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PREVIEW

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Prediction of genetic values across breeds in beef cattle

Núñez-Domínguez, Rafael, Ph.D.

The University of Nebraska - Lincoln, 1993

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PREVIEW

PREDICTION OF GENETIC VALUES ACROSS BREEDS
IN BEEF CATTLE

by

Rafael Núñez-Domínguez

A DISSERTATION

Presented to the Faculty of
The Graduate College at the University of Nebraska
In Partial Fulfillment of Requirements
For the Degree of Doctor of Philosophy

Major: Animal Science

Minor: Biometry

Under the Supervision of Professor L. Dale Van Vleck

Lincoln, Nebraska

December, 1992

DISSERTATION TITLE

Prediction of Genetic Values Across Breeds in Beef Cattle

BY

Rafael Nunez-Dominguez

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PREDICTION OF GENETIC VALUES ACROSS BREEDS
IN BEEF CATTLE

Rafael Núñez-Domínguez, Ph.D.

University of Nebraska, 1992

Adviser: L. Dale Van Vleck

Records of birth (BW), weaning (WW), and yearling (YW) weight on F_1 calves produced in a topcross experiment involving Angus, Hereford, Polled Hereford, Charolais, Limousin, Simmental, Gelbvieh, Maine-Anjou, Chianina, Tarentaise, Shorthorn and Salers bulls mated to Hereford and Angus cows were used in this study. Regressions (b) of crossbred calf performance on expected progeny differences (EPD) of the sires were estimated and used to adjust breed of sire means for genetic trend and sire sampling. Average (b) (kg/kg) of BW, WW, and YW of F_1 calves on EPD of the sire were $1.04 \pm .10$, $.88 \pm .11$, and $1.40 \pm .11$, respectively. The b were similar to the expected values of 1.0 except for YW. Adjusted breed of sire means tended to be regressed toward the average of all breeds, particularly for BW and WW.

Correlations between the expression of genes from sires in purebred (P) and crossbred (C) progeny (r_{PC}), and in Hereford (H)- and Angus (A)-cross F_1 calves (r_{HA}) were estimated treating performance of F_1 calves in P and C, or in H and A as separate traits. A multivariate animal model with birth year-cow age-sex subclasses, random correlated direct and maternal additive genetic effects and maternal permanent

environmental effects was used by breed of sire. Estimates of r_{PC} ranged from .88 to .97, .55 to .94, and .68 to .86 for BW, WW and YW, respectively. Estimates of r_{HA} ranged from .43 to .99, .56 to .95, and .50 to .98 for BW, WW and YW, respectively. Weighted averages of estimates of r_{PC} and r_{HA} across sire breeds were, respectively, .93 and .85 for BW, .77 and .73 for WW, and .76 and .86 for YW.

Predictions of breeding values (PBV) of sires within and across breeds were obtained and the effect of accounting for heterogeneous variances across breed groups was evaluated. Two models differing in their covariance structure were compared. Model I assumed homogeneous variances. Model II accounted for heterogeneous variances. The PBV were obtained for when sires were to be mated to H, A or equally to H and A cows. Sires were ranked based on PBV for each model, and means of selected sires were calculated based on Model II. Effect of heterogeneous variances was most important for YW, and most important when sires are to be mated to H rather than A cows. Gains of 3 to 8 kg of YW may be achieved in the following calf crop if sires are chosen across breeds based on PBV from a model accounting for heterogeneous variances.

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As an animal breeder I have to recognize that a person's success is not only the result of his(her) genetic makeup, but also of the surrounding environment. Although in my case, my parents (no longer living) contributed with excellent genes for important traits in human life, it was the environmental part the one that played a major role in my limited accomplishments. Many people have contributed with their friendship, support, advice and counsel to the successful completion of this phase of my education.

I feel very fortunate to have had the opportunity of doing my graduate studies at the Department of Animal Science of the University of Nebraska, where there exists an excellent working environment. The faculty from this Department together with that from the Roman L. Hruska Meat Animal Research Center encompasses a group of distinguished and internationally respected scientists.

My sincere gratitude, appreciation and respect goes to Dr. Dale Van Vleck for his advise and encouragement during my Ph.D. program. I wish some day I can, at least partially, imitate his ability to explain in an easy way very complex concepts.

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PREVIEW

INTRODUCTION

Genetic improvement for traits of economic importance may be achieved mainly by two kinds of selection; selection among different breeds and selection among individuals within breeds. Effectiveness of genetic improvement relies on adequate evaluation procedures to estimate breed and heterosis effects, and to predict genetic values of animals within a breed.

