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Review

Criollo Coreño cattle in western Mexico: characterization, challenges and outlook

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Abstract:

The National Institute of Forestry, Agricultural and Livestock Research (INIFAP) in Mexico has been studying the Criollo Coreño (C) cattle of the Sierra Madre Occidental for over 20 yr. This review covers productive, genetic and molecular characterization, as well as short-, medium- long-term research challenges and outlooks. Evaluations have been done of 35 growth, carcass quality, fertility and milk production traits in C, Guzerat (G), CG and GC cattle generated through diallelic crossing. Individual heterosis was found to affect reproduction and milk production, while maternal heterosis influenced kilograms of calf weaned per cow exposed. Direct and maternal genetic effects had no relevant influence on the analyzed variables. In other studies, C bulls fed high energy diets were found to produce meat with favorable fatty acid profiles and good quality carcasses, while low doses of FSH can be used for superovulation in C heifers, without affecting embryo production. Overall, the results indicate that GC cows are the best option for calf production, and that the C population maintains significant levels of genetic diversity. Further genetic diversity research is needed on Mexican Criollo cattle populations using molecular genetics; Criollo herds must be included in the systematic recording of phenotypes of productivity and adaptability to be able to identify genes of interest unique to Criollo cattle.

Key words: Beef cattle, Productive characterization, Criollo Coreño, Diallelic cross, Genetic diversity, Heterosis.

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Introduction

There are several populations of Criollo cattle in Mexico, descendants of *Bos taurus* cattle introduced by the Spanish during the Colonial Period. Among them is the Criollo Coreño in the Sierra Madre Occidental. Isolated for over 500 yr in different regions of the country, these populations have been subject to natural selection under adverse conditions, such as low feed availability and lack of health care(1). They have apparently developed the genetic capacity to adapt to difficult conditions and can contribute to the sustainability of cow-calf systems since they do not require radical changes in their rangelands. These populations' hardiness originates in natural selection and is reflected in traits that allow them to overcome random and adverse environmental variations without significant reductions in productive capacity. The genetic diversity of Mexican Criollo cattle is an important genetic resource, which can contribute to design of livestock production systems with low input requirements. Crosses between imported cattle breeds and Criollo populations in Mexico have led to varying degrees of decline or genetic erosion in the latter, although each Criollo population is in a different risk situation.

Successful conservation of Criollo cattle populations depends on the knowledge available about them. The main goal of conservation should be to preserve as much of a breed's genetic diversity as possible. Three types of data are needed to define a strategy for conservation of Criollo cattle populations. First, effective population size depends on the number of males and females used as reproducers in each generation and helps to understand levels of consanguinity and possible loss of genetic diversity. Second, a population's genetic diversity is quantified based on a breed's history and/or molecular genetic data. It can be used to quantify the potential for future evolution and identify genes associated with present or future traits of interest. Third, phenotypic behavior in production and adaptation traits can be used to estimate a population's genetic variability(2).

The Criollo Coreño (C) is found in the Sierra Madre Occidental in indigenous communities in the states of Durango, Jalisco, Nayarit and Zacatecas, in western Mexico. Traditional use of C cattle is for weaned calf production in agroecological regions with limited year round feed availability and difficult environmental conditions. These challenging conditions manifest as declines in productive efficiency. There are approximately 16,000 head of C cattle in this region, which falls within the area of influence of the El Verdineño Experimental Station of the National Institute of Forestry, Agricultural and Livestock Research (Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias - INIFAP)(1,3).

El Verdineño is located in the municipality of Santiago Ixcuintla, Nayarit, Mexico (21º42' N; 105º07' W). Regional climate is tropical warm subhumid (Aw2), altitude is 60 m asl, average annual rainfall is 1,200 mm and average annual temperature is 24 ºC. Vegetation is semi-evergreen tropical forest in secondary succession, and introduced grasses (*Andropogon*, *Megathyrsus* and *Cynodon*).

