

Nurse capacity in crossbred sows and genetic correlation to purebred fertility

B. Nielsen¹, I. Velander¹, T. Ostersen¹, M. Henryon¹ and O.F. Christensen²

¹Pig Research Centre, ²Aarhus University, Denmark

ABSTRACT: This study developed a new trait that describes the nursing capacity (NC) of crossbred sows, traces the genetic effect back to the two purebred lines, and estimates the genetic correlation with fertility in the purebreds. In 2010 to 2013, an experiment was conducted in three large production herds with 11,247 first-parity Danish Landrace x Yorkshire sows (gilts). All terminal sires used were Duroc AI boars. At farrowing, the total number born (TNB) was recorded. During the first three days, after farrowing the number of piglets in each litter was equalized to 14 piglets. The NC was recorded after three weeks as the number of piglets nursed. The NC recorded on crossbred gilts had heritabilities of 0.047 and 0.066 tracing it back to purebred populations of Landrace and Yorkshire. Unfavorable genetic correlations between TNB in purebreds and NC in crossbreds were found.

Keywords: nurse capability; crossbred; purebred

Introduction

In commercial pig production, the number of weaned piglets is a key factor to for productivity, and litter size has been one of the most important traits in pig production the last decades. In the Danish pig breeding program, litter size and survival have increased (Nielsen et al., 2013). Furthermore, in pig production crossbreeding is used taking advantage of the increased performance of crossbred animals compared to purebred animals (heterosis). However, piglet mortality is still a problem in the pig industry, which raises welfare (Jarvis et al., 2005) and economic concerns (Crooks et al., 1992; Serenius et al., 2007). In modern pig production piglet mortality is often as high as 20 to 25%, from birth to weaning (Grandinson et al., 2002; Alonso-Spilsbury et al., 2007). This indicates that there is still room to increase the number of weaned piglets by decreasing the number of dead piglets during the suckling period. During the suckling period the sow has an important role in caring for piglets and there might be genetic differences in this ability between sows. This ability might be captured by measuring the number of piglets from birth to 3 weeks of age, or until weaning. Knol et al. (2002) reported that including the nurse sow effect in a model for piglet survival gave erratic results making it difficult to define an optimal model.

In commercial pig production, sows are mainly produced by two-way crosses of purebred lines. Selection occurs within each of the two purebred lines and is aimed at improving crossbred performance. Even though both purebred and crossbred information is available, the crossbred information is often ignored in the selection of the purebred

lines. In the literature it has been shown how crossbred information might be used for selection in purebred lines (Wei van der Werf, 1994, Christensen et al. 2014).

The aim of this study was to develop a new trait that describes the nurse capacity (NC) of crossbred sows tracing the genetic effect back to the two purebred lines and estimate the genetic correlation to fertility in the two lines that were used to produce the crosses.

Materials and Methods

Data. Crossbred production data were recorded in three herds with Landrace x Yorkshire (F1). All terminal sires used were Duroc AI boars, and sows farrowed in the period from July 2010 to March 2013. The total number born (TNB) piglets (including the number of still born) were recorded for 11,247 crossbred first-parity sows (Table 1). Three days after birth all sows had equal number of 14 piglets. Equalizing the number of piglets per sow was obtained by moving piglets between litters (if needed) during the first three days after farrowing. The experimental sows could receive piglets from any other crossbred sow in the herd. The movement of piglets between litters was kept as low as possible and many sows had their own piglets. The following three weeks piglets could only be removed from the experimental sows if the piglets were dead or deemed too weak to stay with the sow. Three weeks after birth of the piglets the nursing capacity (NC) was recorded as the number of piglet nursed by the sow. Date and number of piglets was recorded. The NC ranged from zero to 14 piglets and high values of NC indicate that the sow had high nurse capacity. Data of NC were recorded for 9,902 crossbred first-parity sows (Table 1).

Table 1: Number of first-parity sows (gilts). All purebred were F1 crosses between Landrace and Yorkshire.

