Utilizing Crossbred Records To Increase Accuracy Of Breeding Values In Pigs

S. Newman[*], L. Wang[*], J. Anderson[*], D. Casey[*]

Introduction

Genetic improvement of pigs is structured as a pyramid where selection occurs in only a small fraction of herds with production occurring in a larger proportion of the total industry (Bichard 1971). Intervening segments (e.g., multiplication, crossbreeding) allow the systematic dissemination of genetic improvements from the apex to permit the flow of genetic material between the selection segment and the production segment. Based on this structure, selection takes place in relatively high-health, well-managed environments that provide a high plane of nutrition. Systematic expansion of these pure lines produces parent breeding stock and commercial (crossbred) parents and progeny at intervening tiers of the pyramid (e.g., Harris 1998).

Progeny of selected individuals are expected to perform under a range of varying production situations. There is a dependent relationship between genotypes and environments in which the difference in performance between two genotypes changes from environment to environment. This is reflected in the correlation between breeding values for purebred and crossbred performance (r_{pc}) deviating from unity for a number of economically important traits (Habier et al., 2007). This bias reduces realized selection response when compared to that estimated from selected animals. That genotype x environment interaction effects are often confounded in the r_{pc} is of no concern if crossbred performance is measured in the same environment as the breeding goal is defined (Wei and van der Werf, 1995).

Genetic improvement should be based on breeding objectives reflecting commercial performance because commercial pigs are invariably crossbred. Thus the collection of crossbred information over a range of environments genetically linked to selected populations, and the further use of this information from purebreds and crossbreds simultaneously, will increase accuracy of breeding value predictions (Bichard and David 1986; Bijma and van Arendonk 1998; Lutaaya et al., 2002). The objective of the current study was to analyze several years of field data to estimate the magnitude of increases in accuracy for some economically important traits in pig breeding programs.

Material and methods

In the present study we define accuracy as the correlation between the true breeding value and the estimated breeding value.

[*]Genus/PIC, 100 Bluegrass Commons Blvd. Suite 2200, Hendersonville, TN 37075 USA

Three traits were chosen: (1) Growth rate (GRT, gm/day) defined as lifetime hot carcass average daily gain in crossbreds; (2) 24-hour postmortem loin pH (LpH) in crossbreds; and (3) grow-finish mortality (GFM) in crossbreds.

Pigs. Herd boars from three PIC sire lines (labeled A, B and C) were used to produce purebred matings (selection candidates for the next generation) at two nucleus farms and for crossbred matings at cooperating commercial farms (providing information on crossbred performance). Semen was sent to multiple commercial farms where single sire matings were made to commercial sows to produce slaughter pigs. Crossbred piglets were ear tagged at birth and various life-cycle measurements recorded, including mortality, congenital defects, and carcass traits when harvested (e.g., hot carcass weight, carcass backfat and loin depth, and loin pH).

Models. The strategy used in the current study for measuring the impact of crossbred records was to run two genetic evaluations for each trait of interest; the only difference in the evaluations was whether crossbred records were included. Production, meat quality and mortality Estimated Breeding Values (EBV) emanate from multi-trait evaluations (conducted by sire line) including both purebred and crossbred traits. For each trait, animal was included as a random effect in the model. For GRT fixed effects included farm, farm x sex and farm x week interactions. For LpH week of slaughter was also included as a fixed effect. For GRT and LpH, a cross (type of dam) x sex interaction and contemporary group (birth year x birth month x finisher) were fit as fixed effects and linear and quadratic effects of days on Paylean®† were fit as covariates. A random effect of litter and the fixed effect interaction of farm x year x sex were included for GFM.

Results and discussion

Means and standard deviations for purebred and crossbred traits are shown in Table 1. Growth rates for purebred animals were higher than crossbreds. Part of the superiority is associated with environment, and also because purebred GRT is actual lifetime (body) average daily gain, while for crossbreds lifetime average daily gain is measured on a hot carcass basis. Differences in LpH between purebred and crossbred animals are likely due to all purebreds being of the same gender (gilts) and also all purebreds being processed at a single abattoir. It was expected that GFM would be greater in crossbreds than purebreds and this is exemplified by smaller mean mortalities measured at the nucleus level for all sire lines as compared to higher mortalities measured in crossbred animals.

Differences in accuracies for the crossbred EBV, with and without crossbred records, are presented in Table 2. For all traits and all lines accuracies were higher when crossbred records were included in the evaluation. The magnitude of the increase was uniform across sire lines by trait, but not within sire line across traits. Relative to the inclusion of crossbred records in the evaluation, accuracy increased for GRT by 23% on average while a 1.5-fold increase was realized for LpH and an over three-fold difference for GFM. When crossbred

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† PayLean® is a ractopamine-based product manufactured by Elanco that enhances growth in meat animals by repartitioning nutrients.

records are missing, crossbred EBVs are predicted only through the r_{pc}. This could also account for smaller accuracies in the absence of crossbred records.

Table 1: Means (standard deviations) for three traits measured in purebreds and crossbreds[a]

	GRT (gm/day)		LpH		GFM (%)	
Sire Line	Pure	Cross	Pure	Cross	Pure	Cross
A	696 (67)	513 (62)	5.73 (0.14)	5.81 (0.24)	1.55 (12.35)	2.49 (15.58)
B	710 (70)	510 (61)	5.66 (0.15)	5.78 (0.23)	2.19 (14.64)	2.89 (16.75)
C	739 (76)	541 (75)	5.69 (0.16)	5.80 (0.24)	1.96 (13.87)	2.84 (16.60)

[a]GRT = Growth Rate [Pure is lifetime (body) average daily gain. Cross is carcass average daily gain]; LpH = 24-hour postmortem loin pH; GFM = Grow-Finish Mortality.

Table 2. Accuracies of crossbred breeding values estimated with and without crossbred records[a]

	GRT		LpH		GFM	
Sire Line	With	Without	With	Without	With	Without
A	0.66	0.54	0.57	0.24	0.56	0.17
B	0.67	0.54	0.57	0.20	0.54	0.18
C	0.66	0.54	0.57	0.24	0.57	0.17

[a]GRT = Carcass average daily gain; LpH = 24-hour postmortem loin pH; GFM = Grow-Finish Mortality.

The correlated response to selection in crossbred performance when selection is based on purebred performance is primarily a function of r_{pc} and the heritabilities of the purebred and crossbred traits. Traits with high r_{pc} (> 0.55) like GRT expressed the smallest increase in accuracy due to the addition of crossbred records. Alternatively a lowly heritable trait like GFM with low purebred and crossbred heritabilities (< 0.15) and low r_{pc} (< 0.35) greatly benefited from the addition of crossbred records. Bijma and van Arendonk (1998) pointed out that the benefit of crossbred information is high when r_{pc} is low because of the reduced effectiveness of selection in purebreds for crossbred response. They also showed that even for very high r_{pc}, crossbred information will still be important for traits with low heritability because of the additional sib information provided.

Conclusion

The structure of pig breeding programs allows for the simultaneous collection of purebred and crossbred records from herd sires given single-sire matings are identified at the commercial level. These records can then be utilized in genetic evaluation to increase the accuracy of EBV for crossbred traits in pure line nucleus sibs to the crossbred sibs. Crossbred records will increase accuracy as a function of heritability of the purebred and crossbred traits as well as the genetic correlation between purebred and crossbred performance. It is of primary importance that pure line genetic improvement be based on breeding objectives reflecting crossbred performance.

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