Influence of Controlled Energy Intake on Body Composition of Beef Steers

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Introduction

Decreasing the amount of fat in beef decreases loss due to trim and the number of calories in a serving. Differences in fat content of cattle are caused by differences in genotype, gender, chemical agents and energy intake relative to functional requirements. An increase in energy intake increases both fat content and body weight. Based on this fact, differences in energy intake cause an association between fat content and body weight. This fact has led some scientists to suggest the hypothesis that fat content of animals of similar genotype and gender can be predicted from body weight even if there are differences in energy intake. In order for this hypothesis to be true, rate of gain for fat must be proportional to rate of gain for body weight. Previous research has demonstrated that this is not the case. Increasing energy intake decreases the days required to reach a constant slaughter weight and increases the fat content of cattle slaughtered at a constant weight. Hence, increased fat content is associated with fewer days required to reach the same final weight when genetically similar cattle consume different amounts of energy.

The contents of the gastrointestinal tract (gut fill) influences body weight. Gut fill varies among measurements of different animals or among repeated measurements of the same animal. For this reason, carcass weight is a better indicator of an animal's "true weight" than body weight.

The objectives of this study were to estimate differences in fat content caused by variation in energy intake and to determine the extent to which these differences are associated with carcass weight or days to slaughter.

Procedure

A total of 161 steers were used in the study. Steers were one of two biological types, 1) a small biological type which consisted of two-way crosses of Red Poll or Angus sires and Angus or Hereford dams or 2) a large biological type which consisted of crosses of Brown Swiss sires with two-way crosses of Angus, Hereford, Simmental, Limousin, and Charolais dams. Average initial weights of the small and large biological type steers were 588 and 696 lb, respectively.

Steers were fed a diet composed of 74% corn grain or a diet composed of 74% corn silage. Steers given the corn silage diet were fed ad libitum or fed to maintain body weight. Steers given the corn grain diet were fed ad libitum, fed a restricted amount of food so they grew at the same rate as steers given ad libitum corn silage, or fed to maintain body weight. Planned growth patterns of the steers for body weight are presented in Figure 1. Steers were slaughtered when they achieved one of four slaughter weight groups (Figure 1). Chemical composition for protein, water, fat and ash was determined for boned-out soft tissue near the 9th, 10th, and 11th ribs.

Results

Average body weights at slaughter were similar to those planned (Table 1). Differences in average hot carcass weight were associated with differences in average body weight at slaughter (Table 1).

Average chemical composition of the boned-out soft tissue near the 9th, 10th, and 11th ribs is presented in Tables 2 and 3. One of the main purposes of the study was to determine if all of the differences in fat content caused by changing energy intake were associated with differences in hot carcass weight or if some of these differences could be associated with time needed to reach the same hot carcass weight. Over half (55%) of the variation in fat content among steers of the same biological type was associated with hot carcass weight. An additional 10% of the variation in fat content was associated with days needed to reach the same hot carcass weight. Diet accounted for a further 10% of the variation in fat. Percentages of variation for protein, water, and ash attributed to weight, days, and diet were similar to those for fat.

How large were differences in chemical composition associated with hot carcass weight and days to reach the same hot carcass weight? For every 100 lb increase in hot carcass weight, there was an associated increase of 5.1% fat and a decrease of 1.0% protein, 4.1% water, and .06% ash of the soft tissues near the 9th through 11th ribs. For each additional 100 days that it took steers consuming ad lib silage or restricted grain to reach the same hot carcass weight as steers fed ad lib grain, their fat decreased 2.5%, protein increased .4%, water increased 1.9%, and ash increased .02%. These relationships should not be used to compare 14 month-old steers weighing 800 lb to 5 year-old steers of the same weight and genotype. However, these relationships should be valid over the normal range of growing and finishing periods because this time span is unlikely to exceed 600 days.

There were some nutritional treatments where the data did not fit the general patterns described above. Steers fed restricted grain in the third slaughter group contained less fat and more protein, water, and ash than the values predicted from hot carcass weight and days required to reach the same hot carcass weight. Conversely, steers fed ad lib grain in the fourth slaughter group contained more fat and less protein, water, and ash than the values predicted from hot carcass weight and days required to reach that weight.

We conclude from these results that that fat content decreases as dietary energy intake is reduced and the days required to reach a given hot carcass weight increase. However, nutritional manipulation can sometimes cause differences in chemical composition among similar steers that are not predictable from hot carcass weight or days on feed. For producers that receive a premium price for low-calorie beef, both energy consumption and slaughter weight can be manipulated to control the fatness of cattle. One of the criticisms of feeding cattle less energy to produce a leaner product is that it takes longer to reach slaughter weight and, hence, requires more feed. Recent research indicates that this may not always be the case. Economical production of lean beef seems possible.

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Table 1—Average hot carcass weight and slaughter body weight

			Hot carcass weight				Slaughter body weight			
			Small		Large		Small		Large	
Level	Diet	Slaughter group	grow	maintain	grow	maintain	grow	maintain	grow	maintain
	grain	1		341		394		588		678
	forage	1		370		432		626		733
Ad lib	grain	2	485	504	579	579	822	846	967	927
Restricted	grain	2	425	489	502	518	700	811	844	883
Ad lib	forage	2	416	498	509	544	729	822	874	989
Ad lib	grain	3	579	500	696	590	956	835	1141	980
Restricted	grain	3	570	544	619	584	903	965	1040	1062
Ad lib	forage	3	553	507	615	509	954	943	1054	1009
Ad lib	grain	4	742		835		1216		1385	
Restricted	grain	4	769		879		1253		1370	
Ad lib	forage	4	747		837		1264		1465	

Table 2—Mean chemical composition(%) of soft tissue near 9th through 11th ribs of small biological type steers

	Fat		Protein		Water		Ash	
Diet	grow	maintain	grow	maintain	grow	maintain	grow	maintain
Slaughter weight group 1								
Grain		20.7		17.0		61.7		.87
Forage		24.5		16.2		58.7		.80
Slaughter weight group 2								
Ad lib grain	36.5	34.4	14.0	14.8	49.3	50.7	.70	.73
Restricted grain	31.9	31.8	15.3	14.7	52.7	53.5	.79	.75
Ad lib forage	29.0	29.1	15.7	15.1	55.5	55.3	.80	.78
Slaughter weight group 3								
Ad lib grain	34.4	26.0	14.7	16.1	50.6	57.2	.75	.83
Restricted grain	29.0	27.1	15.8	15.7	55.1	56.0	.79	.79
Ad lib forage	37.8	21.3	14.2	16.7	48.1	61.0	.72	.83
Slaughter weight group 4								
Ad lib grain	50.0		11.5		38.6		.57	
Restricted grain	46.7		11.4		41.2		.58	
Ad lib forage	45.7		12.1		41.4		.58	

Table 3—Mean chemical composiition (%) of soft tissue near 9th through 11th ribs of large biological type steers

	Fat		Protein		Water		Ash	
Diet	grow	maintain	grow	maintain	grow	maintain	grow	maintain
Slaughter weight group 1								
Grain		12.5		18.9		68.2	1.00	
Forage		18.6		17.6		62.7		1.85
Slaughter weight group 2								
Ad lib grain	29.5	24.8	15.9	16.7	54.4	58.4	.74	.84
Restricted grain	20.1	21.6	17.2	17.4	62.0	61.1	.85	.95
Ad lib forage	24.0	23.6	16.8	17.2	58.8	59.2	.82	.89
Slaughter weight group 3								
Ad lib grain	31.6	20.3	15.4	17.8	52.6	61.6	.78	.82
Restricted grain	22.7	16.3	17.6	17.9	59.4	65.0	.88	.83
Ad lib forage	27.2	12.1	16.5	19.1	55.9	68.1	.80	.96
Slaughter weight group 4								
Ad lib grain	42.1		13.3		44.7		.59	
Restricted grain	32.0		4.6		52.5		.70	
Ad lib forage	36.7		4.0		48.4		.69	

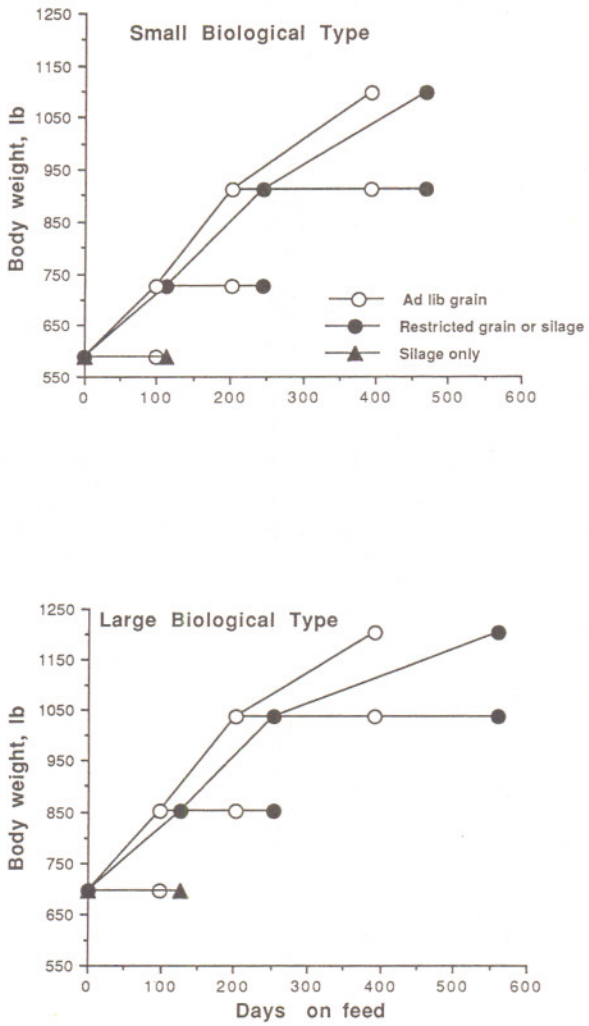

Figure 1—Planned growth patterns.

Management Factors Influencing the Feeding of Young Bulls for Market-Ready Beef

Michael D. MacNeil, Keith E. Gregory, and J. Joe Ford[1]

Introduction

Feed is a major part of the total cost in raising cattle from weaning to market-ready weights. Young bulls convert energy and protein from feeds to lean beef more efficiently than steers. Most consumers would prefer beef with less fat outside the muscle of retail cuts. Carcasses from bulls killed at about 17 months of age and weighing 1,300 to 1,450 pounds have less backfat; less kidney, pelvic, and heart fat; and yield more weight of closely trimmed retail product than carcasses of similarly managed steers. However, at this age carcasses of bulls also have less fat within the muscle and may be less tender. Production of beef from young bulls is a common practice in Europe. However, it remains a largely unused system in the United States. Aggressive and homosexual behaviors of bulls may explain part of the reluctance by U.S. feedlot operators toward feeding bull calves. In these studies we investigated factors under managerial control that might reduce undesirable behavior of young bulls and improve their performance.

Procedure

We conducted three experiments feeding 12 to 14 mo old bulls to marketweight. The feeding period lasted either 56 or 112 days. Factors evaluated were: group size (30-34 vs 60-68 head/pen), mixing bulls from different pens, and tranquilizing bulls before mixing them. Rations contained 1.2 to 1.3 Mcal of metabolizable energy per lb and 12 to 13% crude protein. Each pen of bulls was transported to a packing plant as a group and killed immediately after arrival. Carcass data were recorded 24 hr after slaughter.

Results

Bulls penned in smaller groups grew about 17% faster (2.7 vs 2.3 lb/day) than bulls penned in larger groups. However, feed consumed per day did not differ by group size. Bulls penned in smaller groups also had 17% more backfat (.38 vs .33 in) than their counterparts penned in larger groups. Based on these results, the optimal number of bulls per pen is less than 60. However, finding that optimum requires further research.

Tranquilizing bulls before mixing them reduced butting and riding immediately after that. However, as the tranquilizer wore off butting and riding increased. Over a 3 day period after mixing the bulls, no differences existed between tranquilized and nontranquilized groups in numbers of head butts or mounts. Tranquilized and nontranquilized bulls were similar in all performance and carcass characteristics measured.

Bulls reared from weaning with the same pen-mates can establish a "pecking order" at younger ages and less violently than bulls mixed at 1 yr of age. In comparison with bulls mixed at 1 yr of age, keeping pens intact from weaning had no effect on their growth, feed intake, or carcass attributes. We speculate that the few days needed to establish a "pecking order" in relation to the length of the feeding period offset this treatment effect.

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Evaluation of Four Computer Models for Prediction of Growth and Body Composition

Gary L. Bennett and Ralph N. Arnold[1,2]

Introduction

Leaner, high quality beef can be produced by making good management and genetic decisions. The problem is knowing what is a good decision. Computer models can be used to predict the outcomes of different ways of producing beef. Managers can choose their best system using these predictions combined with their financial and feed resource information.

Several computer models predict growth and body composition as part of an overall evaluation of beef production. Other models predict only growth and body composition. These models predict one or more of the following biological processes: the amount of feed consumed, the partition of consumed feed into nutrients for maintenance and growth, and the partition of nutrients used for growth into fat, lean, and bone.

This research compared growth and body composition prediction from four computer models. Standard situations and experimental results were used for the comparison. The goal was to decide whether any of the models were accurate enough to aid cattle producers who want to increase the leanness of beef. Another goal was to find ways to improve predictions.

Procedure

Three computer models of growth and body composition were extracted from models of overall beef production systems. The developers of these models emphasized feed intake and growth more than body composition. The fourth model evaluated was developed to predict growth and composition when feed intake was known. The four models were then used to make comparisons.

The standard situations compared were lean growth unrestricted by feed intake, forage diet, grain diet, compensatory growth, and medium and large size steers. Feed intake of forage and grain diets was determined several ways, i.e., using model predictions, using the same intake for all models, and as a percentage of body weight.

Three experiments were identified that had both feed intake and body composition available for comparison with model predictions. The experimental treatments included level of feed intake, type of feed, breed, age, and sex. Both actual feed intake and predicted feed intake were used for some comparisons.

Results

The computer models required either direct input of mature wt or other indirect input values that resulted in a mature weight. Direct or indirect input values for mature wt were adjusted so that protein growth rates were the same for the first 900 days following birth assuming growth was not restricted by feed intake. Fat growth rates were similar for all models until about 500 days and then diverged as animals approached maturity.

The four models responded differently to different levels of assumed feed intake. Models also differed when all-grain diets were compared with all-forage diets. Simulated body composition varied with level of feed in three models but only after severe restriction in another model. Two models simulated slight compensatory growth. The predicted effect of 200 days of restricted growth followed by ad lib intake ranged from 0 to 5% body fat at slaughter weight.

Differences among model predictions stemmed from assumptions about feed intake, maintenance requirements, protein:water ratios, and the partition of growth among different tissues. These were the result of differences in the interpretation of the growth process. Equalizing feed intake reduced differences in growth and composition when grain was fed but not when poor quality roughage was fed.

It was apparent from the simulation of standard situations that the evaluation of a beef production system will depend on the computer model chosen, especially if carcass composition is important. Comparisons with experimental results were done to find which situations were accurately predicted by the computer models.

Many predicted and experimental wt differed by more than would be expected by chance. Differences expressed as percentages of their experimental values were generally less for body wt than for fat, water, and protein weight. The accuracy of predicting fat was usually less than protein and water.

Predicted and experimental feed intakes for ad lib treatments were also different in many cases. There was a tendency to over- or underpredict intake for all treatments in an experiment, but this was not always the case.

A consistent pattern of differences, such as finding differences only in one type of cattle or for one kind of feed, was not apparent. This limited conclusions about how to improve the models. Weight gain was more accurately predicted than the composition of the gain. This suggests that more research is needed to determine the partition of gain to fat, lean, and bone. One conclusion reached was that when fat was considered to result from the storage of excess energy, then all errors in predicting feed intake and its utilization for maintenance and growth end up as differences in fat.

These comparisons suggested that other approaches to predicting the effects of nutrition on body composition need to be tried. To be useful in designing and evaluating systems of producing leaner beef, these approaches need to have fewer places where errors can occur or distribute errors more evenly among lean, fat, and bone.

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[1]Bennett is the research leader and Arnold was a research affiliate, Production Systems Research Unit, MARC.

[2]The full report of this work was published in Agricultural Systems 35:401-432 and 36:17-41, 1991.

Conversion Efficiency Through Weaning of Nine Breeds of Cattle

Thomas G. Jenkins and Calvin L. Ferrell[1]

Introduction

Beef cattle production entails the conversion of plant resources not normally considered as part of the food chain for humans into a food resource that partially fulfills human dietary needs. Traditionally, the beef industry has been segregated into production components, each having its own marketing endpoint. The cow/calf component of the industry produces progeny for introduction into the food chain conversion process. Energy and protein requirements of the commercial cow herd should be fulfilled as much as possible through direct harvest of forages by the animals. Within the U.S., a wide range of forage production environments exist.

Commercial producers have the flexibility to identify breeds or breed crosses to be used as producing females and to identify sire breed or breed crosses to mate with these cows. Previous research at MARC has demonstrated variation among and within breeds for traits affecting weight of calf produced at weaning. Cows representative of breeds with greater genetic potential for growth and lactation yield have been shown to produce calves that are heavier at weaning. Additional research at MARC has documented a positive relationship between genetic potential for production and energy requirement to maintain body weight of the cow. Differences in energy required to sustain the producing female suggest that breeds or breed crosses can be identified that are more effective in the conversion of forage resources into amarketable product. Earlier work conducted at MARC indicated that breed crosses more moderate in growth potential and lactation yield, were more effective in preweaning weight production of calves. The objective of the study was to determine if differences exist among breeds of beef cattle in the efficiency of converting food energy to weight of calf at weaning.

Procedures

In 1986, 16 pregnant multiparous cows from Angus, Braunvieh, Charolais, Gelbvieh, Hereford, Limousin, Red Poll, Pinzgauer, and Simmental cows that were 5 yr or older were assigned to the study. Four cows within each breed were assigned to one of four energy availability levels: 130, 170, 210 or 250 Kcal of metabolizable energy (ME) per metabolic body size (wt.^{75}) during nonlactating periods or during lactation fed at the rate of 170, 210, 240, or 290 Kcal ME/wt.^{75}. Individual animals remained at the assigned levels throughout the test period. Daily feed allotments of individual cows (Table 1) were based on the weight of the cow (measured approximately at the seventh month of gestation) at the time of the cow's assignment to the study. Cows were individually fed and received their daily allotment in a single feeding. Feed refused by the cows over a seven day period was measured and recorded. Feed consumed by the cow was determined as the difference between the feed provided for a seven day period minus the feed refusal. In mid-March each year all pregnant cows were transported to drylots for calving. Male calves were castrated at birth. Birth weights were recorded for all calves. Cow/calf pairs were returned to the test facility approximately 10-14 days after calving. Upon return to the test facility, lactating cows' feed allotments were increased.