A herd of C cattle is maintained in El Verdineño for experimental purposes. It was founded in 1982 through acquisition of 50 cows and 10 bulls from rural communities in the Sierra Madre Occidental; no data is available on the origins of these animals. By 1990, the herd included 70 C cows which had been born on site, with known genealogical and production information, as well as management conditions. Diallelic crosses between C and Guzerat (G) animals were begun to evaluate productive capacity. Estimates were made of the direct and maternal genetic effects of the C (*Bos taurus*) and G (*Bos indicus*) breeds, and the effects of individual and maternal heterosis, on economically important traits(4). The first stage of diallelic crossing (1990-1994) involved mating 14 C bulls and 12 G bulls with 70 C cows and 70 G cows to produce pure C and G animals and reciprocal F1 crosses (CG and GC). Beginning in 1993, the second stage of diallelic crossing involved mating of the females of the four breed groups (C, G, CG and GC) produced in the first stage with Red Angus bulls. In both stages, the calves remained with the cows until weaning, which occurred at 7 mo of age on average.

This review summarizes INIFAP research on the productive, genetic and molecular characterization of C cattle from the Sierra Madre Occidental in Mexico, through analysis of the breed groups of the cows produced during diallelic crossing. Research challenges and short-, medium-, and long-term outlooks for Mexico's Criollo cattle populations are addressed.

Productive characterization of Criollo Coreño cattle

Research done at the INIFAP has shown that C cattle can contribute to improving growth calf production in the warm subhumid tropical region of western Mexico(5,6,7). Offspring of C bulls with G or Red Angus cows which are grown and finished in feedlot in the tropical region of Nayarit produce good quality carcasses with good yields(8,9). The following section reviews the productive, genetic and molecular characterization of C cattle from 1990-2019.

Breed, additive and non-additive genetic effects

In a study evaluating reproductive characteristics, C, CG and CG cows exhibited higher ($P<0.10$) rates of estrus (ER) and gestation (GR) than G females. For ER, the G cows were 20 % lower than C, 26 % lower than CG and 33 % lower than GC, while for GR they were 14 % lower than C, 18 % lower than CG and 26 % lower than GC (Table 1). The C, CG and GC cows were reproductively more efficient than the G females. No differences in calving rate (CR) were observed between G and CG cows (Table 1), possibly due to higher embryo or fetus loss in CG cows. This suggests that G cows provide a less favorable uterine environment than do C cows. The CR for GC cows suggests they also have a relatively unfavorable uterine environment for prenatal growth than do GC cows. Compared to G cows, weaning rate (WR) was also higher ($P<0.10$) in C (14%), CG (16 %) and GC (25 %) cows (Table 1). This could be due to lower maternal ability in the G cows during the birth-weaning period, lower calf survival during this period, or a combination of both. Estimated individual heterosis (h_i) had a favorable influence ($P<0.10$) on all reproductive rates, which was manifested in a higher WR ($P<0.10$) in the GC and CG cows than in the C and G cows. In contrast, no differences in direct genetic effects (g_i) were observed between C and G cows for any of the reproductive variables (Table 2). Differences between the four breeds of cows were minimal for maternal genetic effects (g_m) for ER, GR and WR, but clearly favored C cows (15 %, $P<0.10$) for CR (Table 2)(5).

Table 1: Least squared means for reproductive traits, pre-weaning growth, milk production and quality, growth in feedlot and carcass traits for Guzerat (G), Guzerat x Criollo Coreño (GC), Criollo Coreño x Guzerat (CG) and Criollo Coreño (C) cattle from sources published between 2006 and 2012

