

CORRELATION BETWEEN DIFFERENCES IN PARENTAL GENETIC MERIT AND PROGENY VARIABILITY IN ANGUS CATTLE.

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SUMMARY

Calf weight variability is a major concern to cattlemen within the U.S., particularly when considering birth weight. The concern is that two bulls, with similar Expected Progeny Differences (EPD) may both produce calves that average 35 KG at birth, but one bull's calves range from 32 to 38 KG while the other bull's calves range from 28 to 42 KG. A possible source of this variation may result when a bull's parents have very different genetic merit for that trait.

The results of this study show that parental differences in genetic merit (EPDs) does not have an effect on the variation of a bull's offspring. There is very little correlation between parental EPD differences and the variation in weight of a bull's calves or with the Mendelian sampling of the bull or his calves.

The implications of these results are that producers are not reducing variation by mating cattle with like EPDs. Therefore, bulls and cows with complimentary traits can be mated without affecting subsequent calf variation.

INTRODUCTION

A common form of beef cattle breeding in the United States is to mate bulls and cows with similar Expected Progeny Differences (EPD). The thought is that a sire born of parents with similar EPDs will produce progeny with less variation for that trait. If this practice does not reduce variation in a bull's progeny then seedstock producers are limiting their ability to match complimentary mates.

Assuming that quantitative traits are controlled by multiple loci, several genotypes can result in animals with the same genetic merit. The more loci involved the higher the possibilities are of genotypes for a specific genetic value. Therefore, mating two animals with similar genetic merit (EPDs) does not insure that the animals are of similar genotypes and progeny variability may not be reduced.

The purpose of this study was to determine if parental differences in genetic merit, for several quantitative traits, has an effect on the weight variability or Mendelian sampling of that sire's progeny.

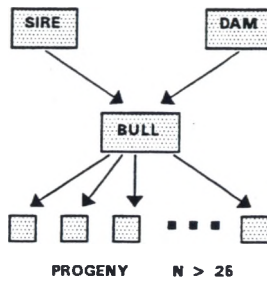
MATERIALS AND METHODS

Field data were provided by the American Angus Association and included records on adjusted birth weight BW, 205 d adjusted weaning weight (WW), adjusted 365 d weight (YW), birth weight EPD (BWE), weaning weight direct EPD (WWE), weaning weight milk EPD (WME) and yearling weight EPD (YWE) for the bull, his parents and progeny. All EPDs were from the National Cattle Evaluation, no pedigree estimates were used.

Figure 1 should assist in understanding the structure of the data. The parental EPD differences for BWE, WWE and YWE were calculated by taking the absolute value of the bull's sire's EPD minus the bull's dam's EPD (BDIF, WDIF and YDIF, respectively). A Mendelian sample for BW, WW and YW were calculated for each bull by taking the absolute value of his EPD minus his parental average EPD for the respective trait (Quaas and Pollak, 1980) (BMSB, BMSW and BMSY, respectively).

Means and variances for several traits were calculated on the progeny of each bull that had a BDIF, WDIF or YDIF value and 25 or greater progeny represented. The traits included: BW, WW, YW, corrected BW (BW minus calf's dam's BWE, CBW), corrected WW (WW minus calf's dam's WWE minus 2 times calf's dam's WME, CWW), corrected YW (YW minus calf's dam's YWE, CYW), Mendelian sampling for BW, WW, and YW (PMSB, PMSW, PMSY, respectively), and Mendelian sampling when only progeny with an accuracy value greater than .30 were considered (PHAB, PHAW and PHAY, respectively).

Figure 1. Data structure.



Pearson Correlations were computed between BDIF, WDIF and YDIF with BMSB, BMSW, and BMSY, BW variance (BWV), WW variance (WWV), and YW variance (YWV), CBW variance (CBWV), CWW variance (CWWV), and CYW variance (CYWV), PMSB mean (MSBM), PMSW mean (MSWM), and PMSY mean (MSYM), PMSB variance (MSBV), PMSW variance (MSWV), and PMSY variance (MSYV), PHAB mean (HABM), PHAW mean (HAWM), and PHAY mean (HAYM), PHAB variance (HABV), PHAW variance (HAWV), and PHAY variance (HAYV), respectively. Correlations were computed using SAS (1989).

RESULTS

The correlations and number of observations between the parental EPD differences with the other traits are presented in Table 1.

Although some values were significantly different from zero all correlations were extremely small in magnitude. This would indicate that a bull produced by parents with similar genetic merit values (EPD) does not sire progeny with less variation for that trait. With the large numbers represented in this study and the tight restrictions placed on bulls included in the analysis, these results should be very representative of the US Angus population.

Table 1. Pearson correlation and number of observations between parental EPD differences and other traits.

TRAIT	BMS	Act WT	Cor WT	PMSM	PMSV	HMSM	HMSV
BDIF	.024* 6694	.015 6694	.013 6688	.029* 6654	.003 6654	.006 1591	-.034 1591
WDIF	-.036** 8833	.041** 8890	.034** 8877	.087** 8760	.067** 8760	.084** 8492	.068** 8492
YDIF	-.071** 3851	-.056** 4147	-.057** 4101	.071** 3736	.025 3736	.027 268	.000 268

BMS = bull Mendelian sampling; Act WT = variance of bull's progeny actual weight; Cor WT = variance of bull's progeny birth weight corrected for dam EPDs; PMSM = progeny Mendelian sampling mean; PMSV = progeny Mendelian sampling variance; HMSM = progeny Mendelian sampling mean when only progeny with an accuracy value greater than .30 were considered; HMSV = progeny Mendelian sampling variance when only progeny with an accuracy value greater than .30 were considered.

* p < .05

** p < .01

DISCUSSION

The correlation between parental differences with the bull's Mendelian sampling and his progeny's mean and variance Mendelian sampling for the respective trait were very low and sometimes negative. This shows that parental differences in genetic merit has very little effect on Mendelian sampling. The amount that a calf's actual genetic merit differs from the average of its parents genetic merit is not influenced by these parental differences, in either the first or second generation. These results would agree with both, the assumption that these quantitative traits are controlled by multiple genes, and these genes segregate randomly.

The result that adjusted actual and corrected weight variation of a bull's progeny were lowly correlated with his parental genetic merit differences has a very practical implication. This would indicate that the practice of mating bulls and cows with similar EPDs for a trait to reduce the resulting bull's variability for that trait, is unfounded. Therefore, producers that are currently utilizing this practice can mate bulls and cows that better compliment each other, without increasing variation in subsequent calf crops.

REFERENCES

- QUAAS, R.L. AND POLLAK, E.J. (1980) J. Anim. Sci. 51 : 1277-1287.
 SAS. (1989) SAS User's Guide: Statistics. SAS Inst. Inc., Cary, NC.