Estimates of heterosis and breed effects for various traits, obtained from crossbreeding experiments in beef cattle, have been published since the middle of the 1960's (Gregory et al., 1965; Gaines et al., 1966; Cundiff et al., 1974a,b; Koger et al., 1975; Gregory et al., 1978; Long, 1980; Wyatt and Franke, 1986). Experimental evidence has indicated that considerable improvement in several important traits can be achieved by commercial beef cattle producers through the use of organized crossbreeding systems (Gregory and Cundiff, 1980), or through the use of composite breeds (Gregory et al., 1992).

Procedures to predict breeding values in beef cattle have been modified over time in order to reduce bias and to increase accuracy. Nielsen (1974) described the evolution of sire evaluation procedures in dairy and beef cattle. Benyshek et al. (1988) presented an overview of the development of methods of genetic prediction in the U.S. beef industry. They listed several major events that greatly influenced beef sire

evaluations: 1) the formation of the Beef Improvement Federation in 1968, which immediately addressed the question of National Sire Evaluation, 2) the development of Guidelines for Uniform Beef Improvement Programs (first published in 1970), 3) the discovery of the simple rules to calculate the inverse of the numerator relationship matrix by Henderson (1975, 1976), 4) widespread use of artificial insemination, and 5) development of more powerful computer hardware. All these factors allowed the application of more sophisticated sire evaluation methods developed by Henderson (1973).

Currently in the U.S., 18 beef cattle breed associations are doing national genetic evaluations and are publishing sire summaries containing predictions of genetic values expressed in terms of expected progeny differences (EPD) mainly for weights at birth, weaning and 365 d, and for net maternal ability (milk) and maternal weaning weight (growth plus milk). Sixteen of those breed associations use either the animal model or the reduced animal model (Quaas and Pollak, 1980), for single or multiple traits. Several breed associations are reporting considerable favorable genetic trends for growth and milking ability (e.g., AAA, 1991; APHA, 1991; ASA, 1991).

One next step in cattle genetic evaluation procedures that would allow commercial beef cattle producers to utilize more effectively genetic differences among and within breeds, would be to predict genetic merit of breeding stock across breeds. Prediction systems for across breed genetic values

depend on the population structure. When limited information on crossbred animals is available for genetic evaluations, procedures such as those suggested by Kinghorn (1982), Notter (1989) and Notter and Cundiff (1991) are more suitable.

Kinghorn (1982) suggested the use of a multibreed selection index, which is basically a function of breed genetic value (breed group effect) and a deviation of an individual's phenotype from its breed genetic value weighted by the within-breed heritability. Notter (1989) discussed the possibility of calculating across-breed EPD and suggested a procedure that uses constants for breed effects, base year of the breed, and heterosis effects, in addition to EPD within breeds.

More sophisticated prediction procedures, i.e., mixed model methods, require that enough purebred and crossbred data to be available, and that perhaps different variance and covariance components will be needed for the various breed groups. Application of mixed model methods to estimate crossbreeding parameters was discussed by Komender and Hoeschele (1989). Procedures to predict breeding values for purebred and crossbred data have been described by Elzo and Famula (1985), Arnold et al., (1992), and Swan and Kinghorn (1992).

Komender and Hoeschele (1989) compared the use of fixed vs mixed models to estimate crossbreeding parameters and concluded that serious underestimates of the true standard

errors of crossbreeding parameters may result when ignoring all genetic relationships among animals via the animal model. They mentioned that the effectiveness of an animal model for computing suitable standard errors and unbiased estimates of crossbreeding parameters increases when analyzing unbalanced experiments and field data.

Elzo and Famula (1985) proposed the use of mixed model procedures with sire-maternal grandsire models to account for sire x breed group of dam interactions, and for heterogeneous variances across breed groups. Their models included additive and nonadditive direct and random effects, assuming that the variance of genetic effects of crossbred animals is a weighted mean of the genetic variances of base breeds represented in the crossbreds. Rules to derive the inverse of the additive genetic covariance matrix with unequal but proportional variances across genetic groups were published for both single traits (Elzo, 1986), and multiple traits (Elzo, 1990).

Procedures to predict genetic values of animals with diverse genetic composition using either the animal model or the reduced animal model were described by Arnold et al., (1992). These models account for heterogeneous variances across breed groups and for nonadditive random effects due to sire x breed of dam or dam x breed of sire interactions.