Cows were exposed to sires identified within their respective breeds for a 90 day period beginning in mid-June of each year. During the breeding season, cows and calves were separated at approximately 4:00 p.m. daily, the cows were penned by breed, and cows remained in these pens until approximately 7:00 a.m. The 1987 calf crop was weaned in a single group at approximately 200 days. Within the two remaining production years, calves were weaned in two groups with average weaning age and range in age similar to 1987. Following weaning of the calves, daily feed allotments of individual cows were reduced to nonlactation levels.

Weekly feed consumptions for individual cows were summed for the three year test period. Individual calf records were used to adjust the weaning weights of calves to 200 days weaning age. Records of individual cows were summed. Biological efficiency is defined as the ratio of weight of calf weaned relative to the feed consumed by cows weaning calves. The efficiency ratio is an index of the effectiveness of converting feed resource to a marketable product. As used in the present evaluation, it is a measure of that amount of feed energy that was consumed that is available for use by the cow to produce a product. For cows weaning calves, total feed consumption, sum of calf weights weaned, and the ratio of biological efficiency were analyzed to evaluate the effects of breed, level of energy availability, and the breed by level of energy availability upon these traits.

Results

For the traits of interest, the interaction of breed by energy availability was not found to be a significant source of variation. This indicates that the rank among the breeds for these traits would be expected to be the same across all four energy availability levels. Both breed and level of energy availability affected total feed consumption, average weaning weight, total weaning weight for the three year period, and biological efficiency ratio.

Estimates for the traits of interest by level of energy availability are reported in Table 2. Productivity and total weight weaned for the 3 yr period increased as level of energy available to the cow increased. Over the test period, cows receiving the highest feed level produced 30% more weight at weaning than did cows fed at the lowest intake level but only 8% more than at the other two levels. Input, feed consumed during the 3 yr period, was 78% greater for cows receiving the highest feed level, and 65% and 39% for the intermediate groups relative to the feed consumed by the cows assigned to the low feed level. Although cows receiving the lowest quantity of feed produced the lowest product yield for the test period, this group of cattle were 27% more effective in converting feed energy consumed to calf weight than the two highest feed available levels and were 7% more efficient than the 170 kcal/wt.^{75} group.

Breeds of cattle previously characterized as having higher genetic potential for growth tended to be of higher rank for this output component. Comparison of weaning weight yield for the 3 yr period among the breeds indicates some reranking among the breeds for output (Table 3).

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Braunvieh and Charolais had the greatest yield and Hereford the lowest. Input information for the purpose of this report represents feed consumed by cows weaning calves. Charolais, as a breed group, consumed the least amount of feed and Braunvieh and Angus consumed the most. Among straightbred cows producing calves of the same breed, two separate groups could be identified: Red Poll, Braunvieh, Limousin, Pinzgauer, Charolais, and Gelbvieh were the most effective in converting feed energy resources to a marketable product (Table 3). Hereford, Angus and Simmental breeds were less effective in converting the energy resource to weaning weights. Among all breeds, approximately 16% difference was observed between the most and least efficient breeds.

These results indicate that differences in the effectiveness of the conversion of food energy resources to marketable product may be affected by level of food energy availability and choice of breeds. From a feed energy standpoint, the producer needs to be aware of the productivity potential of the forage resources available and the desired level of productivity sought for the cow herd. Harvested energy resources tend in general to have higher cost associated with them. Efforts of the cow/calf producer to improve or maximize total weight weaned through use of supplemental feeding programs or through intentional understocking may result in less than optimum production.

When compared on the basis of pounds of calf weaned per unit of food energy consumed by the producing cow, differences exist among the nine beef breeds evaluated in this study. These breeds have been previously characterized with regard to growth potential and ability for milk production. Using productivity information in conjunction with measures of average production efficiencies for breeds should enable a producer to identify a mating system and the breeds of cattle compatible with the mating system for a defined production environment.

Table 1— Composition of diets (percent of dry matter)

Ground alfalfa	77.5	
Corn	17.5	
Corn silage	5.0	
Metabolizable energy	1.03	Mcal/lb
Crude protein	16%	

Table 2—Effect of level of energy availability upon measures of output and input over three years

	Energy availability (Kcal/wt.$^{.75}$)			
	130	170	210	250
Total feed consumed,(Mcal)	14,391	19,701	23,776	25,739
Three year total weaning wt, lb	873	1,126	1,193	1,237
Efficiency, (lb/Mcal)	.061	.057	.048	.048

Table 3—Effect of breed upon measures of output and input over three years

	Total feed consumed (Mcal)	Three year total weaning wt (lb)	Efficiency (lb/Mcal)
Angus	22,435	1,078	.049
Braunvieh	22,624	1,243	.057
Charolais	17,117	1,243	.055
Gelbvieh	22,036	1,170	.055
Hereford	20,890	985	.048
Limousin	21,786	1,199	.056
Red Poll	20,119	1,130	.058
Pinzgauer	20,186	1,102	.056
Simmental	20,975	1,047	.050

Characterization of Lactation Curves for Nine Breeds of Cattle Fed Differing Rations

Thomas G. Jenkins and Calvin L. Ferrell[1]

Introduction

Genetic merit for milk production influences the weight of calf marketed by producers. Higher preweaning weight gains are made by calves from cows that produce high levels of milk. Lactational productivity can influence future levels of herd calf output if the expression of higher genetic potentials for milk production exceeds the nutrient availability for the production environment. For example, if the lactating female energy requirements exceed the available energy resources, then the ability to reinstall the estrous cycle may be delayed. For producers, this delay may result in younger, lighter calves in the following production cycle. Producers using restricted breeding seasons may find that the number of cows conceiving is reduced. If the producer's management strategy includes culling of once open females, more heifers are required to be retained for replacements, thus reducing the number of young animals for sale.

Previous research has documented that differences exist among breed crosses or breeds of cattle for characteristics associated with lactation. Yield at time of peak lactation and total milk yield during the lactation period vary. Among dairy animals, research has shown that the higher producing animals tend to be in negative energy balance during the first part of the lactation cycle, i.e., in an attempt to achieve their genetic potentialor milk production, the cows produce more energy in milk than they can consume. Feeding strategies have been or are being developed to circumvent this problem. It is not argued here that genetic potential for milk production of beef breeds is directly comparable to dairy cattle, rather that the range in feed energy environments in which lactating beef cows produce offers a similar opportunity for a negative energy balance to occur. Current recommended feeding standards make recommendations for supplemental feeding based on level of production but ignore the possibility of breed differences.

The object of this study was to quantify breed differences for component traits describing the lactation curve among beef breeds and to characterize the response of these traits to increasing feed energy availability.

Procedure

As part of a comprehensive project to evaluate life cycle production efficiency, lactation records of mature cows representing nine cattle breeds were collected from 1987 through 1990. Breeds included were Angus, Braunvieh, Charolais, Gelbvieh, Hereford, Limousin, Red Poll, Pinzgauer and Simmental. Sixteen cows of each breed were assigned to the study. All cows had calved a minimum of two times prior to entrance into the study. At the initiation of the study, cow ages ranged from 5 to 8 yr. Cows were housed in open-front barns with concrete flooring. Each year pregnant cows were transferred to grass pastures for calving. Time on pasture ranged from 14 to 90 days. Ten to 16 days postcalving, cow-calf pairs were returned to the intensive facilities.

Cows received a ground alfalfa hay based diet. Composition of the diet is detailed in Table 1. Within each breed, four cows were assigned to one of four energy intake levels during the lactation period: 170, 210, 250 and 290 kcal ME/wt/-.75/day. Each cow's ration was determined by using the weight of the cow at the 6-7 mo of gestation of the year the cow entered the study. The ration was fed daily, with feed consumption summed and recorded weekly for each cow. Samples of feed were taken daily and composited weekly. These composite samples provided material for determination of dry matter and crude protein.

Milk yields were determined approximately five to seven times from 14 to 196 days postpartum by weigh-suckle-weigh techniques. Separation of cows and calves preceded the sampling time by 17 hr. The difference between calf weights prior to and after suckling adjusted to a 24 hr basis provided an estimate of daily milk production of the cow. Suckling continued for approximately 45-60 min following introduction of the calves to their dams. Cow lactation records with fewer than five daily samplings within a production cycle were excluded from the data set. A total of 431 lactations from 179 cows was included in the data set.

To evaluate lactation curve characteristics, individual animal observations were used to develop lactation curves for each cow. From these curves, three traits were determined:

time of peak lactation

yield at time of peak lactation=

210-day total yield

Time of peak lactation (PK), yield at time of peak lactation (PKYD), and total yield for a 30-week lactation period (TOTAL) were analyzed to determine if differences exist among breeds, level of energy intakes, and the interaction between breed and energy intake. One of the objectives of this study was to determine if the response within a breed to increased metabolizable energy (ME) availability during the lactation period for milk production characteristics differed.

Results

Differences were observed among the nine breeds for PK, PKYD, and TOTAL. Increasing energy intake level increased PKYD and TOTAL but the increase in these traits decreased per unit increased energy intake. The largest increases would be realized at the lower energy intake levels.

Least squares means by breed for all traits are reported in Table 2. Estimated PK (wk) for the Hereford breed occurred earlier than for Angus, Braunvieh and Red Poll, but at a similar time postparturition as the remaining breeds. The Red Poll was similar to the Angus, Braunvieh and Gelbvieh, but differed from the remainder of breeds. The remaining breeds were intermediate and did not differ from one another for PK.

Yield at time of peak lactation was similar for Braunvieh, Gelbvieh, Pinzgauer, and Simmental. These four breeds produced more milk at PK than the British breeds (Angus and Hereford) or Limousin, and Charolais. Total yield of the breeds ranged from approximately 2600 to 4000 lb pooled over energy intake level. Braunvieh yield for a 210 day lactation period exceeded all breeds except for Gelbvieh. The Hereford and Limousin production were similar. Intake level of ME affected all the response variables (Table 3). PK was later for cows fed at 210 kcal ME/wt.$^{.75}$/d than for cows receiving 170 kcal ME (8.3 ± .3 and 9.2 ± .3; respectively). Cows fed at the higher energy intakes differed from these levels but not from each other. Positive response to PKYD

[1]Jenkins is a research animal scientist, Production Systems Research Unit; and Ferrell is the research leader, Nutrition Research Unit, MARC.

was observed with increasing levels of energy intake. A similar positive response occurred for TOTAL. TOTAL yields for 290 and 250 kcal ME energy intake levels were greater than 210, which was greater than 170 kcal ME. The difference between 290 and 250 kcal ME/wt.$^{.75}$ was not significant. Pooled across breeds, curvilinear responses in PK, PKYD and TOTAL were observed as ME allowance increased but the rate of increase decreased as the energy allowance was raised.

Information describing the effect of increasing energy allowances upon lactation curve traits in beef cattle is limited. In comparison with previous information provided for dairy cattle, it is evident that beef cattle respond similarly to increasing levels of energy intake. With increased energy allowance, PK was delayed and the yield at that time increased. The rate or degree to which these changes occur depends on previous energy intake. Breeds of cattle differ in lactational characteristics. Information such as this can be used by producers to identify those breeds that fulfill the needs for a specific production enterprise and perhaps partially define the role for a specific breed in the industry.

Table 1— Composition of diets (% of dry matter)

Ground alfalfa	77.5	
Corn	17.5	
Corn silage	5.0	
Metabolizable energy	1.03	Mcal/lb
Crude protein	16%	

Table 2—Means for time of peak yield, yield at time of peak yield, and total yield for nine breeds of cattle

	Traits		
		Yield	
Breed	Time of peak lactation (wk)	At peak lactation (lb/d)	210 d total (lb)
Angus	10.4	20.7	3,130
Braunvieh	10.3	26.2	3,967
Charolais	9.5	21.6	3,152
Gelbvieh	10.0	25.3	3,733
Hereford	8.8	18.7	2,620
Limousin	8.8	20.9	2,968
Red Poll	11.1	22.2	3,445
Pinzgauer	9.6	24.4	3,608
Simmental	9.6	24.0	3,528

Table 3—Means for time of peak lactation, time of peak yield, yield at time of peak yield, and total yield by energy availability levels of metabolizable energy

	Traits		
		Yield	
Energy intake levels kcal/wt $^{.75}$	Time of peak lactation (wk)	At peak lactation (lb/d)	210 d total (lb)
170	8.3	20.4	2,726
210	9.2	22.7	3,271
250	10.7	23.8	3,661
290	10.9	24.2	3,742

Estimates of Mature Weights and Maturing Rates for Breed Crosses

Thomas G. Jenkins, Miroslav Kaps, Larry V. Cundiff, and Calvin. L. Ferrell[1]

Introduction

Recent attempts to increase weight of product marketed for a cow herd have emphasized increasing the weights of progeny that are to be sold. Previous investigations have identified sufficient variation between and within breeds of cattle to enable the producer to set the desired level of genetic potential for size in the cow herd and rate of growth in the progeny. The assumption has been that a positive relationship exists between mature size and productivity. Researchers are beginning to question if this assumption is correct. It has been reported that mature size is negatively related to productivity. However, higher productivity has been related to faster maturing rate (the rate at which an animal attains its mature body mass). Breeds of cattle would be expected to vary with regard to the combination of maturing rate or mature weight that would be most beneficial for production. With the diversity in genetic potential for weights available, today's producers should be able to set the optimum mature weights and maturing rates for their production goals within a defined production environment. Exploitation of genetic differences among the breeds for these traits has been suggested as a way that beef production efficiency could be improved. Exploitation of these differences requires characterization of measures of growth through maturity for a large number of breeds or other uniquely defined populations of cattle. Estimates of growth parameters from birth through 15-18 months are readily obtainable. Estimates of mature weights and rates of maturing for diverse populations are limited. The objective of the present investigation was to estimate means for breeds for several measures of growth through maturity, thus providing an information base characterizing diverse breeds of cattle with regard to mature weights, rates of maturing, and heights.

Procedure

Data that were analyzed for this report were collected as part of the Germ Plasm Evaluation Program conducted at MARC, a comprehensive investigation conducted to characterize production performance for diverse breeds of cattle. The data for weight, height and condition scores of F_1 females from the first three cycles were produced from 1970 through 1976. The F_1 females used in the study were produced by artificially inseminating either Angus or Hereford cows with semen from Angus, Brahman, Brown Swiss (European and American), Charolais, Chianina, Gelbvieh, Hereford, Jersey, Limousin, Maine Anjou, Pinzgauer, Red Poll, Sahiwal, Simmental, South Devon and Tarentaise bulls. More detailed information describing how sires from the different breeds were identified for use has been previously reported. Weights were recorded at birth, weaning, at 28-day intervals from weaning to approximately 24 mo of age and then twice yearly until a cow was removed from the project. Postweaning, heights at the hip, and body condition scores (9 point; 1 = extremely emaciated, 9 = extremely obese) were recorded at each weighing. Calves born into the project were raised on pasture with their dams and weaned at approximately 200 days of age. Following weaning, the heifers were maintained in a drylot for approximately 168 days. Multiparous cows were sustained on cool- and warm-season grass pastures during the summer months. During the winter, legume and grass hay was provided to the cows. Weight, height and condition measurements were recorded prior to initiation of the breeding season and at time of weaning. Records from individuals that were open two consecutive years were removed from the evaluation. Animals dying prior to accumulating a minimum of 24 measurements of weight were deleted from the data set. Animals were not removed based upon a growth criterion. These edits resulted in a set of records collected from 1577 individuals that were used for analyses. The number of sires for each of the breeds were: Angus 32; Brahman 17; Brown Swiss 11; Charolais 25; Chianina 17; Gelbvieh 11; Hereford 32; Jersey 32; Limousin 12; Maine Anjou 15; Pinzgauer 9; Red Poll 16; Sahiwal 6; Simmental 26; South Devon 29 and Tarentaise 6; respectively. For greater detail concerning management protocol of cattle assigned to the Germ Plasm Evaluation Program, see previous progress reports.

Breeds included in the project were identified for evaluation to characterize the diversity in potential for production traits such as growth rate, age at puberty, and milk producing ability. To minimize the effect of variation in body condition on weights of animals within each breed attributable to individual animal differences in milk production, weight measurements recorded after 20 mo of age were adjusted to a constant condition score. Growth curves (weight-age relationship) were estimated for the individual animals using the recorded weights. Nonlinear regression was used to fit animal weights to a growth function commonly referred to as the Brody growth model. An assumption associated with this model is that the rate of growth along the growth curve is proportional to the amount of growth remaining to be attained. Parameters of interest estimated from this model include the asymptote of the curve (A) and the rate constant (k), respectively, which previously have been used to describe mature weight and rate of approach to mature weight of living organisms.

Results

Improvement in production characteristics measured by weight may result from selection within breeds or by using breed substitution to exploit direct genetic variation among breeds. Based upon previous research, immediate improvement could be realized by breed substitution. However, within breed selection represents the beneficial course of action to maintain genetic diversity among our cattle breed populations. Breed means and characterizing traits of interest are reported in Table 1. Information such as this can be used to identify the breed resources for the most appropriate breeding program. In addition to mature weights, maturing rate and height at maturity, weights at birth, 200 day, 365 day, and 500 day are reported for the 16 sire breeds. Weights for the traits averaged over breeds of sire were 77, 427, 645, 741, 1140 lb for birthweight, weaning weight, yearling weight and 500 day weight. The average weight of maturing was 5.6% and the average height at maturity was 50 in. Cows sired by Chianina bulls and those sired by Maine Anjou bulls exhibited heavier mature weights and attained these weights at relatively slow rates (maturing

[1]Jenkins is a research animal scientist, Production Systems Research Unit, MARC; Kaps was a visiting scientist from Yugoslavia; Cundiff is the research leader, Genetics and Breeding Research Unit; and Ferrell is the research leader, Nutrition Research Unit, MARC.

rates approximately 16% less than the average of the 16 breeds). The mature weight average of the Jersey sired cows was approximately 18% less than the pooled breed average and, as indicated by their maturing rate, they attained their mature weight rapidly. The Brahman, Hereford, Sahiwal and Tarentaise sired females grew to a heavier mature weight than the Jersey sired female but the maturing rate averages for these breeds were similar to that of the Jersey. Using information from this study in combination with results from other studies, producers should be able to identify breeds of animals which are most suited to serve a paternal, maternal, or general purpose role in the beef industry today. The ability to exploit differences among breeds to establish desired mature sizes or rates of maturing is evident from the diversity among the sire breeds reported in this study. Using mating systems to effectively use this genetic diversity should provide the producer an effective means to improve the efficiency of beef production.

