Potential Genotypes for Morada Nova Sheep in Northeastern Brazil

E.A.P. Figueiredo, H. D. Blackburn, J. O. Sanders, T. C. Cartwright and J. M. Shelton

The online version of this article, along with updated information and services, is located on the World Wide Web at:
http://www.journalofanimalscience.org/content/67/8/1956

POTENTIAL GENOTYPES FOR MORADA NOVA
SHEEP IN NORTHEASTERN BRAZIL[1]

E.A.P. Figueiredo[2], H. D. Blackburn[3],
J. O. Sanders[3], T. C. Cartwright[3]
and J. M. Shelton[4]

Empresa Brasileira de Pesquisa Agropecuaria
(EMBRAPA), Sobral, Brazil and
Texas Agricultural Experiment Station, College Station 77843

ABSTRACT

A total of 27 combinations of genetic potentials of ewes for mature size (WMA; 30, 40 and 50 kg of body weight), milk production (GMLKL; 1.125, 1.500, and 1.875 kg of milk/ day at the peak day of lactation) and ovulation rate (OVR; 1.65, 2.20, 2.75 ova per ovulation) were simulated. The current genotype was assumed to be 40 WMA, 1.15 GMLKL and 2.2 OVR. Results showed that annual efficiency of meat production for flocks in northeastern Brazil (total live weight sold: total weight of dry matter consumed) increased when genetic potentials for OVR and GMLKL were raised from base, but decreased with increased genetic potential for mature size. The most efficient genotype was a 40 WMA, 1.50 GMLKL and 2.75 OVR, followed closely by the genotypes 40 WMA, 1.125 GMLKL and 2.75 OVR, and 30 WMA, 1.5 GMLKL and 2.75 OVR. Genotypes with 50 WMA were not present in the 11 genotypes ranked above the base genotype.
(Key Words: Simulation, Sheep, Brazil, Optimization.)

Introduction

Computer simulation provides an avenue to evaluate populations of animals with specific genetic compositions a priori. Simulation can help define what the optimal selection criteria is. This approach is appealing because the full impact and ramifications of selection programs are not known until the stated goal has been achieved. The objective of this study was to evaluate the productivity of Morada Nova sheep in northeastern Brazil when their potential mature size (WMA), potential peak daily milk production (GMLKL) and ovulation rate (OVR) were adjusted upward or downward. The results of the simulations could help to determine optimal or nearly optimal combinations that could result in an increase of production efficiency.

Northeastern Brazil is a hot, tropical, semi-arid region and has a population of hair sheep estimated at 5.83 million head (Fitzhugh and Bradford, 1983). In this environment, sheep are raised for meat and skin production. Currently, characterization of domestic sheep is lacking due to the early stages of research projects. Therefore, due to the critical need to increase productivity of sheep in this area, it was important that proper selection objectives be found and utilized. Simulation was used to reduce the time required to estimate optimal combinations of genotypes.

Materials and Methods

The Texas A&M Sheep Simulation Model was used for our simulations (Blackburn et al.,

TABLE 1. AVAILABILITY (AVC), DIGESTIBILITY (DIG),
CRUDE PROTEIN (CP) AND SUPPLEMENTATION AMOUNT AND QUALITY
USED AS FORAGE PARAMETERS FOR THE SIMULATION EXPERIMENT

| Month | AVC[a], kg | DIG, % | CP, % | Supplementation | | |
				Amount, kg	DIG, %	CP, %
JAN	.40	63.0	23.6	.20	57.0	7.0
FEB	.40	62.0	18.0	.20	57.0	7.0
MAR	.60	58.0	18.0			
APR	.80	56.0	18.0			
MAY	.90	53.0	18.0			
JUN	1.65	53.0	17.0			
JUL	1.90	51.0	13.0			
AUG	1.40	52.0	13.0			
SEP	.75	47.0	13.0			
OCT	.60	48.0	13.0	.20	57.0	7.0
NOV	.60	48.0	12.0	.20	57.0	7.0
DEC	.40	48.0	12.0	.20	57.0	7.0

[a]Availability is the amount of forage of the designated digestibility and crude protein available for an individual mature sheep to consume per day.

