

## COMBINING PUREBRED AND CROSSBRED DATA IN MULTIBREED GENETIC EVALUATION OF BEEF CATTLE

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### SUMMARY

A comparison of multiple breed genetic evaluations between a combined population of 1,043,153 purebred and crossbred animals with 412,955 purebred only animals was conducted for direct genetic effects of birth weight (BW), direct and maternal effects of weaning gain (WG and MWG) and postweaning gain in the herd (PWG-H) and at central evaluation stations (PWG-S). Differences in breed effects were similar between the combined and purebred population. Correlations between the evaluations from the combined and purebred population were 0.76, 0.74, 0.74, 0.78 and 0.81 for BW, WG, MWG, PWG-H and PWG-S respectively. Approximate expected correlations were 0.76 for all traits. Mean accuracies for each trait were significantly higher for the combined population than the purebred population. Inclusion of crossbred information would allow for multiple breed evaluations to directly compare animals across breed, increase accuracies associated with economically important traits and increase the genetic base to select potential herd sires.

### INTRODUCTION

Canadian beef sire evaluations are computed for 13 breeds using within breed genetic evaluations. Twenty six percent of records used to nationally evaluate sires within breed are from crossbred animals (Song, 1994). Some Canadian breed associations have been adverse to the inclusion of crossbred data in within breed genetic evaluations of sires and dams because animals could possibly be reranked. Including crossbred information would allow the inclusion of records that are currently eliminated from the evaluation of some beef breeds and provide comparisons between purebred animals of different breeds. Commercial producers are often interested in comparing potential herd sires of different breeds.

Although multibreed evaluations have received much attention in the last few years, to date, only young bulls in centrally evaluated stations are being evaluated simultaneously under a multibreed model (Armstrong et. al., 1990).

### MATERIALS AND METHODS

Data included records on birth weight (BW), gain from birth to weaning (200 day) (WG) and post-weaning gain in the herd (165 day) (PWG-H) and in central stations (140 day) (PWG-S). There were 743,313 records associated with 1,043,153 animals including 412,955 purebred and 630,198 crossbred. There were 33,464 weaning groups, 9,267 yearling groups and 266 central test groups. Purebreds were defined as 7/8 or greater of one breed. Crossbred animals include both crossbred progeny and dams.

The animal model used included the effects of fixed contemporary group, fixed age of dam by sex of calf interaction for preweaning traits and age of dam for postweaning traits, random genetic group effects, random direct additive and maternal additive genetic

effects. The phantom grouping procedure of Quaas (1988) was used to assign unknown purebred parents as random effects. The model is further outlined in Miller et al.,(1994).

Variances and covariances were assumed to be homogeneous. Heritabilities and correlations have been shown to be similar across breeds (Koots et al., 1991, Caron, 1994). Heritabilities and genetic correlations used are shown in Table 1 and residual correlations in Table 2.

Genetic evaluations on a within breed basis were calculated as EPDs (Expected Progeny Difference) by subtracting the average animal (or maternal) estimated breeding value (EBV) for the breed over the most recent 3 year period from each purebred animal EBV and dividing by two. Genetic evaluations were calculated as ABCs (Across Breed Comparisons) by subtracting the average animal (or maternal) EBV for the entire multibreed population in the most recent three year period from each individual's EBV and dividing by two and then setting relative to a Hereford base of zero. Accuracies were associated with genetic evaluations for each animal and were calculated using a procedure of Misztal and Wiggans (1988). Correlations were calculated and compared to approximate expected correlations.

## RESULTS AND DISCUSSION

Mean ABCs were highest for Simmental for all traits for both the combined evaluation and the purebred only evaluation (Table 3). Differences in genetic evaluations between the combined population and the purebred only population were small although maternal breed differences are larger than expected. These larger maternal breed differences may be due to the incorrect breed of sire and breed of dam assumptions for crossbred calves when parental information was missing. Similar genetic evaluations indicate that crossbred data can be used within breed and in multiple breed evaluations to directly compare animals across breeds.

EPDs estimated from the combined data were highly correlated with the EPDs from the purebred data. Estimated correlations were very similar to the expected correlation coefficients (Table 4). Nunez-Dominguez et al. (1993) found average correlations between purebred and crossbred progeny from sires to be 0.93, 0.77 and 0.76 for birth weight, 200-d weight and 365-d weight, respectively. Expected correlations suggest that including crossbred data results in sires still being evaluated similarly.