Table 1— Mature weight, maturing rate, height at maturity, and weights at various ages by sire breed

Sire breed	N	Weight (lb)[a]					Maturing rate[a] (k*100)	Height at maturity(in)
		Birth	200 d	365 d	500 d	Maturity		
Angus	122	75	394	613	715	1126	96.4	49.2
Brown Swiss	107	84	427	638	743	1144	98.2	50.4
Brahman	94	81	462	715	823	1210	108.9	52.0
Charolais	100	81	451	651	750	1219	89.0	50.8
Chianina	67	87	429	653	770	1296	83.9	53.5
Gelbvieh	65	84	440	649	761	1185	94.6	50.4
Hereford	173	73	431	653	737	1100	107.1	48.4
Jersey	99	62	376	552	634	935	108.9	48.4
Limousin	136	75	422	618	704	1135	89.3	50.4
Maine Anjou	67	90	429	667	779	1283	87.5	51.2
Pinzgauer	85	92	451	719	805	1155	117.8	50.4
Red Poll	81	81	403	592	695	1124	87.5	49.2
Sahiwal	83	75	431	658	748	1069	110.7	50.0
Simmental	132	81	444	661	752	1131	101.2	50.8
South Devon	93	77	416	627	719	1126	96.4	52.0
Tarentaise	73	75	442	701	783	1142	112.5	49.6
Pooled	1577	77	427	645	741	1409	5.6	50.0

[a] Maturing rate of each sire breed is expressed relative to the pooled estimate of 5.6.

Simulated Effects of Herd-Level Management Strategies on Efficiency of Beef Production

Michael D. MacNeil, Don D. Kress, and Gordon E. Dickerson[1]

Introduction

Beef producers make some decisions that affect production at the herd level. In many cases these decisions are not supported by data, since resources needed to obtain experimental data are limited. Computer modeling is a logical way to evaluate herd level effects. Here we examine options for culling cows based on age and pregnancy status under four crossbreeding systems.

Procedure

We used a computer model to calculate inputs and outputs needed for beef production. This model followed from earlier work at Texas A&M University and at MARC. Monthly estimates of diet digestibility for each class of stock described the production environment. Classes of cattle included cows, replacement heifers, and steers and surplus heifers destined for slaughter. We summed all inputs and outputs needed to produce, on avg, low choice carcasses. Conclusions from these results apply to herds where management retains ownership until steers and surplus heifers are marketed at a grade constant (low choice) endpoint.

Input costs for cows and replacement heifers were obtained from a survey of production costs per cow unit in the ranching area of Nebraska. Costs for inputs included: grazing at $13/animal unit mo, native hay at $35/ton, protein supplement at $190/ton, other cash costs (including interest) $98/cow, and labor at $6/hour. Input costs for feeding calves were from a similar survey associated with feeding steers from weaning to market weight on corn-based high concentrate rations. These costs included: corn at $2.25/bushel and other cash costs including interest at $79/head. We used ten-yr (1977-1986) avg prices paid for beef cattle in Nebraska to calculate returns. These avg prices per lb were: $0.61 for choice market-ready steers, $0.59 for choice market-ready heifers, and $0.39 for cull cows.

We examined four mating systems to study gains obtained from either separately or jointly using heterosis and breed differences. A straightbred system makes the most use of breed differences, using only the single "best" breed, but does not capitalize on heterosis. A three-breed rotation captures 87% of available heterosis, but takes less advantage of breed differences than the straightbred system. Terminal sire systems use both heterosis and breed differences to varying degrees. We simulated a roto-terminal system and a specific cross system. The roto-terminal system is a maternal two-breed rotation with terminal sires bred to cows 4 yr old and older. First-cross females are produced and then bred to terminal sires in the specific cross system. Except for the straightbred system, all systems require three breeding pastures. Cows simulated had 1,100 lb genetic potential for mature weight and 33.7 lb/day maximum milk yield. Genetic potential of terminal sires for mature size was 40% greater than for the females.

Cows and yearling heifers were bred during June and July. Culling options varied in severity of culling open females. They were: 1) no culling based on pregnancy status, 2) open heifers culled, 3) open heifers and open 2-yr-olds culled, 4) open cows, 2-yr old and older culled, and 5) all open females culled. We also simulated culling of cows as they reached maximum ages of 7, 9, 11, 13, or 15 years. All imposed culling took place at weaning, on November 1. Model calculations set equilibrium age distributions so that 1,000 simulated females always entered the breeding season.

Biological efficiency was defined as total TDN input to the production system divided by total slaughter wt equivalent output. Slaughter wt equivalent output was total slaughter wt of steers and surplus heifers plus .63 times the slaughter wt of cull cows. Thus, slaughter wt of cull cows is valued at 63% of slaughter wt of steers and heifers. Economic efficiency was total cost attributed to the production system divided by total value of its outputs. Net return was the difference between total value of outputs from the production system and total cost of its inputs.

Results

Relative importance of mating system, culling option, and maximum cow age depended on whether the evaluation was at a biological or economic endpoint. The five options for culling based on pregnancy status were the largest contributor (40%) to differences in biological efficiency. Mating systems (27%) and culling at different maximum ages (28%) were also important contributors to biological efficiency. However, mating systems had the greatest effects on economic efficiency and net return, 56% and 60%, respectively. Culling options based on pregnancy accounted for only 21% of variation in economic efficiency or net return. Culling at a prescibed maximum age contributed only 20% and 16% to differences in economic efficiency and net return. Within this simulated production environment and with avg production costs and prices received, optimal management resulted in $1.02 of expense for every $1.00 of income.

Interactions of culling strategies and mating systems were not important to understanding differences in either measure of efficiency or in net return. Therefore, the consequences of culling strategies and mating systems can be discussed separately. Likewise, interpretations of differences among mating systems, among culling strategies based on pregnancy status, and among maximum ages were consistent across both efficiency measures and net return. Therefore, graphical presentations were limited to economic efficiency or cost per $1 of income.

Among the mating systems studied, the straightbred system was least efficient (Fig. 1). It required 10.05 lb of TDN for every lb of slaughter wt equivalent output. Economically, inputs costing $1.68 returned $1.00 in income and the net return per cow was -$105 for the straightbred system. By using heterosis, but not breed differences, the three-breed rotation system improved biological efficiency to 9.65. For the three-breed rotation, economic efficiency was 1.60 and net return was -$86. Using a terminal sire with a two breed maternal rotation was most efficient. In that system with bio-

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logical efficiency at 9.16, economic efficiency was 1.43 and net return was -$29. The three-breed specific cross system was intermediate between the three-breed rotation and using terminal sires in combination with a two-breed rotation.

In Figure 2, we present simulated effects of culling based on pregnancy status. Culling open females at all ages improved herd-level efficiency and profitability. When keeping open females, 9.96 lb TDN produced a lb of slaughter wt equivalent output. Economically, inputs costing $1.61 returned $1.00 and net return per cow was -$82 when not culling open females. Culling all open females improved biological efficiency to 9.07. Economic efficiency was 1.48 and net return per cow was -$48 when culling all nonpregnant females.

Shown in Figure 3 are effects of maximum cow age on economic efficiency. Results for biological efficiency and net return were similar. We did not find an optimal maximum age at which to cull cows in this study. Keeping cows as long as they remain sound was the most efficient and profitable strategy simulated. However, the decreasing rate of improvement in efficiency probably results from the relatively small number of cows remaining at the older ages. These results may be sensitive to assumptions about involuntary culling at older ages.

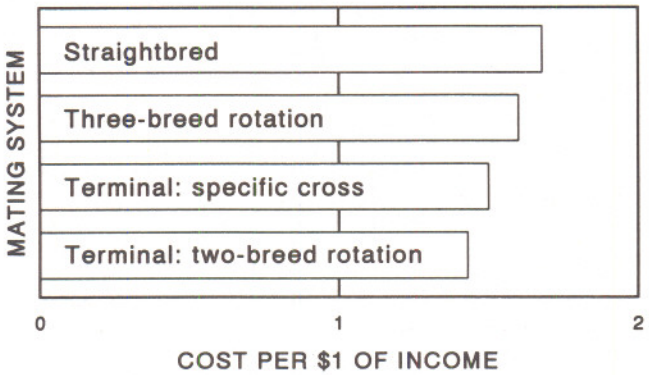

Figure 1 – Mating system effects on economic efficiency.

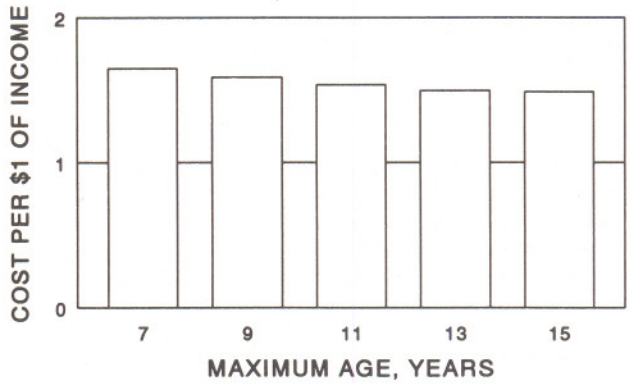

Figure 3 – Effects of maximum cow age on economic efficiency.

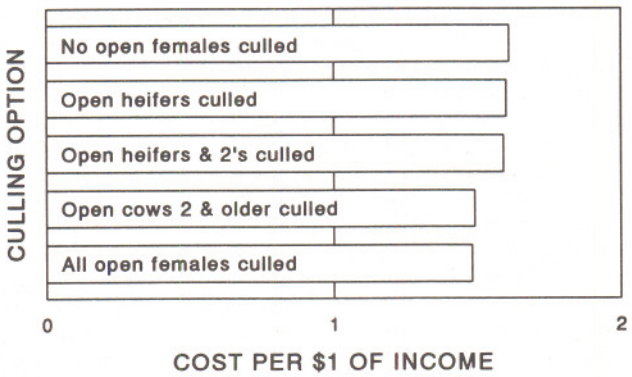

Figure 2 – Effects of culling open females on economic efficiency.

Using Crossbreeding Systems to Produce Beef

Michael D. MacNeil, Larry V. Cundiff, Keith E. Gregory, and Robert M. Koch[1]

Introduction

Crossbreeding provides an opportunity to improve performance by beef cattle. Breed differences are heritable and can be used to produce superior crossbred cattle. Heterosis results from bringing together unlike genes from different breeds to produce an animal with a level of performance that exceeds the average of the parent breeds. We develop crossbreeding systems to make the greatest improvement in performance possible consistent with a sustainable breeding program. Heterosis and differences among breeds are tools of the trade. In this paper, we combine the results from earlier studies to investigate their practical applications.

Procedure

Angus, Hereford and Shorthorn cows produced straightbred and two-breed cross calves. Resulting straightbred heifers were bred to bulls of the other breeds to produce additional two-breed cross calves. Two-breed cross heifers resulting from the original matings produced three-breed cross and backcross progeny at the same time. The three-breed cross and backcross heifers formed the foundation for two- and three-breed rotation systems. These rotation systems continued for two more generations. Straightbred calves were produced along with backcross, three-breed cross, and rotation calves. All calves grazed with their dams until weaning and had no access to creep feed.

Steer calves were fed a growing-finishing ration containing 1.18 Mcal metabolizable energy per lb for 252 days after weaning. Then they were slaughtered and carcass data collected.

Breed group differences resulted from breed effects of the individual, its dam, or its maternal grandam. Heterosis at each generation also may contribute to differences among breed groups. Data analyses quantified the effects of substituting one breed for another and the effects of heterosis on weaning wt, final wt, carcass wt, and retail product wt per cow exposed.

Terminal sires express genetic effects only through direct influences on their offspring. For this study, we characterized a generic terminal sire breed using results from the Germ Plasm Evaluation Program. Traits of a terminal sire affecting wt produced per cow exposed include: calf mortality to weaning, calving date, birth wt, preweaning daily gain, postweaning daily gain, carcass wt, marbling score, and retail product weight. The basis for the terminal sire breed was expression of these traits by calves from Brown Swiss, Gelbvieh, Maine Anjou, Simmental, Limousin, Charolais, and Chianina sires compared with calves from Hereford and Angus sires.

Thus, Angus, Hereford, Shorthorn, and terminal sire breed resources were available. Using these resources, we then predicted performance of five mating systems. The systems considered were: straightbred, two-breed start rotation (Fig. 1), three-breed rotation, and two- and three-breed maternal rotations with a terminal sire (Fig. 2).

Results

The mating system of choice depends on several resources that are specific to each cattle operation. These resources include: number of cows, number of breeding pastures, availability of labor, and amount and quality of feed and forage. We assume breeding of all cows was by bulls in natural service. Compromising a system by failing to meet its requirements reduces the benefits that can be expected from it. Resources required to put the mating systems into place are reviewed here.

The straightbred system is the simplest to carry out. Its success requires appropriate matching of available feed resources and environment with an adapted breed. Numbers of cows and breeding pastures, managerial ability, and availability of labor are least restrictive to the straightbred system of all mating systems.

A two-breed rotation requires enough cows to employ two bulls, two breeding pastures, and identifying all females by the breed of their sire. A three-breed rotation requires a correspondingly greater commitment of resources. In either rotation, bulls are bred to cows that are most distantly related to the breed of the bull. Rotation systems provide limited opportunity to take advantage of breed differences. Environmentally well adapted breeds that are comparable in birth weight, growth, and lactation potentials should be used.

Terminal sire based systems allow use of breeds in specialized roles. Young cows bred in a rotation among breeds that are superior for maternal traits and adapted to the environment produce the replacement heifers. Mature cows are bred to breeds with high genetic potentials for growth rate and lean-to-fat ratio of the carcass. All progeny of the terminal sire are sold for slaughter. Using a terminal sire with a two-breed maternal rotation requires three breeding pastures and enough cows to use four bulls.

All crossbreeding systems produced more lb of product per cow exposed than the straightbred system. Products considered were weaning wt (Fig. 3), final wt (Fig. 4), carcass wt (Fig. 5), and wt of retail cuts (Fig. 6)

Heterosis increased weaning wt per cow exposed from the two-breed rotation by 59 lb and from the three-breed rotation by 75 lb over the straightbred system. Adding a terminal sire to a rotation system yielded only small increases in weaning wt per cow exposed. Three-breed rotation and terminal sire on two-breed maternal rotation systems require similar numbers of breeds. Yet the latter system produced only 3.7 lb more weaning wt per cow exposed. We conclude cow-calf producers should evaluate a terminal sire system carefully before deciding to use it.

Comparing among endpoints preceding slaughter, the various crossbreeding systems were similar to the weaning endpoint. Only when we examined retail product wt per cow exposed did important advantages (26 lb or 18%) lie with the terminal sire systems over the rotation systems. If consumers want leaner meat products, then economic benefits from producing calves using terminal sires need to be transferred from consumers back to cow-calf producers.

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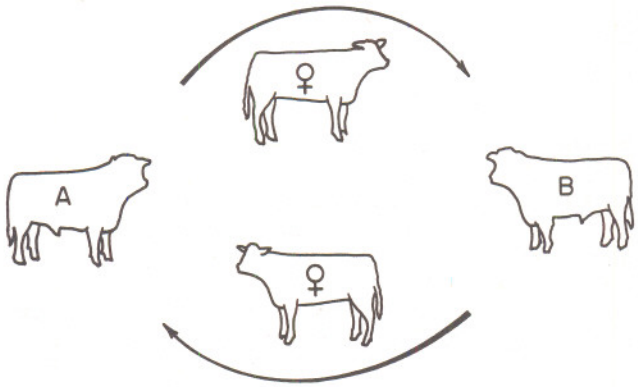

Figure 1 – Two-breed rotation. Bulls of breed A are bred to females sired by bulls of breed B. Bulls of breed B are bred to females sired by bulls of breed A.

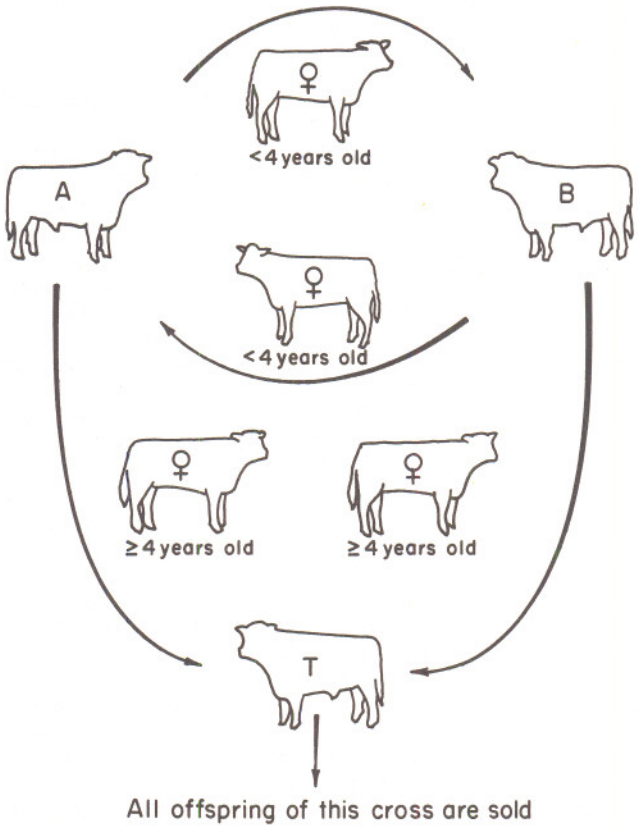

Figure 2 – Terminal sire incorporated with two-breed rotation. Heifers and cows less than four years old are bred in a two-breed rotation. Older cows are bred to bulls of the terminal sire breed and all offspring from the terminal sire breed are marketed.

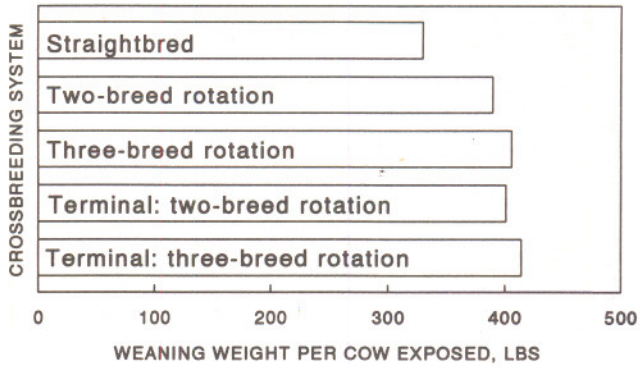

Figure 3 – Effects of crossbreeding system on weaning weight per cow exposed.

