Sire Re-ranking and Analysis Methods for Sow Lifetime Reproductive Traits

L. Engblom[*], K. Stalder[*], M. Nikkilä[*], J. Holl[†], S. Tsuruta[‡],
W. Herring[†], M. Culbertson[†] and J. Mabry[*]

Introduction

Today, 30% or more commercial sows are removed before parity three (Engblom *et al.*, 2007) resulting in lost economic opportunity and reduced production efficiency. Sow longevity may be improved by selection for highly prolific sows over several parities in existing production systems. Recent studies have shown that selection for longevity should consequently lead to improvement in annual replacement rates (Heusing *et al.*, 2005; Serenius *et al.*, 2006; Tarrés *et al.*, 2006).

Sow longevity is an economically important trait in pig production which may be improved by selection (Heusing *et al.*, 2005; Serenius *et al.*, 2006; Tarrés *et al.*, 2006) but including this trait in genetic evaluations presents challenges. One challenge is elongated time intervals required to collect complete lifetime data resulting in extended generation intervals. This problem can be addressed by programs handling incomplete data records (censoring). In addition, indicator traits expressed earlier in life which have high genetic correlations with longevity may enhance longevity genetic evaluations.

The objectives of the present study were to investigate the effect of censoring programs on sire rankings of lifetime reproductive traits measured on crossbred daughters and to identify linear and nonlinear early indicator traits for inclusion in sow longevity genetic evaluations.

Material and methods

The data were from pedigreed crossbred Landrace × Large White sows at a single farm. Sows with a first farrowing recorded before 290 days or after 500 days were excluded to remove questionable records. After restricting the data to only include contemporary groups (entering month within year) with at least 100 sows, the final data set included 12,725 sows entering the farm between December 2004 and March 2009. The data included 30% incomplete (censored) data records.

Several early indicator traits for longevity were constructed; number born alive in first parity (NBA1) and accumulated number of piglets born alive up to 2nd (ABA2), 3rd (ABA3) and 4th (ABA4) parity were calculated for all sows, even if they were removed at a lower parity

---

[*] Department of Animal Science, Iowa State University, Ames, IA 50011, USA
[†] Smithfield Premium Genetics Group, Rose Hill, NC 28458, USA
[‡] Department of Animal and Dairy Science, University of Georgia, Athens, GA 30602, USA

number. This novel indicator trait, accumulated born alive up to a specified parity, was evaluated for its potential as an early indicator of sow longevity. Four stayability traits were created as indicator traits; stayability for the gilts entering the farm up to farrowing parity 1 to 4 (ST1F to ST4F). The stayability traits were assigned a value of 0 for a sow removed before the event and 1 for a sow surviving up to the event. One longevity traits was created, lifetime number born alive (LBA) was determined as the number of piglets born from birth to removal or end of data collection and only included sows with complete records (data from all parities) at removal or end of data collection. Phenotypic averages for the traits are shown in Table 1.

Statistical analyses: First, co(variance) components were estimated using the average information (DMU AI) restricted maximum likelihood (REML) algorithm based on mixed linear models using the DMU Software package (Madsen and Jensen, 2008). Secondly, it was investigated whether fitting nonlinear, binomial and threshold models would fit stayability traits better than linear models that assume a normal distribution. Binomial models were fit to stayability traits using the GLMM (Generalized Linear Mixed Model) feature in DMU fitting logit link (standard logistic probability distribution) and probit link functions (assuming an underlying normal distribution). To fit a threshold model, THRGIBBS1F90 (Tsuruta and Misztal, 2006) with Bayesian inference using Gibbs sampling was used. Univariate analyses, ignoring censoring were performed to estimate the heritabilities and effect of common litter shown in Tables 1 and 2. LBA was analyzed with DMU using two different variables, ignoring censoring (LBA_IC; N=11,882) and only including complete lifetime records (LBA_CR; N=8916) to evaluate the impact of implementing censoring in the analysis. In addition, LBA was analyzed using GIBBS2CEN which accounts for censoring using Bayesian inference and Gibbs sampling (LBA_C). Estimated breeding values on sires with at least 30 daughter records were compared using Spearman rank correlations to investigate the effect of censoring and relationships between LBA and indicator traits (Table 3). The number of sires that met this criterion was 124 (103 for LBA_CR).