1987; Blackburn and Cartwright, 1987). Briefly, the model simulates the performance of each sheep in the nutritional environment provided. Animal weight, reproduction, milk production, forage intake, mortality and offtake are simulated for each animal across time. The model uses a time step of 15 d. Input parameters for the model include genotype, nutrition and management options. Genotype is characterized by genetic potential of ewes for mature size (WMA), number of ova at each ovulation (OVR), milk production at peak day of lactation (GMLKL) and seasonality of breeding. Forage parameters are crude protein and digestibility percentages of the diet and forage availability (kg·hd^{-1}·d^{-1}), which sets the upper limit for feed intake. Management specified includes breeding season, supplementation, weaning weight or age, replacement and culling policy and sales.

Inputs for the nutritional environment (Table 1) were available from Pfister (1983) and Kirmse (1984) for the region around Sobral, Ceara, Brazil. In these experiments, the sheep were allowed to graze and(or) browse in a native type of brush called caatinga. The caatinga vegetation is a deciduous woodland with a heterogeneous mix of deciduous trees and shrubs with an annual herbaceous understory noted by its density and diversity, as well as by an absence of perennial grass cover (Pfister, 1983). Such brush remains green from January to June and then loses its leaves, forming a litter on the ground. The animals were allowed to graze reserved paddocks during the dry season and received approximately 200 g of chopped Napier grass per day as a supplement. The model was parameterized to mimic this type of forage and grazing system. The baseline genetic parameters included WMA, GMLKL, OVR, and seasonality of breeding. These parameters were obtained from data on the Morada Nova breed ovulated at Sobral (Figueiredo, 1986). Management was specified to emulate that in northeastern Brazil. Management included breeding in November and lambing in March. Lambs were weaned at 105 d of age. Lambs not kept as replacements were sold when they reached a minimum of 24 kg. Ewes were culled for age at 8 yr.

The simulation model was used to run a 3 × 3 × 3 factorial experiment in which three levels of WMA (30, 40 and 50 kg; L, M and H, respectively) by three levels of GMLKL (1.125, 1.500 and 1.875 kg; L, M and H, respectively) and three levels of OVR (1.65, 2.20 and 2.75 ova/ovulation; L, M and H, respectively) were examined. In this paper, notation for a genotype will be expressed in the order of WMA, GMLKL and OVR as L, M or H for each. Genetic potentials were derived by adjusting the base genotypic (MMM) values up or down by 25% for each parameter. The base genotype represents input parameters used for the validation of simulated results with the actual experimental data. A flock of approximately 175 ewes was simulated for each genotype. Flock size remained

FIGUEIREDO ET AL.

Genotype[a]	No. of ewes		Lambing, %		Lambing rate, %	
	Avg	CV[b]	Avg	CV	Avg	CV
LLL	185.5	2.8	97.6	1.3	142.5	2.6
LLM	187.0	1.6	97.7	1.0	182.5	2.1
LLH	188.7	1.7	96.7	1.3	216.7	1.6
LML	181.0	1.2	96.0	1.7	138.2	1.2
LMM	186.0	1.8	97.2	1.0	179.5	2.3
LMH	182.5	.7	96.7	.5	211.2	.4
LHL	180.5	1.8	97.2	.5	135.2	2.1
LHM	179.2	.5	97.7	.6	177.2	.7
LHH	188.7	2.1	97.2	1.0	209.5	1.1
MLL	175.7	1.9	94.0	2.4	132.2	2.8
MLM	178.0	1.0	93.5	2.0	173.5	3.3
MLH	182.5	2.1	92.7	2.2	207.2	2.8
MML	177.7	3.5	95.0	2.6	127.5	.8
MMM	177.5	1.3	93.2	1.3	166.0	2.9
MMH	180.2	1.4	92.2	2.4	204.5	1.3
MHL	179.5	1.0	94.5	2.8	124.5	.8
MHM	176.0	1.5	93.7	1.6	165.7	.6
MHH	173.2	2.0	92.0	.9	199.2	.9
HLL	169.5	3.2	81.7	1.5	123.2	2.8
HLM	173.7	.5	79.5	4.1	159.7	3.7
HLH	171.5	1.5	77.2	1.9	195.0	1.4
HML	166.2	1.3	83.2	1.1	119.5	1.1
HMM	168.0	1.9	79.7	4.3	163.0	3.8
HMH	175.2	1.3	80.2	3.7	191.5	3.0
HHL	169.5	2.8	82.7	5.9	118.7	3.0
HHM	166.7	2.9	79.5	3.0	157.2	1.6
HHH	174.0	3.1	81.2	1.6	188.5	2.0