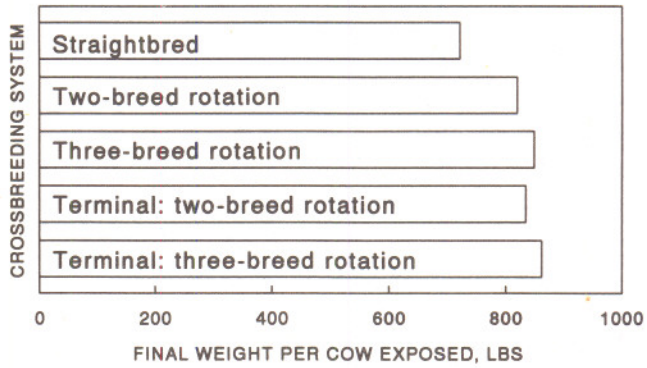

Figure 4 – Effects of crossbreeding system on final weight per cow exposed.

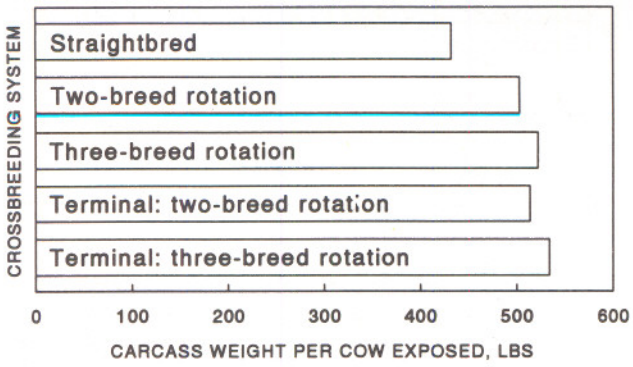

Figure 5 – Effects of crossbreeding system on carcass weight per cow exposed.

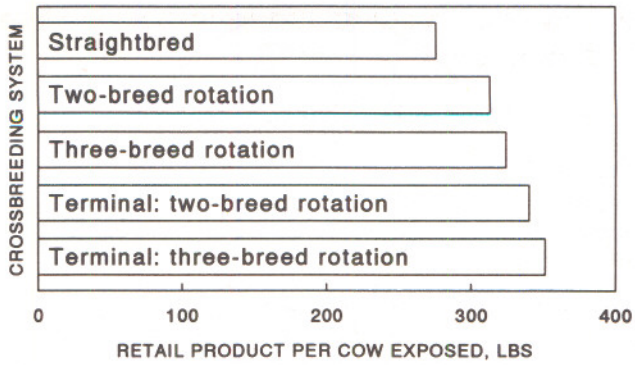

Figure 6 – Effects of crossbreeding system on retail product weight per cow exposed.

Effects of Inbreeding and Heterosis in Hereford Lines on Reproduction and Maternal Performance

Michael D. MacNeil, Delwyn D. Dearborn, Larry V. Cundiff, Chris A. Dinkel, and Keith E. Gregory[1]

Introduction

Two genetic mechanisms have been described as potential explanations for heterosis. The first mechanism is dominance. Dominance occurs when there are two differing forms of a gene (alleles) at a given position (locus) on a pair of chromosomes and where one of the pair of alleles masks or over powers the effect of the second. Having two different alleles at a locus is referred to as heterozygosity and the affected individual is heterozygous. Whether an individual has one or two copies of a dominant allele makes little difference in its superiority over others having two copies of the recessive allele. A higher degree of heterozygosity is expected when one population carrying the dominant allele in high frequency is crossed with a second population carrying the recessive allele in high frequency. Alternatively, heterosis may result from joint effects of genes at several loci. This alternative mechanism is called epistasis.

Previous research documents reduced performance resulting from the mating of closely related individuals (inbreeding). Inbreeding generally reduces growth and reproductive rates and delays maturity. This inbreeding depression arises from increasing the frequency with which two alleles at a locus are identical (homozygous) and again coupled with dominant gene action. Thus, effects of inbreeding and heterosis are of similar size but opposite in direction, if dominance at individual loci causes both.

In this study, we used inbreeding and linecrossing of Hereford cattle in an attempt to distinguish between these two explanations for heterosis influencing maternal traits. Answering this question sheds light on the amount of heterosis to be expected in composite breeding schemes.

Procedure

Scientists with the South Dakota Agricultural Experiment Station created four inbred lines. Each inbred line started from 1 bull and 15 cows. The same 4 bulls and 60 cows were the basis for a contemporary control line. The control line was maintained as a single herd. Mating bulls from each inbred line with cows from the other inbred lines resulted in production of linecross females. Mating inbred bulls to control line cows produced topcross females. Mating of related cows and bulls was avoided in producing topcross females. Replacement females (control, inbred, linecross, and topcross) were transported to MARC and evaluated for reproductive and maternal performance over an eight-yr period.

Results

Performance of females from the four lines as 2-yr-old heifers and at all ages is shown in Table 1. The topcross breed group can be used to separate effects of inbreeding of sire and dam. In this study, the topcross breed group did not differ in performance from either the linecross or control breed groups.

If performance of inbred and control lines differs, then effects due to inbreeding exist. Inbreeding depressed survival of calves from pregnancy testing to calving of first calf heifers. Birth weights of calves from inbred cows were also lighter than from control line cows. Except for pregnancy rate, other comparisons of inbred and control line cows were also negative. However, they were not large enough to establish conclusively the existence of inbreeding effects.

Heterosis exists if performance by linecrosses differs from that of the parental inbred lines. Survival rates for calves from linecross females exceeded those from inbred females both from pregnancy testing to calving and from calving to weaning. Linecross cows also had heavier calves than inbred cows, both at birth and at weaning.

Comparing effects of heterosis and inbreeding, we find no differences in their size for any trait except birth weight. For birth weight, inbreeding depression was larger than heterosis. This result may stem from the heavier than expected birth weights of calves from control line cows. Results of this study indicate that effects of inbreeding are detrimental to reproduction and maternal performance in cattle. Crossing inbred lines results in significant heterosis. Performance levels of linecrosses apparently are restored to the level of noninbred contemporaries.

Table 1—Levels of inbreeding, reproductive traits of two-year-old heifers and maternal performance of inbred, linecross, topcross, and control line cows

	Breed group			
Traits	Inbred	Linecross	Topcross	Control
Level of inbreeding, percent				
Individual	27	0	0	7
Sire	31	34	27	4
Dam	24	27	7	6
2-yr-old				
Pregnant, percent	76	79	70	76
Prenatal survival, percent	85	97	97	100
Birth rate, percent	66	78	68	77
Postnatal survival, percent	70	90	80	83
Weaning rate, percent	46	70	55	65
All ages				
Birth wt, lb	72	75	76	82
Weaning wt, lb	400	429	432	431

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Postpartum Interval Is Influenced by Nutritional Environment and Biological Type

Russell A. Nugent III, Thomas G. Jenkins, Andrew J. Roberts, and John M. Klindt[1]

Introduction

Reproduction is a major component of production efficiency for a cow-calf system. Failure of a cow to conceive is the most important factor reducing net calf crop. The interval from parturition to estrus, or postpartum interval, greatly influences the chances of a cow becoming pregnant during a restricted breeding season. Breeds can differ in length of postpartum interval and further, postpartum interval is influenced by numerous environmental factors including nutritional value of available feedstuffs. Inadequate energy availability increases postpartum interval in suckled beef cows, but energy requirements differ among biological types. The level at which energy begins to limit reproductive performance may not be constant for all biological types of cattle. The objective of this study was to test the effects of biological type and daily metabolizable energy availability on length of postpartum interval of mature beef cows.

Procedure

Mature, multiparous purebred Angus, Braunvieh, Charolais, Gelbvieh, Hereford, Limousin, Pinzgauer, Red Poll, and Simmental cows were randomly assigned within breed (four cows per level, 144 total females) to be fed for 4 yr at either 130, 170, 210, or 250 kcal of metabolizable energy x body weight$^{-.75}$ per day during nonlactational periods, with an increase in ration size of 25% during lactation. The diet is outlined in Table 1. Body condition scores (1 = very thin to 9 = very fat) averaged over breeds were approximately 1.5 to 3.5 for cows fed at 130 kcal and 7.0 to 8.5 for cows fed at 250 kcal. The other two energy levels yielded intermediate condition scores.

Prior to treatment, cows were grazed on mature smooth brome pasture, and the body weight of a cow at the time she entered the study (avg day of gestation: 210; range: 189-231) was used to establish her individual ration throughout the remaining time on the study. Average age of cows was 9 yr (range: 5-13), and avg age did not differ between nutritional treatment X biological type subclasses.

Prior to the study, breeds were assigned to biological types based on genetic potential for mature size (growth) and daily yield of milk at time of peak lactation (milk). Genetic potentials for growth and milk were determined from previous studies at MARC. The four biological types were: moderate genetic potential for milk and growth (Angus, Hereford, Red Poll), moderate genetic potential for milk and high genetic potential for growth (Charolais, Limousin), high potential for milk and moderate potential for growth (Braunvieh, Pinzgauer), and high genetic potential for milk and growth (Gelbvieh, Simmental).

Cows of the same breed and treatment were housed together in 760 square ft open front barns. Individual feeding was accomplished through use of electronic headgates. Two wk before the expected earliest calving date, all pregnant cows were transferred to pasture for calving. Cow-calf pairs were returned to feeding pens at approximately 2 wk after calving. Calves were weaned at approximately 200 days of age (range was 175 to 225 days). Prior to statistical analysis, effects of calf date of birth were removed from the data.

In 1991, the 121 (out of 144) cows that calved were bled once per wk starting 3 wk postpartum. Blood samples were collected for 27 wk postpartum on 31 cows and for 15 wk postpartum on 90 cows. Cows were not exposed to bulls following calving in 1991. Circulating concentration of the reproductive hormone progesterone was then determined from each blood sample by radioimmunoassay procedures. Postpartum interval was defined as the number of wk from parturition to the beginning of the first normal length luteal phase (the first wk that baseline progesterone preceded 2 wk of elevated progesterone).

Results

Biological type interacted with nutritional treatment to influence postpartum interval (Table 2). Increased energy availability tended to decrease postpartum interval in all biological types, but the magnitude of the decrease depended upon biological type. The interaction between type and nutritional level was, therefore, not one of reranking but rather one of differences among types in magnitude of the decrease in postpartum interval from the lowest to higher energy availability levels. Averaged over type, the 130 kcal energy availability level yielded the longest interval from calving to resumption of cyclicity and 210 and 250 kcal the shortest interval.

Biological types with a high genetic potential for growth exhibited the longest postpartum intervals, but also showed the greatest positive response to increased feed availability. Averaged over treatments, postpartum intervals were longest for the moderate milk, high growth type and were intermediate and shorter for high milk, high growth type cows. Further, increasing energy from 130 kcal to 250 kcal decreased postpartum interval the most for the moderate milk, high growth type. When feed availability was lowest, high genetic potential for peak milk yield decreased postpartum interval by 39 days when associated with high growth potential but increased the interval by 1 day for moderate growth types.

Efficient production dictates that calving intervals and thus postpartum intervals be relatively short. In the present study, the length of the postpartum interval varied between cows that were fed for long periods at specified levels of energy availability. Decreases in postpartum interval in response to increasing energy availability depended upon genetic potential for both mature size and level of peak milk yield. At the lowest level of energy availability, biological types with the greater genetic potential for mature weight exhibited extended postpartum intervals. However, in types with higher genetic potential for milk as well as growth the effect of low energy availability on postpartum interval was greatly reduced.

Thus it appeared that if daily energy availability was limiting, breeds that were historically selected for large mature size and growth (draft and beef) with no accompanied selection for milk (e.g., Charolais, Limousin) may partition a greater portion of their energy intake towards basal metabolism, growth, and lactation before any remaining nutrients are used for resumption of estrous cycles. Conversely, historical selection of a breed for dual-purpose as a milk-beef type (large mature size and high milk output, e.g., Gelbvieh, Simmental) may have resulted in a biological type that partitioned relatively more energy towards reproduction under

[1]Nugent is a research associate and Jenkins is a research animal scientist, Production Systems Research Unit, MARC; Roberts is a research physiologist, Reproduction Research Unit, MARC; Klindt is a research physiologist, Nutrition Research Unit, MARC.

conditions of limited energy availability and therefore returned to estrus earlier.

In cattle populations developed for meat and milk, timely reproductive performance was apparently considered a favorable attribute and presumably selection for milk output was accompanied by direct or indirect selection for other maternal characteristics as well (i.e., age at puberty and postpartum interval). It should be noted that sampling could have influenced results and conclusions should not be interpreted as being necessarily indicative of all cattle from the breeds and biological types used.

Increased genetic merit for level of milk yield had a less marked influence on the effect of energy restriction upon postpartum interval in types with a more moderate weight at maturity. This observation was supported by previous work that showed no difference in postpartum interval among breed crosses with similar moderate mature size, but different genetic potentials for milk production.

Effective production systems require the matching of genetic potential for performance (output) to the environment. Breeds or breed-crosses used to generate and maintain a cow herd must be chosen to some degree for the specific nutritional environment in which they will be producing. Differences among biological types for some component(s) of reproduction appeared to be especially important when energy availability was restricted. Important genotype environment interactions can influence reproductive potential and thus the efficiency of a cow-calf production system.

Table 1 – Composition of diet on a dry matter basis

Ground alfalfa	77.5%
Whole shelled corn	17.5
Corn silage	5.0
Metabolizable energy	1.0 Mcal/lb
Crude protein	16%

Table 2 – Mean postpartum interval by biological type and nutritional environment

Biological type	Daily energy availability[a] 130	170	210	250	Average by type
Moderate growth - moderate milk	88	83	46	59	69
High growth - moderate milk	146	69	58	66	85
Moderate growth - high milk	89	91	47	32	65
High growth - high milk	107	70	63	49	72
Average by energy availability	108	78	54	52	73

[a] kcal metabolizable energy x body weight$^{.75}$ during nonlactational periods: energy availability was increased by 40 kcal during lactation.

Computer Simulation of Body Composition in Growing and Finishing Beef Cattle

Charles B. Williams, John W. Keele, and Gary L. Bennett[1,2]

Introduction

The National Institute of Health Consensus Development Conference in 1985 recommended that Americans eat a diet with no more that 30% of the calories coming from fat, to reduce the risk factors associated with cardiovascular disease. Beef with a low-fat content could compose a greater portion of this recommended diet than beef with a high-fat content. There is a large base of experimental results on the effects of various factors such as genetics, feeding level, sex condition, exogenous biological growth stimulants, time on feed, and postweaning management on growth, composition and palatability of beef carcasses. Systems analysis through the use of computer models is an excellent means of integrating this existing knowledge. Computer models can be used to help identify feeding systems to produce leaner beef, provided these models are general enough to predict body composition with reasonable accuracy. Results from previous research have shown that some differences in body composition of cattle of the same breed and body weight may be predicted by rate of gain. Our objective was to develop and evaluate a dynamic computer simulation model that uses rate of gain to predict differences in body fat caused by plane of nutrition and to identify the model's range of applicability.

Procedures

Previous models that account for differences in body composition among cattle of similar genotype and weight caused by differences in energy intake require nutrient intakes as inputs. Nutrient intakes are difficult to predict and expensive to measure when animals are grazing. Our model is based on the premise that it is easier to predict or measure the growth patterns of cattle on a given nutritional regimen based on past experience or data than it is to predict or measure their nutrient intakes. The model assumes that protein is adequate for the amount of energy consumed. This restriction is based on the assumption that the costs relative to benefits of achieving protein adequacy are small compared to the costs relative to benefits of achieving energy adequacy.

Previous research has shown that daily gains for fat free matter and fat respond to increasing amounts of energy consumption as shown in Figure 1. Assuming the relationships in Figure 1, the percentage of fat free matter in gain decreases with increasing rate of empty body gain in a curvilinear fashion (Figure 2). The relationship shown in Figure 2 was used as a basis for developing a model that uses differences in rate of empty-body gain (caused by differences in energy consumption) to predict differences in body composition. The shape of the curve in Figure 2 depends on genotype, sex, stage of maturity (fraction of mature fat free matter in the body) and previous growth pattern. The model incorporates adjustments for these factors.

The model was evaluated with data from one unpublished and seven published experiments (Table 1). These experiments used several breeds of cattle, growing at rates that varied from small daily losses to high daily gains and various combinations of these growth rates. Ability of the model to simulate animal responses was first evaluated with respect to the accuracy with whichthe model simulated treatment means for fat percentage observed in the experiments. If the model simulated the observed animal responses closely, then paired values (experimental and simulated) should have a relationship which is close to one to one. Second, if there were important differences in body composition of animals at the same body weight, and these differences were associated with differences in nutrition, we wanted to evaluate the ability of the model to account for these nutritional effects.

Results

Observed and simulated treatment means for body fat percentage for the experiments listed in Table 1 are plotted in Figure 3. Data points lie close to the 45 degree line, which supports a one to one relationship between observed and simulated treatment means. However, the data plotted in Figure 3 do not distinguish between differences associated with weight and nutritional effects on body composition beyond those associated with body weight. To address this problem, observed and simulated nutritional effects on percentage body fat were obtained after adjusting for body weight differences. These nutritional effects are plotted in Figure 4. The results show that for experiments in which nutritional treatments had a significant effect on observed composition, the simulated data from the model also showed a similar significant effect. The results depicted in Figure 4 provide evidence that the model can predict differences in fatness of cattle caused by nutrition.

One of the outliers in Figure 4 represents a treatment in which a low protein diet was fed. In this case the model did not predict a significant nutritional effect on composition. One of the underlying assumptions of the model is that dietary protein is adequate, so inadequate protein may be responsible for the conflicting results obtained in simulating this experiment. Large effects of nutrition independent of changes in body weight are probably slightly underpredicted by the model, and the model will haveapproximately the same degree of accuracy in predicting composition as body weight alone in cases for which there are no nutritional effects on composition.

The following is a description of several areas where this model may be appropriate as a research/management tool.