Animal x breed of mate interactions, and particularly sire x breed of dam interactions, may be seen as genotype x environment interactions if performance in different maternal

environments (dam genotypes) is regarded as a different trait (Falconer, 1952). The correlation between traits is an indicator of the importance of genotype x environment interaction. Under these circumstances, a multiple trait model may be used (Swan and Kinghorn, 1992). Although interaction models are equivalent (Henderson, 1985) to multi-trait models to study animal x breed of mate interactions when variances are the same for all traits and covariances are the same for all pairs of traits, the second approach has a more flexible covariance structure and will result in more accurate predictions. However, when the number of traits increases, the analyses become more prohibitive to compute.

An important limitation to obtain predictions of genetic values across breeds is the lack of enough information on crossbred cattle either from designed crossbreeding experiments, or from industry crossbreeding programs. One comprehensive breed evaluation program that has used a large number of AI sires with current EPD's is the Germ Plasm Evaluation Program of the Roman L. Hruska U.S. Meat Animal Research Center. Data from this Program were used in this dissertation.

Before considering implementation of a particular prediction system accommodating animal x breed of mate interactions, more information about reranking of sire's breeding values across genotypes of the dams, studied through correlations, are needed (Swan and Meyer, 1991). The

importance of accounting for heterogeneity of variances across breed groups is also needed.

Notter and Cundiff (1991) calculated the regression of performance of crossbred progeny on EPD of the sires. If these regressions differ significantly from their expectation, then interactions of sire x breed of dam are present. If accuracy of sire's EPD is high, Notter and Cundiff (1991) suggested a procedure to find out if reranking of breeding values of sires is causing sire x breed of mate interactions. The first part of this dissertation consists of an update of the study of Notter and Cundiff (1991), including records from additional breeds of sires. Part II of the dissertation deals with the importance of sire reranking of breeding values of sires when mated to Hereford and Angus cows, measured in terms of correlations. In Part III, the importance of adjusting for heterogeneous variances on prediction of breeding values within and across breeds is evaluated.

LITERATURE CITED

- AAA. 1991. Spring Sire Evaluation Report. American Angus Association, St. Joseph, MO.
- APHA. 1991. Polled Hereford Sire Summary. American Polled Hereford Association, Kansas City, MO.
- Arnold, J. W., J. K. Bertrand, and L. L. Benyshek. 1992. Animal model for genetic evaluation of multibreed data. J. Anim. Sci. 70:3322.
- ASA. 1991. Simmental Sire Summary. American Simmental Association, Bozeman, MT.
- Benyshek, L. L., M. H. Johnson, D. E. Little, J. K. Bertrand, and L. A. Kriese. 1988. Applications of an animal model in the United States beef cattle industry. J. Dairy Sci. 71(Supplement 2):35.
- Cundiff, L. V., K. E. Gregory and R. M. Koch. 1974a. Effects of heterosis on reproduction in Hereford, Angus and Shorthorn cattle. J. Anim. Sci. 38:711.
- Cundiff, L. V., K. E. Gregory, F. J. Schwulst and R. M. Koch. 1974b. Effects of heterosis on maternal performance and milk production in Hereford, Angus and Shorthorn cattle. J. Anim. Sci. 38:728.
- Elzo, M. A. 1986. Inverse of single trait additive genetic covariance matrix with unequal variances across additive genetic groups. J. Dairy Sci. 69:569.

- Elzo, M. A. 1990. Recursive procedures to compute the inverse of the multiple trait additive genetic covariance matrix in inbred and noninbred multibreed populations. *J. Anim. Sci.* 68:1215.
- Elzo, M. A. and T. R. Famula. 1985. Multibreed sire evaluation procedures within a country. *J. Anim. Sci.* 60:942.
- Falconer, D. S. 1952. The problem of environment and selection. *The American Naturalist* 86:293.
- Gaines, J. A., W. H. McClure, D. W. Vogt, R. C. Carter and C. M. Kincaid. 1966. Heterosis from crosses among British breeds of beef cattle: Fertility and calf performance to weaning. *J. Anim. Sci.* 25:5.
- Gregory, K. E. L. A. Swiger, R. M. Koch, L. J. Sumption, W. W. Rowden and J. E. Ingalls. 1965. Heterosis in preweaning traits of beef cattle. *J. Anim. Sci.* 24:21.
- Gregory, K. E., L. V. Cundiff, R. M. Koch, D. B. Laster and G. M. Smith. 1978. Heterosis and breed maternal and transmitted effects in beef cattle. I. Preweaning traits. *J. Anim. Sci.* 47:1031.
- Gregory, K. E. and L. V. Cundiff. 1980. Crossbreeding in beef cattle: Evaluation of systems. *J. Anim. Sci.* 51:1224.
- Gregory, K. E., L. V. Cundiff, and R. M. Koch. 1992. Composite breeds to use heterosis and breed differences to improve efficiency of beef production. ARS-USDA.
- Henderson, C. R. 1975. Rapid method for computing the inverse of a relationship matrix. *J. Dairy Sci.* 58:1727.