[a]The first letter represents WMA, the second GMLKL and the third OVR; L = low, M = medium and H = high.

[b]Coefficient of variability between years.

constant, but based on DM consumption of this flock, productive efficiency was calculated to compare genotypes.

The simulation for a genotypic combination was for 8 yr. The last 4 yr were averaged and used in the analysis. Using the last 4 yr allowed the initial flock, which had its genotype altered, to reach an equilibrium. Averaging the last 4 yr was performed to reduce the effects of stochastic variation, which could occur within a simulation run.

Results and Discussion

The simulated 4-yr average and respective coefficients of variation for the number of breeding ewes, the lambing percentage and the lambing rate according to genotype are presented in Table 2. The number of breeding ewes was intended to be fixed in every run by replacing 20% of the breeding ewes per year. As a result, 35 new breeding ewes were incorporated into the flock every year. The difference in the number of breeding ewes, therefore, reflects the differential fertility and mortality rates in each genotype. In general, the number of breeding ewes was approximately 184, 178 and 170 for L--, M-- and H-- genotypes, respectively. A similar trend was observed between lambing percentage (ewes lambing per ewe breed $\times$ 100) and size. For lambing rate (the number of lambs born per ewe lambing $\times$ 100), the genotypes ranked L--, M-- and H-- with an 8- to 10-point difference between the genotypes in their respective order. This trend can be seen by comparing genotypes with the same GMLKL and OVR and different genetic potentials for WMA. Therefore, these results indicate that, in terms of reproduction, there was little interaction between WMA, GMLKL and OVR and that smaller animals are better suited for the extensively managed flocks in Northeast Brazil when forage production and stocking rates are

TABLE 3. FOUR-YEAR AVERAGE FOR WEANING WEIGHT (kg), NUMBER OF
LAMBS SOLD PER EWE, TOTAL WEIGHT (kg) AND AVERAGE WEIGHT (kg)
OF THE LAMBS SOLD OF SIMULATED GENOTYPES

| Genotype[a] | WWS[b] | | WWM[b] | | NOS[c] | TWS[c] | AWS[d] |
	Avg	CV[e]	Avg	CV	Avg	Avg	Avg
LLL	15.3	.2	9.9	2.3	.86	24.6	28.6
LLM	14.6	4.2	9.8	1.1	1.11	30.4	27.4
LLH	12.6	4.0	9.6	.9	1.28	33.5	26.2
LML	16.4	.6	11.4	.8	.88	25.5	29.0
LMM	15.9	1.1	11.3	.5	1.14	32.1	28.2
LMH	14.5	3.0	11.0	1.7	1.35	36.9	27.3
LHL	16.8	.2	12.1	2.1	.87	25.8	29.7
LHM	16.3	.5	11.6	4.9	1.18	33.5	28.4
LHH	15.2	.7	11.7	2.6	1.31	36.3	27.7
MLL	16.9	.5	10.7	2.7	.73	23.8	32.6
MLM	15.3	1.3	10.6	.9	.93	30.2	32.5
MLH	13.7	4.0	10.5	1.6	.99	32.2	32.5
MML	17.8	1.6	12.1	1.0	.73	25.3	34.7
MMM	16.2	2.0	11.9	1.2	.88	29.4	33.4
MMH	18.8	.6	12.1	1.5	1.07	34.7	32.4
MHL	19.4	.6	12.6	2.0	.71	24.0	33.8
MHM	18.4	1.3	12.5	1.8	.91	29.8	32.8
MHH	16.8	3.8	12.3	1.8	1.11	35.5	32.0
HLL	18.3	1.1	11.7	4.0	.49	17.3	35.4
HLM	16.7	1.5	11.7	5.9	.60	20.0	33.3
HLH	15.0	2.2	12.4	4.7	.62	20.5	33.1
HML	20.5	1.7	12.5	4.2	.56	17.5	31.3
HMM	18.8	3.9	12.7	1.6	.60	19.4	32.4
HMH	17.5	1.3	12.5	1.1	.72	24.3	33.7
HHL	21.4	1.5	12.5	1.3	.55	16.8	30.5
HHM	19.4	1.9	12.5	2.9	.62	20.3	32.8
HHH	17.3	3.8	12.4	1.0	.72	23.9	33.2