Variables	Breed Group			
	G	GC	CG	C
[1]Estrus rate, %	49[a]	82[b]	75[b]	69[b]
[1]Gestation rate, %	46[a]	72[b]	64[b]	60[b]
[1]Calving rate, %	42[a]	71[b]	56[ac]	59[bc]
[1]Weaning rate, %	38[a]	63[b]	54[b]	52[b]
[2]Birth weight, kg	31.72[a]	30.44[ab]	31.11[a]	28.86[b]
[2]Weaning weight, kg	177.42[a]	187.45[a]	183.34[a]	153.50[b]
[2]Weight of calf at birth per cow exposed, kg	17.69[a]	19.73[a]	18.21[a]	16.38[a]
[2]Weight weaned per cow exposed, kg	98.44[ac]	143.50[b]	116.15[ab]	83.97[c]
[2]Gestation length, days	283.25[ab]	283.87[ab]	280.98[a]	284.10[b]
[3]Total milk production, kg	949[a]	1,059[b]	990[ab]	805[c]
[3]Daily milk production, kg	4.50[a]	5.00[b]	4.70[ab]	3.90[c]
[3]Peak production, kg	6.50[a]	7.30[b]	6.70[ab]	5.80[c]
[3]Day peak production, days	76[a]	74[a]	77[a]	70[a]
[3]Lactation persistance, days	147[a]	147[a]	149[a]	143[a]
[4]Milk fat, %	2.80	2.98	3.09	2.81
[4]Milk fat, kg	25.90	29.50	28.80	22.30
[4]Milk protein, %	3.56[a]	3.83[b]	3.72[b]	3.88[b]
[4]Milk protein, kg	33.90	38.20	37.20	31.60
[4]Lactose, %	4.79	4.82	4.75	4.71
[4]Lactose, kg	47.10[a]	52.10[a]	48.60[a]	39.50[b]
[4]Milk non-fat solids, %	9.09	9.36	9.19	9.29
[4]Milk non-fat solids, kg	88.20[a]	98.90[a]	93.20[a]	76.90[b]
[5]Initial weight in the feedlot, kg	226.00[a]	206.70[ab]	208.90[b]	164.60[c]
[5]Yearling weight, kg	359.50[a]	338.50[ab]	329.50[b]	279.40[c]
[5]Final weight in the feedlot, kg	405.60[a]	388.60[ab]	377.10[b]	335.20[c]
[5]Daily weight gain in the feedlot, kg	1.15[a]	1.13[a]	1.07[a]	1.09[a]
[5]Feed efficiency in the feedlot, kg	0.105[a]	0.114[b]	0.103[a]	0.109[ab]
[5]Rib-eye area, inches	10.73[a]	11.83[a]	9.66[b]	8.40[c]
[5]Fat thickness, inches	0.37[a]	0.48[a]	0.38[a]	0.40[a]
[5]Hot carcass weight, kg	241.70[a]	249.60[a]	210.60[b]	187.50[b]
[5]Dressing percentage, %	60.20[a]	58.60[ab]	58.20[b]	54.20[c]
[5]Kidney and pelvis fat, kg	8.06[a]	2.91[b]	5.34[b]	7.95[a]
[5]Yield grade, units	2.61[a]	2.92[ab]	2.62[a]	3.21[b]
[5]Cutability, %	50.79[a]	50.06[ab]	50.80[a]	49.48[b]
[5]Retail yield, %	76.58[a]	75.12[ab]	76.61[a]	73.97[b]

[a,b,c] Different letter superscripts in the same row indicate difference: [1,2]($P<0.10$); [3,4,5]($P<0.05$).

Sources: [1]Martinez *et al.*(5); [2]Martinez *et al.*(6); [3]Martinez *et al.*(11); [4]Martinez *et al.*(12); [5]Martinez *et al.*(8).

Reproductive performance in cows and pre-weaning growth in calves

Aspects of superovulation in C cows were evaluated in a study using reduced doses of FSH applied in three treatments (T1= 280 mg, T2= 200 mg and T3= 140 mg) to C cows (Exp 1) and C heifers (Exp 2). Treatment 1 produced higher ($P<0.05$) values for recovered corpuscles

