Sow Reproductive Stayability and Lifetime Traits

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Summary and Implications

Sow longevity can be improved by selection, but genetic evaluations are challenged for implementation due to the long time interval required to collect complete lifetime data and low reliability of early indicator traits. Present study evaluated genetic parameters for several sow reproductive, stayability and longevity traits. Heritabilities for sow reproductive and longevity traits were estimated from 0.03 to 0.09. Heritabilities of the binary stayability traits were estimated from 0.00 to 0.14. Common litter effect had largest impact in early recorded traits. The results show that fitting the binary stayability traits to normal variance function give the lowest heritability estimates and the binomial variance function with logit function resulted in the highest estimates.

Introduction

Sow longevity is an important economic and animal well-being trait which can be improved by selection for more robust animals. Selection for sow longevity could be performed indirectly by selection for improved fertility or directly by implementing a longevity trait. The longevity trait could be either longevity (e.g. days in herd), stayability (removal or not after certain parity) or lifetime production (measured in no of piglets or piglet weight). In addition, it is possible to construct additional traits, e.g. lifetime productivity per herd time. The objective of the present study is to evaluate the data from F1 sows with known pedigree to estimate variance components and heritabilities for several longevity traits and other reproductive traits. The analyses were performed using different statistical tools to try to analyze the data including the binary stayability traits as accurate and efficient as possible.

Materials and Methods

Data included 12,725 pedigreed commercial F1 (LR×LW) sows with first farrowing between 2004 and 2009 on a single farm. Records were treated as complete, ignoring the 30% censoring (non complete records since the sows were still alive). Data was analyzed with DMU6 (AI REML) and THRGIBBSF90 (Gibbs sampling). Univariate analyses were performed and the pedigree included information about five generations. The model included the fixed effect of year-month and the random effects of animal and common birth litter. Phenotypic mean, heritability (h^2) and effect of common litter (l^2) were calculated and are presented for analyzed traits.

Several reproductive and lifetime traits were analyzed fitting normal distribution in DMU: age at first farrowing (AFF), number born alive parity 1 (NBA1), number weaned parity 1 (NW1), accumulated born alive to parity 2- 4 (ABA2 to ABA4), removal parity (RPAR), length of productive life (LPL), accumulated lifetime born alive (LBA), lifetime number weaned (LNW) and lifetime born alive by parity (LBA/P). In addition, stayability (removal or not after certain parity/event) traits were analyzed. This binary trait was assigned a value 0 for a sow removed before an event and 1 for a sow staying until that specific event. The events were if the animals were mated as gilts (STAY0M), after farrowing parity 1 to 3 (STAY1M to STAY3M) and if they farrowed a parity 1 to 4 (STAY1F to STAY4F). In DMU the stayability traits were analyzed both with normal and binomial variance functions fitting Generalized Linear Mixed Model. The binomial variance function was fitted with both logit and probit link functions. In THRGIBBSF90 a threshold model was fitted for the stayability traits. The Gibbs sampler ran 300,000 rounds, 100,000 burn-ins, sampling every 100 giving results based on 2,000 samples.

Results and Discussion

Heritabilities for reproductive and longevity traits were estimated from 0.03 to 0.09 and corresponding figures for common litter effect was 0.01 to 0.06, see Table 1. The common litter effect was largest in early recorded traits and decreased with higher parity numbers. Table 2 show heritability and common litter effect for stayability traits. Heritabilities were estimated from 0.00 to 0.14 and common litter effects were estimated from 0.00 to 0.09. The results show that heritability estimated when fitting a normal distribution is about at the same level as binomial distribution with probit function. Threshold model resulted in higher heritabilities and binoimial distribution with logit function gave the highest heritability estimates, except for the STAY0m event where the threshold model gave the highest estimates. The results show that the non-normal variance functions all gave higher heritability estimates than the normal variance function for the analyzed stayability traits.

Table 1. Estimates of mean, heritability and common litter effect for reproductive and lifetime traits[1].

	AFF	NBA1	NW1	ABA2	ABA3	ABA4	RPAR	LPL	LBA	LNW	LBA/P
Mean[2]	363	11.0	10.0	16.6	19.8	28.8	2.7	409	34.0	29.3	9.71
h^2	0.04	0.09	0.03	0.04	0.04	0.05	0.06	0.07	0.07	0.06	0.05
l^2	0.06	0.04	0.01	0.03	0.03	0.03	0.02	0.01	0.02	0.02	0.03

[1]AFF=age at first farrowing; NBA1=number born alive parity 1; NW1=number weaned parity 1; ABA2-ABA4=accumulated born alive to parity 2-4; RPAR=removal parity; LPL=length of productive life; LBA=accumulated lifetime born alive; LNW= lifetime number weaned; LBA/P=lifetime born alive by parity
[2]Phenotypic mean

Table 2. Estimates of mean, heritability and common litter effect for stayability traits[1].

Program, distr.		STAY0M	STAY1F	STAY1M	STAY2F	STAY2M	STAY3F	STAY3M	STAY4F
	Mean[2]	0.90	0.78	0.70	0.58	0.53	0.46	0.42	0.35
DMU, normal	h^2	0.03	0.03	0.04	0.03	0.04	0.02	0.03	0.04
	l^2	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.02
DMU, binomial logit function	h^2	0.00	0.14	0.14	0.11	0.12	0.07	0.09	0.12
	l^2	0.00	0.04	0.04	0.04	0.03	0.04	0.03	0.03
DMU, binomial probit function	h^2	0.00	0.05	0.05	0.04	0.05	0.03	0.04	0.05
	l^2	0.00	0.01	0.01	0.02	0.01	0.02	0.01	0.01
THRGIBBSF90 threshold	h^2	0.07	0.07	0.08	0.06	0.07	0.04	0.05	0.08
	l^2	0.09	0.04	0.04	0.04	0.03	0.03	0.03	0.03

[1]STAY0M=stayability from entering herd to being mated as gilt; STAY1M-STAY3M=stayability from entering herd to being mated after parity 1 -3; STAY1F-STAY4F=stayability from entering herd to farrow a litter in parity 1-4
[2]Phenotypic mean, proportion of sows remaining for the event of all sows entering the herd