

## **Estimated genetic parameters for number born alive between nucleus and commercial herds in swine**

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### **Summary**

Genetic evaluation for number born alive (NBA) between nucleus and commercial herds were estimated by ASREML using a sire model. Data for 8,191 nucleus herd litters and 21,538 commercial herd litters were obtained. Fixed effect testing of both herds showed significant difference for contemporary group, farm and parity. Additive genetic relationship among animals by sire were included. Heritability estimates for NBA were  $0.12 \pm 0.01$  for nucleus herd and  $0.23 \pm 0.01$  for commercial herd. Genetic and phenotypic correlations for NBA between both herds were  $0.64 \pm 0.03$  and  $0.37 \pm 0.03$ , respectively.

### **Introduction**

Genetic evaluations for reproductive traits like number born alive (NBA), are included in selection criteria to accelerate genetic gain for economically important traits in swine breeding programs. This progress requires monitoring genetic parameters for the traits evaluated and periodically estimating the genetic parameters specific for a given population (See *et al.*, 1993). Under the classic genetic pyramid model, nucleus herds supply genetically improved breeding stock to multipliers, which disseminate genetic gain through producing hybrid parent stock for use in commercial breeding herds. Dekkers (2007) stated that one of the main limitations of this system is that purebred performance in nucleus farm can be a poor predictor for the future crossbred performance from commercial herds. Wei & van der Steen (1991) proposed to use phenotypic data from crossbred relatives to estimate breeding values (BV) for purebred, nucleus relatives. This requires accurate recording performance and pedigree at the crossbred performance level occurring on commercial pork operations. The present dataset included purebred Landrace from a nucleus herd and data from Landrace x Large White crossbred sows from a commercial herd. Genetic evaluation would be concerned with connectedness for sires in both herds and contemporary groups within herds. The objective of this study was to estimate genetic parameters for NBA for sires between nucleus and commercial herds.

## Materials and methods

### Data Structure

The performance and pedigree records validated and any errors identified were corrected or omitted from the data set. Animals in the pedigree were born from 2003 through 2012. Data structure details for nucleus and commercial herds were summarized in Table 1. Records from Landrace sows farrowing in the nucleus herd and records from Landrace x Large White crossbred sows in commercial herd were included in the present analysis. Contemporary group defined as season-year of farrowing date (range: 113 to 119 days). Season was defined as 4 seasons (winter: December to March, spring: April to June, summer: July to September, and fall: October to November). Sows records in the present analysis included parities 1 to 11. However, the number of sows in parities 8, 9, 10, and 11 were small and hence they were grouped into a single 8+ parity classification. Frequency of parity 1, 2, and 3 in nucleus herd was 51, 27, and 12 percent, respectively and in commercial herd was 27, 22, and 18 percent, respectively. The preliminary analysis shows that mean NBA phenotypic values from the commercial herd was significantly greater when compared to the nucleus herd values.

*Table 1. Details of data structure and descriptive statistics from nucleus and commercial herds*

	Number born alive	
	Nucleus herd	Commercial herd
No. of litter records	8,191	21,538
No. of animals	5,133	5,390
No. of daughter	4,245	4,207
No. of parity	1 to 9	1 to 11
No. of contemporary groups	27	18
Litter per female	1.88	3.38
Means±SD (piglets)	11.0±0.04 <sup>a</sup>	12.8±0.02 <sup>b</sup>
Range (piglets)	1-21	1-25

<sup>a, b</sup> significant difference between column ( $P < 0.05$ )

Sire information was shown in Table 2. Number active sires connecting the nucleus and commercial herds was approximately 6 percent from total number active sires (424 sires) in this dataset and average of daughters per sire in the commercial herd was greater than average of daughters per sire in the nucleus herd.

*Table 2. Sire information in the dataset*

	Nucleus herd	Commercial herd
Number of sire ancestor	3,810	12,088
No. of sire with daughter record	325	126
Average of daughters per sires	26	45
Number of connected sire		27
Average of daughters per connected sire		64

### Genetic parameter estimates

A sire model was fitted to the data including all pedigree information. Fixed effects for model used to analyze the nucleus and commercial herds included contemporary group, farm, breed and parity. These fixed effects were tested by using generalized linear model (Proc GLM, SAS v. 9.4, SAS Inst., Cary, NC). The final model was used to estimate the variance components for nucleus and commercial data used for this study. Variance and covariance components were estimated by the average information restricted maximum likelihood (AI-REML) and where a full sire model was implemented throughout using ASREML software (Gilmour *et al.*, 2009). Estimated variance components including the sire genetic and the residual error variances were used to calculate heritability. Additionally, the genetic and phenotypic correlations estimates were obtained (Falconer & Mackey, 1996).

### Results and Discussion

Fixed effect evaluation showed highly significant differences between contemporary groups, farm, breed, and parities ( $P < 0.01$ ) from both the nucleus and commercial herds. Number born alive in 3<sup>rd</sup> and 4<sup>th</sup> ( $13.1 \pm 0.05$  piglets) were greater than other parities ( $P < 0.05$ ) and NBA in parity 8 was the lowest ( $10.9 \pm 0.04$  piglets) of all parities. These results were in agreement with Quiniou *et al.* (2002) who reported that when sows reached the 4<sup>th</sup> parity and greater, prolificacy decreased.

Variance components and the heritability estimates for NBA are shown in Table 3. Heritability estimates for NBA were 0.12 and 0.23 from the nucleus and commercial herds, respectively. Sire genetic variance for NBA from the commercial herd was greater when compared to the genetic variance observed from the nucleus herd and may be the result of continued selection and rapid generation turn over that occurs in the nucleus herd in order to genetically improve economically important traits. Results indicated that the heritability for this trait is sufficiently great enough so that swine producers can improve this trait through traditional selection methods. The current heritability estimates were within range of those published in a literature review by Ferrez, & Johnson (1993), and from the finding reported by Kim *et al.* (2002) and Noppibool *et al.* (2016).

Genetic and phenotypic correlations for the nucleus and commercial herd NBA were relatively high and positive (0.64 and 0.37). In other words, if NBA genetic improvement occurs in the nucleus, the producer would expect genetic improvement at the commercial herd level of the production pyramid. Analysis when the data set has a greater number of records across a greater number of years may improve genetic parameter estimates to even a higher value.

*Table 3 Variance components and heritability estimates for NBA between nucleus and commercial herds*

	Nucleus herd	Commercial herd
Sire genetic variances (piglets <sup>2</sup> )	0.28	0.53
Residual variances (piglets <sup>2</sup> )	9.15	8.64
Total variances (piglets <sup>2</sup> )	9.43±0.17	9.17±0.12
Heritabilities <sup>1</sup>	0.12±0.01	0.23±0.01
Genetic correlation		0.64±0.03
Phenotypic correlation		0.37±0.03

<sup>1</sup> Heritability estimates by

(Falconer & Mackey, 1996)

## Conclusion

Average NBA were 11 and 12.8 piglets in nucleus and commercial herds. Heritability estimates for NBA in both herds were 0.12 and 0.23 by using sire model implemented using ASREML. Genetic and phenotypic correlations for NBA between nucleus and commercial herds were 0.64 and 0.37. The genetic parameter estimates including genetic correlations could be used by nucleus and commercial herds to formulate better breeding strategies to improve genetic improvement in both levels of the breeding pyramid for NBA.

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