

# Utilization of commercial female data in maternal genetic improvement programs

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## Introduction

Maternal performance is encompassed in several of the key profitability drivers in commercial swine units. Purebred breeders and commercial breeding stock companies strive to improve reproductive performance in their maternal lines through genetic selection programs implemented in their nucleus herds. Maternal breeds or lines are crossed at the multiplication level to maximize heterosis in the resulting parent-stock female. The genes of genetically superior animals are passed to the multiplication level and ultimately the commercial level as quickly as possible to reduce genetic lag.

However, genetic selection programs are implemented at the nucleus level in high-health, intensely-managed herds of typically purebred/pureline animals. There may exist a genotype x environment interaction that limits the expression of purebred genetic improvement at the commercial level. The genetic improvement at the nucleus level does not always translate into improved performance at the commercial level.<sup>1</sup> The genetic correlation between reproduction at the nucleus level and the same traits at the commercial (purebreds and crossbred) level has been estimated to be less than 1 (in broilers), indicating selection for traits at the nucleus level will not maximize genetic improvement for the same traits at the commercial level.<sup>2</sup>

Genetic improvement programs in swine may indeed be missing an opportunity for additional genetic improvement by not including commercial crossbred data.<sup>3</sup> Additional records, in the form of commercial F1 daughters, will lead to improved accuracy of Estimated Breeding Values (EBV); one of the key components of genetic improvement programs. Ehlers et al. reported an increase in accuracy of EBV for reproductive traits on the order of 8% and significant reranking of both sires and dams when commercial crossbred data was included in the evaluation.<sup>4</sup> These results indicate a need to make nucleus selections utilizing a genetic evaluation system which includes reproductive records from pedigreed females at the commercial level.

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## Materials and Methods

A data set including 30,355 purebred Yorkshire and Landrace litter records from 2010-2015 from the National Swine Registry's (NSR) Swine Testing and Genetic Evaluation System (STAGES™), 20,304 litter records from purebred Yorkshire and Landrace females producing F1 litters, and 31,915 litter records from pedigreed commercial parent-stock females was utilized to estimate variance components for a combined purebred and crossbred maternal genetic evaluation.<sup>5</sup> Purebred records included were Number Born Alive (P\_NBA), Number Weaned (P\_NW), and Litter Weaning Weight (P\_LWT). Each of these traits were pre-adjusted according to NSR breed specific guidelines (P\_NBA for parity and age at breeding; P\_NW for parity, age at breeding, and number after transfer; P\_LWT for age at weaning, parity, and number after transfer). The same traits were utilized from purebred sows farrowing pedigreed F1 litters; these traits were pre-adjusted as well. Commercial records utilized were Number Born Alive (C\_NBA), Number Weaned (C\_NW), and Litter Weaning Weight (C\_LWT) and were unadjusted.

All traits were evaluated in a six-trait evaluation using REMLF90. Breed of sow (Yorkshire, Landrace, or F1) and breed of litter (Yorkshire, Landrace, F1, or Commercial) were included as fixed effects in the model. Contemporary group was defined as litters born in the same month in the same herd and included as a fixed effect for all traits. Parity, age at breeding, number after transfer and age at weaning were included in the six-trait evaluation as needed for the unadjusted commercial records. Service sire was included as a random effect for number born alive. Table 1 shows the summary statistics for the dataset used in this analysis.

**Table 1. Summary Statistics**

Litter Breed	Litter Records	NBA <sup>1</sup>	NW <sup>1</sup>	LWT, kg <sup>1</sup>
Landrace	11,199	11.28	11.37	66.3
Yorkshire	19,156	11.25	11.80	64.4
F1	20,304	11.59	11.66	69.2
Commercial	31,915	11.92	10.77	71.5

<sup>1</sup>Number born alive, number weaned, litter weaning weight raw means - pre-adjusted for pure and F1 litters, unadjusted for commercial litters

Genetic parameters estimated from the study data were implemented into a daily genetic evaluation program for maternal line genetic improvement using BLUPF90. A Bio-economic selection index was calculated for maternal lines using EBV from the combined six-trait evaluation and economic values for traits from the NSR genetic evaluation system (STAGES™). Results from a sub-set of animals (one NSR firm with the largest number of records in the commercial crossbred dataset; 2,363 Yorkshire boars and 8,479 gilts; 1,797 Landrace boars and 5,951 gilts) were further examined for changes in sire and dam ranking and differences in mean commercial index value when ranked on either the purebred or combined purebred and crossbred index.

## Results and Discussion

Table 2 shows heritability and genetic correlations from the six-trait analysis for purebred and crossbred reproductive traits.