Type of animal	Trait	Number of gilts
Crossbred gilts	TNB	11247
	NC	9902
Purebred Landrace gilts	TNB	59884
Purebred Yorkshire gilts	TNB	37495
Animals in pedigree		133205

For the crossbred sows, the related dams and half-sib sisters of purebred Landrace and Yorkshire sows in multiplier herds were identified and recordings of TNB in their first parity were obtained. Thus, for related animals of both purebred and crossbred first-parity sows data for TNB was included in the data set.

Only recordings of first-parity sows were included in the analysis to avoid bias affected by phenotypic selection (culling) of sows after first litter.

Statistical analyses. A multivariate mixed model approach was applied to combine purebred and crossbred information. The model was developed as a so-called reduced animal model according to Wei van der Werf (1994), i.e

$$\begin{bmatrix} y_{TNB,L} \\ y_{TNB,Y} \\ y_{TNB,L,Y} \\ y_{NC,L,Y} \end{bmatrix} = \begin{bmatrix} X_{TNB,L} & 0 & 0 & 0 \\ 0 & X_{TNB,Y} & 0 & 0 \\ 0 & 0 & X_{TNB,L,Y} & 0 \\ 0 & 0 & 0 & X_{NC,L,Y} \end{bmatrix} \begin{bmatrix} b_{TNB,L} \\ b_{TNB,Y} \\ b_{TNB,L,Y} \\ b_{NC,L,Y} \end{bmatrix} + \begin{bmatrix} Z_L & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & Z_Y & 0 & 0 \\ 0 & Z_{L-LY} & 0 & 0 & Z_{Y-LY} & 0 \\ 0 & 0 & Z_{L-LY} & 0 & 0 & Z_{Y-LY} \end{bmatrix} \begin{bmatrix} a_{TNB,L} \\ a_{TNB,L-LY} \\ a_{NC,L-LY} \\ a_{TNB,Y} \\ a_{TNB,Y-LY} \\ a_{NC,Y-LY} \end{bmatrix} + \begin{bmatrix} e_{TNB,L} \\ e_{TNB,Y} \\ e_{TNB,L,Y} \\ e_{NC,L,Y} \end{bmatrix}$$

where y_i , X_i , b_i , and e_i , $i=\{TNB,L; TNB,Y; TNB,L,Y; NC,L,Y\}$, are the vectors of recordings, the associated incidence matrices, the vectors of fixed effect, and the vectors of residuals of TNB, recorded in Landrace (L), Yorkshire (Y), crossbred population (LY), and the NC recorded in crossbred population. The incidence matrices Z_L and Z_Y link the recording of purebred to genetic effect in purebred Landrace and Yorkshire, and Z_{L-LY} and Z_{Y-LY} link recording in crossbred to genetic effects of the two purebred populations of Landrace and Yorkshire. The non-zero elements of Z_{L-LY} and Z_{Y-LY} are multiplied by 0.5 as only the half of the breeding values is transmitted from purebred parents to crossbred progeny.

The residual variances were assumed to be Gaussian distributed i.e.

$$\begin{bmatrix} e_{TNB,L} \\ e_{TNB,Y} \\ e_{TNB,L,Y} \\ e_{NC,L,Y} \end{bmatrix} \sim N(0, R)$$

and

$$R = \begin{bmatrix} \sigma_{e,TNB,L}^2 & 0 & 0 & 0 \\ 0 & \sigma_{e,TNB,Y}^2 & 0 & 0 \\ 0 & 0 & \sigma_{e,TNB,L,Y}^2 & \sigma_{e,TNB-NC,L,Y}^2 \\ 0 & 0 & \sigma_{e,TNB-NC,L,Y}^2 & \sigma_{e,NC,L,Y}^2 \end{bmatrix}$$

in which some off-diagonal elements were assumed to be zero as no purebred animals were recorded for crossbred traits and vice versa.