(RC) and unfertilized ovules (UFO). However, no differences were observed between treatments for transferable embryos (TE), non-transferable embryos (NTE), corpora lutea (CL), ovary volume (OV), serum progesterone concentration (P4), fertilization percentage (F%) and recovery percentage (R%). Considering the average values for NTE, CL, UFO, OV and R%, T1 was deemed the best treatment for promoting superovulation in C cows. As FSH dose decreased so did RC, most notably in T1 (10.3 RC) which differed ($P<0.05$) from T3 (4.1 RC). The number of UFO was also higher ($P<0.05$) in T1 than in T3, suggesting that T3 promoted a lower superovulatory response in the cows than T1. However, T1 did not result in higher embryo production, due to the high UFO in this treatment. In contrast to the C cows, no differences were detected between treatments for any of the variables in the C heifers. This highlights the feasibility of using reduced FSH doses in heifers without affecting their response to superovulation. A positive correlation ($P<0.05$) between CL and P4 was observed in all the C females, reflecting the fact that females with the highest CL also had the highest P4. Another positive correlation ($P<0.05$) was also detected between OV and P4, again indicating that those with the highest OV had the highest P4. Considering the results of the three treatments in both experiments, it was observed that the cows responded better to superovulation by producing higher CL (10.4, 9.1 and 8.8 for T1, T2 and T3, respectively) than the heifers (5.8, 5.5 and 4.5 for T1, T2 and T3, respectively); in contrast, cows had lower F% (44.6, 52.5 and 36.9 % for T1, T2 and T3, respectively) than heifers (96.5, 95.7 and 97.3 % for T1, T2 and T3, respectively). Overall, the results of the three treatments in both experiments showed that the cows had higher OV, CL and P4 than the heifers. Ovulatory response in terms of RC was also lower in the heifers (3.8 in T1, 2.3 in T2 and 2.0 in T3) than in the cows (10.3 in T1, 7.2 in T2 and 4.0 in T3). However, no differences were present for TE (2.3 in T1, 1.8 in T2 and 1.7 in T3) and NTE (1.3 in T1, 0.3 in T2 and 0.2 in T3) in heifers, and TE (1.2 in T1, 2.9 in T2 and 1.1 in T3) and NTE (2.0 in T1, 1.8 in T2 and 0.8 in T3) in cows. Average TE and NTE values in the cows and heifers indicated that both had similar embryo production levels, probably due to the higher fertility of heifers. No differences between treatments were detected for TE in either experiment. The results show that low FSH doses can be used to induce superovulation in C heifers, thus reducing the costs of superovulation and embryo production. The C cows responded better to superovulation than the C heifers, although the heifers had a higher F%(10).

Table 2: Estimators of direct (g_i), maternal (g_m) and grandam (g_n) genetic effects, and individual (h_i) and maternal (h_m) heterosis for reproductive traits, pre-weaning growth, milk production and quality, growth in feedlot, and carcass traits estimated from a diallel generated from Criollo Coreño (*Bos taurus*) and Guzerat (*Bos indicus*) cattle, and published between 2006 and 2012

Variables	**Genetic effect**				
	h_i	**h_m**	**g_i**	**g_m**	**g_n**
[1]Estrus rate, %	**20.00**$^{\beta}$		-14.00	-6.00	
[1]Gestation rate, %	**15.00**$^{\beta}$		-6.00	-7.00	
[1]Calving rate, %	**13.00**$^{\beta}$		-2.00	**-15.0**$^{\beta}$	
[1]Weaning rate, %	**13.00**$^{\beta}$		-5.00	-9.00	
[2,4]Birth weight, kg		0.48	**3.80***	0.74	
[2,4]Weaning weight, kg		**19.93***	**37.60***	8.45	
[2]Weight of calves at birth per cow exposed, kg		1.93			
[2]Weight weaned per cow exposed, kg		**38.62***			
[2]Gestation lenght, d	-1.25				
[3]Total milk production, kg	**147.00***				
[3]Daily milk production, kg	**0.60***				
[3]Peak production, kg	**0.80***				
[3]Day of peak production, d	2.50				
[3]Lactation persistance, d	3.00				
[4]Milk fat, %	0.23		-0.12	-0.11	
[4]Milk fat, kg	**5.07***		4.34	0.68	
[4]Milk protein, %	0.05		**-0.21***	0.11	
[4]Milk protein, kg	**4.97***		3.38	1.06	
[4]Lactose, %	0.03		0.15	0.07	
[4]Lactose, kg	**7.04***		**11.08***	3.48	
[4]Milk non-fat solids, %	0.09		-0.03	0.17	
[4]Milk non-fat solids, kg	**13.48***		**16.98***	6.64	
[5]Initial weight in the feedot, kg		12.51			2.26
[5]Yearling weight, kg		14.60			-9.05
[5]Final weight in the feedot, kg		12.40			-11.47
[5]Daily weight gain in the feedot, kg		-0.02			-0.06
[5]Feed efficiency in the feedot, kg		0.02			**-0.01**$^{\beta}$
[5]Rib-eye area, inches		**1.18**$^{\beta}$			**-2.20**$^{\beta}$
[5]Fat thickness, inches		0.04			
[5]Hot carcass weight, kg		15.5			**-39.02**$^{\beta}$
[5]Dressing percentage, %		1.16			
[5]Kidney and pelvis fat, kg		**-3.88**$^{\beta}$			
[5]Yield grade, units		-0.14			
[5]Cutability, %		0.30			
[5]Retail yield, %		0.59			