1. Identification of postweaning systems of beef cattle production which would result in leaner carcasses at slaughter.
2. Characterizing the postweaning biological efficiency of different breed types when grown under different postweaning systems of production.
3. Identification of production systems to produce beef for different speciality markets.

In addition to these applications the model can be integrated into larger system models of the entire beef production system.

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[1]Williams and Keele are research animal scientists, and Bennett is the research leader, Production Systems Research Unit, MARC.

[2]The full report of this work was published in J. Anim. Sci. 70:841-866, 1992.

Table 1—Brief description of the experiments used to evaluate the model

Category	n	No. dietary treatments	No. slaughter groups per treatment	No. in initial slaughter group
Holstein steers	47	4	1	8
Angus steers	29	3	4	2
Hereford steers	37	4	2	0
Hereford females	35	4	2	0
Holstein steers-1	54	6	3	4
Holstein steers-2	48	4	3	4
Angus steers	71	2	5	0
Holstein steers	69	2	5	0
Angus steers	42	2	2	12
Charolais steers	41	2	2	12
Small frame	120	6	2,3	0
Large frame	120	6	2,3	0
Small frame	79	5	2,3	10
Large frame	82	5	2,3	10

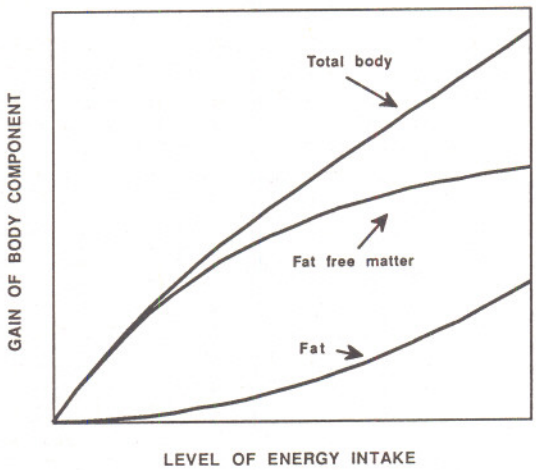

Figure 1 – Relationship between energy intake and daily gain of body chemical components when energy is the most limiting nutrient.

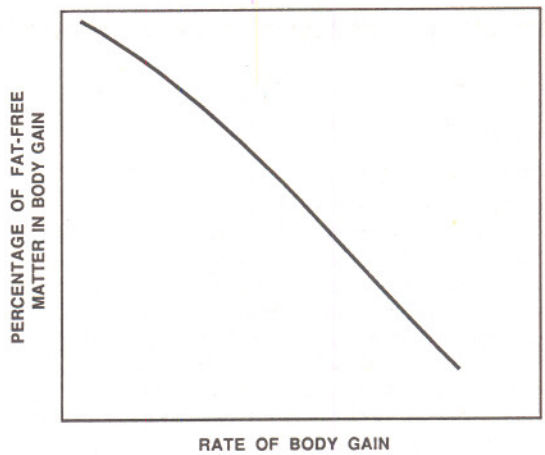

Figure 2 – Relationship between percentage fat free matter in gain and rate of body gain when differences in rate of body gain are caused by differences in energy consumption and energy is the most limiting nutrient.

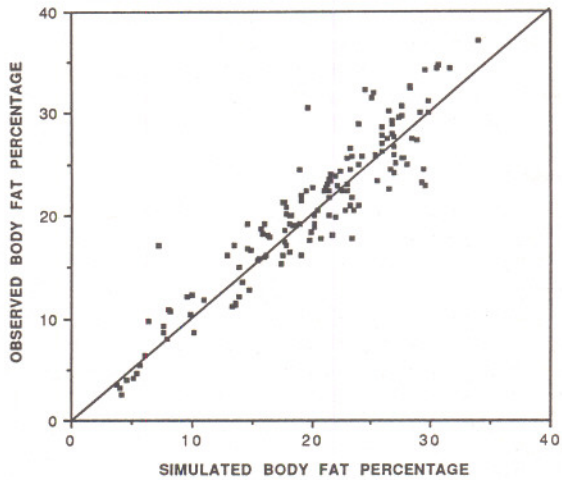

Figure 3 – Relationship between treatment means for observed body fat percentage and simulated body fat percentage.

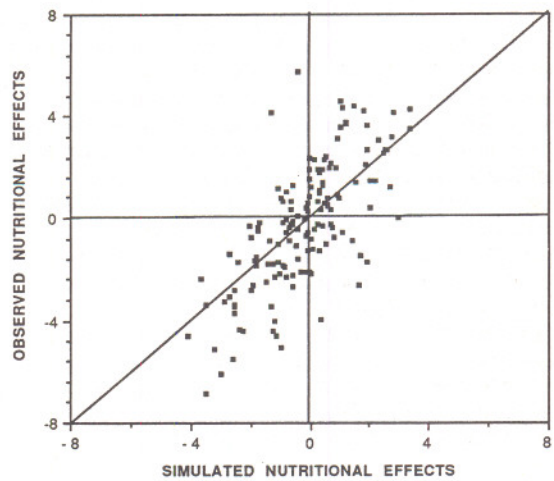

Figure 4 – Relationship between observed and simulated nutritional effects on body fat percentage.

A New Approach to Estimating Empty-Body Weight in Growing and Finishing Beef Cattle

Charles B. Williams, John W. Keele, and Dale R. Waldo[1]

Introduction

Animals require nutrients for maintenance and production. A large part of the calculated nutrient requirements is based on body weight, which includes the contents of the gastrointestinal tract (gut). Ruminants have a large gut capacity, and for a 1000 lb steer, gut contents can account for 50 to 250 lb of its body weight. These contents are not a part of the animal and should not be considered when calculating maintenance requirements. Therefore to translate nutrient requirements for each unit of empty-body weight (body weight minus the weight of gut contents) gain into requirements per unit gain in body weight, we need an accurate method of estimating the weight of gut contents. Several systems have been proposed to estimate empty-body weight. The National Research Council and the Agricultural Research Council used equations to calculate empty-body weight as a constant fraction of shrunk-body weight, or a constant fraction of body weight within three discrete dietary classes, respectively.

Results of previous research have demonstrated that in addition to body weight there is a continuous relationship between weight of gut contents and dietary characteristics such as percentage of dietary concentrates and neutral detergent fiber (indigestible and slowly digested fractions of the feed). Other work has also shown that weight of gut contents is much higher when animals consume hay vs silage prepared from the same forage source. Our objective was to develop and evaluate a method to estimate weight of gut contents and use this estimate to convert body weight to empty-body weight. To achieve this objective a model was developed to predict weight of gut contents in cattle as a function of forage neutral detergent fiber, physical form of forage dry matter (hay vs silage and pasture), proportion of dietary concentrates and body weight.

Procedures

Experimental data were used to develop an equation to predict the fraction of body weight associated with gut contents, from the percentage neutral detergent fiber in the forage. Factors were then developed using data from other experiments to adjust this fraction for the effects of body weight, percentage of dietary concentrates and the physical form of forage dry matter. The adjusted gut contents fraction was then multiplied by body weight to obtain the weight of gut contents. This weight was subtracted from body weight to obtain empty-body weight. All body weights used in model development represented weight recorded early in the morning with animals having access to feed and water overnight. Hay and silage were the physical forms of forage dry matter used in the model. It was assumed that green pasture and dormant pasture were physically the same as silage or hay, respectively.

Data from 11 published experiments with 64 treatments (Table 1) were used to evaluate the model. Empty-body weight predictions obtained with the models used by the Agricultural Research Council (ARC) and the National Research Council (NRC) were also evaluated with these experimental data, and compared to the present model's predictions. The accuracy with which these three models (our present model, Agricultural Research Council, and National Research Council) predicted empty-body weight was evaluated by comparing observed to predicted values.

Results

The model to predict the weight of gut contents was:
weight of gut contents = Body weight x(53.54 + 3.29 x percentage neutral detergent fiber of forage) x (correction factor for body weight) x (correction factor for fraction of concentrates in diet) x (correction factor for forage physical form), where

correction factor for body weight = $(\text{body weight} / 200)^{-.332}$
correction factor for fraction of concentrates = 1 - .246 x (fraction of concentrates) - 1.481 x $(\text{fraction of concentrates})^2$ + 1.107 x $(\text{fraction of concentrates})^3$, and

correction factor for forage physical form was 1.35 for hays and 1 for silages.

Empty-body weight was calculated from the predicted weight of gut contents and the observed body weight. The model empty-body weight values calculated from predicted gut contents for the treatments using hay in Experiments 2, 4, and 5 were very different from observed values. In these experiments ammoniated stargrass and perennial ryegrass hay were used, and previous results have suggested that for ammoniated hays the correction factor for forage physical form should be 1. With this modification the calculated empty-body weight values using the present model predictions of gut contents were much closer to the observed values.

Observed empty-body weight is plotted in Figure 1, against the empty-body weight calculated with the present model, and empty-body weight predicted with the ARC and NRC models. For cases where the observed and predicted values are the same, then the points representing these paired values would lie on the 45 degree line shown in this figure. Points above the line mean that the predicted values underestimates the observed, and the opposite would be true for points below the line. Empty-body weight values calculated with the present model tended to be smaller than observed values for weights less than 400 lb. The method used by the ARC consistently overpredicted empty-body weight, and the NRC's method overpredicted empty-body weight for 50 of the 64 treatment means. These results confirm that the present model would be accurate in calculating empty-body weight from predicted weight of gut contents for weaned cattle, and suggest that it may not be appropriate between birth and weaning. This is understandable since these animals would be consuming milk, and their rumens have not been fully developed.

Referring to Figure 1, equations can be developed to adjust the empty-body weight predicted with the systems used by the ARC and NRC. It is possible that these adjusted predictions may be more accurate than the present model. These equations were developed, and the adjusted predictions of empty-body weight using the ARC and NRC models were compared to the present model's calculated empty-body weight values. The results of this analysis showed that the present model was still more accurate than the other two models.

[1]Williams and Keele are research animal scientists, Production Systems Research Unit, MARC; Waldo is a research animal scientist, Ruminant Nutrition Laboratory, Beltsville, MD.

The present model was developed with data on cool-season grasses, legumes and corn silage and it has not been fully tested with warm-season grasses, however, preliminary results with stargrass show no inconsistencies. Also it is possible that the correction factor for the fraction of dietary concentrates may not be appropriate in cases where very low-quality forages are supplemented with either cereals of high-protein byproducts, or protein supplements that differ in ruminal degradability. As more data become available, the model needs to be tested under these experimental conditions. Data used to develop and evaluate the model were obtained from animals that were on a specific plane of feeding for over three weeks, and model predictions of empty-body weight may not be accurate in the early period when animals are switched from restricted to full feeding or vice versa. Model inputs are dietary characteristics that can be obtained from routine forage analyses and unfasted body weight. This makes the model easy to use. It can be incorporated into diet formulation programs and systems models of cattle production.

Table 1—Summary of data from 64 treatments in 11 published experiments used to evaluate the model

Exp.	Number of treatments	Number of animals	Forage type	Neutral detergent fiber, %	Concentrate fraction in diet
1	3	54	Hay	40	.0
2	6	102	Hay	75-82	.0-.23
3	2	24	Silage	51.0	.38
4	8	48	Silage, hay & pasture	51	.0
5	12	66	Hay	66	.0-.44
6	4	24	Straw	80	.59-.87
7	4	40	Hay	42	.0
8	3	36	Hay	66	.6-.95
9	12	29	Straw	80	.83-.88
10	4	40	Silage	44-59	.0-.28
11	6	32	Silage	51.9	.0-.08

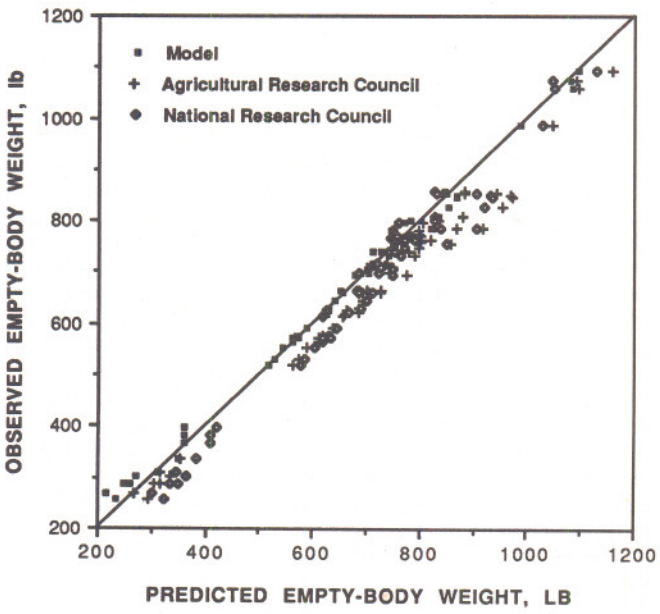

Figure 1 – Observed and predicted empty-body weight treatment means for 64 treatments in 11 published experiments.

Beef Cattle Salmonellosis: A Study of Oral *Salmonella typhimurium* and Topical *Salmonella newport* Inoculations

Ed K. Daniels, Neal E. Woollen, James S. Dickson, and E. Travis Littledike[1]

Introduction

Cattle are frequently infected with salmonellae by fecal-oral transmission or by being fed contaminated animal protein byproducts (40% are reported contaminated in the U.S.). Both could propagate salmonellosis in feedlots.

Research indicates that stress can induce shedding of salmonellae by asymptomatic carriers. Stress factors associated with salmonellosis include: transportation, starvation, changes in ration, overcrowding, age, pregnancy, parturition, exertion, anesthesia, surgery, intercurrent disease, and oral treatment with antibiotics and anthelmintics.

In this study, we have attempted to correlate dosage of *S. typhimurium* inoculum with disease, persistence of infection, and environmental contamination. The persistence and spread of *S. newport* placed on the skin of cattle was also studied.

Procedure

Inoculation procedures. Three groups of four steers each were inoculated orally with marker *S. typhimurium.* Groups 1, 2, and 3 were inoculated orally with 40,000,000, 7,000,000, and 1,000,000 units of *S. typhimurium*, respectively. The inoculum for each steer was placed in a gelatin capsule and administered with a balling gun. Ages of the steers were 19 mo (group 1), 8 mo (group 2), and 12 mo (group 3).

Group 2 steers were also inoculated topically with a strain of *S. newport.* Each hindfoot was placed in a plastic bag containing bovine feces inoculated with 1,100 salmonellae per lb.

Sampling procedures. Fecal samples were collected from the rectum and frozen at -4°F. At each sampling, rectal temperatures were recorded and observations of general appearance and clinical signs were noted.

In group 1, fecal samples were collected from two calves twice daily for 9 days after inoculation and then necropsied following euthanasia. The remaining two animals were sampled twice daily from 1 to 64 days, then once daily from 64 to 103 days, and, thereafter, once a day 3 days a wk (Monday, Wednesday, and Friday) from 103 to 365 days after inoculation.

In group 2, fecal samples were collected once daily for 39 days after inoculation and then once a day 3 days a wk to day 109. Rectal mucosa scrapings, using a wooden applicator stick, were collected from this group from day 5 to day 36 after inoculation. Microbiological samples of each foot were taken once a day (Monday through Friday) for 17 days after inoculation and then once a wk for two additional weeks. Foot samples were collected by scraping and swabbing the hoof walls with a sterile wooden applicator stick and then a piece of sterile gauze. On day 21 after inoculation, hair clippings from above the hoof were collected. Blood samples were taken for bacterial culture once a wk for 4 weeks.

In group 3, fecal samples were collected once daily for 43 days after inoculation and then once a day 3 days a wk to day 68.

Ground samples of the pens, as well as feed and water samples, were taken once during clinical signs for groups 1 and 3, and four times (once a wk for the first 4 wk) for group 2.

Tissue samples were harvested from all steers at necropsy following euthanasia. Sampling included brain, spinal cord, tonsil, various muscles, heart, lung, liver, spleen, kidney, urinary bladder, gall bladder, rumen (and contents), omasum (and contents), abomasum (and contents), duodenum (and contents), jejunum (and contents), cecum (and contents), colon (and contents), rectum (and contents), mesenteric lymph nodes, peritoneal fluid, pericardial fluid, and blood. Two steers in group 1 were necropsied 9 days after inoculation and the remaining two at approximately 1 year. Group 2 steers were necropsied 125 days after inoculation and group 3 steers were necropsied 80 days after inoculation. Tissue samples were frozen at -94°F.

Microbial analysis. Suspect colonies from all samples were identified by genus and species using a computerized microbiology system. *Salmonella typhimurium* isolates were also checked to verify compatibility with the marker inoculum. The salmonella isolates were also sent to the National Veterinary Services Laboratory for further verification.

Results

Group 1. Three steers showed severe clinical signs of diarrhea, elevated rectal temperatures (102 to 104°F), and ataxia 1 day after inoculation. The marker strain of *S. typhimurium* was found in fecal samples from two of the clinically ill steers 1 day after inoculation. The other clinically ill steer shed the marker bacteria on day 2. Fecal shedding of salmonellae persisted for 4 days in two of the steers and 6 days in the third. Clinical signs in two of the steers increased in severity and euthanasia was necessary on day 9. Salmonellae were never isolated from the feces of the steer showing no clinical signs.

Two steers were necropsied on day 9 and the marker strain of salmonella was found in the distal jejunum of both, in the proximal jejunum of one, and in the rectum of the other. *Salmonella infantis* was found in the urinary bladder, a mesenteric lymph node, and the caudal lumbar spinal cord of one steer. The other steer had *S. infantis* in contents of the middle jejunum, abomasal fluid, and the liver. This wild strain of salmonella was never isolated from fecal samples during the experiment.

Clinical signs of the surviving affected steer gradually decreased during the year; however, the steer developed signs of laminitis. Laminitis was not noted in any of the other steers (groups 1, 2, or 3). At necropsy, tissues and gastrointestinal contents of the two surviving steers were salmonella negative.

Group 2. Mild clinical signs of ataxia, slightly elevated rectal temperatures (102 to 103°F), and diarrhea were noted in all steers. Marker salmonellae were found in the fecal sample of one steer on day 4 after inoculation and in the fecal sample of another steer 13 days after inoculation.

[1]Daniels is a research microbiologist, Animal Health Systems Research Unit, MARC; Woollen is a veterinary medical officer, Animal Health Systems Research Unit, MARC; Dickson is a research food technologist, Meats Research Unit, MARC; and Littledike is the research leader, Animal Health Systems Research Unit, MARC.

