FUTURE BREEDING SYSTEMS FOR BEEF CATTLE

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SUMMARY

A deterministic simulation model was developed to predict % heterozygosity, breeding values and expected phenotypes in conjunction with an innovative beef cattle breeding program utilizing composite sires. CASH (23% Hereford, 23% Angus, 34% Brown Swiss, 20% Charolais), RX3 (25% Hereford, 25% Red Holstein, 50% Red Angus), and MARC III (25% each of Hereford, Angus, Red Poll and Pinzgauer) were mated to Hereford cows with MARC III bulls being used on heifers only and mature cows being mated to the least related of CASH and RX3. The model records each mating and characterizes progeny by the percent blood from each of their contributing foundation breeds. Individual and maternal heterozygosity values, relative to F1 values, were summarized by year for fifteen years. Breeding values for individual animals were estimated from breed means of foundation animals weighted by percent of each breed. Estimated heterosis values were combined with breeding values to obtain expected phenotypic values of progeny.

INTRODUCTION

Research in applied beef cattle breeding is increasing its use of systems analysis in an attempt to combine and match genetic and environmental resources. The continued improvement in computer efficiency and increased memory allows development of large scale simulation models to monitor interactions of genotype and environment. Optimum combinations of growth, milk production, fertility and mature size can be explored under a variety of environmental and economic conditions through simulation.

Properly managed genetic (breed) resources can provide for increased production efficiency through complementarity and heterosis. The development and use of composite breeds of cattle is consistent with a systems approach to genetic resource management. Composite animals represent an attempt to combine the superior performance of two or more breeds in a complementary fashion to produce an overall superior biological type. In addition to combining additive breed effects, preliminary results show retention of heterosis in composite populations to be linearly related to retained heterozygosity for growth traits (Gregory, 1986). The level of relative F1 heterozygosity retained in composite populations is proportional to $1 - \Sigma Pi^2$, where Pi is the fraction of each of n breeds used in formation of the composite (Wright, 1922; Gregory, 1980).

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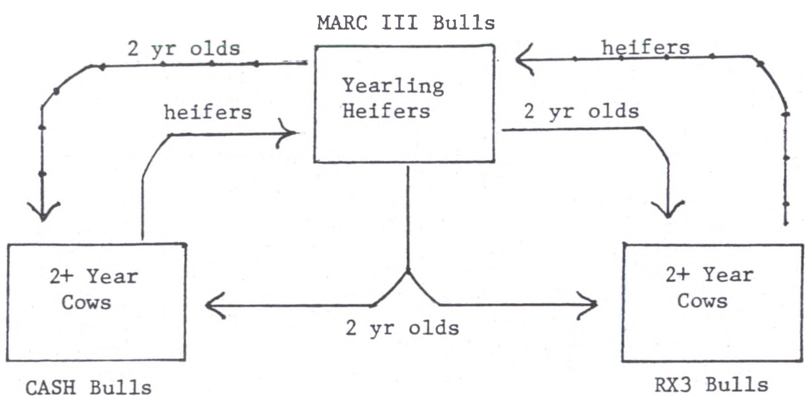
The objective of this study was to develop a deterministic computer model to calculate percent blood of parental breeds which is used in calculating percent heterozygosity and estimating breeding values. In addition, heterosis was estimated relative to F1 values and used to obtain expected phenotypic values for individual animals for any crossing scheme. Results of the model are described for a crossing system using three phenotypically similar but genetically diverse composites.

PROJECT DESCRIPTION

Breeding research recently initiated at the San Juan Basin Research Center, Hesperus, CO involves the use of composite sires on straightbred Hereford cows in an innovative crossbreeding program. The composite breeds selected are MARC III (25% Hereford, 25% Angus, 25% Pinzgauer, 25% Red Poll), RX3 (25% Hereford, 25% Red Holstein, 50% Red Angus) and CASH (23% Hereford, 23% Angus, 34% Brown Swiss, 20% Charolais) all of which are solid red and polled. The MARC III has been designated for use on heifers only and 2-yr-old and older cows will be bred to the least related of CASH or RX3. Initially, straightbred Hereford cows are randomly assigned to either CASH or RX3. Heifers are selected from all three sire groups. Simulation models are being developed in conjunction with this program in a systems approach to beef cattle breeding.

