Genetic parameter of sow longevity and sow lifetime prolificacy traits using purebred swine censored record

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ABSTRACT: The purpose of the present study was to investigate the indicators for improved sow longevity in a Thailand swine commercial nucleus herd. The sow longevities in this study were stayability in the 2nd - 5th parity (STAY2, STAY3, STAY4, and STAY5), lifetime (LT), lifetime production (LP), Productive per lifetime (PD%) and number born alive per lifetime day (NBA/LT). Lifetime and prolificacy records were from 3,148, 2,354, and 1,176 daughters of 306, 273 and 158 sires in purebred Landrace, Yorkshire, and Duroc, respectively. Sow records were collected between 2008 and 2016. Genetic parameters were estimated with a threshold model for stayability traits with THRGIBBS1F90. Genetic parameters for LT, LP, PD% and NBA/LT traits were estimated by Bayesian linear models with GIBBS2F90 and GIBBS2CEN considering censored records (record which animal are still alive when data collection occurred). The longevity and lifetime prolificacy were analyzed with bivariate analysis. Posterior means of heritability of stability were 0.14-0.28, 0.10-0.31, 0.10-0.39 and 0.14-0.38 in STAY2, STAY3, STAY4, and STAY5 respectively. Genetic correlations among these traits is positive 0.32-0.94 (STAY2-STAY5) and 0.77-0.98 (STAY3-STAY5). Heritability of longevity and lifetime prolificacy traits using GIBBS2F90 and GIBBS2CEN were 0.03-0.13 and 0.03-0.24 in LT, 0.21-0.29 and 0.21-0.29 in LP, 0.03-0.21 and 0.03-0.12 in PD% and 0.12-0.24 and 0.12-0.24 in NBA/LT. Heritability estimated with censored records was not only higher than it was when ignoring the censored records, but the -2log (p) was lower also. Thus, STAY3 and LP and NBA/LT breeding value estimated with ignoring the censored records are indicators for improved sow longevity and lifetime prolificacy in this commercial herd.

Keywords: genetic parameter, sow longevity, sow prolificacy, censored record

Introduction

The economic standpoint of commercial sow herds is improving sow longevity (Stalder et al., 2003). Sow longevity was the sow's ability to survive and still produce in the herd (Nikkilä et al., 2013). Many previous studies indicate that 30% of commercial sows were removed at early parity three (Engblom et al., 2007; Stalder et al., 2003) and 50% of sows are culled annually (Engblom et al., 2016). Mathur (2002) reported that the high culling rate was related to the average number of piglets per litter having decreased, the number of non-reproductive days having increased and selection intensity limiting genetic progress having decreased. Sow longevity is an important factor to increase the production and

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profitability of a commercial sow herd which can be improved by genetic selection (Serenius et al., 2006). Noppibool et al. (2015) reported that sire and dam population in a Northern Thailand farm were improved in length of productive life and lifetime production by a selection program. In several studies sow longevity was defined as the number of days between birth date and cull or removal date or stayability and lifetime piglets produced (Abell, 2013; Engblom et al., 2016). Usually, data of sow longevity are needed to collect complete lifetime data (uncensored) but Engblom et al. (2016) suggested that not ignoring the incomplete data records (censored) due to breeding value estimation was correct rather than including only complete records. For a young sire, their daughter's length of productive life or lifetime prolificacy records would be mostly incomplete. So estimation of breeding values of sires can be improved by including the censored records for their daughter (Guo et al., 2001).

There are many methods for estimating the breeding value of sow longevity such as Bayesian or survival analysis, linear models and the REML approach. In the past, survival analysis and linear model analysis were the most widely used analyses (López-Serrano et al., 2000; Serenius and Stalder, 2006). Different approaches are used for genetic evaluation of sow longevity such as THRGIBBS1F90 for linear-threshold models by Bayesian approach with Gibbs sampling for binary stayability traits, GIBBS2F90 and GIBBS2CEN for Bayesian analysis with linear model but GIBBS2CEN for use with censored data. (Engblom et al, 2016). The objectives of this study were (i) to estimate the genetic parameters for stayability in the 2nd - 5th parity (STAY2, STAY3, STAY4, and STAY5); (ii) compare genetic parameters from different methods (censored and uncensored data) for lifetime (LT), lifetime production (LP), Productive per lifetime (PD%) and number born alive per lifetime day (NBA/LT). Finally, identify which indicator can be used to determine the value of adding the trait into a selection program.