These were the only positive fecal samples in this group. Salmonella contamination persisted between the claws for 8 days on one steer, for 3 days on another, and for 7 days on two steers. Attempts to isolate salmonellae by scraping the hoof wall or from clipped hair was unsuccessful. In all four animals, the marker strain of salmonella was found on one front foot and no positive ground samples were found.

Group 3. No clinical signs were observed. At necropsy 3 wk later, no gross lesions were noted and no salmonellae were isolated from tissues or gastrointestinal contents.

Conclusions

Severity of clinical signs was variable. Severity of disease appeared to be related to the infectious dosage, but individual variability was also observed.

Fecal shedding of salmonellae was also not consistent. Individual variability of both onset and duration was observed in groups 1 and 2. The fact that no fecal shedding of salmonellae was observed in group 3 suggests that there is a minimal infectious dose required to induce fecal shedding of salmonella. Long-term persistence of enteric *S. typhimurium* infection with recurrent shedding was not observed. A wild strain of salmonella, *S. infantis*, was recovered from various tissue samples of clinically ill steers, but never recovered from rectal fecal samples. This microorganism was not recovered from fecal samples of clinically normal pen-mates.

Ground, feed, and water samplings were not reliable in evaluating fecal shedding of *S. typhimurium* in the cattle pens. In spite of the spread of *S. newport* infection between the claws of the hindfeet to the forefeet, this microorganism was never recovered from ground samples. Even during periods of known fecal shedding, salmonellae could be recovered only from one sample of damp soil at the base of a watering unit.

It was demonstrated that active infection of the gastrointestinal tract can be present with no shedding of salmonellae in the feces. This observation suggests that isolation of salmonella from fecal material is a poor indicator of the salmonella infection status of beef cattle. Most of the time during clinical signs of salmonellosis, we were unable to isolate the organism in rectal samples or rectal mucosal scrapings. It was shown that even if fecal sampling is negative, carcass tissues may be contaminated with salmonellae and could possibly serve as a potential source of contamination to processing facilities, employees, and consumers.

Determination of Passive Immunity in Calves[1,2]

Louis J. Perino, R. James Sutherland, and Neal E. Woollen[3,4]

Introduction

Calves passively acquire a significant and vital portion of their immune protection from disease through consumption of the first milk (colostrum). The immunoglobulins (antibodies) that are contained in colostrum will help protect the calf from disease for the first several months of life. This process is called passive immunoglobulin transfer.

Failure of passive immunoglobulin transfer (FPT) is a serious and ongoing problem in calves. Although many factors that contribute to FPT have been examined, it continues to be an obstacle to profitability. Calves that do not receive adequate colostrum are at increased risk of infection from a variety of disease-causing organisms.

Several methods of detecting FPT have been described. Evaluating the status of passive immunity in calves is hindered by deficiencies in the available testing technologies. The most accurate means to assess FPT is determining concentrations of serum immunoglobulin. The predominant type of immunoglobulin transferred from the cow to the calf through colostrum is immunoglobulin G (IgG). Direct measurement of serum concentrations of IgG is usually accomplished using radial immunodiffusion. The value of this test is limited by the high cost involved, the technical expertise required, and the lack of relevance of the test results after the 24 to 48 hr required for the test to run.

Several indirect methods of determination are available. These include zinc sulfate turbidity, sodium sulphite precipitation, glutaraldehyde coagulation, and serum refractometry. These are indirect measurements of the immunoglobulin levels of the calf and therefore are subject to artifactual readings due to aberrations in hydration status, total blood protein levels, and other blood attributes. Some of the above tests (zinc sulfate turbidity, sodium sulphite precipitation, and glutaraldehyde coagulation) require the transport of test tubes and reagents to the field. These three tests are semiquantitative and provide estimates of minimal levels or ranges of serum immunoglobulin levels. Refractometry is simple, quick, and inexpensive, but considered the most inaccurate estimator of immunoglobulin status.

Gamma-glutamyltransferase (gamma-GT) is a membrane associated enzyme located in multiple sites throughout the body. Gamma-GT is located primarily in cells that have absorptive or secretory functions. Serum level of gamma-GT is recognized as a useful clinical indicator of liver disorders in many species. Activity of gamma-GT in colostrum has been reported to be high in a number of species, including dogs, sheep, cattle, and human beings. In many of these species, serum activity of gamma-GT in neonates that have consumed colostrum is elevated. However, this is not true in all species, with horses being a reported exception.

The purposes of this study were to characterize the activity of serum gamma-GT in newborn calves before and after suckling and to explore the usefulness of serum gamma-GT as an indicator of FPT in calves.

Procedure

Blood samples were collected from the calves of 48 fourbreed composite heifers (1/4 Red Poll, 1/4 Hereford, 1/4 Pinzgauer, 1/4 Angus) at the time of birth and at 1 day of age. Serum was harvested from the blood, frozen, and stored for later assay.

At birth, calves received an ear tag, oral rotavirus and coronavirus vaccine, and their navels were treated with iodine. At approximately 60 days of age, and 3 wk before weaning (approximately 5 mo of age), the calves were vaccinated with multivalent clostridial and leptospiral vaccines. A modified-live virus vaccine containing infectious bovine rhinotracheitis and bovine virus diarrhea viruses was also given 3 wk before weaning.

Health status of the calves and cause of morbidity were determined by trained animal caretakers under veterinary supervision. Unusual cases were referred to the veterinary staff for diagnosis.

Serum concentrations of IgG were determined using a commercial radial immunodiffusion kit (VMRD RID Kits, VMRD, Pullman, Washington). The upper and lower limits of detection were 3,300 and 412 mg/dl, respectively. Serum total protein values were assessed with a refractometer. Activity of gamma-GT in serum was measured by automated spectrophotometry using a commercially available kit (gamma-GT reagent 44074, Ciba-Corning Diagnostics Corp, Oberlin, Ohio).

Correlation coefficient, means, percentages, and standard deviations[5] were generated with a commercial microcomputer spreadsheet program (Lotus Development Corp, Cambridge, Massachusetts). Mantel-Haenszel Chi-squares, relative risk, and Kappa values were calculated using a public-domain microcomputer epidemiologic statistic program (USD Inc, Stone Mountain, Georgia).

Results

Paired serum samples were obtained from 48 calves. Activity of gamma-GT was elevated in calves that suckled colostrum. The degree of elevation was proportional to the amount of colostrum consumed, as indirectly indicated by serum concentrations of IgG. Calves suckling colostrum had 10.0 and 1.3 times greater serum concentrations of IgG and protein, respectively, and a 26 times greater serum activity of gamma-GT, compared to concentrations at birth. At birth the avg serum concentrations of IgG and protein were 131 mg/dl[6] and 3.9 g/dl, respectively, and serum activity of gamma-GT was 28 IU/L. After 24 hr these values had increased to 1,400 mg/dl,[6] 5.0 g/dl, and 734 IU/L, for the same respective parameters.

Calves were classified as having FPT, PFPT, and normal passive transfer, on the basis of concentration of serum

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[2]Published as a research bulletin of the University of Nebraska-Lincoln Agricultural Research Division.

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[4]Appreciation is expressed to the cattle operations staff, W. Gordon Hays, manager, for assistance in collection of samples and to Jill Boyum and Tammy Sorenson for technical assistance.

[5]Standard deviations were corrected to provide unbiased estimates of standard deviation.

[6]Averages at birth and 24 hr include 14 and 8 calves, respectively, with serum IgG concentrations below 412 mg/dl for which 411 mg/dl was used to determine the mean.

IgG detected by radial immunodiffusion. Twenty-one percent of calves had FPT (Table 1).

Serum IgG concentrations, serum protein concentrations, and serum activity of gamma-GT were related (Figure 1). The correlation coefficient between IgG and gamma-GT was 0.41. The correlation coefficient between IgG and protein was 0.77.

Significant differences were detected in the morbidity between calves classified as having FPT, PFPT, and normal passive transfer (Table 2). The calves with FPT had a 9.5 times greater risk of becoming classified as sick prior to weaning compared with calves with PFPT and normal passive transfer (P=0.0004). The causes of morbidity were variable (Table 2), suggesting a generalized immunodeficiency.

The sensitivity and specificity of a cut-off value of 200 IU gamma-GT/L serum for diagnosing FPT were 80% and 97%, respectively. The sensitivity and specificity of a cut-off value of 4.2 g protein/dl serum for diagnosing FPT were 80% and 100%, respectively. The Kappa values for diagnosis of FPT using serum concentrations of IgG versus serum activity of gamma-GT, IgG versus protein, and gamma-GT versus protein were 0.72, 0.86, and 0.79, respectively.

In summary, serum activity of gamma-GT is elevated in 24 hr old calves that have consumed colostrum; therefore diagnostic value of elevations of gamma-GT for hepatic pathology is limited during at least the first wk of life for a calf that has received an adequate amount of colostrum.

The least expensive and most rapid indicator of passive immune status in this study was determination of concentration of serum total protein. However, refractometric total serum protein can be misleading as other plasma analytes such as glucose, urea, and creatinine contribute to the refractive index. Thus, sick and/or dehydrated calves can render spuriously high total serum protein values.

Table 1—Number of calves and avg serum IgG, gamma-glutamyltransferase (gamma-GT), and total protein (TSP) values at 24 hr after birth for calves classified as failure of passive transfer (FPT), partial failure of passive transfer (PFPT), and normal

Classification serum IgG levels	FPT <800 mg/dl	PFPT 800-1,600 mg/dl	Normal >1,600 mg/dl
Total calves	10	18	20
Avg IgG mg/dl	449.0[a]	1,272.0	1,990.0
Avg gamma-GT IU/L	154.0	706.0	1,049.0
Avg TSP g/dl	4.0	5.0	5.5

[a]Includes eight calves with IgG concentrations below 412 mg/dl for which 411 mg/dl was used to determine the mean.

Table 2—Clinical diagnoses of sick calves classified as failure of passive transfer (FPT), partial failure of passive transfer (PFPT), and normal at 24 hr after birth

Classification serum IgG levels	FPT <800 mg/dl	PFPT 800-1,600 mg/dl	Normal >1,600 mg/dl
DIAGNOSIS:			
Diarrhea	2	0	1
Keratoconjunctivitis	1	0	0
Arthritis	1	0	0
Pneumonia	1	0	0
Omphalophlebitis	0	0	1
TOTAL SICK	5[a]	0	2
TOTAL AT RISK	10	18	20

[a] Values differ from other values in row (P<.05).

Serum activity of gamma-GT also gave reliable indications of concentration of passive immunity but such determinations were more costly and time consuming to determine than those used for serum protein. Serum activity of gamma-GT is not susceptible to changes in other serum analytes and is less susceptible to artifacts caused by dehydration.

Determination of either gamma-GT serum activity or protein serum concentration was less expensive and gave results sooner than radial immunodiffusion for IgG. Determination of both would be useful in determining the success or failure of colostral management in groups of bovine neonates. The value in applying these tests lies in evaluation of groups of calves. Failure of passive transfer is a management problem and the prevalence of subsequent infection depends largely on the success of the colostral management. The role of these tests lies in testing healthy calves in the range of one to seven days of life. A minimum of ten calves should be sampled since the greater the sample size the less sensitive and more specific a test can afford to be.

Once effective methods of identifying calves that have experienced failure of immunoglobulin transfer have been validated, cattle producers can use these methods as management tools. If too many calves are found to have experienced failure of immunoglobulin transfer, producers can alter their management. Individual calves that have experienced failure of immunoglobulin transfer can receive special treatments such as supplementary colostrum and additional vaccinations. Evaluation of the efficacy and cost effectiveness of such interventions are part of the ongoing research in this project.

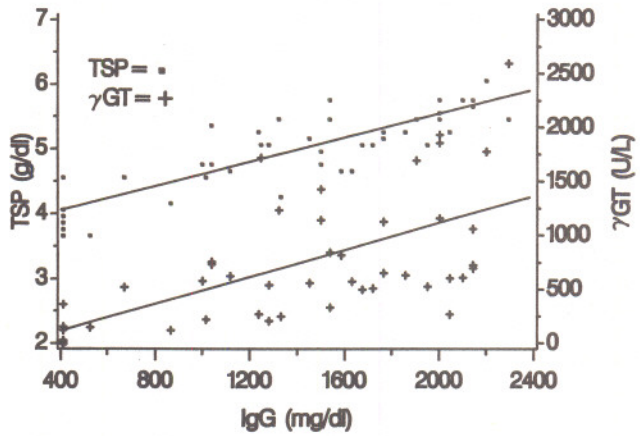

Figure 1 – Serum IgG concentrations vs serum protein concentrations (TSP) or serum activity of gamma-glutamyltransferase (gamma-GT) for calves 24 hr after birth.

Development of a Method for the Serological Differentiation Between Animals Either Vaccinated with Killed Virus Vaccine or Infected by Bovine Viral Diarrhea Virus (BVDV)

Jimmy Kwang and E. Travis Littledike[1]

Introduction

Bovine viral diarrhea (BVD), caused by the BVD virus, has been recognized in many parts of the world and is considered to have a marked economic impact on the cattle industry. In the U.S. alone, serological surveys indicated that 60 to 80% of the cattle population have antibodies to the virus. There are many strains of bovine viral diarrhea virus (BVDV) which differ in their ability to cause changes in cell culture. Thus, cytopathic and noncytopathic biotypes of BVDV are identified. The cytopathic strains induce a vacuolation of the infected cultured cells, where noncytopathic strains do not.

Control of BVDV has been attempted for many years by use of either modified-live or killed virus vaccines. The killed virus vaccine is more commonly used. The modified-live virus vaccine is known to cause complications during pregnancy, potentially fetopathogenic effects being a major concern. There is evidence that vaccination of persistently infected cattle with modified-live virus vaccine can result in severe mucosal disease. Due to the ubiquitous nature of BVDV, producers may find advantages in designing BVD control procedures for a herd to be able to differentiate between cattle that 1) have received modified-live BVD virus vaccination, 2) have received killed BVD virus vaccination, or 3) were naturally infected. This study explored the potential of BVDV protein, p80, to allow differentiation of the above three conditions.

The genome of an isolate of a BVDV strain has been sequenced. Encoded within the genome are at least four primary gene products (proteins): p20, gp116, p125, and p133. There is evidence that p125 polypeptide precursor gives rise to p80 polypeptide due to the breakdown of this precursor protein in cells infected with BVDV. The p80 area of the BVDV genome is well conserved in the many BVDV strains that have been isolated.

Procedure

New molecular biology techniques permitted the manipulation of the BVDV genome to allow isolation and recombination of the p80 gene into a DNA structure designed for production of the p80 specific protein. The recombinant p80 protein was produced, expressed, and purified in sufficient quantities to develop a specific immuno-blot assay for BVDV antibodies in cattle sera. Twenty-four cattle sera were tested: eight of the cattle were vaccinated with modified-live virus vaccine, eight were vaccinated with killed virus vaccine, and eight were naturally infected with BVD.

Results

The immuno-blot assay that was developed was tested for BVDV-p80 antigen-antibody reaction. When the BVDV-p80 protein was reacted with the cattle sera in the immuno-blot test, the following results were obtained: all sera from modified-live virus vaccinated cattle were positive; all sera from killed virus vaccinated cattle were negative, and all sera from naturally infected cattle were positive (Table 1). Since p80 is not a structural protein of the virus and the killed virus doesn't replicate in the host cell, there is not sufficient p80 antigen in cattle vaccinated with killed BVD vaccine to cause production of p80 antibodies in cattle. Therefore, cattle vaccinated with the killed BVD vaccine either do not make antibodies or do not produce detectable levels of antibodies to the p80 region of the virus. Thus, the cattle test negative. However, modified-live virus used for vaccination replicated in the host cell after vaccination and produced large amounts of p80; therefore, antibodies were produced in the cattle to the p80 and the cattle tested positive.

The significance of this finding is two-fold. First, p80 is capable of differentiating between the modified-live and killed virus vaccines. Second, if a herd was vaccinated only with killed virus vaccine and tested with p80 immuno assay, the expected results would be negative—if the herd was clean of BVDV. Any positive results would indicate that a source of natural infection must be present in the herd. This source could be from persistently viremic BVD carriers, that may or may not exhibit signs of the infection, but would spread BVD throughout the herd and give birth to carrier calves which would continue the spread of BVD in the herd. To ultimately control BVDV, carriers of the BVD virus must be identified and eliminated from the herd and no new carrier cattle added. In addition, effective vaccination of the cattle before breeding would protect the fetal calves from becoming carriers and perpetuating BVD in the herd.

Table 1—Comparison of BVDV p80 antibody response in cattle vaccinated with either MLVV, KVV, or NI with virus

Animal no.	BVDV exposure	Serum neutralization test	p80 immuno-blot assay
1	MLVV	32	+
2		16	+
3		64	+
4		16	+
5		32	+
6		32	+
7		32	+
8		32	+
9	KVV	4	-
10		8	-
11		4	-
12		<2	-
13		<2	-
14		<2	-
15		4	-
16		8	-
17	NI	>256	+
18		>256	+
19		>256	+
20		>256	+
21		128	+
22		>256	+
23		>256	+
24		128	+

BVDV = Bovine viral diarrhea virus.
MLVV = Modified-live virus vaccine.
KVV = Killed virus vaccine.
NI = Naturally infected.

[1]Kwang is a research microbiologist, Animal Health Systems Research Unit, MARC, and Littledike is the research leader, Animal Health Systems Research Unit, MARC.

Development of a Sensitive Antibody Detection Method to Bovine Viral Diarrhea Virus (BVDV) Infection

Jimmy Kwang and E. Travis Littledike[1]

Introduction

Bovine viral diarrhea virus (BVDV) is a RNA virus and a prototype member of the pestivirus genus in the genetic family Flaviviridae. Due to the rapid growth of BVDV molecular biology in the last 4 yr, our understanding of the genomic organization of BVDV has greatly increased, and a protein encoding map of the BVDV genome has been established. According to this map, it is generally accepted that a glycoprotein, identified as gp116, is the precursor which gives rise to gp62 and gp53 proteins through a proteolytic process. Further protein break down of gp62 yields glycoproteins gp48 and gp25. The order of these genes in the BVDV genome would thus be gp48-gp25-gp53. Based on the serological testing results of cattle to individual BVDV proteins, a strong immune response to glycoproteins gp53 and gp48 has been found.

Although considerable literature exists on the diagnosis of BVD disease, the methodologies (virus isolation, serum neutralization, etc.) are either time consuming, expensive, inconsistent, or unsuitable for use in large populations of cattle. Recently, recombinant techniques have found wide application in a second-generation assay for the detection of viral disease infection. We have produced recombinant gp48 in large amounts using these recombinant techniques. The large-scale production of the recombinant gp48 protein provided a convenient and economical source of immunobiologically useful material. This recombinant protein demonstrated great sensitivity and specificity for BVD antibody detection.