Crossbred data is readily available in Canada. Inclusion of crossbred data into analyses can provide comparison between purebred animals of different breeds. The number of sires evaluated doubled with the inclusion of crossbred data (from 5389 with purebred only to 10961 with purebred and crossbred combined). The genetic base to select potential sires is increased when crossbred data is included in analyses.

Mean accuracies for each trait were significantly higher ( $P < 0.05$ ) for the combined population than the purebred population (Table 5). The inclusion of crossbred data can significantly increase the accuracy of evaluations and should be included in genetic evaluations of beef cattle.

Table 1. Heritabilities and genetic correlations

BW <sub>d</sub>	WG <sub>d</sub>	PWG-H <sub>d</sub>	PWG-S <sub>d</sub>	BW <sub>m</sub>	WG <sub>m</sub>
.48	.10	.10	.10	-.20	0
	.32	.35	.35	0	-.20
		.28	.79	0	0
			.43	0	0
				-.20	0
				.21	.10
					.26

Table 2. Residual correlation

	WG	PWG-H	PWG-S
BW	.36	.17	.18
WG		-.10	0
PGH			0

Table 3. Average ABC (Standard Deviation) by breed<sup>1</sup> 1990-92 relative to Hereford under two evaluations, 1. Including purebred and crossbred data and 2. Including purebred data respectively

Breed	BW	WG	WGM	PWG-H	PWG-S
Angus	-0.5 (1.14)	4.4 (5.15)	1.6 (2.39)	3.8 (4.73)	5.9 (4.52)
Purebred	-0.2 (0.80)	4.4 (4.81)	2.5 (2.20)	3.3 (3.10)	5.8 (3.51)
n	1865	4614	4614	1023	180
Charolais	1.6 (1.45)	10.9 (5.56)	0.6 (5.23)	6.8 (4.37)	11.2 (5.46)
Purebred	0.6 (0.92)	8.3 (5.81)	3.8 (4.04)	5.9 (3.54)	12.0 (3.66)
n	3891	10580	10580	1543	462
Limousin	0.7 (0.95)	4.9 (4.99)	-0.4 (4.53)	2.7 (4.39)	2.0 (4.78)
Purebred	-0.4 (0.62)	3.1 (4.72)	2.0 (2.66)	3.4 (2.91)	1.5 (3.09)
n	3437	7732	7732	1140	378
Simmental	2.6 (1.90)	14.8 (6.22)	5.0 (3.14)	8.3 (4.65)	11.6 (4.92)
Purebred	1.0 (1.52)	15.2 (6.14)	8.4 (2.87)	9.7 (3.64)	12.4 (3.73)
n	5340	8366	8366	889	267

BW = birth weight direct (kg), WG = weaning gain direct (kg), WGM = weaning gain maternal (kg), PWG-H = 165 day post-weaning gain in herd (kg), PWG-S = 140 day post-weaning gain in station

<sup>1</sup> Base is average ABC in multibreed population over most recent three year period (1990-92)

Table 4. Correlation between two genetic evaluations, 1. Including purebred and crossbred data and 2. Including purebred data only.

Trait	Correlation Coefficient	Expected Correlation
Birth Weight (Direct)	0.76056	0.76303
Weaning Gain (Direct)	0.74034	0.76312
Weaning Gain (Maternal)	0.73641	0.76403
Post-Weaning Gain (Home)	0.77541	0.75761
Post-Weaning Gain (Station)	0.81045	0.75775

Animals included in correlation had minimum weaning gain accuracies of 0.60 in both evaluations

Table 5. Mean ABC Accuracies (in percent) by trait under two evaluations, 1. Including purebred and crossbred data and 2. purebred data respectively.

Trait	Combined	Purebred
Birth Weight (Direct)	77.945	73.496
Weaning Gain (Direct)	77.952	73.521
Weaning Gain (Maternal)	78.056	73.478
Post-Weaning Gain (Home)	77.412	72.857
Post-Weaning Gain (Station)	77.426	72.872

Animals included in mean accuracies had minimum weaning gain accuracies of 0.60 in both evaluations

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