**Table 2. Heritability and Genetic Correlations**

	Trait	Pure			Cross		
		Number Born Alive	Number Weaned	Litter Weaning Wt.	Number Born Alive	Number Weaned	Litter Weaning Wt.
Pure	Number Born Alive	0.10	0.29	0.18	0.85	0.04	0.08
	Number Weaned		0.06	0.53	0.15	0.56	0.38
	Litter Weaning Wt.			0.12	-0.11	0.47	0.86
Cross	Number Born Alive				0.10	-0.14	-0.25
	Number Weaned					0.03	0.59
	Litter Weaning Wt.						0.06

<sup>1</sup>Heritability on diagonal; Genetic correlation above diagonal

Results indicate heritability is low for each trait, being consistent with previous results.<sup>6</sup> The genetic correlation between purebred and crossbred traits is less than 1, indicating selection based on an index that includes only purebred data will not maximize the rate of genetic improvement in number born alive, number weaned, and litter weaning weight at the commercial level. Heritability for C\_NW and C\_LWT were lower than their purebred counterparts, possibly due to differences in on-farm management between nucleus and commercial farms. Number born alive, whether purebred or crossbred showed similar heritability; indicating number born alive may be a straightforward measure and counted the same way across herds. Interestingly, the genetic correlation of C\_NBA with C\_NW and C\_LWT were negative. This, combined with the heritability near zero (0.03) for C\_NWN, may be an indication of management differences between nucleus and commercial farms, where litter size is generally standardized to allow each female to nurse an approximately equal number of pigs. Cross-fostering, or the (lack of) record of cross-fostering at the commercial level, may also contribute to these observed differences.

Table 3 shows the number of sires represented and daughter records per sire utilized in the daily genetic evaluation process.

**Table 3. Summary statistics from daily genetic evaluation**

Litter Breed	Sires	Average <sup>1</sup>	Minimum <sup>1</sup>	Maximum <sup>1</sup>	Total Records
Purebred	9,311	23.6	1	1,690	219,740
F1	1,486	30.0	1	1,759	44,580
Commercial	327	175.6	1	4,201	57,421

<sup>1</sup> Number of daughter litter records per sire

Sires with daughters producing purebred and F1 litters average approximately 25 and 30 records, respectively. For sires with commercial F1 daughters in production, the number increases substantially to ~175. Additional daughter records in the form of commercial females add significant accuracy to Breeding Value estimation, further improving genetic gain.<sup>7</sup> Increasing the number of half-sib progeny from 20 to 100 improves accuracy of a sires' EBV from 0.45 to 0.75 for lowly heritable traits (0.05), such as number born alive, number weaned, and litter weaning weight.<sup>8</sup> In broilers, it has been shown that genetic gain is greater when more crossbred progeny are tested, regardless of varying family structures tested, due to the improved accuracy of selection.<sup>2</sup>

Of the 9,311 sires with purebred daughter records, 1,311 have records from purebred daughters farrowing F1 litters, and 194 have records from F1 daughters. Fewer boars are represented at the commercial level, due to the lack of concern over inbreeding typically accounted for in nucleus boar selection and use and the fact not all NSR members have customers with pedigreed F1 females.

In the subset of data from one NSR firm that accounted for >90% of the commercial crossbred records, significant reranking of both sows and boars occurred when commercial data was included. Significant reranking did occur across breeds and genders, with Spearman rank correlation coefficients ranging from 0.77 to 0.85. Results are consistent with previous work utilizing purebred and crossbred swine reproductive data.<sup>4</sup>

We also see a marked difference in selection index value between the top 5% boars or 25% gilts when ranked using the purebred versus combined purebred crossbred index.

**Table 4. Differences in maternal selection index value and rank correlations when selecting purebred boars and gilts incorporating either purebred or purebred and crossbred combined data**

Breed	Gender	Number <sup>a</sup>	Percentage <sup>b</sup>	Index1 <sup>c</sup>	Index2 <sup>d</sup>	Rank Correlation <sup>e</sup>
Yorkshire	Boars	2,363	5%	121.00	117.96	0.77
Yorkshire	Gilts	8,479	25%	117.33	116.10	0.83
Landrace	Boars	1,797	5%	121.85	119.95	0.81
Landrace	Gilts	5,951	25%	116.61	115.60	0.85

<sup>a</sup> Number of animals in the selection candidate pool

<sup>b</sup> Percentage selected

<sup>c</sup> Mean commercial index value of selected animals when ranked by commercial index

<sup>d</sup> Mean commercial index value of selected animals when ranked by purebred index

<sup>e</sup> Rank correlation coefficient between purebred and crossbred selection index value

Differences in selection differential between the two ranking methods for boars are approximately 3 units for Yorkshires and 2 units for Landrace. With a value of \$1.25 per commercial daughter litter, per index unit, the value of this difference may not appear to be significant. With an average of 175 F1 daughter records per boar in this data set, the value would be \$656.25 per Yorkshire sire and \$437.50 per Landrace sire. However, assuming a normal working life in a boar stud, a purebred maternal boar could impact closer to 20,000 F1 commercial litters, indicating the value of the selection differential would be \$75,000 for a Yorkshire sire and \$50,000 for a Landrace sire. Differences in selection differential for the sows is roughly half the difference seen in the boars, more than likely due to the selection of five times as many sows compared to boars.

## Summary

These analyses demonstrate maternal genetic evaluation systems should be updated to include pedigreed commercial female records to enhance selection programs for reproductive traits. The added expense and workload to manage and track multiplication and commercial performance should be off-set by the added improvement in reproduction at the commercial level.

## References

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