

## A GENETIC ANALYSIS OF SOW LONGEVITY

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### **SUMMARY**

Sow longevity, measured in terms of final parity attained, was analysed by a variety of methods, including survival analysis, linear model and generalised linear mixed model approaches. Heritability estimates ranging from 0.11 to 0.21 were obtained from the different analyses. Non-survival analysis methods did not perform well as alternatives to survival analysis. Evidence of low, unfavourable genetic correlations with average daily gain and ultrasonic backfat depth was found.

**Keywords:** pigs, sow longevity, survival analysis.

### **INTRODUCTION**

Sow longevity (SL) can be thought of as a composite trait containing information about all traits on which voluntary and involuntary culling takes place. It has been shown (Dijkhuizen *et al.* 1989; De Vries 1989) that there is an economic benefit to increasing SL. Tholen *et al.* (1996) and Yazdi *et al.* (2000) carried out genetic parameter estimation of different measures of SL and found it to be heritable. An appropriate analysis of SL would take account of the presence of incomplete records on sows, changes in the environmental effects associated with a sow during her lifetime and the distribution of the data. This can be achieved with survival analysis. Software to perform survival analysis on large data sets with animal breeding models has been developed by Ducrocq and Sölkner (1999). In this study SL was analysed using survival analysis, linear model (LM) and generalised linear mixed models (GLMM) techniques. The aim was to obtain genetic parameters and compare predictors of genetic merit for SL.

### **MATERIALS AND METHODS**

**Data.** Information on sow longevity, in terms of latest parity recorded, was available for 6402 sows from an 800 sow synthetic line. Sows had to have a first parity record to be included in the data and had between one and 12 parities recorded. The last 814 sows to farrow were regarded as being censored. For censored sows it was not possible to tell whether or not they had left the breeding herd from the data. The distribution of final recorded parity for uncensored sows is given in Table 1. As part of the routine herd recording, data were available on average daily gain from birth to approximately 150 days of age (ADG) and ultrasonic backfat depth (BF) as well as various sow reproduction observations including number born alive (NBA). Estimated breeding values for ADG, BF and NBA were used as selection criteria for this line.

**Traits.** Sow longevity traits were defined according to the method used for their analysis. Final parity for all sows (both censored and uncensored) was analysed using survival analysis (trait SLS). Alternatively, for uncensored sows a linear model was applied to final recorded parity (SLLP) and

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the Normal score of this value (SLLN). Finally, a series of binomial traits were defined with censored and uncensored sows receiving a 1 if they farrowed in parity  $n$  and a 0 otherwise (SLT $n$ , where  $n$  is a value between 2 and 5), these traits were analysed using a GLMM. Bivariate analyses also considered the traits ADG, BF and NBA.

**Table 1. Distribution of final recorded parity for uncensored data**

Parity	Number of sows	% of sows	Cumulative %
1	1121	20.1	20.1
2	1019	18.2	38.3
3	1064	19.0	57.3
4	829	14.8	72.1
5	629	11.3	83.4
6	422	7.6	91.0
7...12	504	9.0	100.0

**Analyses.** Survival analysis of final recorded parity number was carried out using the grouped data model of Prentice and Gloeckler (1979) as implemented in the Survival Kit version 3.1 (Ducrocq and Sölkner 1999). Linear model and GLMM analyses were performed using average information residual maximum likelihood as found in the ASREML computer package (Gilmour *et al.* 1999). A probit link function was used in all GLMM analyses assuming an underlying threshold model.

Sire was included as a random effect in all analyses, and relationships among sires were accounted for. Fixed effects were determined by preliminary survival analysis of the data. Farrowing group (FG) and a linear regression of age at first farrowing were included as fixed effects in all analyses. Farrowing group was defined as the three-month period in which a sow farrowed. For the survival analysis (trait SLS), FG was fitted as a time-dependent effect; ie the sow appears in a different FG at each farrowing. Fitting FG as a time-dependent effect makes best use of the information collected on a sow. For LM and GLMM analyses (traits SLLP, SLLN and SLT $n$ ) time-dependent effects could not be fitted, so FG in the first parity of the sow was used.

Bivariate analysis of SLLP with ADG, BF and NBA were carried out using a linear sire model in ASREML. The model for the analysis of SLLP was as for the univariate analysis. NBA in each of parities one to five was analysed alongside SLLP, fitting farrowing group in the current parity as a fixed effect. For ADG and BF contemporary group was included as a fixed effect and litter of birth was included as a random effect uncorrelated with the sire effect. In addition, linear and quadratic regressions on weight at measurement were fitted for BF.

## RESULTS AND DISCUSSION

**Univariate analyses.** Table 2 contains heritability estimates from the univariate analyses. For survival analysis and GLMM analyses these values are on the underlying scale. The residual variance in the survival analysis is fixed to be  $\pi^2/6$ , and in the GLMM analyses to be one. The Normal scoring process results in SLLN having an approximate phenotypic variance of one, while the variance

components for SLLP are fully data dependent. As a result the variance components are not comparable across analyses and are not presented here.

The levels of heritability indicate that genetic progress could be made in SL. Heritability increases across parities for the binomial traits (SLT2...SLT5). The trend in heritability could result from herd management decisions and was also observed by Tholen *et al.* (1996). Additional analyses including linear regressions on ADG, BF and NBA produced lower estimates of the heritability (e.g. the heritability for SLS reduced to 14% of the phenotypic variance), indicating that only some of the genetic variation in SL in this population was due to the selection criteria. The heritability of SLS was higher than those reported by Yazdi *et al.* (2000) for survival analysis of age in days at culling (or censoring), but probably not significantly so.