Materials and Methods

Data description

This project uses 3,191, 2,354, and 1,176performance records from Landrace, Yorkshire and Duroc sows, respectively. There were 4,416 Landrace, 3,118 Yorkshire, and 1,547 Duroc animals for this study. This population was purebred swine in a nucleus herd at the Eastern part of Thailand. Data on purebred sow records collected over the period from 1 January 2008 through the end of data collection on 29 February 2016 with at least one farrowing record will be used. Sows with a first farrowing record before 300 days or after 500 days were deleted from the dataset. The records from sows still alive in the herd were censored data. There were 15-25% censored data for longevity and lifetime prolificacy traits included in this dataset. Pedigree information for at least three generations was known for every sow with performance data.

Traits analyzed

Longevity trait;

- Stayability in the 2nd-5th parity (STAY2, STAY3, STAY4, and STAY5) is defined as the ability of the sow to survive. The record of stayability traits were set to code 1 for sows culled or code 2 for sow surviving up to the 2nd - 5th parity. Also including sows which are still in production at the data collection date and coding 2 in parity 2 to 5 for them due to having a chance for success at parity 5. Four stayability traits were evaluated as indicator traits for true lifetime production (Engblom et al, 2016; Knauer et al, 2010).

- Lifetime (LT) is the number of days from first conception date to last weaning date. LT was considered as starting from first conception date due to the period from gilt entry to farm until conception being short or long term depending on farm management and is not genetic.

- Lifetime production (LP) is the total calculated days (gestation day + lactation day) during a sow's life.

Lifetime prolificacy trait;

- Productive per lifetime (PD%) is (Lifetime of production day / Lifetime day) x100

- Number born alive per lifetime day (NBA/LT) is the total number of piglets born alive / lifetime day.

Statistical analyses

Mixed model methodology and generalized linear mixed model (SAS, Inst. Inc., Cary, NC) was used for developing models for variance component estimation of the traits evaluated in this study. For all traits in each sow breed, statistical analyses used the Bayesian method for estimating variance components. This method was based on the empirical distribution of the Markov chain Monte Carlo approach and Gibbs sampling procedure (Engblom et al, 2016). Univariate analysis was performed to estimate heritability (h^2) and multivariate analyses to estimate correlations.

The stayability traits were evaluated on a threshold model assuming an underlying normal distribution. Univariate and multivariate analyses were performed with THRGIBBS1F90 (Tsuruta and Misztal, 2006) with Bayesian inference using Gibbs sampling. The statistical model for stayability traits was

$$y_{ij} = \mu + \mathrm{YBD}_i + b_1 \mathrm{AFF}_j + a_j + e_{ij}$$

in which y_{ij} = the trait measured on sow j, μ = intercept, YBD_i = fixed effect of year of birth date i (i = 1 to 8), AFF_j = age at first farrowing of sow j, b_1 is a regression coefficient, a_j = additive genetic effect of sow j with $a_j N{\sim}(0,\sigma_a^2)$, and e_{ij} = random residual with $e_{ij} N{\sim}(0,\sigma_e^2)$.

Following analysis, LT, LP, PD%, and NBA/LT traits were evaluated with 2 different linear model methods: (i) all data were analyzed by ignoring censor (i.e. incomplete records were treated as complete records), Univariate analyses were performed using GIBBS2F90 (Misztal et al., 2002); and (ii) all data were analyzed by censored data, end date (censoring) was the last weaning date for a culled sow or the end of data collection (February 29, 2016) for the sow that was still productive. Univariate and multivariate analyses with censored data were implemented using Markov chain Monte Carlo approach and Gibbs sampling procedures in GIBBS2CEN (S. Tsuruta, University of Georgia, Athens, GA, personal communication).

In analysis with GIBBS2CEN, the censored data was set to negative value. A reason to use negative values was that the program recognizes censored records when they are negative. The program still uses positive values to estimate variance components. The only differences between non-censored and censored records were the range of the distribution when sampling.

The statistical model for analyzing LT and LP traits were

$$y_{ij} = \mu + \mathrm{LPar}_i + b_1 \mathrm{AFF}_j + a_j + e_{ij}$$

in which y_{ij} = the trait measured on sow j, μ = intercept, LPar_i = fixed effect of last parity i (i

= 1 to 9), AFF_j = age at first farrowing of sow j, b_1 is a regression coefficient, a_j = additive genetic effect of sow j with $a_j N\sim(0,\sigma_a^2)$, and e_{ij} = random residual with $e_{ij} N\sim(0,\sigma_e^2)$.