[a]The first letter represents WMA, the second GMLKL and the third OVR; L = low, M = medium, and H = high.

[b]WWS and WWM = weaning weight of single and multiple born lambs.

[c]NOS and TWS = number and total weight of lambs sold per ewe in the flock.

[d]AWS = average weight of lambs sold.

[e]CV = coefficient of variability between individuals within a genotypic combination.

equivalent to those measured by Pfister (1983) and Kirmse (1984).

Weaning weights (Table 3) decreased linearly from L to H OVR and increased approximately linearly from L to H for GMLKL and WMA. The heaviest weaning weight was produced by the HHL and the smallest by the LLH. For number of lambs sold per ewe in the flock, as a measure of offtake, genotypes ranked from high to low as L--, M-- and H--. The lowest figure was .49 lambs sold from genotype HLL and the highest 1.35 from genotype LMH.

The average total weight of lamb sold per ewe in the flock was highest for L-- genotypes, intermediate for M-- and lowest for H-- genotypes. The lowest offtake was 17.3 kg of lambs sold from genotype HLL and the highest was 36.8 kg of lambs sold from genotype LMH. For average weight of lambs sold, the genotypes L--, M-- and H-- were 28.1, 33.0 and 32.6 kg, respectively. The lightest lambs were sold from genotype LLH (26.2 kg) and the heaviest from the genotype HLL (35.4 kg).

There was no increase in weight of the lambs sold from genotype H-- in relation to those of genotypes M--, but there was an increase of approximately 5.0 kg from genotypes L-- to M--. This increase indicates that there is potential for increasing size from L-- to M--; i.e., M WMA can be supported, but the zero increase from M-- to H-- indicates that M WMA is near the limit for that environment and, therefore, an increase in mature size is not recommended.

Preweaning mortality increased as WMA became larger (Table 4) and ranged from 11.2% for LML to 43.4% for HLH. This is a

TABLE 4. FOUR-YEAR AVERAGE AND COEFFICIENT OF VARIABILITY (%)
FOR PREWEANING AND ADULT MORTALITY AND AMOUNT OF MILK
CONSUMED BY SINGLE AND MULTIPLE LAMBS OF
DIFFERENT SIMULATED GENOTYPES

Genotype[a]	Preweaning		Adult		Milk, g	
	Avg	% CV[b]	Avg	% CV	Singles	Multiples
LLL	14.2	26.7	9.7	18.5	390	473
LLM	19.8	11.3	14.6	24.5	380	456
LLH	23.5	9.2	12.3	26.3	360	439
LML	11.2	7.9	12.0	13.6	464	559
LMM	17.3	16.0	13.3	19.2	464	548
LMH	16.5	28.5	19.7	12.4	447	525
LHL	11.3	26.4	12.6	19.9	532	609
LHM	15.9	9.4	15.7	23.2	512	555
LHH	16.9	9.0	15.9	9.4	485	569
MLL	20.1	7.1	12.6	32.5	355	427
MLM	26.9	8.1	14.2	25.1	344	433
MLH	29.6	11.1	14.6	17.2	366	433
MML	14.3	13.1	14.7	10.2	454	523
MMM	22.4	7.2	13.5	19.5	442	521
MMH	25.4	10.7	16.6	26.9	417	504
MHL	15.8	13.4	11.0	12.9	505	552
MHM	20.7	7.9	15.1	25.2	489	556
MHH	25.1	22.3	19.1	23.9	470	550
HLL	19.2	3.8	13.5	13.7	315	418
HLM	28.9	10.4	13.9	8.6	333	438
HLH	43.4	4.9	13.6	26.6	322	423
HML	15.7	22.4	13.1	10.9	421	492
HMM	30.1	11.6	13.2	23.0	409	496
HMH	37.0	5.0	13.3	17.6	391	471
HHL	14.9	30.3	12.2	11.0	473	473
HHM	28.7	9.9	14.4	23.9	448	494
HHH	39.7	9.8	13.1	14.2	424	490

