

rogued block of F₉ plants increased for four generations as a bulk from a single F₄ plant. This seed was further increased to about 3900 bushels of Foundation seed at North Dakota Branch Stations during 1976 and 1977. This seed was allocated to the North Dakota County Crop Improvement Associations for further multiplication in 1978. Other states also had access to limited supplies of the new cultivar, if they wished to increase it, in compliance with the policy of mutually sharing new cultivar seedstocks.

The North Dakota Agricultural Experiment Station will maintain purified seedstocks of Calvin durum wheat for foundation seed growers as long as the cultivar is in commercial demand.

Summary

Calvin, a new durum wheat cultivar, has been developed and released by the North Dakota Agricultural Experiment Station, in cooperation with the U.S. Department of Agriculture. Calvin is the second semidwarf durum cultivar released by the Agricultural Experiment Station and represents a continuous research effort over a 20-year period. It has a high yield capability similar to Cando and had higher test weight, kernel weight and kernel size. Calvin has been equal or superior to Cando in agronomic and quality characteristics. Cando has had disease reactions similar to Cando and Rolette.

Milling and spaghetti processing performance of Calvin were satisfactory, providing good semolina yield and

spaghetti of high yellow color when evaluated over a 3-year period (1975-77). Test weight of Calvin was higher than those of Ward and Cando but slightly lower than that of Rolette. Vitreous kernel content was lower than the three check cultivars. Kernel distribution was more similar to Cando, but wheat protein was slightly lower than the three checks.

Acknowledgements

The authors are grateful to all cooperators who have contributed to the development of Calvin durum. Several scientists, technicians and secretaries in the Departments of Agronomy, Cereal Chemistry and Technology, and Plant Pathology at NDSU, the Cooperative Rust Laboratory at St. Paul, Minnesota, and Agricultural Research Center, Beltsville, Maryland, the USDA Hard Red Spring and Durum Wheat Quality Laboratory at NDSU, and the NDSU Branch Experiment Stations cooperated in the development of Calvin. The winter increases of Calvin at CIANO (Experiment Station), Ciudad Obregon, Sonora, Mexico, and near Yuma, AZ, were accelerated through cooperation of the Crop Quality Council, Minneapolis, MN, the Mexican Ministry of Agriculture and CIMMYT.

References

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WITHIN-HERD GENETIC EVALUATION OF BEEF CATTLE FOR WEANING WEIGHT

W. D. Slanger, M. L. Buchanan,
C. N. Haugse and P. T. Berg

A new procedure for reducing the computing time of within-herd genetic evaluation of beef cattle for weaning weight was tested using 503 weaning weight records of the North Dakota State University Angus herd. The new procedure was compared with a previously known method. The genetic evaluations obtained by the two methods were very similar. The new method took 37% less computer time. The data indicated that a slight genetic improvement took place in the herd. The study indicated that a viable procedure exists for obtaining sophisticated, within-herd genetic evaluations of beef cattle for weaning weight at considerable savings in computer time.

INTRODUCTION

Managers of beef cattle herds are faced with the problem of deciding which animals in the herd will con-

Dr. Slanger is assistant professor, the late Mr. Buchanan was professor and chairman, Haugse is professor and chairman and Dr. Berg is assistant professor, Department of Animal Science.

tribute most to the genetic improvement of the herd. Genetic improvement results when animals with high genetic values are retained in the herd and animals with low genetic values are culled from the herd. Within-herd genetic evaluation is the prediction of the genetic values of the animals in the herd based on production and pedigree information.

The purpose of this research was to develop a progressive and efficient within-herd genetic evaluation procedure of beef cattle for weaning weight based on weaning weight records and pedigree information. As faster computers become more available, the practical and regular application of sophisticated genetic evaluation techniques approaches reality. Such techniques are now being used in national beef sire evaluation procedures. This study was aimed at applying these techniques to individual beef herds. These procedures are different from the general type of within-herd genetic information now available in that they are more accurate, take into account all known pedigree relationships, and provide an accurate record of the genetic, environmental, and phenotypic changes that take place in the herd with time.

