Estimates of Additive and Dominance Genetic Effects for Sow Longevity

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Summary and Implications

The purpose of current study was to estimate variance components, especially dominance genetic variation, for overall leg action, length of productive life, and sow stayability until third and fifth parity. This project evaluated the data from Finnish litter recording scheme. The variance components were estimated in two purebred (Landrace, n=23,602 and Large White, n=22,984) and crossbred (Landrace x Large White, n=17,440) datasets. The fixed effect of herd-year, and random effects of additive sire, parental dominance, and litter were included in the statistical model of all the traits. Moreover, the fixed effect of breeding consultant, and linear regression of test weight were also included in the statistical model for overall leg action. The estimated heritabilities of these traits ranged between 0.04 and 0.06, and were very similar between the different breeds. Similarly, the estimates for ratio of dominance variance to phenotypic variance (d^2) varied between 0.01 and 0.17, the highest from the crossbred dataset. Moreover, all the d^2 estimates in crossbred population were higher than the corresponding heritability estimates. However, in purebred populations, d^2 estimates were generally lower than the corresponding h^2 estimates. All the genetic correlations between same traits from purebred and crossbred were high. This indicates that the genetic gain in purebred populations will be passed on to the commercial crossbred sows. Based on current results, we suggest considering accounting for the effect of dominance in the breeding value estimation of sow longevity, especially when data from crossbred animals are included. Moreover, because dominance genetic variation for sow longevity exists, it should be possible to use that variation by planning the mating pairs to produce sows for commercial production.

Introduction

In general, the objective of breeding program is to improve genetic material of animals utilized in commercial production. In modern pork production units, the production is based on crossbred Landrace x Large White sows. Thus, the breeding objective in Landrace and Large White populations is to improve efficiency of crossbred sows, and their offspring.

Genetic gain of crossbred progeny through selection in purebred populations is dependent on the genetic correlation between same trait of purebred and crossbred population (Bijma et al., 2001). If that correlation is low, genetic gain in "purebred traits" is not realized in crossbred production. In that case, selection should be based on information collected from crossbred sows and their progeny. When the correlation appears to be lower than one, it is likely the result of genetic x environment interaction and non-additive (e.g. dominance) genetic effects. The correlation estimates between "same" trait in purebred and crossbred populations has varied between traits and populations studied. For example, Lutaaya et al. (2001) estimated genetic correlations of daily gain and backfat thickness between purebred (A, B) and their reciprocal cross (C) populations. They found daily gain was closely (0.99) correlated between A and C, whereas the corresponding correlation between B and C was only 0.62. Both the backfat correlations were clearly lower than one (A-C: 0.32, B-C: 0.70).

As sow longevity is considered as a 'fitness trait', it may be assumed to be affected highly by crossbreeding and non-additive genetic effects (Falconer and Mackay, 1996). The knowledge about genetic correlation between sow longevity in crossbred and purebred sows, and dominance genetic variation is needed in optimization of breeding program and breeding value estimation for sow longevity. Thus, the objective of this study was to estimate these parameters and to discuss the proper way to utilize crossbred vs. purebred information in breeding value estimation.

Materials and Methods

Data from Finnish litter recording scheme was utilized to estimate dominance genetic variation, and additive genetic correlations between "same" longevity related traits (stayability until 3rd and 5th parities, length of productive life and overall leg action) of crossbred and purebred populations. Stayabilities were recorded as a binary trait, i.e., whether sow has reached the parity (3 or 5) or not. Length of productive life was recorded as an interval from first farrowing to culling or death of sow. Overall leg action was scored with the scale from one to five by a breeding advisor. Records were utilized only from largest farms and it contained information on 23,602 Landrace, 22,984 Large White, and 17,440 Crossbred sows.

To study how "same traits" in purebred (LR, LW) and crossbred (LR x LW) populations are genetically correlated, the same trait in different populations were treated as different traits in three trait model. Five different analyses were carried out for all the traits to compare the effect of accounting sows inbreeding (F), sows common litter environment (L), and parental dominance (D) in the statistical model on these correlations. In all the models, fixed effect of farm and year interaction and random additive genetic effect of sire were included for all the traits. Similarly, the fixed effect of scorer (farm advisor) and fixed regression of on-farm test weight was included in the

statistical models of overall leg action in all the analyses. In matrix notation, the most complicated statistical model for records of crossbred sows can be written as:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z_{LR}u_{LR}} + \mathbf{Z_{LW}u_{LW}} + \mathbf{Wl} + \mathbf{Hd} + \mathbf{e},$$

where $\mathbf{b}$ is the vector of fixed effects, $\mathbf{u_{LR}}$ and $\mathbf{u_{LW}}$ are the vectors of additive genetic sire effects, $\mathbf{l}$ is the vector of common litter effect, $\mathbf{d}$ is the vector of parental dominance effect, $\mathbf{e}$ is the vector of residual effects, and $\mathbf{X}$, $\mathbf{Z_{LR}}$, $\mathbf{Z_{LW}}$, $\mathbf{W}$, and $\mathbf{H}$ are the corresponding incidence matrices. Only one additive genetic sire effect, either LR or LW, was included in the statistical model for purebred records. Covariance matrices of random effects were assumed to be $\mathbf{A} \otimes \mathbf{G_0}$, $\mathbf{I} \otimes \mathbf{L_0}$, $\mathbf{D} \otimes \mathbf{F_0}$, and $\mathbf{I} \otimes \mathbf{R_0}$ for additive genetic, litter, parental dominance, and residual, respectively.