[a]The first letter represents WMA, the second GMLKL and the third OVR; L = low, M = medium, H = high.

[b]CV = coefficient of variability between years.

result of decreasing quantities of milk available for lambs. Average milk consumptions for single and multiple birth lambs for L, M and H WMAs were 448.2, 426.9 and 392.9 g/d and 525.9, 499.9 and 466.1 g/d, respectively. There also was a trend for preweaning mortality to increase as prolificacy increased within a WMA. However, this was most evident when WMA had the lowest level of potential milk production. Mortality in adult sheep was approximately equal for all genotypes, except for LLL, LMH and MHH, which deviated most from the average of 14%. The low level of mortality of the LLL genotype was attributed to its low level of performance, allowing the ewes to maintain a higher body condition during lambing and lactation. Higher ewe mortality for LMH and MHH genotypic combinations was due to ewes staying in lower body condition during lactation than other tested combinations did. Although mortalities were higher for these combinations, it was not severe enough to decrease total flock performance, as evidenced by their ranking for biological efficiency.

The average amount of milk produced by ewes with single and twin lambs per day increased with GMLKL (Table 4). The amount of milk produced decreased when OVR increased for all genotypes as a function of the lower body condition in genotypes of higher OVR. Milk production was higher for genotypes L--, intermediate for genotypes M-- and lowest for genotypes H--. As WMA became larger, milk production, averaged across genotypes, decreased 4.8% (L-- vs M--) and 8.0% (M-- vs H--) for ewes nursing single lambs. The reduction in milk production as WMA increases is a direct result of larger ewes' not being able to consume adequate amounts of forage to meet their nutritional requirements. If this nutritional limitation were reduced (e.g.,

TABLE 5. FOUR-YEAR AVERAGE AND COEFFICIENT OF VARIABILITY (%)
FOR TOTAL WEIGHT SOLD (WT), TOTAL DRY MATTER CONSUMED (DM)
AND EFFICIENCY IN DIFFERENT SIMULATED GENOTYPES

Genotype[a]	WT, kg		DM, kg		Efficiency[b]	
	Avg	CV[c]	Avg	CV	Avg	CV
LLL	5,449	2.4	116,606	1.4	47	1.3
LLM	6,552	.8	127,182	1.0	51	1.5
LLH	7,255	2.4	135,398	1.5	54	1.8
LML	5,480	3.5	116,483	1.2	47	3.2
LMM	6,871	2.6	131,936	.8	52	2.4
LMH	7,569	4.3	138,608	1.4	55	2.9
LHL	5,550	5.8	116,048	1.5	48	4.9
LHM	6,818	2.5	129,157	1.1	53	2.0
LHH	7,656	3.3	141,237	2.7	54	1.2
MLL	5,206	4.2	109,594	.2	48	3.0
MLM	6,308	4.2	120,259	1.0	52	1.6
MLH	6,858	10.2	126,375	.0	55	2.3
MML	5,585	3.0	116,771	1.5	48	2.3
MMM	6,208	6.4	119,895	2.3	51	3.9
MMH	7,247	4.5	130,238	.6	56	4.7
MHL	5,401	5.2	111,686	2.9	48	4.0
MHM	6,251	2.0	120,416	.6	53	3.2
MHH	7,143	1.6	129,041	1.9	54	8.3
HLL	3,974	8.5	96,000	1.9	41	7.9
HLM	4,653	5.1	103,376	1.1	45	4.4
HLH	4,667	7.7	102,645	2.4	45	5.4
HML	4,065	6.2	92,145	2.2	44	4.3
HMM	4,408	5.5	98,205	1.6	45	5.3
HMH	5,206	14.2	109,766	3.1	47	12.0
HHL	4,017	6.6	92,711	1.6	43	6.1
HHM	4,436	7.3	97,883	1.3	45	7.2
HHH	5,376	9.2	108,476	5.0	50	6.1