Figure 1. System I Mating Scheme.



MODEL DESCRIPTION

A deterministic model has been developed on the Cyber 205 computer to simulate fifteen years of mating as outlined above. The model records each mating and characterizes potential progeny by their percentage of blood from each of the contributing breeds. Individual heterozygosity is computed using the percent of each parental breed.

All individuals have a probability of existence in the breeding herd, and summary and herd statistics were weighted by these values. Herd size was kept constant in the model and heifers were retained for breeding at a predetermined rate. Culling based on genotype was practiced initially with increased pressure placed on straightbred cows.

The breed percentage, as computed in the first phase of the model, was used to estimate breeding values and combined with heterozygosity values to estimate expected phenotypes of animals produced. Parental breed means for birth weight, weaning weight direct, weaning weight maternal, yearling weight and mature weight were used as breeding values for breeds represented in the composites used. These means were expressed as deviations from the foundation Hereford cow herd and are presented in table 1. Weaning weight maternal was expressed as an expected change in pounds of calf at weaning due to milk production of the dam.

TABLE 1. PARENTAL BREED MEANS AS DEVIATIONS FROM HEREFORD BASE (kg)

	Trait[a]				
Breed	BW	WWD	WWM	YW	MW
Hereford	0.	0.	0.	0.	0.
Angus	-2.3	0.	11.3	4.5	0.
Red Poll	-3.2	-2.3	4.5	-9.1	-45.4
Pinzgauer	0.	2.3	4.5	12.2	22.7
Red Angus	-2.3	0.	11.3	4.5	0.
Red Holstein	3.6	3.6	13.6	26.0	90.7
Charolais	3.6	11.3	4.5	30.8	90.7
Brown Swiss	3.6	3.6	13.6	26.0	90.7
	Base Phenotypic Means				
	BW		WW	YW	MW
Hereford	36.3		193	306	476

[a]BW = birth weight, WWD = weaning weight direct, WWM = weaning weight maternal, WW = weaning weight, YW = yearling weight, MW = mature weight.

Individual breeding values were estimated by weighting the breed means of those breeds represented in an individual by the percent of each breed and summing over all breeds for each trait. In this manner, a set of "composite" breeding values were computed and reported as deviations from Hereford for all potential progeny.

Expected phenotypes for birth weight, weaning weight, yearling weight and mature weight were then estimated by combining breeding values with non-additive effects. Percent heterosis expressed by an individual for a particular trait was estimated by multiplying maternal and individual F1 heterosis estimates for that trait by the relative F1 heterozygosity level of the dam and calf, respectively. Individual and maternal F1 heterosis estimates used are presented in table 2. Expected phenotypes were computed by adding a calf's expected breeding value for a trait to the overall mean for that trait and multiplying by the heterosis values estimated for the calf and its dam.

$$EP_{ij} = (M_j + BV_{ij})(1 + HI_{ij})(1 + HM_{ij})$$

EP_{ij} = expected phenotype of the ith calf for the jth trait
M_j = mean Hereford additive genetic value for the jth trait
BV_{ij} = breeding value of ith calf for jth trait
HI_{ij} = individual heterosis (F1 heterosis * % F1 heterozygosity)
HM_{ij} = maternal heterosis (maternal heterosis * % F1 heterozygosity of dam)

TABLE 2. PERCENT INDIVIDUAL AND MATERNAL HETEROSIS

	Trait[a]				
	BW	WWD	WWM	YW	MW
individual	.04	.05		.04	.025
maternal	.017		.06		

[a]See Table 1 for abbreviations

MODEL RESULTS

Results from the heterozygosity model are presented in table 3. These values represent a replacement strategy in which 90% of heifers are retained until all straightbred cows have been replaced, after which 40% of the heifers are retained. Heterozygosity levels of the calf crop increased steadily from .76 in year 1 to .86 in year 15. Maternal heterozygosity values also reached .86 by year fifteen which appears to be an equilibrium level for the system. The approach to equilibrium using composite breeds avoids the fluctuations inherent to rotational crossbreeding programs.

