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Estimates of additive and dominance genetic effects for sow longevity

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ABSTRACT 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 study was conducted by analyzing the data from Finnish litter recording scheme. The variance components were estimated in two purebred (Landrace and Large White) and crossbred (Landrace x Large White) datasets. There were information on 23 602, 22 984, and 17 440 sows in the Landrace, Large White, and crossbred datasets, respectively. 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 ranged between 0.04 and 0.06, being 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, being highest in crossbred dataset. Moreover, all the d^2 estimates in crossbred population were higher than the corresponding heritability estimates. In purebred populations, d^2 estimates were generally lower than the corresponding h^2 estimates. Based on current results, reliability of crossbred breeding values would increase by accounting dominance in the breeding value estimation.

Introduction

In general, the objective of breeding program is to improve genetic merit of animals utilized in commercial production. In modern pork production units, crossbred Landrace x Large White sows are the predominant breed or line used as parent females. Thus, the breeding objective in Landrace and Large White populations is to improve efficiency of crossbred sows and their offsprings.

Genetic gain of crossbred progeny through selection in purebred populations is dependent of 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 such case, selection should be based on information collected from crossbred sows and their progeny. The correlation appears to be lower than one mainly because of genetic x environment interaction and non-additive (e.g. dominance) genetic effects. Therefore the correlation estimates between the “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 being very 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 should 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 order to optimize breeding programs and breeding value estimation for sow longevity. Thus, the objective of this study was to estimate these parameters and to discuss about proper methods to utilize crossbred vs. purebred information in breeding value estimation.

Material and Methods

Data from Finnish litter recording scheme, collected by Finnish Animal Breeding Association (FABA), was utilized to estimate dominance genetic variation, and additive genetic correlations between the "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 indicating whether sow has reached a pre-determined parity (3 or 5) or not. Length of productive life was recorded as a interval from first farrowing to culling or death of sow. Overall leg action was scored by the breeding adcisors in a scale of one to five, one being worst and five indicating sow free of leg problems. Records were utilized only from largest farms and it contained information on 23 602 Landrace, 22 984 Large White, and 17 440 Crossbred sows (Table 1).

Table 1. Number of observations ($N_{records}$), number of sires in pedigree (N_{sire}), and averages with their standard deviations (S.D.) for the traits studied in Finnish Landrace (LR), Large White (LW) and crossbred (CB = LR or LW x LW or LR) sows.

	LR	***LW***	***CB***
$N_{recorded}$	23602	22984	17440
N_{sire}		4373	
average (± S.D)			
Overall leg action	3.54 (.53)	3.54 (.53)	3.55 (.53)
Stayability, 3rd parity	0.57 (.49)	0.56 (.50)	0.67 (.47)
Stayability, 5th parity	0.31 (.46)	0.29 (.45)	0.43 (.49)
Length of productive life	466 (380)	438 (366)	539 (413)

Two different sire models were fitted on the data. First, the genetic correlations between the "same" trait of purebred and crossbred populations were estimated including only additive sire and residual as random effects. Second, common litter and parental dominance effects were also included in the statistical model. In addition of random effects, the fixed effect of farm sow was born was also accounted in the statistical model for all of the traits, and the fixed effect of scorer and fixed regression coefficient of on-farm test weight was included in the statistical models of overall leg action. In matrix notation, the statistical model for records of crossbred sows can be written as:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_{\mathbf{LR}}\mathbf{u}_{\mathbf{LR}} + \mathbf{Z}_{\mathbf{LW}}\mathbf{u}_{\mathbf{LW}} + \mathbf{Wl} + \mathbf{Hf} + \mathbf{e} \quad ,$$

where **b** is the vector of fixed effects, $\mathbf{u}_{\mathbf{LR}}$ and $\mathbf{u}_{\mathbf{LW}}$ are the vectors of additive genetic sire effects, **l** is the vector of common litter effect, **d** is the vector of parental dominance effect, **e** is the vector of residual effects, and **X**, $\mathbf{Z}_{\mathbf{LR}}$, $\mathbf{Z}_{\mathbf{LW}}$, **W**, and **H** are the corresponding incidence matrices. Naturally 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, proportions of dominance variance, and genetic correlations between the 'same' traits in different breeds are presented in Table 2. First of all, it can be said that estimated heritabilities are very similar between the different analyses, and in agreement with previous studies presented in the literature. All studied sow longevity related traits are relatively lowly heritable, heritability estimates ranging between 0.04 and 0.09. However, sufficient genetic variation exists to select for sow longevity in efficient breeding program.

Estimated proportions of dominance variance from total variance ranged between 0.03 and 0.12, being somewhat higher in crossbred than purebred populations. More specifically, the d^2 estimates were close to two times higher than the corresponding h^2 estimates in crossbred populations.

In general, estimated genetic correlations between the 'same' trait in purebred and crossbred populations were high (over 0.85). Thus, the current data indicates that selection based only on purebred information would be effective to improve the trait in crossbred sows. However, the correlations tend to increase while common litter environment and parental dominance was accounted in the statistical model, i.e., the reliability of breeding value estimation might increase by also accounting for the dominance and litter effects in the statistical model.

A general tendency exists where the correlations between Landrace and crossbreds are lower than those between Large White and crossbreds. Moreover, the increase in the correlation due to more accurate modeling is also higher between Landrace and crossbreds than between Large White and crossbreds.

Table 2. Heritabilty h^2, proportions of dominance variance d^2 and genetic correlations (r_g) of same trait between purebred and crossbred records for Finnish Landrace (LR), Large White (LW) and their crosses (CB).

	h^2_{LR}	h^2_{LW}	h^2_{CB}	d^2_{LR}	d^2_{LW}	d^2_{CB}	$r_{g\_LR,\ CB}$	$r_{g\_LW,\ CB}$
additive								
leg action	0.06	0.09	0.12	-	-	-	0.88	0.94
stay3	0.07	0.06	0.08	-	-	-	0.85	0.91
stay5	0.07	0.07	0.08	-	-	-	0.90	0.92
LPL	0.09	0.08	0.06	-	-	-	0.94	0.99
additive + litter + dominance								
leg action	0.04	0.06	0.08	0.03	0.03	0.09	0.88	0.94
stay3	0.05	0.05	0.06	0.03	0.03	0.09	0.93	0.95
stay5	0.05	0.05	0.06	0.04	0.04	0.09	0.94	0.91
LPL	0.07	0.06	0.04	0.11	0.10	0.12	0.96	0.99

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