[a]The first letter represents WMA, the second GMLKL and the third OVR; L = low, M = medium and H = high.

[b]Efficiency is expressed as the total weight sold per year per total DM consumed by the flock per year.

[c]CV = coefficient of variability between years.

stocking rate lowered), higher levels of performance could occur.

The 4-yr averages and respective coefficients of variability for total weight sold, total dry matter consumed by the flock per year and the ratio of total weight sold per ton of dry matter consumed, a measure of the efficiency of each genotype, are given in Table 5. Generally, total weight sold increased with increased OVR and GMLKL in all genotypes but decreased with increases in WMA, largely due to the number of ewes in the flock. The highest figure was 7,656 kg of weight sold from genotype LHH, and the lowest was 3,974 kg from genotype HLL.

The amount of dry matter consumed by the flock per year decreased with increases in WMA, due to decreased flock size. The lowest figure was 92,145 kg for genotype HML, and the highest figure was 141,237 kg for genotype LHH.

The efficiency increased as OVR was raised, but it decreased from genotypes M-- to H-- and it increased only slightly from genotype L-- to M--. The lowest efficiency figure was 41.3 for genotype HLL and the highest was 55.6 for genotype MMH, although several other efficiencies approached this level, namely 54.6, 54.2, 55.4 and 54.2 for genotypes LMH, LHH, MLH and MHH, respectively. Any of these genotypes therefore could be used as the goal to be achieved through genetic improvement. The efficiency of MMM, the base genotype (50.9), was lower than for LLM (51.5), LLH (53.6), LMM (52.1), LMH (54.2), LHM (52.8), LHH (54.2), MLM (51.9), MLH (55.4), MMH (55.6), MHM (52.6) and MHH (54.2). This would indicate that there may be some advantages in altering the genetic composition of the Morada Nova. The genotypes listed above include six of the nine genotypes of low WMA and five of the genotypes with

medium WMA. The sixth medium WMA genotype is the base genotype. These simulations suggest that large WMA genotypes would not perform well in such environment; therefore, selection for high WMA should be avoided. However, if stocking rate is reduced, thereby allowing forage availability to increase, sheep with larger WMAs may become a more viable option.

Another observation is that genotypes with low OVR are not present among the 11 most efficient combinations. Therefore, OVR and (or) prolificacy should be kept at the current levels or be increased through selection. A third important finding is that all levels of GMLKL are present among the nine most efficient genotypes in equal proportions. This indicates that the GMLKL variations used in the experiment were not so critical in the test conditions. Probably the lower level was enough to support adequate growth of the offspring. In addition, increased ewe fertility and ewe survival of lower GMLKL compensated for decreased lamb weights.

The monthly weights of breeding ewes were highly influenced by levels of GMLKL. Within the same WMA, ewes with higher GMLKL had lower body condition from the beginning of lactation until 2 to 3 mo after weaning. Lactation occurs during the best forage production phase of the year; therefore, the detrimental effect of low body condition was buffered. Another important factor contributing to the success of the higher GMLKL was that only one breeding season per year was used; therefore, the ewes had time to regain body reserves.

Higher GMLKL results in faster preweaning growth. Faster preweaning growth would mean that lambs could reach slaughter weight, on pasture, 2 or 3 mo after weaning. This could be a management improvement policy adopted in this sheep production system, because it would require less forage inputs to the system at the most critical time for forage production in the region, the second half of the dry season. If such lambs could be sold with adequate slaughter weight by mid-September to mid-October, the forage resources of the dry season could be directed entirely toward breeding ewes. This point deserves further investigation through specific simulation studies as well as through experimentation to test the efficacy of such an approach.