Average breeding values and expected phenotypes of calves are presented by year in table 4. Breeding values increased steadily over time for all traits except birth weight. The slight decline in breeding values for birth weight the first three years was offset by heterosis to yield a .9 - 1.3 kg increase in expected phenotype from the 36.3 kg base. Breeding values and expected phenotypes for birth weight remained stable after year six while these values for all other traits continued to increase.

The expected phenotype for weaning weight combines the breeding values for weaning weight direct and weaning weight maternal with individual and maternal heterosis. Over the fifteen year period, an increase in expected phenotype of 27 kg was realized for weaning weight. Expected phenotypes for yearling weight and mature weight increased by 21 and 37 kg respectively from the Hereford base to year 15.

MODEL APPLICATION

Although the model is currently being used for a specific composite crossing project, it has universal application to any crossbreeding program. Various crossing schemes can be compared beginning with any base cow herd. The formation of new composites can also be evaluated.

The breeding values for parental breeds as described herein can be replaced by estimated breeding values for individual animals as computed from separate analyses. We plan to obtain and incorporate estimated breeding values for all foundation Hereford females based on previous production. In a continuous effort to update and validate the model, estimated breeding values will also be obtained for sires and crossbred dams based on progeny data as it becomes available.

This model can be used by cattlemen to formulate and update breeding plans, which, when combined with results from other models can aid in maximizing economic return.

TABLE 3. PERCENT OF PARENTAL BREED AND PERCENT INDIVIDUAL AND MATERNAL HETEROZYGOSITY BY YEAR

	% of Breed								% Heterozygosity		
Year	HE	AN	RP	PZ	RA	RH	CH	SW	high	low	avg
1											
individual	.62	.08	.04	.04	.09	.05	.03	.05	.77	.75	.76
maternal	1.0	0.	0.	0.	0.	0.	0.	0.			0.
3											
individual	.55	.10	.06	.06	.09	.05	.04	.06	.84	.75	.78
maternal	.85	.03	.02	.02	.04	.02	.01	.02			.29
6											
individual	.41	.12	.05	.05	.15	.07	.06	.10	.89	.75	.85
maternal	.57	.09	.05	.05	.09	.05	.04	.06			.77
9											
individual	.37	.12	.05	.05	.16	.08	.06	.11	.92	.75	.85
maternal	.50	.10	.05	.05	.12	.06	.05	.08			.80
12											
individual	.33	.13	.05	.05	.17	.09	.07	.12	.93	.75	.86
maternal	.41	.12	.05	.05	.14	.07	.06	.10			.84
15											
individual	.30	.13	.05	.05	.19	.09	.07	.12	.94	.75	.86
maternal	.36	.12	.05	.05	.17	.08	.07	.11			.86

TABLE 4. AVERAGE BREEDING VALUES AND EXPECTED PHENOTYPES OF PROGENY BY YEAR (kg)

Year	Breeding Values (Deviations)[a]					Expected Phenotypes			
	BW	WWD	WWM	YW	MW	BW	WW	YW	MW
1	-.05	.73	3.8	4.5	11.2	37.2	201	320	497
3	-.09	.82	4.4	5.0	11.9	37.6	206	321	498
6	.14	1.3	6.1	7.8	20.4	38.1	216	325	507
9	.14	1.4	6.5	8.4	21.9	38.1	218	325	509
12	.14	1.5	7.0	9.1	23.8	38.1	219	326	510
15	.14	1.6	7.3	9.6	25.5	38.1	220	327	513

[a]See Table 1 for abbreviations

REFERENCES

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