Estimates for dominance variance were based on method inverting paternal dominance relationship matrix described by Hoeschele and VanRaden (1991). All the analyses were carried out using EM-algorithm with REMLF90 package (Mizstal, 1998).

Results and Discussion

Estimates for heritability, proportion of variance due to common litter environment and the proportion of variance due to parental dominance of the sow longevity related traits (stayabilities 3 and 5, length of productive life and overall leg action) are presented in Table 1. Estimated heritabilities are all low, and in the same magnitude between the different analyses. However, there is a tendency for the heritability estimates from the simplest model, containing only additive genetic sire as a random effect (not including sow's inbreeding) to be higher (0.06 – 0.12) than heritability estimates from the more complex models, which account for different combinations of sow's inbreeding, common litter environment and parental dominance effects (0.03 – 0.09).

The estimated proportions of variance due to common litter environment varied between 0.02 and 0.14 (Table 1). Although l^2 estimates from different statistical models in general are all in the same magnitude, it seems that the effect of common litter environment, sow's inbreeding and dominance genetic effects are confounded. In general, l^2 estimates from AL and ALF models were lower that the corresponding estimates from ALFD model, especially in crossbred population (l^2 average 0.06 in both AL and ALF models, and 0.03 in ALFD model). Thus, these estimates indicate that common litter environment accounts part of the variation due to dominance genetic effects in ALFD model.

Estimated genetic correlations of same traits between crossbred and purebred populations are presented in Table 2. In general, all the correlations were very high (all over 0.75), Large White – crossbred correlations being somewhat higher than Landrace – crossbred correlations. There is a tendency for the correlations to increase as more information is accounted for in the statistical model. This increase appears to be larger among the correlations between Landrace and crossbred breeding values than between Large White and crossbred. For example, the average correlation between Landrace and crossbred population increased from 0.89 (model A) to 0.94 (model AFLD). The corresponding increase between Large White and crossbred population was from 0.94 to 0.95. However, the lowest average correlation between Large White and crossbred population was resulted by AF model (0.92).

Substantial dominance effects (d^2 ranged between 0.03 and 0.12) was found to impact these traits. The dominance effects of this magnitude should be accounted for in the statistical model of routine breeding value estimations. Possible benefits appear simply by obtaining more reliable breeding values through more correct statistical modeling, and by accounting for dominance effects in selection. Moreover, the estimated genetic correlations of same traits between purebred and crossbred populations increased by accounting the common litter environment and parental dominance in the statistical model. In addition to the benefits of accounting dominance effect in the statistical model of breeding value estimation, the potential to utilize predicted dominance effects to make planned matings in multiplier level also exists.

Table 1. Estimates for heritability (h^2), proportion of variance due to common litter environment (l^2) and proportion of dominance variance out of phenotypic variance (d^2) of leg score, stayabilities until 3rd and 5th parities (Stay3, Stay5), and length of productive life (LPL) for Finnish Landrace, Large White and Landrace x Large White populations. Estimates are obtained using five different statistical models[1].

	h^2					l^2			d^2
	A[1]	A,F[1]	A,L[1]	A,L,F[1]	A,L,F,D[1]	A,L[1]	A,L,F[1]	A,L,F,D[1]	
Landrace									
Leg score	0.06	0.04	0.04	0.04	0.04	0.10	0.14	0.09	0.03
Stay3	0.07	0.07	0.05	0.06	0.05	0.05	0.06	0.04	0.03
Stay5	0.07	0.04	0.05	0.04	0.05	0.05	0.06	0.04	0.04
LPL	0.09	0.06	0.07	0.05	0.07	0.05	0.03	0.02	0.11
Large White									
Leg score	0.09	0.05	0.06	0.03	0.06	0.11	0.13	0.10	0.03
Stay3	0.06	0.03	0.05	0.03	0.05	0.05	0.07	0.04	0.03
Stay5	0.07	0.06	0.05	0.05	0.05	0.05	0.03	0.04	0.04
LPL	0.08	0.08	0.06	0.07	0.06	0.06	0.05	0.03	0.10
Crossbred									
Leg score	0.12	0.09	0.08	0.09	0.08	0.08	0.01	0.05	0.09
Stay3	0.08	0.07	0.06	0.06	0.06	0.05	0.07	0.02	0.09
Stay5	0.08	0.08	0.06	0.07	0.06	0.05	0.03	0.03	0.09
LPL	0.06	0.07	0.05	0.07	0.04	0.05	0.05	0.02	0.12

[1] Different combinations of additive genetic sire (A), inbreeding coefficient of sow (F), common litter environment of sow (L), and parental dominance (D) were included in the statistical models

Table 2. Genetic correlations between the same traits (leg score, stayabilities until 3rd and 5th parity [Stay3, Stay5], and length of productive life [LPL]) of from crossbred (Landrace x Large White) or purebred populations. The estimates are obtained using five different statistical models[1].

	A	A+F	A+L	A+L+F	A+L+F+D
Landrace					
Leg score	0.88	0.93	0.88	0.93	0.92
Stay3	0.85	0.76	0.89	0.90	0.93
Stay5	0.90	0.95	0.92	0.96	0.94
LPL	0.94	0.94	0.92	0.95	0.96
Large White					
Leg score	0.94	0.93	0.94	0.93	0.93
Stay3	0.91	0.83	0.93	0.94	0.95
Stay5	0.92	0.93	0.89	0.93	0.91
LPL	0.99	0.99	0.98	0.99	0.99

[1] Different combinations of additive genetic sire (A), inbreeding coefficient of sow (F), common litter environment of sow (L), and parental dominance (D) were included in the statistical models