The statistical model for analyzing PD% trait was

$$y_{ij}= \mu+\mathrm{YBD}_i+b_1\mathrm{AFF}_j+a_j+e_{ij}$$

in which y_{ij} = the trait measured on sow j, μ = intercept, YBD_i = fixed effect of year of birth date i (i = 1 to 8), AFF_j = age at first farrowing of sow j, b_1 is a regression coefficient, a_j = additive genetic effect of sow j withv $a_j N\sim(0,\sigma_a^2)$, and e_{ij} = random residual with $e_{ij} N\sim(0,\sigma_e^2)$.

The statistical model for analyzing NBA/LT trait was

$$y_{ij}= \mu+\mathrm{YBD}_i+b_1\mathrm{AFF}_j+b_2\mathrm{TB1Par}_k+a_{jk}+e_{ijk}$$

in which y_{ij} = the trait measured on sow j, μ = intercept, YBD_i = fixed effect of year of birth date i (i 1 to 8), AFF_j = age at first farrowing of sow jk, $\mathrm{TB1Par}_k$ = total born piglets in first parity of sow jk, b_1 and b_2 are a regression coefficient, a_{jk} = additive genetic effect of sow jk with $a_{jk} N\sim(0,\sigma_a^2)$, and e_{ijk} = random residual with $e_{ijk} N\sim(0,\sigma_e^2)$.

Variance components, genetic standard deviations (SD) and genetic correlations were performed in THRGIBBS1F90, GIBBS2F90, and GIBBS2CEN, the Gibbs sampling was run as a single chain of 220,000 cycles with burn-in period of the first 20,000 cycles. After samples in burn-in period are considered removed, the remaining 10,000 samples (every 20th cycle was stored) were used to calculate posterior means and standard deviations of variance and covariance components using POSTGIBBSF90 (Misztal et al., 2002).

Finally, The Spearman rank correlation for longevity and lifetime prolificacy traits between censored data and ignoring censored data calculated using SAS software for comparison order of breeding values of sows were still in production.

Results and Discussion

Descriptive statistics

Descriptive statistics for the traits in this study are shown in **Table 1** These data include the records of sows that are still alive in the herd (i.e., incomplete record or right-censored record) and were 15-25% (data not shown). The mean of LT was 500 to 530 days, they were similar with other studies that have calculated from first farrowing to removal after including the number of gestation days (Lucia et al., 2000; Yazdi et al., 2000). Noppibool et al. (2015) found that the length of productive life (LPL) of commercial purebred sows in Northern Thailand was 680.35 ± 420.53 days

Heritabilities

The heritabilities estimated for STAY2 to STAY5 traits ranged from 0.10 to 0.39 in this study (**Table 2**), they were higher in Duroc sows compared with Landrace and Yorkshire sows. These estimates were higher compare to previous research showing that heritabilities for stayability to mating and farrowing in parity 1 to 4 were 0.05 to 0.08, estimated with THRGIBBS1F90 (Engblom et al., 2016). Engblom et al. (2009) found that heritabilities for STAY12 and STAY13 were 0.03 to 0.06. Heritability estimated for LT and LP were higher in Duroc sow than Landrace and Yorkshire sows, respectively (**Table 3**). In Yorkshire, the heritability for LT was lowest but it was similar with Swedish crossbred sows (0.03 to 0.08) (Engblom et al., 2009). PD% was higher in

Table 1 Phenotypic descriptive[1] statistics for longevity and lifetime prolificacy traits of 3 purebred sows in a study

Traits[1]	Number of records	Mean	SD	Min	Max
Landrace					
LT	3191	511.52	302.02	111	1316
LP	3191	493.05	287.92	111	1236
PD%	3191	97.14	3.40	61.10	100.00
NBA/LT	3191	0.089	0.02	0.01	0.20
AFF	3191	368.54	29.71	300	500
Yorkshire					
LT	2354	534.24	307.85	114	1260
LP	2354	513.85	292.82	114	1229
PD%	2354	97.03	3.37	67.70	100.00
NBA/LT	2354	0.087	0.02	0.01	0.20
AFF	2354	373.45	29,91	305	498
Duroc					
LT	1176	501.19	289.44	111	1265
LP	1176	478.76	273.40	111	1217
PD%	1176	96.52	4.42	64.10	100.00
NBA/LT	1176	0.069	0.02	0.01	0.17
AFF	1176	371.48	26.25	304	498

[1]LT = Lifetime; LP = Lifetime production ; PD% = Productive per lifetime; NBA/LT Number born alive per lifetime day.