The genetic evaluation procedure of this study was directed at obtaining predictions of the genetic values of two different traits. One trait was the genetic ability of the animal to have a heavy or light weaning weight. This trait is the direct genetic ability for weaning weight. The second trait was the genetic ability of the animal to affect weaning weights via maternal influences. Maternal influences refer to the mothering ability of the dam of the calf. Every animal has a genetic value for both traits. The heritabilities of direct and maternal genetic traits were assumed to be .25 and .37, respectively. The genetic correlation between the two traits was assumed to be $-.28$.

The essence of this research was to test the practicality of a theory (Slanger, 1977, 1979) for obtaining within-herd genetic evaluations of beef cattle at reduced computing costs. The sample data used to test this theory were 503 weaning weight records of the North Dakota State University Angus herd. Years 1958 through 1976 were represented in the data. Two sets of genetic evaluations were obtained. One set was obtained by a previously known method (Henderson, 1976). The second set was obtained by applying the method of Slanger. The latter procedure reduces computing costs because extraneous genetic evaluations are eliminated. The two sets of evaluations were compared to see how similar they were and to determine the savings in computer time. Both procedures took into account all known pedigree relationships among the animals.

RESULTS AND DISCUSSION

The essential result was that the two sets of genetic evaluations were very similar and that the new procedure took 37% less computer time than the previously known method. The two procedures are very similar because both took into account the same weaning weight and pedigree information. They are not exactly alike because of arithmetic rounding error that results when large numbers of evaluations are obtained.

Table 1 shows the types and numbers of animals in the pedigree. The previously known procedure (method 1) obtained a prediction of both the direct and maternal genetic value of each animal in the pedigree. This means 1274 (2×637) genetic evaluations. The procedure which eliminated extraneous genetic evaluations (method 2) obtained 587 direct genetic value predictions and 241 maternal genetic value predictions, for a total of only 828

TABLE 1. Types and Numbers of Animals in Pedigree

25 unidentified dams
25 identified dams with no individual weaning weight records and only one progeny each
55 identified dams with no individual weaning weight records and with two or more progeny each
503 animals with records
<u>29</u> sires with no individual weaning weight records
637
Of the 503 animals with records there were:
215 steers
31 bulls with no progeny
150 heifers with no progeny
100 heifers with progeny
7 bulls with progeny

genetic evaluations. Because there were 446 fewer evaluations ($1274 - 828$), less computer time was needed to obtain method 2 evaluations. One type of extraneous evaluation was that for the direct genetic value of an unidentified dam or of an identified dam which had no individual weaning weight record and had only one progeny. In other words, 50 ($25 + 25$) direct genetic evaluations were eliminated. The second type of extraneous genetic evaluation was that for maternal genetic evaluation of steers, heifers, and bulls that had individual weaning weight records but left the herd before leaving any progeny, presumably as market animals. This means 396 ($215 + 31 + 150$) maternal genetic evaluations were eliminated.

The two sets of genetic evaluations were compared in two ways. One was to calculate the rank correlation between the two and the second was to compare the genetic, environmental, and phenotypic trends. The rank correlations were very high. The rank correlation between the two sets of direct genetic evaluations was .996. This means that the order of the animals' predicted direct genetic values from highest to lowest was almost the same with both methods. A perfect correlation would be 1.0. The rank correlation between the two sets of maternal genetic evaluations was .999.