- Henderson, C. R. 1976. A simple method for computing the inverse of a numerator relationship matrix used in prediction of breeding values. *Biometrics* 32:69.
- Henderson, C. R. 1973. Sire evaluation and genetic trends. In: *Proceedings of the Animal Breeding and Genetics Symposium in Honor of Dr. Jay L. Lush*. Am. Soc. of Anim. Sci., Champaign, IL. pp 10-41.
- Henderson, C. R. 1985. Equivalent linear models to reduce computations. *J. Dairy Sci.* 68:2267.
- Kinghorn, B. 1982. Genetic effects in crossbreeding. II. Multibreed selection indices. *Z. Tierz. Zuechtungsbiol.* 99:315.
- Koger, M. F. M. Peacock, W. G. Kirk and J. R. Crockett. 1975. Heterosis effects on weaning performance of Brahman-Shorthorn calves. *J. Anim. Sci.* 40:826.
- Komender, P. and I. Hoeschele. 1989. Use of mixed-model methodology to improve estimation of crossbreeding parameters. *Livest. Prod. Sci.* 21:101.
- Long, C. R. 1980. Crossbreeding for beef production: Experimental results. *J. Anim. Sci.* 51:1197.
- Nielsen, M. K. 1974. An examination of analysis procedures for national beef sire evaluation programs. Ph.D. Dissertation. Iowa State University.
- Notter, D. R. 1989. EPD for use across breeds. 21st Meeting of the Beef Improvement Federation. p 63. Nashville, TN.

- Notter, D. R. and L. V. Cundiff. 1991. Across-breed expected progeny differences: Use of within-breed expected progeny differences to adjust breed evaluations for sire sampling and genetic trend. *J. Anim. Sci.* 69:4763.
- Quaas, R. L. and E. J. Pollak. 1980. Mixed model methodology for farm and ranch beef cattle testing programs. *J. Anim. Sci.* 51:1277.
- Swan, A. A., and K. Meyer. 1991. Prediction and estimation of non-additive genetic effects within and across breeds. *Proc. 9th Conference "Genetics for Profit and Prophets for Genetics" of the Austr. Assoc. Anim. Breed. Genet.* pp 488-495.
- Swan A. A. and B. P. Kinghorn. 1992. Evaluation and exploitation of crossbreeding in dairy cattle. In *Symposium: Dairy Crossbreeding. J. Dairy Sci.* 75:624.
- Wyatt, W. E. and D. E. Franke. 1986. Estimation of direct and maternal additive and heterotic effects for preweaning growth traits in cattle breeds represented in the Southern region. *Southern Cooperative Series, Bull. No.* 310.

PART I.
BREED COMPARISONS FOR GROWTH TRAITS ADJUSTED FOR WITHIN
BREED GENETIC TREND USING EXPECTED PROGENY DIFFERENCES

ABSTRACT

Records (2,910) of birth (BW), weaning (WW), and yearling weight (YW) on F_1 calves produced in a top-cross experiment involving Angus, Hereford, Polled Hereford, Charolais, Limousin, Simmental, Gelbvieh, Maine-Anjou, Chianina, Tarentaise, Shorthorn, and Salers bulls mated to Hereford and Angus cows and records (4,592) of WW on three-breed-cross calves out of 986 F_1 females of the same breed crosses were used in this study. The purposes were to estimate how much of the expected progeny differences (EPD) of the sires was realized in crossbred calves and to estimate sire breed effects for the traits adjusted for genetic trend and sire sampling. Published EPD for BW, WW, YW, net maternal ability (MLK), and maternal WW (MAT) were used. Average regressions (kg/kg \pm SE) of BW, WW, and YW of F_1 calves on EPD of the sire were $1.04 \pm .10$, $.88 \pm .11$, and $1.40 \pm .11$, respectively. The regressions (b, kg/kg) were similar to the expected values of 1.0 except for YW. For WW of three-way-cross calves on MLK EPD of the maternal grandsire, b was $1.02 \pm .11$, which was not different from the expected value of 1.0. Estimated sire-breed means were adjusted to a 1982 genetic base by adding b times the difference of the 1982-breed-mean EPD and mean EPD of sires used in the study. Three different adjustments were compared: the pooled across breeds b, a separate b for each breed, and the expected b of 1.0. In general, the adjustments