The genetic variances of breeding values were also assumed to be Gaussian distributed, thus

$$\begin{bmatrix} a_{TNB,L} \\ a_{TNB,L-LY} \\ a_{NC,L-LY} \\ a_{TNB,Y} \\ a_{TNB,Y-LY} \\ a_{NC,Y-LY} \end{bmatrix} \sim N(0, G), \quad G = \begin{bmatrix} G_L \otimes A_L & 0 \\ 0 & G_Y \otimes A_Y \end{bmatrix}$$

where A_L and A_Y are the animal relationship matrices in purebred Landrace and Yorkshire populations, respectively, \otimes is the Kronecker product, and G_L and G_Y are matrices of variances denoted as follow

$$G_L = \begin{bmatrix} \sigma_{TNB,L}^2 & \sigma_{TNB-TNB,L-LY}^2 & \sigma_{TNB-NC,L-LY}^2 \\ & \sigma_{TNB,L-LY}^2 & \sigma_{TNB-NC,L-LY}^2 \\ & & \sigma_{NC,L-LY}^2 \end{bmatrix}, \quad G_Y = \begin{bmatrix} \sigma_{TNB,Y}^2 & \sigma_{TNB-TNB,Y-LY}^2 & \sigma_{TNB-NC,Y-LY}^2 \\ & \sigma_{TNB,Y-LY}^2 & \sigma_{TNB-NC,Y-LY}^2 \\ & & \sigma_{NC,Y-LY}^2 \end{bmatrix}$$

The three diagonal elements in G_L represent the genetic variances of TNB in purebred Landrace, and TNB and NC in crossbreds. The two off-diagonal elements in first row in G_L describe the co-variances between TNB in purebred and TNB and NC in crossbreds. The off-diagonal element in the second row i.e., $\sigma_{TNB-NC,L-LY}^2$ denotes the genetic correlations between TNB and NC in crossbreds traced back to purebred Landrace population. Similarly the elements in G_Y denote the genetic variances and co-variances traced back to the purebred Yorkshire population.

Selection on TNB in purebreds affects TNB in crossbreds by the coefficients $\beta_{TNB-TNB,L-LY} = \sigma_{TNB-TNB,L-LY}^2 / \sigma_{TNB,L}^2$ and $\beta_{TNB-TNB,Y-LY} = \sigma_{TNB-TNB,Y-LY}^2 / \sigma_{TNB,Y}^2$. Also, the selection on TNB affects the NC in crossbreds by the coefficients $\beta_{TNB-NC,L-LY} = \sigma_{TNB-NC,L-LY}^2 / \sigma_{TNB,L}^2$ and $\beta_{TNB-NC,Y-LY} = \sigma_{TNB-NC,Y-LY}^2 / \sigma_{TNB,Y}^2$, respectively for the Landrace and Yorkshire populations.

Phenotypic variances ($\sigma_{p,i,j}^2$) of trait $i=\{TNB,NC\}$ in purebred $j=\{L,Y\}$ were obtained by combinations of the variances in R , G_L and G_Y . In purebreds the phenotypic variances were obtained by $\sigma_{p,TNB,j}^2 = \sigma_{e,TNB,j}^2 + \sigma_{TNB,j}^2$. In crossbreds $j=\{LY\}$ $e_{i,LY}$ are the residuals within full-sib families which contains half of the genetic variances (Mendelian sampling) and thus the phenotypic variances were obtained by $\sigma_{p,i,LY}^2 = \sigma_{e,i,LY}^2 + 1/4\sigma_{i,L-LY}^2 + 1/4\sigma_{i,Y-LY}^2$.

Results and Discussion

The recordings in crossbred first-parity sows show that NC ranged from five to 14 (Figure 1).

The recordings of crossbred sows were obtained in the experimental setup, but the recordings of purebreds were obtained from historical data of multiplier herds. Therefore the number of purebred sows was 4 to 6 times larger than the number of recorded crossbred sows (Table 1).