Figures 1 and 2 show the direct and maternal genetic trends, respectively. The fact that the two lines of each type of trend are almost parallel emphasizes the similarity of the two sets of evaluations. The slight genetic improvement indicated for both traits is consistent with the type of selection that had been practiced in the herd. The environmental and phenotypic trends are shown in table 2. The environmental trend shows the differences among years for weaning weight caused by differences in such things as rainfall, management, weather, etc. The

Figure 1. Trends for Direct Genetic Value

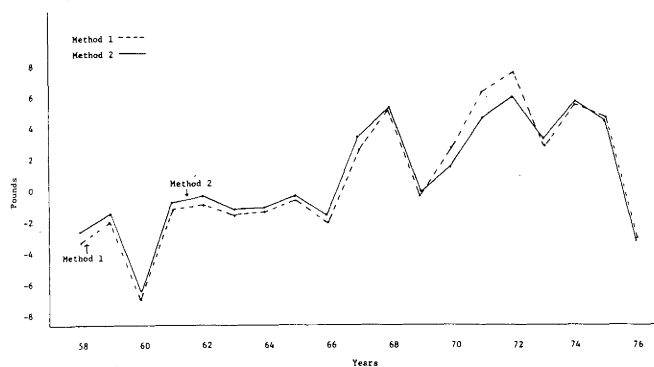


Figure 2. Maternal Genetic Trends

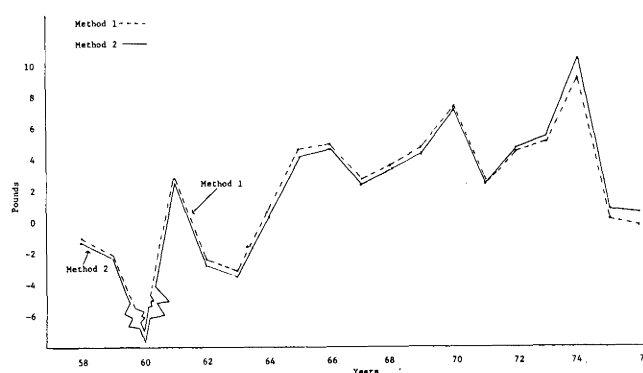


TABLE 2. Environmental and Phenotypic Trends (1958-76) From Method 1 and Method 2

Environmental		No. Rec.	Phenotypic		Ave. of Records
Method 1	Method 2		Method 1	Method 2	
528.31	527.81	13	523.69	523.69	523.76
472.27	472.01	14	468.07	468.07	468.07
512.87	512.68	3	484.00	484.00	484.00
468.13	468.16	12	469.58	469.58	469.58
420.30	419.90	21	416.67	416.67	416.66
454.36	454.16	20	449.15	449.15	449.15
439.12	438.99	21	438.09	438.09	438.09
452.17	452.12	18	455.89	455.89	455.88
441.66	441.58	15	444.33	444.33	444.33
465.08	464.67	23	470.17	470.17	470.17
473.83	473.90	24	482.50	482.50	482.50
459.78	459.66	44	463.75	463.75	463.75
455.33	456.50	32	465.00	465.00	465.00
465.96	467.55	59	474.51	474.51	474.50
445.06	446.54	32	456.97	456.97	456.96
502.22	501.40	44	510.00	510.00	510.00
416.45	415.21	17	431.18	431.18	431.17
440.88	440.38	43	445.58	445.58	445.58
497.62	497.24	48	493.98	493.98	493.97

TABLE 3. Predictions of Direct and Maternal Genetic Values of Sires Used in the Herd With 10 or More Progeny

Sire	Direct ¹	Maternal ¹	Years in Which Sire had Progeny	Number of Progeny
1	21, 21	-2, -2	68, 69	17
2	-5, -4	3, 1	58	11
3	-4, -3	-10, -11	59, 60	10
4	13, 11	12, 14	71	11
5	6, 0	39, 44	70, 71, 72	59
6	-50, -48	23, 23	72, 73	19
7	7, 8	-18, -16	67, 69, 70	47
8	-12, -11	4, 4	75	17
9	40, 40	-50, -46	71, 72, 73	48
10	-75, -74	35, 25	75, 76	29
11	7, 9	-20, -19	74	13
12	-1, 0	0, -1	64, 65, 66, 67, 68	29
13	-11, -11	14, 14	69, 70	20
14	-6, -6	4, 3	59, 61, 63, 64, 66	28
15	4, 5	-6, -7	61, 62, 63, 64, 65	45
16	65, 62	-23, -20	76	22
17	36, 35	-14, -12	75	18