Procedure

A total of 175 bovine sera were included in this study. Eighty samples were from MARC, where a BVDV vaccination program has been practiced with both killed and modified-live virus vaccines during the last 10 years. The remaining 95 samples were from an isolated commercial ranch in north-central Nebraska that had never been vaccinated for BVDV. Therefore, antibody-positive individuals may represent the outcome of either, or various combinations of, natural infection, killed virus vaccine, modified-live virus vaccine, or passive immunity from the mother. In addition, five serum samples were used as the negative control and two cattle sera immunized with BVDV previously were used for the positive control.

To allow study of the role of BVDV-gp48 during infection and the subsequent immune response in cattle, we developed a specific immune assay (immuno-blot assay) by incorporating the recombinant gp48 protein into the test.

Results

The serum neutralization tests identified the 175 bovine samples as follows: 89.1% (156/175) of the sera had antibodies to BVDV and 10.9% (19/175) did not. When subjected to the recombinant-gp48 immuno-blot assay, sera from the 156 animals with serum neutralization titer equal to or greater than 1:4 reacted positively, indicating a gp48 antigen-antibody reaction was present. The 19 sera that did not have antibodies to BVD (serum neutralization titer less than 1:4) were negative in the immuno-blot. To verify the 19 negative sera samples did not have gp48 antibodies, a third test (radioimmunoprecipitation) was performed. The results of these tests were in complete agreement with the serum neutralization and immuno-blot assays. The gp48 protein was readily recognized by the BVDV-gp48 positive serum and the five negative control sera showed no reactivity. Thus, the gp48 recombinant protein proved to be both specific and sensitive when used in this immuno-blot assay.

To determine if the antibody response to gp48 differs in cattle with 1) natural infection, 2) killed virus vaccine, or 3) modified-live virus vaccine, we used three pair of sera from calves before and 4 wk after exposure to these treatments. Their serum neutralization titers and immuno-blot reactivity are shown in Table 1. This information shows the calves developed an immune response to gp48 following exposure to all three treatments. This further indicated that gp48 is a major structural protein of BVDV.

Progress in understanding the molecular biology of BVDV and the role of individual proteins in infection and immunity has been slow. Procedures have only recently been developed which increase the ease and efficiency of producing such proteins in quantity and quality to allow in-depth study. Bovine viral diarrhea virus-gp48 can be readily produced by the method described in this report and it can be used in an immuno-blot assay to detect the presence of antibodies produced by natural infection and vaccination with killed or modified BVD virus. Bovine viral diarrhea virus-gp48 is a highly conserved and recognized gene across the spectrum of BVDV strains tested. Therefore, the use of BVDV-gp48 recombinant protein may prove to be a strong candidate for developing a BVDV antibody detection test kit. The rapid, sensitive nature of such a test, and its low cost, could prove to be an effective tool for diagnosis and control of BVD in large and small cattle herds.

Table 1— Pair serum samples examined for antibody reactivity before and after different forms of virus exposure

Pair	Sera	Form of exposure	SN titer	Immuno-blot assay
1	a		<2	-
	b	NI	256	+++
2	a		<2	-
	b	MLVV	64	+++
3	a		<2	-
	b	KVV	16	++

SN = Serum neutralization.
a = Before exposure.
b = After exposure.
NI = Natural infection.
KVV = Killed virus vaccine.
MLVV = Modified-live virus vaccine.

[1]Kwang is a research microbiologist, Animal Health Systems Research Unit, MARC, and Littledike is the research leader, Animal Health Systems Research Unit, MARC.

Consequences of Antigenic Diversity of Bovine Viral Diarrhea Virus

E. Travis Littledike, Steven R. Bolin, and Julia F. Ridpath[1,2]

Introduction

Two main biotypes of bovine viral diarrhea virus (BVDV) have been identified based on their ability to cause changes in tissue culture cells. The cytopathic biotype multiplies in tissue culture and kills cells, while the noncytopathic biotype slowly multiplies in tissue culture and has much less ability to kill tissue culture cells. In general, cytopathic BVDV biotypes cause acute infections that often kill the bovine fetus, while noncytopathic BVDV biotypes often result in chronic infection of the fetus which, subsequently, develops in calves and adults that carry and shed noncytopathic viruses at high levels for the rest of their lives.

Previous studies have indicated that cytopathic and noncytopathic viruses are antigenically similar. Also, after vaccination of cattle with modified-live or killed BVDV vaccines, antibodies are induced that neutralize a broad range of BVDV. However, very significant antigenic diversity among BVDV has been described. Also, studies indicated that some neutralizing antibodies from cattle that have recovered from BVDV react differently with several BVD isolates. In addition, monoclonal antibodies developed against specific BVDV isolates can differentiate BVDV into several groups and, when cattle which are persistently infected with noncytopathic BVDV are challenged with cytopathic BVDV, the antibodies they produce have a very narrow range of viral neutralizing activity.

Thus, some antigenic diversity among BVDV, as detected by neutralization tests, is well established. However, there is little information that shows the practical consequences of this antigenic diversity relative to the disease in cattle.

The primary purpose of this study was to identify cattle in MARC's herd that were persistently infected with BVDV and test the isolates of BVDV from the MARC herd to determine if these natural field viruses could be neutralized by serum obtained from MARC cows vaccinated with killed BVDV.

Procedure

Source of sera. Serum was obtained over a 5-wk period in the fall of 1988 from 5,726 cows maintained as a semi-closed herd on pasture. At that time, the herd had been on a killed virus vaccination program for BVD for more than 7 years. The vaccine used was of bovine-cell origin and contained the Singer isolate of cytopathic BVDV. The vaccination program consisted of calfhood vaccination with the first dose given 1 mo before weaning and the second dose given 4 wk later at the time of weaning. Thereafter, cows were revaccinated with a single dose of vaccine 2 to 3 wk before breeding. Approximately, 80% of cows calved in April and May and the remaining 20% calved in August and September. At the time samples of serum were obtained, cows calving in the spring were at approximately 3 mo of gestation and had been vaccinated approximately 4 mo previously. Cows that calved in the late summer had calved approximately 2 mo previously and were vaccinated approximately 12 mo previously. The herd was managed as several groups of varying numbers maintained on separate pastures. At weaning, calves from all groups were moved to a feedlot. Performance of a calf in the feedlot was one of the criteria used to select herd replacements and cull dams. The replacement rate for the herd was approximately 20% per year.

Viral neutralization tests. Sera were tested for neutralizing antibodies against one or more of the following viruses: cytopathic viral isolates BVD-TGAC and BVD-Singer, and noncytopathic viral isolates BVD-3659, BVD-2541, BVD-9789, BVD-NEB, BVD-7443, BVD-639, and BVD-VM. Noncytopathic viruses 9789, NEB, 7443, and VM were isolated from persistently infected cattle, BVD-639 was isolated from the uterus of a cow that aborted, and BVD-3659 and BVD-2541 were isolated from persistently infected cattle identified during this study. With the exception of BVD-3659 and BVD-2541, the viruses used were antigenically distinct from each other when tested against a panel of monoclonal antibodies that had neutralizing activities. Viruses 3659 and 2541 were antigenically similar to each other, but distinct from the other viruses.

Neutralization tests against BVD-TGAC virus were performed on all samples of serum. Those samples of serum that had neutralized antibody titers of less than 2, 2, 4, or 8 were tested for neutralizing antibody titer against BVD-Singer virus. In addition, 18 selected samples of serum that had neutralized antibody titers of less than 2, 2, or 4 against BVD-TGAC virus were tested for neutralizing antibodies against the aforementioned seven noncytopathic BVD viruses. All samples of serum (n=56) that had neutralized antibody titers of eight against BVD-TGAC virus were tested for neutralizing antibodies against noncytopathic BVD-3659 virus.

Immunoprecipitation. In selected samples of serum from killed virus vaccinates that had neutralized antibody titers of less than 2 to 256 against BVD-TGAC virus, antibody specificity for polypeptides induced by BVD-Singer virus (vaccine virus) was identified by immunoprecipitation. For comparison, viral induced polypeptides were immunoprecipitated with samples of serum obtained from modified-live virus vaccinates that had neutralizing titers of 2 to 16 against BVD-TGAC virus.

Results

Virus was isolated from 3 of 448 samples of serum that had neutralized antibody titers of 64 or less against BVD-TGAC virus (Table 1). In those three samples of serum, the neutralizing antibody titers against BVD-TGAC virus were less than 2, 2, and 32. The corresponding neutralizing antibody titers against BVD-Singer virus were 32, 64, and 256. Persistent infection was subsequently confirmed in two cows (ages 2 and 3 yr) by isolation of virus (designated BVD-3659 and BVD-2541) from a second sample of serum obtained at least 4 wk before or after the original sample of serum. Due to poor performance, a third cow (2 yr of age) had been sold soon after the original sample of serum was obtained. It was not possible to confirm persistent infection in that cow. Virus was not isolated from sera obtained from siblings of one persistently infected cow or the dam of the other persistently infected cow.

Neutralizing antibody titers of four or less against BVD-TGAC virus were detected in samples of serum obtained

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[2]The full report of this work was published in Am. J. Vet. Res. 52(7):1033-1037.

from 91 and 40 cows that calved in the fall and spring, respectively. In each of those 131 samples of serum, neutralizing antibody titers against BVD-Singer virus were greater than the corresponding neutralizing antibody titers against BVD-TGAC virus (Table 1). From those 131 samples of serum, 18 were selected and further tested for neutralizing antibodies against seven noncytopathic BVD viruses. None of these 18 samples of serum contained neutralizing antibodies against all seven noncytopathic viruses (Table 2). Noncytopathic BVD-3659 virus was not neutralized by any of the selected samples of serum. The BVD-3659 virus was neutralized by 18 of 56 samples of serum that had neutralized antibody titers of eight against BVD-TGAC virus (data not shown).

Conclusion

Although the herd surveyed in this study had been on a killed BVDV vaccination program for 7 yr, two persistently infected cows were identified. Persistent BVDV infection is lifelong and occurs in calves born to dams that have an acute, transient viral infection during the first 4 mo of gestation or to dams that are themselves persistently infected. The two persistently infected cows likely represented failure of vaccination to protect against fetal infection under natural conditions. That finding supported previous studies in which experimental, killed BVDV vaccines failed to prevent transplacental transmission of virus in challenged, exposed cows.

Failure of vaccination to protect the fetus might be explained by antigenic differences among BVD viruses. In several sera from this herd, the titer of neutralizing antibodies against the vaccine virus was relatively high (64 to 256); however, several isolates of BVD virus were identified that escaped neutralization by those same sera. Those data clearly indicate antigenic diversity among BVD viruses. Included among the viruses that escaped neutralization were noncytopathic viruses BVD-3659 and BVD-2541 that were isolated from persistently infected cows in this herd. Thus, the persistently infected cows likely represented a practical consequence of antigenic diversity among BVD viruses.

Natural decay of viral-specific antibody likely contributed to the lack of detectable antibodies against certain BVD viruses. Data from this study support this hypothesis. Approximately, 80% of the cows were given a booster dose of vaccine 4 mo before samples of sera were obtained and the remaining 20% of cows were boostered with vaccine 12 mo before sampling. A disproportionately high 91 of 131 samples of serum (70%) that had neutralizing antibody titers of four or less against BVD-TGAC virus were obtained from cows vaccinated 12 mo before sampling. Thus, failure to detect neutralizing antibodies against certain BVD viruses several mo after vaccination may have been attributable to viral antigenic diversity and natural decay of antibodies.

On the basis of the large number of samples of sera that had high titers of neutralizing antibodies against a BVD virus antigenically distinct from the killed vaccine virus, and on the pattern of immunoprecipitated viral-induced polypeptides associated with those sera, we speculate that most of the cattle in this herd had been infected with BVD virus. Identification of only two persistently infected cows might seem trivial; however, the rate of persistent infection probably would have been higher if newborn calves were tested instead of cows. Subsequent to completion of this study, eight calves in this herd (approximately 2 yr old) were identified as persistently infected with BVD virus. The persistently infected cattle in this herd likely were born to vaccinated cows that were infected with field virus during early gestation. Consequences of antigenic diversity among BVD viruses are not likely limited to fetal infections in vaccinated dams. Newborn calves with colostral antibody or vaccinated feedlot calves might be susceptible to disease induced by certain antigenic variants of BVD virus.

Table 1—Distribution of neutralizing antibody titers ($-\log_2$) against bovine viral diarrhea (BVD)-TGAC virus in all samples of serum and range of titers and geometric mean titers of neutralizing antibodies against BVD-Singer virus in samples of serum that had neutralized antibody titers of three ($-\log_2$) or less against BVD-TGAC virus

Number of sera	Neutralizing antibody titer to TGAC virus	Geometric mean titers to Singer virus	Range of neutralizing antibody titers to Singer virus
48	0	4.09	1 to 8
42	1	5.25	3 to 8
41	2	6.11	3 to 8
56	3	5.21	3 to 8
61	4	ND	ND
70	5	ND	ND
130	6	ND	ND
253	7	ND	ND
5,025	8	ND	ND

ND = Not done.

Table 2—Neutralizing antibody titers (-log2) in select sera against bovine viral diarrhea (BVD)-TGAC virus, corresponding titers of neutralizing antibodies against BVD-Singer virus, and presence (+) or absence (-) of detectable concentrations of neutralizing antibodies against seven antigenically distinct noncytopathic BVD viruses

Neutralizing antibody titer		Neutralizing activity against noncytopathic viruses[a]						
TGAC virus	Singer virus	3659[b]	2541[b]	9789	NEB	7443	639	VM
0	1	-	-	-	-	-	-	-
0	1	-	-	-	-	+	+	-
0	3	-	-	-	-	-	+	-
0	4	-	-	-	-	-	-	-
0	6	-	-	-	-	-	-	-
0	6	-	-	-	-	+	+	+
0	7	-	-	-	-	-	-	+
0	7	-	-	-	+	+	-	+
0	8	-	-	-	-	+	-	-
1	7	-	-	-	+	+	+	+
1	7	-	+	+	+	+	+	+
1	8	-	-	-	-	-	+	+
1	8	-	-	-	+	+	+	+
2	3	-	-	-	-	-	-	+
2	6	-	+	+	+	+	+	+
2	8	-	-	-	+	+	+	+
2	8	-	-	+	+	+	+	+
2	8	-	+	-	+	+	+	+

[a] Serum was diluted 1:1 with fluid containing virus.

[b] Viral isolates from MARC herd.

Brachygnathia in Simmental Cattle

Neal E. Woollen[1]

Introduction

Brachygnathia is a deficit in mandibular length causing the incisor teeth to meet the upper dental pad behind its anterior angle. It is a problem to breeders of both red and black Simmental cattle, as well as other breeds. The condition has been considered inherited as a simple autosomal recessive trait. It has also been observed as one part of a lethal, multiple-defect syndrome in Simmentals caused by the calf being born with an extra chromosome (Trisomy 17). Intrauterine infection with bovine viral diarrhea-mucosal disease virus (BVD-MD) also can cause the defect, but usually in this case the calf is also born with a variety of additional problems. In Angus cattle, the defect has also been observed accompanying osteopetrosis, an inherited bone defect.

Selective culling and breeding practices designed to remove an undesirable genetic trait have been unsuccessful for a number of producers of both red and black Simmentals. For that reason, we have been studying the inheritance of this condition in more detail.

Procedure

An affected and distantly related red bull and heifer were selected as the foundation for this project. Following superovulation and embryo transfer, 14 calves were produced from this mating. One affected heifer was selected to mate back with her sire. Eleven calves have been produced from this mating. The same bull was mated to an affected Angus cow. Six calves have been produced from this mating. Semen has been collected from a black Simmental bull. To evaluate the source of deleterious genes in black Simmental cattle, he will be mated to the same females.

Results

The initial mating produced three (21%) affected calves. The father- daughter mating produced two (18%) affected calves. The Angus-Simmental mating has produced no affected calves. Affected calves have had no additional significant defects, and have been of both sexes.

In a recessive mode of inheritance, two affected cattle should produce 100% affected calves if penetrance is complete. It is clear that there are significant factors affecting penetrance, or that the condition is not due to recessive gene action.

There is no significant difference in the percentage of affected calves produced from either Simmental mating. It is reasonable to assume that if enough calves were produced, the affected percentage would be roughly 25%. This pattern of inheritance is compatible with overdominance at two gene loci (locations) involving four genes. In overdominant inheritance, the heterozygote (Aa) is different from either the homozygous dominant (AA) or recessive (aa). Overdominance at one locus would produce 50% affected calves, and overdominance at two loci would produce 25% affected calves.

The fact that no affected calves have been produced from the Simmental-Angus mating suggests that inheritance of the condition is different between the two breeds. However, with only six calves produced to date, this is only an assumption. If this pattern continues, we also can assume the condition in black Simmentals is of either Simmental or Angus origin and not combined genetic action. Identical matings using the black Simmental bull should clarify this matter.

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Transmission of Bovine Leukosis Virus[1]

Louis J. Perino, E. Travis Littledike, Larry V. Cundiff, and Catherine E. Dewey [2,3,4]

Introduction

Bovine leukosis virus is an exogenous retrovirus (Retroviridae, Oncovirinae) that infects lymphocytes of cattle. Infection with bovine leukosis virus and the concomitant antibody response are lifelong. Infection can result in several outcomes, including production of antibodies against bovine leukosis virus without other evidence of infection, inversion of the T:B lymphocyte ratio, persistent lymphocytosis, and clinical lymphosarcoma.

The prevalence of an infection in a population of animals is the proportion of the group infected at any given time. Surveys have shown the prevalence of bovine leukosis virus infection in cattle populations ranging from 0 to nearly 100%. This wide range of prevalence levels is likely due to variations in risk factors such as husbandry practices, insect vectors, and genetic resistance. For example, prevalence tends to be higher in dairy than beef cattle and in cattle in Southern vs Northern states.

The relative importance of the known modes of transmission of bovine leukosis virus has not been established in beef cattle. Also, the economic impact of bovine leukosis virus infection in beef cattle has not been examined. However, the presence of cattle infected with bovine leukosis virus in a herd drastically reduces opportunities to export cattle and/or semen to many countries.