The model fitted for all analyses included the random animal effect (a), entering year × month fixed effect combination and the random birth litter effect (l). The pedigree was traced five generations back when possible and the final pedigree file included 20,099 animals. Standard errors for DMU heritability estimates were calculated using Taylor series approximations. The Gibbs samplers were run 550,000 rounds with 50,000 burn-ins, sampling every 50th sample resulting in 10,000 samples from which the estimates and standard deviations were calculated. Autocorrelations between samples and effective sample sizes were evaluated by using POSTGIBBSF90 (Misztal *et al.*, 2002).

Results and discussion

Heritability estimates and common litter effects analyzed with linear models ignoring censoring are shown in Table 1. All heritability estimates were low, but are in agreement with previous studies (Serenius *et al.*, 2006; Engblom *et al.*, 2009). The present study analyzed LBA as the main measurement for longevity instead of the more commonly used productive life (measured in days). The reason for using LBA is that it is the trait having economic importance in piglet production. Additionally, length of productive life may include non-productive days which we do not want to select for since these are undesirable from a productivity standpoint. LBA analyzed with linear models resulted in heritability estimates from 0.06 to 0.07 and LBA_C which accounted for censoring at 0.05 (SD: 0.01).

Table 1: Phenotypic averages, estimates of common litter effect (l^2) and heritability (h^2)

	Average	l^2	$h^2_{st.err}$
NBA1^{1}	11.1	0.04	0.09$_{.02}$
ABA2^{1}	16.6	0.03	0.04$_{.01}$
ABA3^{1}	22.8	0.03	0.04$_{.01}$
ABA4^{1}	27.5	0.03	0.05$_{.01}$
ST1F^{1}	0.78	0.02	0.03$_{.01}$
ST2F^{1}	0.58	0.02	0.03$_{.01}$
ST3F^{1}	0.46	0.02	0.02$_{.01}$
ST4F^{1}	0.35	0.02	0.04$_{.01}$
LBA_CR^{1}	34.2	0.03	0.06$_{.01}$
LBA_IC^{1}	33.9	0.03	0.07$_{.01}$

Table 3: Sire (spearman) rank correlations between indicator traits and LBA analyzed with and without accounting for censoring*

	LBA_CR^{1}	LBA_IC^{1}	LBA_C^{3}
NBA1^{1}	0.13$^{n.s.}$	0.23**	0.25**
ABA2^{1}	0.70***	0.81***	0.83***
ABA3^{1}	0.81***	0.92***	0.93***
ABA4^{1}	0.87***	0.97***	0.97***
ST1F^{2}	0.56***	0.60***	0.62***
ST2F^{2}	0.68***	0.79***	0.80***
ST3F^{2}	0.79***	0.86***	0.85***
ST4F^{2}	0.79***	0.86***	0.85***
LBA_CR^{1}	1	0.92***	0.88***
LBA_IC^{1}	0.92***	1	0.99***

* Significance levels are given as superscripts; [1] Analyzed in DMU6, normal distr., ignoring censoring; [2] Analyzed in THRGIBBS1F90, ignoring censoring; [3] Analyzed in GIBBS2CEN, accounting for censoring
NBA1=number born alive in parity 1; ABA2 to ABA4=accumulated born live up to parity 2, 3 and 4; ST1F to ST4F=stayability farrowing parity 1 to 4; LBA_IC and LBA_CR=Lifetime born alive ignoring censoring and including complete records, respectively

Table 2: Estimates of common litter effect (l^2) and heritability (h^2) for stayability traits analyzed with binomial distribution (logit and probit) and threshold-linear model

	Binom.distr; logit^{1}		Binom.distr; probit^{1}		Threshold-linear ^{2}	
	l^2	$h^2_{st.err}$	l^2	$h^2_{st.err}$	l^2	$h^2_{st.dev}$
ST1F	0.04	0.14$_{.13}$	0.01	0.05$_{.05}$	0.04	0.07$_{.02}$
ST2F	0.04	0.10$_{.10}$	0.01	0.04$_{.04}$	0.04	0.06$_{.02}$
ST3F	0.04	0.07$_{.07}$	0.02	0.03$_{.03}$	0.03	0.04$_{.02}$
ST4F	0.03	0.12$_{.11}$	0.01	0.05$_{.05}$	0.03	0.08$_{.02}$