¹The method 1 prediction is listed first, the method 2 prediction is listed second.

phenotypic trend is the sum of the genetic and environmental trends. The phenotypic trend is almost identical to the yearly averages of the records. The environmental and phenotypic trends of the two methods are almost identical.

Table 3 shows the genetic evaluations of sires used in the herd with 10 or more progeny. The years in which each had progeny is indicated. The prediction by method 2 of the direct genetic value of sire 5 was 0 pounds. This means that his genetic ability, within the herd, for weaning weight was 0 pounds. It also means that, if he is mated randomly to the cows in the herd, the resulting weaning weights of his progeny are predicted to average 3 pounds above the average weaning weight of the progeny of a sire with a predicted genetic value of -6 pounds. The prediction by method 2 of the sire's maternal genetic value was 44 pounds. This means that the average mothering ability of the sire's daughters is predicted to be 22 pounds above the average mothering

ability of the daughters of a sire with a maternal genetic evaluation of 0. Animals with high predicted genetic values should be selected to remain in the herd.

CONCLUSION

A viable procedure exists for obtaining sophisticated, within-herd genetic evaluations of beef cattle for weaning weight at considerable savings in computer time.

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LARVICIDAL AND OVIPOSITIONAL DETERRENT ACTION OF UNSLAKED LIME AGAINST THE HOUSE FLY

Odell A. Johnson and I. A. Schipper

The presence of lime in the potential house fly larval rearing medium has a twofold action against the fly. The lime discourages the female house fly from laying eggs. It also has a significant effect on reducing the number of house flies that complete development in medium with lime on or mixed into it. The addition of water such as might occur in rainfall did not significantly reduce the effectiveness of lime as a larvicide. Advantages of utilizing a nontoxic house fly oviposition inhibitor are discussed.

INTRODUCTION

Fly control in and around feedlots and dairy barns has become a serious problem because many effective but potentially hazardous chemicals have been removed from use. Several methods of population control have been proposed which include alternatives to the use of such materials. It has been demonstrated in preliminary experiments that lime spread in feedlots is an effective deterrent to foot rot. A literature search indicated that various researchers have used lime as a repellent against insects. It has been used as a repellent to the Narcissus fly (2) and on apple and pear trees to kill bark beetles (4). It has also been effective against thrips and aphids (4). Lime also acts as an ovipositional repellent against the moth *Euzaphuss* (3) and against *Rhagoletis pomonella* (Walsh), the apple maggot (1).

Johnson is entomologist, Metabolism and Radiation Research Laboratory (USDA), and Dr. Schipper is professor, Department of Veterinary Science.

EXPERIMENTAL PROCEDURE

The project was undertaken to determine possible ovipositional deterrent and larvicidal effects of lime against house flies. The house flies used in these tests had been reared for 35 generations in the laboratory on a standard CSMA larval medium. CSMA is a commercial preparation of alfalfa meal, wheat bran, and malting grains used to rear house fly larvae. The adults were fed reconstituted dry milk (fresh daily) and sugar cubes. Aged 1-day-old medium was placed in cages to induce egg deposition.

Initial tests were conducted to determine the larvicidal activity of lime by inoculating 50 eggs into 14.5 gm of CSMA. Six cartons of CSMA were utilized for each test: a control, one with lime on top of the media, and one with lime stirred into the upper 1.5 cm of CSMA. The three other cartons were treated the same but 5 cc of water was added on the third day after inoculation.

A separate investigation was conducted to determine the effect of the presence of lime on house fly oviposi-