Increases in GMLKL slightly increased efficiency within WMA. Increases mainly were due to the shorter time the lambs remained in the flock after weaning until slaughter. It is recommended locally that lambs should not be slaughtered before they reach at least 24.0 kg of live weight to avoid reduced skin size. That was the minimum weight at which lambs were sold in this simulation study. The age of the lambs from high GMLKL to achieve the required weight was reduced and such lambs were sold earlier, therefore consuming less DM. This consideration should be emphasized, and simulations should be extended to study the optimal age and weight for selling the lamb crop if the genetic potential of the ewes for milk production is increased.

The higher efficiency of the lower WMA genotypes is different from the results reported by Blackburn (1984) for a simulation experiment conducted in Kenya with the same model. He found that the genotype 45/1.75, (WMA/GMLKL), almost always ranked first for efficiency for several measures of efficiency studied. His second most efficient genotype was 35/1.30, the medium levels of both parameters. An explanation for this difference is that Blackburn (1984) simulated ewes of low genetic potential for prolificacy and a different forage environment. The reproductive rate of his ewes was 118%. The ewes simulated in this study ranged from 123 to 216% lambing rate (i.e., the former study did not cover the range of reproduction level covered in this study). Another potential source for discrepancy is the large difference between forage resource of the two studies. The present study used forage parameters of Pfister (1983) and Kirmse (1984), who reported low forage availability during the dry season and different crude protein and digestibility contents in the forage (Table 1). According to these authors, the limiting forage parameters in the region were availability and(or) energy. The forage availability listed in Table 1 shows that there is a forage availability restriction from mid-September through mid-February. The Kenya simulations for nomadic herds mimicked a different situation; that is, the flock was moved to fresh pastures whenever the vegetation in the campsite had been consumed. This tended to provide less limiting forage availability than in Northeast Brazil, where the animals simulated were in native caatinga pastures under a stocking rate

of 1.7 ha per head of sheep of 35.0 kg live weight, which imposes restricted availability during the dry season. Blackburn's (1984) simulations also considered year-around breeding instead of a restricted breeding season, as in this study. The different results between studies reflects the sensitivity of the simulation model to different production systems. It also emphasizes the need to design specific breeding and management programs for different production environments.

The simulated results reported here provide a basis for directing the selection goals of animal breeders in northeast Brazil. By narrowing the criteria for selection and providing direction, a genetic optimum should be obtained more easily.

Literature Cited

Blackburn, H. D. 1984. Simulation of genetic and environment interaction of sheep production in Northern Kenya. Ph.D. Dissertation. Texas A&M Univ., College Station.

Blackburn, H. D. and T. C. Cartwright. 1987. Description and validation of the Texas A&M sheep simulation model. J. Anim. Sci. 65:373.

Blackburn, H. D., T. C. Cartwright, G. M. Smith, N. McC. Graham and F. Ruvuna. 1987. The Texas A&M Sheep and Goat Simulation Models. Texas Agric. Exp. Sta. B-1559, College Station.

Figueiredo, E.A.P. 1986. Potential breeding plans developed from observed genetic parameters and simulated genotypes for Morada Nova sheep in northeast Brazil. Ph.D. Dissertation. Texas A&M Univ., College Station.

Fitzhugh, H. A. and G. E. Bradford. 1983. Hair sheep of western Africa and the Americas: A Genetic Resource for the Tropics. Westview Press, Boulder, CO.

Kirmse, R. D. 1984. Effects of clearcutting on forage production, quality and decomposition in the caatinga woodland of Northeast Brazil: Implications to goat and sheep nutrition. Ph.D. Dissertation. Utah State Univ., Logan.

Pfister, J. A. 1983. Nutrition and feeding behavior of goats and sheep grazing deciduous shrub-woodland of Northeastern Brazil. Ph.D. Dissertation. Utah State Univ., Logan.