached lower values (35 %, 28 %, 26 %, 25 % and 24 % for AFF_o and $FI1_o$–$FI4_o$, respectively) compared to those of the transformed ones (37 %, 38 %, 38 %, 39 % and 39 % for AFF_t and $FI1_t$–$FI4_t$, respectively). The highest portion of phenotypic variability was explained by the HYS effect for age at first farrowing (90.5 % for original and 92.1 % for transformed age at first farrowing). The herd, year, and season effects also explained the high proportion of variability for other traits (generally more than 60 %) when they were considered as one joint effect. The relatively large differences in the explained variability between pairs of the original and the transformed traits were observed for the length of lactation (higher for the transformed observations) and for the mating type (higher for the original observations), especially for farrowing interval traits. All the effects were highly significant with $p < 0.001$; the breed of service sire for both age at first farrowing traits and the mating type for the third and the fourth farrowing interval were significant with $p < 0.05$.

The variance components for the original and the

Table 2: Descriptive statistics for the transformed data

	AFF_t [1]	$FI1_t$ [2]	$FI2_t$ [3]	$FI3_t$ [4]	$FI4_t$ [5]
Total number of sows	24,094	17,910	13,643	10,028	7,142
Minimum	286.00	121.00	120.00	120.00	123.00
Mean	375.73	158.63	154.65	153.88	153.11
Median	362.00	153.00	151.00	150.00	150.00
Maximum	438.00	186.03	182.00	180.00	177.00
Standard deviation	36.57	13.33	11.12	10.39	9.59
Skewness	0.09	0.31	0.56	0.54	0.50
Kurtosis	−0.42	−0.24	−0.76	−0.74	−0.71

[1] transformed age at first farrowing, [2] transformed first farrowing interval, [3] transformed second farrowing interval, [4] transformed third farrowing interval, [5] transformed fourth farrowing interval.

Table 3: *Relative proportion of phenotypic variance explained by effects for all traits*

	AFF_o	AFF_t	$FI1_o$	$FI1_t$	$FI2_o$	$FI2_t$	$FI3_o$	$FI3_t$	$FI4_o$	$FI4_t$
LL	-	-	6.56	13.02	12.83	22.31	11.24	21.49	17.67	30.33
HYS	90.51	92.12	74.98	72.38	69.90	68.53	68.97	69.54	60.64	60.39
BSS	0.12*	0.10*	2.09	2.01	2.34	1.64	1.21	0.91	1.07	0.50
MT	6.68	5.37	12.84	9.83	13.62	6.66	17.47*	7.43*	17.94*	7.23*
TNB	2.69	2.40	3.52	2.76	1.31	0.85	1.10	0.64	2.68	1.55

* ($p < 0.05$). All other effects are highly significant ($p < 0.001$). LL: Length of lactation, HYS: Herd-Year-Season, BSS: Breed of service sire, MT: Mating type, TNB: Total number of born piglets. For traits abbreviations, see Tables 1 and 2.

transformed traits are shown in Tables 4 and 5. The estimated heritabilities for the original traits were low with a tendency for heritability of the first farrowing interval to be greater than that at the subsequent intervals. Similar values were reported by Serenius *et al.* in 2003, with similar inclination (0.13, 0.06, 0.00, and 0.04 from the first to the fourth farrowing intervals). Serenius *et al.* claimed that this tendency might have been caused by

was 0.10, 0.03, and 0.02 from the first to the third farrowing intervals, respectively, when the length of lactation was assumed as an effect in the model (0.00, 0.02, and 0.00 from the first to the third farrowing intervals, respectively, when lactation length was not considered as an effect in the model). Cavalcante-Neto *et al.* (2009) also estimated a heritability of 0.02 for the first farrowing interval in a Brazilian commercial hybrid when the

Table 4: *Variance components for the original traits*

	AFF_o	$FI1_o$	$FI2_o$	$FI3_o$	$FI4_o$
Additive genetic effect (Heritability)	0.17 ± 0.011	0.11 ± 0.010	0.07 ± 0.009	0.06 ± 0.010	0.06 ± 0.011
Proportion of variance for HYS effect	0.16 ± 0.007	0.06 ± 0.006	0.05 ± 0.005	0.05 ± 0.005	0.03 ± 0.005
Proportion of variance for residual effect	0.67 ± 0.012	0.83 ± 0.010	0.88 ± 0.010	0.89 ± 0.010	0.91 ± 0.011

For traits abbreviations, see Table 1.

the decreasing numbers of observations in later parities, leading to a deterioration of the data structure, i.e., fewer observations per HYS class leading to poorer connectedness of the data. However, in our case, it is likely that it was caused because the total number of observations decreased but the number of observations within a joint HYS effect class did not decrease (average number of observation per class was 24, 23, 22, 22, and 22 for AFF and FI1–FI4) due to flexible HYS class formation. In addition, genetic relationship among herds is sufficient in the Czech Large White population, as observed in our previous study (Krupa *et al.*, 2016). Our results for the original farrowing interval are also consistent with the outcomes reported by Tholen *et al.* (1996), where the heritability

permanent effect was not considered in the model, and estimated it to be 0.00 when this effect was added to the model. All the above-mentioned results were estimated for non-transformed data.