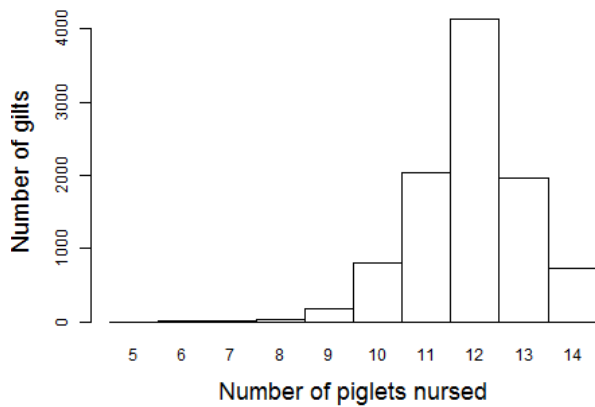


Figure 1: Distribution of number of piglets nursed per litter recorder on gilt in crossbred population (Landrace and Yorkshire crosses).

The genetic variances of TNB were 1.42 and 1.02 in Landrace and Yorkshire (Table 2 and 3). The genetic variances estimated for TNB in crossbreds were lower (0.55 and 0.90) and reflect that TNB are different traits in purebreds and crossbreds, e.g. the direct effect of piglets vitality and piglet survival in two-way crosses at purebred sows and three-way crosses at crossbreds sows is different. Moreover, fertility and piglet survival traits might be different in commercial herds of crossbred sows producing slaughter pigs because the environmental variance and the genetic level due to genetic progress might differ from purebred herds.

Table 2: Estimated genetic variances, covariances (lower part) and genetic correlations (above diagonal) for total number of born (TNB), nurse capacity (NC) in purebred Landrace and crossbred animals (crosses with Yorkshire, LY).

Trait	TNB-L	TNB-LY	NC-LY
TNB in Landrace	1.42	0.73	-0.26
TNB in crossbred	0.64	0.55	-0.12
NC in crossbred	-0.06	-0.02	0.05

Table 3: Estimated genetic variances, covariances (lower part) and genetic correlations (above diagonal) for total number of born (TNB), nurse capacity (NC) in purebred Yorkshire and crossbred animals (crosses with Landrace, LY).

Trait	TNB-Y	TNB-LY	NC-LY
TNB in Yorkshire	1.02	0.51	-0.38
TNB in crossbred	0.49	0.90	-0.11
NC in crossbred	-0.10	-0.03	0.07

The genetic variances of NC observed in crossbreds were 0.05 and 0.07 tracing the effect back to purebred Landrace and Yorkshire (Table 2 and 3). The genetic effect on NC was low compared to the genetic effect of TNB and the potential for genetic gain in NC is therefore low compared to the genetic gain by selection for TNB. Selection on TNB has been widely used the last decades, but the genetic correlations between TNB (here observed in both purebreds

and crossbreds) and NC was unfavorable ranging from -0.11 to -0.38 (Table 2 and 3). The unfavorable genetic correlations between TNB and NC might be explained by unfavorable correlations related to the direct effects of TNB, e.g. selection for TNB reduce the mean birth weight of piglets and increases mortality (Grandinson *et al*, 2002, Su *et al* 2007, Strange *et al*, 2013, Nielsen *et al*, 2013).

The phenotypic variances of NC in crossbreds was $\sigma_{p,NC,LY}^2=1.081$ (not shown) and the heritabilities of NC were 0.047 and 0.066 when tracing NC back to purebred populations of Landrace and Yorkshire, respectively.

The genetic gain for TNB in crossbreds, affected by selection on TNB in purebreds, was $\beta_{TNB-TNB,L-LY}=0.45$ and $\beta_{TNB-TNB,Y-LY}=0.48$. This shows that a bit less 50% of the genetic gain obtained in each of purebreds were transferred to the commercial pig production of crossbred gilts.

Conclusion

The results shows that NC recorded on crossbred gilts was heritable and had heritability of 0.047 and 0.066 tracing NC back to purebred populations of Landrace and Yorkshire, respectively. Thereby, the number of weaned piglets from sows depends on genes. Sows with good "weaning genes" weaned more pigs than sows with inferior genes.

The genetic correlations between TNB in purebreds and crossbreds show that a bit less 50% of genetic gain in each purebred population was transferred to crossbreds. The genetic correlations between TNB in purebreds and NC in crossbreds were unfavorable indicating that selection on TNB in purebred populations reduces the NC in the crossbred population.

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