Excluding an early transient viremia, the virus locates in lymphocytes as a DNA provirus. Because of its cell-associated nature, transmission is believed to occur by movement of infected lymphocytes to susceptible animals. Intradermal, subcutaneous, intramuscular, or intravenous inoculation of as little as one microliter of blood or intracutaneous inoculation of 2,500 lymphocytes from an infected animal (equivalent to .5 microliter of blood) results in transmission of bovine leukosis virus.

Transmission of an infectious agent in this manner is a form of horizontal transmission. Other means of horizontal transmission have been investigated, including casual contact in common housing; animal husbandry procedures such as dehorning without sanitizing the dehorner between cattle, tattooing with common pliers, rectal palpations with common sleeves, and injections with common needles; and blood feeding arthropods. In addition, transmission from the dam to calf, termed vertical transmission, has also been shown to occur with bovine leukosis virus.

The purpose of these studies was threefold: 1) to characterize the bovine leukosis virus status of the MARC cattle population, 2) to investigate the extent and significance of vertical transmission of bovine leukosis virus in the MARC cow herd, and 3) to investigate the role of specific management practices in horizontal transmission of bovine leukosis virus in the MARC cattle herd.

Procedure

Bovine leukosis virus infection detection. Bovine leukosis virus infection status was assessed by the presence of serum antibodies against bovine leukosis virus. Blood samples were collected from cows by jugular or coccygeal venipuncture. Serum was harvested from the blood, frozen, and stored for later testing. Serum antibodies to bovine leukosis virus were detected using agar gel immunodiffusion.

Phase I. A sample size was determined for each area of the MARC that was large enough to detect at least one positive animal with 95% confidence if infection rates were at or above 5% in a group (Figure 1). A random sample of the 1989 adult cattle at each area was identified. The 1989 sera collected from these cattle were retrieved and the bovine leukosis virus infection status was determined. All adult cattle in the twinning project (area 52 and 391 of 821 head at area 73) were tested because of a previous history of bovine leukosis virus infection followed by an eradication program.

Based on results of this survey and analysis of cattle movement patterns, all adult cattle from areas 12, 25, 58, 67, and 73 (non-twinning project) were tested. In addition all cattle in the disease resistance herd (area 18) and all area 18 Angus were tested.

The serum collected in 1988 was tested from any cow found positive in 1989. Sera from all available dams and progeny of infected cattle were also tested.

Phase II. Area 12, having been determined to have the largest number of bovine leukosis virus infected cows, was selected for more intensive monitoring. All positive cows were sampled for hematologic determination of peripheral lymphocyte numbers and T:B lymphocyte ratios. The order in which cows were processed was recorded. Processing activities included injection with common needles, rectal palpation with common sleeves, replacement of ear tags with common pliers, hair clipping over brands, and blood sampling with individual needles. All cattle were sampled yearly, in the fall, for determination of bovine leukosis virus infection status. All calves born to infected cows were sampled to determine bovine leukosis virus infection status after six mo of age, when colostral antibodies to BLV were no longer present.

Results

Phase I. Results of the initial survey are shown in Table 1. A total of seven cattle in four areas were found to be infected during the initial screen. This sample size was designed to determine the presence of at least one infected animal with 95% confidence if infection rates were at or above 5% in the group. The detection of one or more positive animals gives no estimate of the true prevalence of infection in the population. Thus, further testing was required to determine the prevalence of bovine leukosis virus infection in these areas.

All cattle in the twinner population (areas 52 and 73) were negative. This suggests that the BLV eradication program undertaken following assembly of this herd was successful.

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[1]Published as a research bulletin of the University of Nebraska-Lincoln Agricultural Research Division.

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[3]Appreciation is expressed to the cattle operations staff, W. Gordon Hays, manager, for assistance in collection of samples and to Jill Boyum and David F. Heilman for technical assistance.

[4]The authors acknowledge the contribution of Dr. Dennis Wilson in the design of Phase II of this project.

Further testing of cattle in positive areas and areas where positive cattle may have lived revealed additional positive cattle (Table 2). This included areas 12, 25, 58, 67, 73, and two subpopulations of area 18, the disease resistance and Angus herds. The prevalence rates were 3.9%, .7%, .2%, .5%, .2%, 0%, and 9%, respectively.

Infection status of all dams and progeny of infected cows was determined to assess the possibility of vertical transmission. Infected cows had produced 139 calves. Of seven dams and 48 offspring for whom serum samples were available, two infected dam-daughter pairs were found. In one dam-daughter pair both individuals were infected prior to 1988, thus year of seroconversion could not be determined. In the other pair, the dam seroconverted in 1989 and the daughter seroconverted prior to 1988. Thus, in the first pair the possibility of vertical transmission cannot be ruled out. In the latter pair, vertical transmission is not possible. None of the other 46 offspring showed evidence of vertical transmission.

Of the 30 cows in area 12 found to be infected in 1989, analysis of their 1988 sera showed that six of these cows were negative in 1988, suggesting that active transmission was occurring in area 12.

A summary of the location, population size, number of cattle tested, and number of cattle found infected in 1989 is provided in Figure 1.

Phase II. This project is currently in phase II, yet some preliminary results are available. Blood samples were collected from all positive cows in area 12. Total lymphocyte numbers and T:B lymphocyte ratios were determined to characterize the current status of the animals with respect to bovine leukosis and to help estimate the relative potential of the individual for infectivity to other animals. No evidence of peripheral lymphocytosis or aberrant T:B lymphocyte ratios was detected.

Samples collected from all area 12 cows in the fall of 1990 (n=915) and 1991 (n=953), revealed 8 and 17 newly infected cows, respectively. This further suggests that active transmission is occurring via some means at area 12.

All calves born in 1990 to infected cows (n=32) were sampled in the summer of 1991 and none were found to be infected. Sampling of calves born in 1991 is pending.

Information about the order in which cattle are processed is being collected. This data, combined with determination of the identity of newly infected cows, will be used to evaluate whether or not cattle processed directly after bovine leukosis virus- positive cattle were at greater risk to seroconvert than those processed prior to bovine leukosis virus-positive cattle. This will assess the risk of routine husbandry procedures such as injection with common needles and rectal palpation with common sleeves.

In summary, cows infected with bovine leukosis virus are present in several MARC beef cattle herds, but the prevalence rate is low. The highest concentration of infected cows is in one area at MARC. The management factors that have contributed to this are not known. There is active transmission of bovine leukosis virus in at least one population of cattle. The means of transmission has not been determined. It appears that vertical transmission is not an important contributor.

While the low infection rate present in this population of cattle does not afford the opportunity to evaluate production parameters, it may allow us to identify factors that contribute to field transmission of bovine leukosis virus. The practical implication is that knowledge of how this virus is transmitted allows producers to minimize high risk husbandry techniques, thus reducing the number of newly infected cows.

Table 1—Results of initial screening of adult cattle with a sample size, per area, large enough to detect at least one positive cow if infection rates were 5% or greater. All twinner cattle in areas 52 and 73 were tested.

Area	Number present	Number sampled	Number positive
12	760	56	4
18	754	56	0
25	291	53	1
46	587	56	0
52	361[a]	361	0
53	371	54	0
58	850	56	1
67	950	57	0
73	821[b]	447	1
82	186	50	0
84	150	48	0
99	48	31	0
Total	6,129	1,325	7

[a]Includes 166 adult bulls, all of which were screened, that were not part of the twinner herd.

[b]Includes 430 adult cattle, 56 of which were screened and 1 of which was positive, that were not part of the twinner herd.

Table 2—Results of additional testing of cattle in positive areas and areas where positive cattle may have lived

Group	Number tested	Number positive
Area 12	760	30
Area 25	291	2
Area 58	850	2
Area 67	950	5
Area 73 non-twinner project cows	430	1
Area 18 disease resistance herd	155	0
Area 18 Angus	88	5
Total	3,524	45

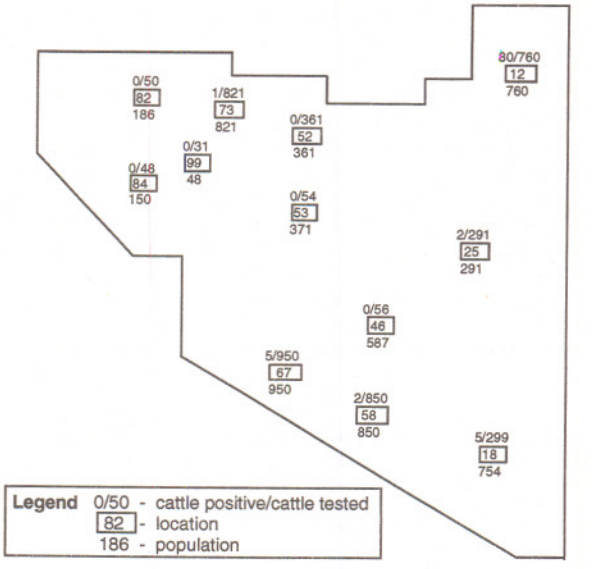

Figure 1 – Summary of the location, population size, number of cattle tested, and number of cattle found infected in 1989.

Isolation of *Pasteurella* spp. from Sick and Healthy Feedlot Calves Using Four Different Sampling Techniques[1]

Keith A. Gilmore, D. Dee Griffin, and Louis J. Perino[2,3]

Introduction

Bovine respiratory disease is the most common disease complex of feedlot cattle. The peak incidence of the disease occurs within the first few weeks of arrival at the feedlot. Bovine respiratory disease is attributed to a complex interaction between bacteria, viruses, environment, stress, and managerial practices. *Pasteurella hemolytica*, and to a lesser extent *Pasteurella multocida*, are considered to be the most common bacterial isolates from cases of bovine respiratory disease.

The purpose of this study was threefold: 1) compare the ability of four different sampling techniques to isolate *Pasteurella* spp. from the respiratory tract of calves, 2) compare the prevalence of *Pasteurella* spp. in the respiratory tract of sick calves and clinically normal cohorts, and 3) evaluate the feasibility and practicality of performing nonsurgical tracheal washes in a feedlot setting.

Procedure

In the fall a group of 64 spring born calves ranging in age from four to six mo were weaned and transported to the MARC feedlot. All of the calves were born and raised at MARC. The calves were vaccinated three wk prior to weaning with a modified live infectious bovine rhinotracheitis virus and bovine viral diarrhea virus (IBR-BVD), polyvalent *Clostridium* spp., and polyvalent *Leptospira* spp. vaccines. Calves were boostered with IBR-BVD and given ivermectin 30 days after weaning and transport to the feedlot. In the feedlot the calves were fed chopped brome hay for the first three days, 40% ground alfalfa hay was added to the diet for the following five days, and silage was introduced after eight days.

The calves were monitored for 28 days in the feedlot. The cattle were observed daily for signs of disease and were removed from the pen when signs of disease became apparent. Calves which exhibited rapid breathing, a runny nose, coughing, inappetence, depression, or isolation were removed to the hospital facility. If a removed calf had a rectal temperature of 103°F or above and the illness could not be referred to any other body system, the calf was treated for respiratory disease. The treatment protocol was intravenous tylosin (8 mg/lb) and oxytetracycline (7 mg/lb) daily for four days, oral sulfadimethoxine boluses (62.5 mg/lb) on the first day and intramuscular vitamin B complex (1 ml/100 lb) on the first day. For each sick calf removed from the pen, sampled, and treated a clinically normal cohort of the same approximate age, gender, and disease history was removed from the pen and sampled but not treated.

Sick and cohort calves were sampled on the day they were removed from the pen before the initiation of treatment and on the last day of the initial respiratory disease treatment. The calves were restrained in the treatment chute and a six inch sterile cotton swab was inserted into the nostril. The swab was then placed into a sterile tube with one milliliter of sterile phosphate buffered saline (PBS). A 13.25 inch guarded nasal swab was then inserted into the nostril. A mouth speculum was used to open the mouth and a sterile 26.25 inch guarded tracheal swab was inserted through the mouth and into the trachea. Both the 13.25 and 26.25 inch guarded swabs were closed systems that contained transport media. Finally, a 36 inch piece of eight millimeter diameter rigid plastic tubing was inserted through the mouth and into the trachea. A sterile length of flexible tubing was threaded down the plastic tube into the trachea. Using a 60 milliliter syringe, approximately 120 milliliters of sterile PBS was injected down the flexible tubing into the distal trachea and quickly aspirated back to obtain a tracheal wash. The total sampling time for each calf was approximately two minutes.

The samples were transported four miles to the Great Plains Veterinary Educational Center Clinical Microbiology Laboratory and plated on blood agar with 5% sheep blood and McConkey II agar. The plates were incubated at 98.6°F in 5% CO_2 and examined at 24 and 48 hr for growth. *Pasteurella* spp. were identified using standardized isolation procedures.

Mantel-Haenszel Chi-squares were calculated using a public-domain microcomputer epidemiologic statistic program (USD Inc, Stone Mountain, Georgia).

Results

Of the 64 calves included in the study, 19 developed clinical bovine respiratory disease within the first 28 days of their arrival at the feedlot. Each of the cohorts remained healthy during the sampling period with the exception of one calf which developed respiratory disease and was then included in the sick group. The morbidity rate was 31% and the mortality rate was 0% for this group of calves during the study period. The results of the *Pasteurella* spp. isolation for each sampling technique are summarized in Table 1.

When the four different sampling techniques were compared on each day for cohort and sick calves there was not a significant difference in the number of *Pasteurella* spp. isolates obtained by any of the techniques.

This information is significant because there is a great difference in the degree of difficulty of sample collection between the four techniques. The performance of all four techniques required minimal time, thus all of the techniques can be performed in the feedlot. The easiest and least expensive of the four is carefully placing a six inch cotton swab into the nasal passage, placing it in PBS, and transporting it to the laboratory. Other techniques involved more elaborate and expensive collection systems.

All of the techniques required handling and restraint of the head of the calf, thus all likely caused some degree of psychological distress. Collection of the two nasal samples required a lesser degree of restraint and manipulation than collection of the two tracheal samples, with the tracheal wash requiring the longest and most vigorous restraint.

Care must be taken with all four techniques to properly restrain the calf. If restraint is inadequate the wooden shaft

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[3]Appreciation is expressed to the staff of the MARC feedlot for assistance in collection of samples and to Jill Boyum and Karen Shuck for technical assistance.

of the six inch nasal swab could break, resulting in loss of the cotton tip in the nasal passage. Epistaxis (nosebleed) could be induced if the guarded deep nasal swab was not introduced with care. The mucosal covering of the lyssa of the tongue could be torn if the tongue was restrained too vigorously during collection of tracheal samples. No other adverse effects that could be attributed to sample collection were noted in any calves.

The main consideration for the selection of a sampling technique is its ability to isolate relevant pathogenic microorganisms. Other important considerations include practicality in a field setting, lack of complications, skill required, ease of sample collection, degree of calf distress induced, and cost of sample collection. These data suggest that when all of these factors are considered, a six inch nasal swab is the most effective sample collection system.

It is not known if isolates were *Pasteurella multocida* or *Pasteurella hemolytica*, as only the genus of isolates was characterized. Additionally, if isolates were *Pasteurella hemolytica*, it is not known if isolates were serotype 1 or 2. This information would allow us to better assess the pathogenic relevance of the *Pasteurella* isolates since pneumonic pasteurellosis in cattle is typically associated with *Pasteurella hemolytica* A1.

Samples were collected after calves were identified as sick. Differences in the microflora between the upper and lower respiratory tract may have been overlooked because the sample was taken after the disease process was well advanced. However, these data suggest that during an outbreak of bovine respiratory disease there is no difference between the sampling techniques examined.

On the first day of treatment there was not a significant difference in the number of calves from which *Pasteurella* spp. was isolated between the sick and cohort groups. Also, there was not a significant difference in the number of calves from which *Pasteurella* spp. was isolated in the cohort calves on day one and day four. For the sick calves there was a significant drop in the number of calves from which *Pasteurella* spp. was isolated from day one to day four of treatment. This is likely a result of antimicrobial therapy.

Differentiation of sick and cohort calves was based on subjective criteria. Since nontreated controls were not included in the sick group, it is possible that healthy calves were erroneously included in the sick group. Misclassification of calves could have affected the outcome of this trial. However, as only one of the cohort calves became sick and none died, misclassification seems less likely.

The treatment protocol used was effective in causing a shift in the microflora of the nasopharynx and trachea. All the calves diagnosed as having bovine respiratory disease and undergoing treatment did recover and remained clinically healthy during the remainder of the study period.

These findings are consistent with and extend previous research. The lower respiratory tract of a normal, unstressed calf is usually sterile. Normal, unstressed calves carry low numbers of *Pasteurella* spp. as part of their nasal flora. Due to changes in the respiratory tract induced by husbandry practices such as weaning and transport, or infection with viruses or mycoplasmas, floral shifts occur that result in an increase in the numbers of pathogenic *Pasteurella* in the respiratory tract. This increase in the challenge dose presented to the defenses of the lower respiratory tract, along with compromise of the defense mechanisms of the lower respiratory tract, results in pneumonic pasteurellosis. Antibiotic therapy does not "cure" the animal. Rather it suppresses bacterial proliferation to such a degree that the pneumonic defenses of the calf can clear the infection.

In summary, there was no significant difference in the ability to isolate *Pasteurella* spp. from sick or cohort calves using either a short nasal swab, a long guarded nasal swab, a guarded tracheal swab, and tracheal lavage. There was no significant difference in the isolation of *Pasteurella* spp. between the sick and cohort calves on the first day of treatment. There was no significant difference in the samples obtained from the cohort calves on day 1 and day 4. There was a significant difference in the ability to isolate *Pasteurella* spp. in the sick calves on day 1 compared to day 4 that is likely a result of antimicrobial therapy.

Table 1—Isolation rate for four sampling techniques used on sick and cohort calves on day found sick and after therapy

	Sampling Technique			
Group	Nasal swab	Guarded nasal swab	Tracheal swab	Tracheal wash
Sick				
Day found sick	12/19 (63)[a]	13/19 (68)	10/19 (53)	8/19 (42)
After therapy	2/19 (11)[b]	1/19 (5)[b]	2/19 (11)[b]	1/19 (5)[b]
Cohort				
Day found sick[c]	8/18 (44)	10/18 (56)	9/18 (50)	8/18 (44)
After therapy	9/18 (50)	7/18 (39)	6/18 (33)	5/13 (28)

[a] Data are expressed as number of *Pasteurella* spp. isolates/number of samples (%).

[b] Values differ from other values in column ($P<.05$).

[c] Cohort calves were removed from their home pen and sampled on the same day as sick calves. They received no treatments. They were held in hospital pens and sampled again the last day of the initial respiratory disease treatment of the sick calves.

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