The transformation procedure had negligible influence on the heritability of age at first farrowing, and the heritability of the transformed AFF was very similar to that of the original one (0.17 and 0.19 for AFF_o and AFF_t, respectively). Transformation of the farrowing interval had a higher positive impact: heritability of $FI1_t$–$FI4_t$ was 0.14, 0.11, 0.11, and 0.12, respectively. Proportions of the variances of the HYS effect were low (0.03–0.18) and were similar in the original and transformed traits. Proportions for residual variances reached high values

Table 5: *Variance components for the transformed traits*

	AFF_t	$FI1_t$	$FI2_t$	$FI3_t$	$FI4_t$
Additive genetic effect (Heritability)	0.19 ± 0.011	0.14 ± 0.010	0.11 ± 0.011	0.11 ± 0.012	0.12 ± 0.013
Proportion of variance for HYS effect	0.18 ± 0.008	0.08 ± 0.006	0.08 ± 0.007	0.08 ± 0.008	0.06 ± 0.008
Proportion of variance for residual effect	0.63 ± 0.011	0.78 ± 0.010	0.81 ± 0.010	0.81 ± 0.012	0.82 ± 0.013

For traits abbreviations, see Table 2.

Table 6: Genetic correlations (above the diagonal) with standard errors and phenotypic correlations (below the diagonal) for the original traits

	AFF_o	$FI1_o$	$FI2_o$	$FI3_o$	$FI4_o$
AFF_o		0.35 ± 0.044	0.43 ± 0.057	0.23 ± 0.075	0.32 ± 0.069
$FI1_o$	0.03		0.69 ± 0.059	0.87 ± 0.070	0.74 ± 0.072
$FI2_o$	0.05	0.09		0.72 ± 0.092	0.94 ± 0.053
$FI3_o$	0.02	0.12	0.06		0.89 ± 0.091
$FI4_o$	0.04	0.07	0.12	0.06	

All the phenotypic correlations are highly significant ($p < 0.001$). For traits abbreviations, see Table 1.

for all the traits. The phenotypic and genetic correlations between the analysed traits are summarised in Tables 6 and 7. The phenotypic correlations were slightly higher for the transformed traits, but had very low values. The genetic correlations between AFF and FI1–FI4 traits were low or moderate, whereas those between the FI1–FI4 traits showed high values (0.66–0.94); all the values were clearly lower than one. The phenotypic Pearson's correlation coefficients between a pair of original and transformed traits were also calculated. The correlation coefficients reached values of 0.93, 0.83, 0.82, 0.81, and 0.80 for the original and transformed AFF and FI1–FI4, respectively. All the phenotypic correlation coefficients were highly significant ($p < 0.001$). Previously, Serenius *et al.* (2003) reported phenotypic and genetic correlations of farrowing interval between different parities. The genetic correlations estimated in their study varied between parities from −0.28 to 0.84, but with large standard errors and correlations between the fourth and previous farrowing intervals fluctuating around zero. Consistent with our results, Serenius *et al.* (2003) also found low phenotypic correlations between parities, and based on the fact that the genetic correlations between farrowing intervals were estimated to be lower than one, concluded that farrowing intervals over parities should be treated as different traits. This is in agreement with our results for the farrowing intervals. Further, Hanenberg *et al.* (2001) also evaluated farrowing interval and its parts as gestation length, interval from weaning to first mating, and

interval from first mating to farrowing on different parities and observed high genetic correlations among parities for all the studied traits, except for interval from first mating to farrowing.

4 CONCLUSIONS

Using the transformation formula decreased the skewness and kurtosis of the original farrowing interval data. The presented heritabilities of farrowing interval on different parities indicated that farrowing interval for the first and subsequent parities should be considered as different traits. Our findings show that selection on transformed traits instead of on original (untransformed) traits should be beneficial for achieving a higher genetic gain.

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Table 7: Genetic correlations (above the diagonal) with standard errors and phenotypic correlations (below the diagonal) for the transformed traits

	AFF_t	$FI1_t$	$FI2_t$	$FI3_t$	$FI4_t$
AFF_t		0.25 ± 0.039	0.38 ± 0.046	0.14 ± 0.054	0.29 ± 0.058
$FI1_t$	0.04		0.70 ± 0.052	0.85 ± 0.051	0.66 ± 0.043
$FI2_t$	0.06	0.18		0.75 ± 0.061	0.94 ± 0.051
$FI3_t$	0.02	0.23	0.21		0.79 ± 0.076
$FI4_t$	0.04	0.17	0.27	0.21	

All phenotypic correlations are highly significant ($p < 0.001$). For traits abbreviations, see Table 2.

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