ST1F to ST4F=farrowing parity 1 to 4
[1] Analyzed in DMU6, binomial distribution, ignoring censoring; [2] Analyzed in THRGIBBS1F90, ignoring censoring

All heritabilities for stayability were greater when analyzed with nonlinear models compared to linear models (Tables 1 and 2). This response was in agreement with theoretical expectations as outlined by Gianola (1979). Although, heritability standard errors were also higher with nonlinear models, binomial models yielded standard errors similar in magnitude as the heritability estimates. Threshold models resulted in standard deviations that were half the magnitude or less of the corresponding heritability estimates. These results indicate there is no advantage to analyze stayability as a binomially distributed trait when compared to analyzing the trait in a linear model. However, it may be beneficial to analyze these traits with other traits in a joint threshold-linear multi-trait model.

Sire rank correlations for the three different LBA and the early indicator traits including stayability traits analyzed with THRGIBBS1F90 are shown in Table 3. The LBA_CR had high correlations with LBA_IC and LBA_C but LBA_IC had a higher correlation with LBA_C, which indicated that it was better to include all available records than to include only complete records when not accounting for censoring in the analyses. The sire rank correlation between LBA_C and LBA_IC is almost unity and showed that the sires were ranked very similarly regardless if the program handled censoring when all available data in the present study with 30% censored records was included.

The sire rank correlations between LBA and the indicator traits are shown in Table 3. All sire rankings of indicator traits were significantly correlated with LBA_C. The results show that sire rankings of stayability up to parity 1 were more similar to LBA_C than sire rankings on parity 1 litter size. Conversely, ranking sires on parity 2 to 4 accumulated born alive was more similar to LBA_C than stayability to second, third and fourth parities, respectively. Sire rank correlation to LBA_C was higher for ABA2 to ABA4 (0.83 to 0.97) than for ST1F (0.62). For accumulated born alive and stayability, correlations between these traits and LBA_C increased with each additional parity. The largest increase in correlations was between the first and second parities. Increasing the parity from 3 to 4 resulted in a marginal sire ranking correlation increase for accumulated born alive, but no increase for stayability.

Conclusion

The results of this study show that stayability traits benefit from being analyzed with a threshold model compared to analyzing with a normal linear model. Sire re-ranking was very small when comparing lifetime born alive with a program accounting for censoring to a program including all available data but ignoring censoring. Furthermore, accumulated born alive in parities 2 to 4 resulted in low sire re-ranking when compared to lifetime born alive analyses and were the strongest indicators for lifetime born alive. Although stayability traits were not the strongest indicators of lifetime born alive, they still had significant association with it. Therefore, accumulated born alive and stayability traits should be considered for inclusion in sow longevity genetic evaluations.

References

Engblom, L., Lundeheim, N., Dalin, A.-M., *et al.* (2007). *Livest. Sci.*, 106: 76-86.

Engblom, L., Lundeheim, N., Schneider, M. D., *et al.* (2009). *Animal*, 3: 783-790.

Gianola, D. (1979). *Genetics*, 93: 1051-1055.

Heusing, M., Hamann, H. and Distl, O. (2005). *Züchtungskunde*, 77: 15-34.

Madsen, P. and Jensen, J. (2008). *A user's guide to DMU.*

Misztal, I., Tsuruta, S., Strabel, T., *et al.* (2002). In *Proc 7th WCGALP*, 28-07.

Serenius, T., Stalder, K. J. and Puonti, M. (2006). *J. Anim. Breed. Genet.*, 123: 355-61.

Tarrés, J., Bidanel, J. P., Hofer, A., *et al.* (2006). *J. Anim. Sci.*, 84: 2914-24.

Tsuruta, S. and Misztal, I. (2006). In *Proc 8th WCGALP*, http://www.wcgalp8.org.br/wcgalp8/articles/paper/27_367-1895.pdf.