Landrace sows and heritability for NBA/LT was higher in Yorkshire sows. Most of the heritabilities estimated from data account censoring were higher than ignoring censored data due to the inclusion of censored records usually creating more genetic variance (higher heritability) (S. Tsuruta, University of Georgia, Athens, GA, personal communication). This research shows that the Duroc sow can improve longevity faster than another breed due to the heritability of sow longevity being higher than that another breed.

Longevity and lifetime prolificacy traits heritabilities estimates in this study ranged from 0.03 to 0.29, the value are barely distinguishable from Nikkilä et al. (2013) who studied in US commercial sows and analyzed with REML and Gibbs sampling (censoring record). In earlier findings Engblom et al. (2009), López-Serrano et al. (2000), and Serenius and Stalder (2004), they found heritabilities estimates for length of productive life analyzed with linear model ranged from 0.02 to 0.11. Therefore the levels of heritability indicated that Longevity and lifetime prolificacy traits would respond to genetic selection in this commercial swine population and worldwide swine population.

LP is an indicator of longevity trait and NBA/LT is an indicator of prolificacy trait for improved sow longevity production due to heritability is higher and -2log (p) is lower than LT and PD%. Thus, sow longevity in this herd will progress when including LP and NBA/LT in breeding selection program. Meanwhile we consider from the definition and benefit of trait; LP focus the total of production day in lifetime. And NBA/LT is the number born alive per lifetime

Table 2 Estimates[1] of heritability (on diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlation for stayability traits of 3 purebred sows in a study.

	Traits[2]			
	STAY2	STAY3	STAY4	STAY5
Landrace				
STAY2	0.17 (0.05, 0.26)	0.99	0.89	0.71
STAY3	0.96	0.22 (0.13, 0.30)	0.81	0.79
STAY4	0.98	0.95	0.27 (0.16, 0.34)	0.99
STAY5	0.98	0.98	0.95	0.30 (0.21, 0.38)
Yorkshire				
STAY2	0.14 (0.02, 0.24)	0.94	0.49	0.32
STAY3	0.93	0.10 (0.01, 0.18)	0.94	0.77
STAY4	0.98	0.98	0.10 (0.02, 0.18)	0.99
STAY5	0.97	0.96	0.91	0.14 (0.05, 0.21)
Duroc				
STAY2	0.28 (0.13, 0.38)	0.99	0.96	0.94
STAY3	0.95	0.31 (0.15, 0.41)	0.99	0.98
STAY4	0.92	0.94	0.39 (0.22, 0.50)	0.99
STAY5	0.92	0.93	0.94	0.38 (0.23, 0.47)

[1] Means and the 95% highest posterior density intervals (HPD95) for the posterior distributions.

[2] STAY2, STAY3, STAY4, STAY5 = Stayability in the $2^{nd} – 5^{th}$ parity

day, it can improve the number born alive and non-productive day indirectly.

Correlations

The genetic correlations between STAY2 to STAY5 were very high positive correlation (0.81-0.99) in closely traits. Our results have similarities in genetic correlation with Engblom et al. (2009) who studied in crossbred sows. **Table 3** shows the STAY3 was a benefit indicator because of genetic correlation between STAY3, STAY4 and STAY5 being high (0.77-0.99). The important point, the farmer or breeding staff can select production sow and replacement gilt with estimated breeding value of STAY3 for improved sow stability. The farmer can guess which sow will stay in the farm until parity 5. The genetic correlation between STAY2 to STAY5 in Duroc breed was highly positively correlated (0.94-0.99) more than Landrace and Yorkshire breed. Because in this farm the Duroc sow is a good robust structure so the chance of being culled by lameness is low. And it feed a small group of piglets in a lactation period so it will have fewer reproductive problems than Landrace and Yorkshire. As reported by Fernandez de Sevilla (2008). The percentages of failure (culled or dead sows) of Duroc was less than Landrace and Large White purebred breeds from 4 swine companies registered in the Associación Nacional de Criadores de Ganado Porcino Selecto due to Duroc having better leg and hoof conformation than other breeds. So Duroc sows still alive until parity 2 will survive until parity 5.

