

DISTRIBUTIONS OF GENETIC EVALUATIONS OBTAINED WITH A MULTI-BREED ANIMAL MODEL

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SUMMARY

A multibreed genetic evaluation of 1,043,153 animals including 412,955 purebred and 630,198 crossbred was performed for direct and maternal genetic effects of calving ease, birth weight, weaning gain and post weaning gain in the herd and at central test stations. A multiple trait animal model with maternal effects was used with breed accounted for by tracing all pedigrees to purebred parentage and grouping unknown purebred ancestors into phantom groups by breed-year. The distribution of evaluations by breed indicate that breed effects are adequately handled through phantom groups in a multibreed evaluation.

INTRODUCTION

Within breed genetic evaluations of sires have been computed in Canada for over 20 years. Records of crossbred progeny are included through the inclusion of a breed of dam-age of dam-sex of calf subclass effect in the model (Schaeffer and Wilton, 1974; Schaeffer and Wilton, 1975). Evaluations across breeds have also been carried out for over 20 years for bulls measured for post-weaning performance in central evaluation stations in Ontario (Wilton et al., 1975). Simultaneous within breed expected progeny differences (EPD) and across breed comparisons (ABC) have now been introduced for bulls in central evaluation stations (Armstrong et al., 1990).

Within herd ratios of individual performance relative to herd average have been computed for many years in the Beef Herd Improvement Program in Ontario. These ratios have also been used for across breed comparisons in commercial herds because ratios were calculated relative to herd average regardless of breed.

There has been considerable interest in an integrated herd test and bull test program, with the flexibility of providing both EPDs and ABCs to producers. The developments described in this paper relate to simultaneous EPD and ABC calculations across herds for all breeds and crosses possible. The distribution of genetic evaluations obtained is presented.

MATERIALS AND METHODS

Data included records on calving ease (CE), 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.

The model was as follows:

$$y = cg + as + (Qg+a) + (Rg+m) + p + e,$$

where y = a vector of observations on the traits measured, pre-adjusted for multiple births and direct and maternal heterosis. Pre-adjustments for multiple births were increases of 30% and 20% for individual birth weights and weaning gains respectively. Pre-adjustments, for heterotic effects were; 5% for birth weight and weaning gain, 3% for post-weaning gain in the herd and at station direct and 5% for maternal weaning gain.

cg = contemporary group, defined as herd-year-management group for pre-weaning traits, herd-year-management group-sex for PWG-H and test group for PWG-S (fixed).

as = age of dam x sex of calf interaction for pre-weaning traits and age of dam for post-weaning traits (fixed).

g = a vector of genetic (phantom) group effects (random).

Q and R link animals and dams respectively to ancestral phantom groups.

$Qg+a$ = direct additive genetic effect (random)

$Rg+m$ = maternal additive genetic effect (random)

p = permanent environmental effect of dam (random).

e = residual error.

Breed effects were identified by tracing pedigrees to purebred ancestors (7/8 or higher). The concept of phantom parent grouping (Quaas et al., 1988) was applied to unknown purebred parents treating phantom groups as random effects. Purebred phantoms were grouped by breed-year combination and treated as animals with unknown parents. Phantom linking parents were used to link unknown crossbred parents to purebred parentage. Purebred sires were assessed to have been used in cases of unknown combinations of sire and dam breeds, following patterns in commercial Ontario beef breeding.

Variances and covariances were assumed to be homogeneous across the multibreed population. Heritabilities and correlations have been shown to be similar across breeds (Koots et al., 1991). 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 EPD (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 across breed comparisons (ABC) 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.

RESULTS AND DISCUSSION

The average ABC by breed are shown in Table 3 along with the standard deviations. Differences were generally similar for weaning gain and post-weaning gain for most breeds. Differences in birth weights were generally proportional to differences in weaning gain.

The within breed distributions of ABC and EPD are identical except for the breed mean. Breed mean, for example, for Charolais post-weaning gain is equal to zero for the most recent 3 year EPD distribution and +7.7 for the equivalent ABC distribution. A complete distribution of ABC for the entire multibreed population in the most recent three years would centre on zero.

Multi-breed evaluations can be used directly for comparisons of animals of various breeds and crosses (ABC) or for comparison of animals within breeds (EPD). A by-product of calculations is a current set of breed differences.

Commercial producers can use multibreed evaluations to directly compare animals in their herds across breeds and crosses for additive genetic merit. Ranking for total genetic merit could be achieved by re-adjusting for heterotic effects, and for producing ability by adding in permanent environment solutions.

Multi-breed genetic evaluation of animals is now feasible and possible from large scale data sets consisting of purebred and crossbred cattle.

Table 1. Heritabilities and genetic correlations

CE_d	BW_d	WG_d	$PWG-H_d$	$PWG-S_d$	CE_m	BW_m	WG_m
.15	-.10	0	0	0	-.10	0	0
	.48	.10	.10	.10	0	-.20	0
		.32	.35	.35	0	0	-.20
			.35	.79	0	0	0
				.43	0	0	0
					.10	-.20	0
						.21	.10
							.26

Table 2. Residual correlations

	BW	WG	PWG-H	PWG-S
CE	0	0	0	0
BW		.33	.21	.25
WG			.21	.25
PWG-H				0

Table 3. Average ABC (Standard Deviation) by breed¹ 1990-92

Breed	BW	WG	WGM	PWG-H	PWG-S
Angus n	-1.1 (1.14) 1865	-1.2 (5.15) 4614	0.6 (2.39) 4614	0.1 (4.73) 1023	2.4 (4.52) 180
Blonde d-Aquitaine	0.7 (1.21) 545	2.2 (5.94) 735	0.5 (2.74) 735	3.7 (5.41) 53	1.6 (4.99) 71
Charolais n	1.0 (1.45) 3891	5.3 (5.56) 10580	-0.4 (5.23) 10580	3.1 (4.37) 1543	7.7 (5.46) 462
Hereford n	-0.6 (1.25) 6318	-5.6 (5.34) 17656	-1.0 (2.86) 17656	-3.7 (4.25) 2725	-3.5 (4.58) 327
Limousin n	0.1 (0.95) 3437	-0.7 (4.99) 7732	-1.4 (4.53) 7732	-1.0 (4.39) 1140	-1.5 (4.78) 378
Maine Anjou n	1.3 (1.66) 242	1.5 (6.03) 395	2.7 (2.66) 395	2.0 (3.08) 17	5.8 (5.96) 19
Salers n	0.5 (1.55) 347	-0.7 (5.41) 621	3.1 (2.82) 621	-1.6 (3.26) 82	0.8 (3.78) 10
Shorthorn n	0.2 (2.06) 333	-4.7 (6.03) 750	0.8 (2.37) 750	-1.1 (3.70) 199	-0.2 (4.36) 58
Simmental n	2.0 (1.90) 5340	9.2 (6.22) 8366	4.0 (3.14) 8366	4.6 (4.65) 889	8.1 (4.92) 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

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

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