Pearson correlation coefficients between sire solutions from the various analyses are given in Table 2. Survival analysis was expected to give the best predictions of genetic merit, as it takes account of data censoring, changes in environmental effects and the distribution of the data. The appeal of non-survival analysis predictors is the ease with which they could be incorporated into a multivariate genetic evaluation. The correlations of the other predictors with the SLS predictor indicate that none of them would be a very good alternative to the SLS predictor, SLLP being the best with a correlation of -0.8. The binomial predictors do reasonably well at predicting survival at the next parity, but early binomial predictors (SLT2 and SLT3) are poor approximations of the SLS predictor. The advantage of using SLT2 in a genetic evaluation system would be that a complete observation would be available relatively early in a sow's life.

**Table 2. Results of univariate analyses of SL traits under a sire model**

Trait	Analysis <sup>A</sup>	$h^2 \times 100 \pm \text{s.e.}^B$	Correlation ( $\times 100$ ) between sire solutions					
			SLLN	SLT2	SLT3	SLT4	SLT5	SLS
SLLP	LM	21 $\pm$ 4	99	60	75	81	77	-80
SLLN	LM	19 $\pm$ 4		72	79	80	72	-78
SLT2	GLMM	11 $\pm$ 6			65	46	32	-43
SLT3	GLMM	16 $\pm$ 5				70	45	-52
SLT4	GLMM	17 $\pm$ 5					65	-61
SLT5	GLMM	21 $\pm$ 6						-64
SLS	SA	18 <sup>C</sup>						

<sup>A</sup> Method of analysis; linear model (LM), Generalised linear mixed model (GLMM) or survival analysis (SA); <sup>B</sup> Estimated heritability and associated standard errors; <sup>C</sup> No standard errors were available from the survival analysis

**Bivariate analyses.** It was not possible to estimate the genetic correlations of SLS with the production traits. Because SLLP gave the best approximation of SLS genetic merit in the univariate analyses, Table 3 contains the results of bivariate analyses of SLLP with ADG, BF and NBA.

Heritability estimates for SLLP are consistent with the univariate estimate. Heritabilities for ADG, BF and NBA are consistent with the literature. Standard errors of the genetic correlation estimates are relatively large. The genetic correlations indicate small, unfavourable genetic relationships of ADG and BF with SLLP. That is, genetically fatter, slower-growing sows will tend to survive longest. There is a positive genetic relationship between NBA and SLLP, and this relationship may be stronger in later parities.

**Table 3. Results of bivariate analyses of SLLP with traits in the selection criteria**

Trait <i>i</i>	$h_{SLLP}^2$ <sup>A</sup>	$h_i^2$ <sup>B</sup>	$c_i^2$ <sup>C</sup>	$r_g$ <sup>D</sup>	$r_p$ <sup>E</sup>
ADG	20 ± 4	23 ± 2	10 ± 3	-10 ± 13	-13 ± 2
BF	21 ± 4	50 ± 3	4 ± 0	8 ± 10	8 ± 2
NBA1 <sup>F</sup>	21 ± 4	7 ± 3	NA	10 ± 20	12 ± 1
NBA2	21 ± 4	16 ± 4	NA	43 ± 15	16 ± 2
NBA3	21 ± 4	22 ± 5	NA	37 ± 15	20 ± 2
NBA4	21 ± 4	7 ± 5	NA	28 ± 29	21 ± 3
NBA5	21 ± 4	14 ± 8	NA	98 ± 29	25 ± 3

<sup>A</sup> heritability of SLLP; <sup>B</sup> heritability of trait *i*; <sup>C</sup> common litter of birth effect variance of trait *i* as a proportion of the phenotypic variance; <sup>D</sup> genetic correlation; <sup>E</sup> phenotypic correlation; <sup>F</sup> NBA<sub>*j*</sub> is NBA in parity *j*.

Inclusion of SL in genetic evaluation and selection decisions would be feasible, with survival analysis methodology to be preferred. Simultaneous genetic progress in ADG, BF, NBA and SL should be achievable. Incorporating SL along with production traits in selection indexes allows selection for profitability, rather than just production.

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#### REFERENCES

- De Vries, A.G. (1989) *Livest. Prod. Sci.* **21**: 49.  
 Dijkhuizen, A.A., Krabbenborg, R.M.M. and Huirne, R.B.M. (1989) *Livest. Prod. Sci.* **23**: 207.  
 Ducrocq, V. and Sölkner, J. (1999) "The Survival Kit V3.1 User's Manual"  
<http://www.boku.ac.at/nuwi/popgen/softskit.htm>  
 Gilmour, A.R., Cullis, B.R., Welham, S.J. and Thompson, R. (1999) "ASREML Reference Manual"  
 NSW Agriculture Bulletin No. 3.  
 Prentice, R. and Gloeckler, L. (1978) *Biometrics* **34**: 57.  
 Tholen, E., Bunter, K.L., Hermes, S. and Graser, H.-U. (1996) *Aust. J. Agric. Res.* **47**: 1261.  
 Yazdi, M.H., Rydhmer, L., Ringmar-Cederberg, E., Lundeheim, N. and Johansson, K. (2000) *Livest. Prod. Sci.* **63**: 255.