Comparison of difference record

Table 3 includes both GS and GScen results. Some heritabilities estimate obtained for longevity and lifetime prolificacy traits using GIBBS2F90 (ignoring censored record) were lower than using GIBBS2CEN (account for

Table 3 Estimates[1] of heritability for longevity and lifetime prolificacy traits analyzed with and without accounting censoring and sow (spearman) rank correlation of 3 purebred sows in a study.

Traits[2]	GS[3]	-2log(p)[3]	GScen[4]	-2log(p)[4]	Spearman rank
Landrace					
LT	0.08 (0.06, 0.15)	28856.98	0.11 (0.06, 0.15)	28334.32	0.97
LP	0.24 (0.20, 0.27)	21469.22	0.24 (0.20, 0.27)	21454.70	0.99
PD%	0.11 (0.09, 0.15)	31400.09	0.12 (0.10, 0.16)	31309.06	0.98
NBA/LT	0.19 (0.14, 0.24)	25962.21	0.19 (0.14, 0.24)	25871.43	0.98
Yorkshire					
LT	0.03 (0.03, 0.06)	21273.97	0.03 (0.03, 0.06)	21269.11	0.97
LP	0.21 (0.16, 0.25)	17045.50	0.21 (0.16, 0.25)	17016.55	0.99
PD%	0.03 (0.01, 0.05)	23035.66	0.03 (0.01, 0.05)	23025.92	0.98
NBA/LT	0.24 (0.18, 0.29)	18885.88	0.24 (0.18, 0.29)	18870.25	0.95
Duroc					
LT	0.13 (0.06, 0.19)	11053.39	0.14 (0.07, 0.20)	11051.03	0.98
LP	0.29 (0.23, 0.34)	8657.42	0.29 (0.23, 0.34)	8652.40	0.99
PD%	0.09 (0.01, 0.15)	11913.07	0.10 (0.01, 0.15)	11902.04	0.98
NBA/LT	0.12 (0.06, 0.17)	9130.12	0.12 (0.06, 0.17)	9125.93	0.98

[1] Means and the 95% highest posterior density intervals (HPD95) for the posterior distributions.
[2] LT = Lifetime; LP = Lifetime production; PD% = Productive per lifetime; NBA/LT Number born alive per lifetime day.
[3] GS = Analyzed in GIBBS2F90 with ignoring censoring record.
[4] GSCEN = Analyzed in GIBBS2CEN accounting for censoring record.
-2log (p) = -2log (the height of marginal probability density function)

censoring record). Even though these results differ from some previously published studies (Engblom et al., 2016; Nikkilä et al., 2013). Most of the heritabilities estimates with both GS and GScen were of similar value, these results correlate fairly well with Garcia et al. (2016) who studied the age at first calving in Nellore cattle. Heritability from GScen was higher than GS mostly because the GIBBS2CEN program recognizes censored records. The difference between ignoring censored and not ignoring censored records is the range of the distribution when sampling. GIBBS2CEN will sample the record based on mean to mean plus square root of residual variance (S. Tsuruta, University of Georgia, Athens, GA, personal communication). Result in Smore genetic variance then the heritability will be higher and the -2log (p) value was lower than the estimate by ignoing the censored record. For this reason it will iincrease the accuracy of evaluation and rate of response to selection for sow longevity. The Spearman rank test correlation between estimated breeding value (EBV) from ignore censored and censored records from sows still in production in the herd for longevity and lifetime prolificacy traits were highly correlated (0.95-0.99). Ranking of EBV from production sow is similar but not the same so it will still have a chance to select a poor sow for mating.

Conclusions and Suggestions

Genetic parameters estimated with the censored records showed the best prediction ability due to heritability was higher and -2log (p) was lower than estimated with ignoring censored records. STAY3 and LP will be indicators of longevity trait and NBA/LT will be indicator of prolificacy trait to add in the index selection for improved sow longevity production.

Even though the sows in the nucleus herd will not be allowed to stay in the herd for long. Because the new replacement gilt will increase genetic progress. But do not forget that every farm still has an involuntary culling sow problem waiting to be solved. Selection with longevity trait can deal with this problem and include it in the selection index with other economic traits such as reproductive and growth traits.

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