Direct genetic effect = Guzerat-Criollo.
Maternal genetic effect = Criollo-Guzerat.
Bold type indicates significant genetic effects: *****($P<0.05$); $^{\beta}$($P<0.10$).
Sources: [1]Martínez *et al*(5); [2]Martínez *et al*(6); [3]Martinez *et al*(11); [4]Martínez *et al*(12); [5]Martínez *et al*(8).

In a study of pre-weaning productive traits, birth weight (BW) in the calves of G and CG cows was 2.9 kg heavier ($P<0.05$) than those of C cows, while BW for the calves of GC cows was intermediate (Table 1). Compared to the calves of C cows, weaning weight (WW) was heavier ($P<0.05$) in those of G (24 kg), CG (30 kg) and GC (34 kg) cows. In contrast, no differences ($P>0.05$) were observed in weight of calf at birth per cow exposed (CWB) between these breed groups. The GC cows produced more ($P<0.05$) weight weaned per cow exposed (CWW) than the G and C cows, while the CG cows only produced more ($P<0.05$) than the C cows. Gestation in the C cows was 3.1 d longer ($P<0.05$) than in the CG cows, while the CG and G cows had intermediate gestation length (GL) (Table 1). Individual heterosis (h_i) had no effect ($P>0.05$) on GL, and maternal heterosis (h_m) had no effect ($P>0.05$) on BW or CWB. However, h_m did affect ($P<0.05$) WW and CWW (Table 2). The effect of h_m on WW was reflected in an increase of 19.93 kg ($P<0.05$). For CWW, the h_m estimator indicates that, on average, GC and CG cows produced 38.6 kilograms more calf at weaning ($P<0.05$) than G and C cows (Table 2). More specifically, GC cows produced between 45 and 60 kg more CWW than G or C cows ($P<0.05$), highlighting the advantage of using GC cows to increase productivity at weaning in G or C herds in calf-cow systems(6).

Milk production and quality

Another study compared milk production and WW in C, G, CG and GC cows. Compared to C and G cows, the GC cows had higher ($P<0.10$) total milk production (TMP; 1,059 *vs* 805 and 949 kg, respectively), daily milk production (DMP; 5.0 vs. 3.9 and 4.5 kg, respectively) and peak production (PEAK; 7.3 vs. 5.8 and 6.5 kg, respectively); the CG cows had intermediate values. Guzarat (G) cows had higher ($P<0.10$) values for TMP (144 kg) and DMP (0.6 kg) than C cows. No differences were observed between the genetic groups for day of peak production (DPEAK) and lactation persistence (LP) (Table 1). Individual heterosis (h_i) influenced ($P<0.05$) TMP, DMP and PEAK, but not DPEAK or LP. The g_i estimator identified higher values ($P<0.05$) for G cows than C cows in TMP, DMP and PEAK. In contrast, g_m did not identify any differences between genetic groups for any of the milk production variables (Table 2). The TMP-WW correlation was significant ($P<0.05$) with all the estimators and for all genetic groups; however, the correlation was stronger for GC (r= 0.49) than CG (r= 0.25). Based on the estimator values, the authors observe that use of GC or CG cows for weaner calf production should incorporate different strategies for feeding management during lactation for each genetic group. The estimator of the overall TMP-WW correlation for all four genetic groups was 0.44 ($P<0.05$). The highest regression coefficients of WW over TMP corresponded to C and GC ($P<0.05$), which suggests that the offspring of C mothers or grandams had a lower nutritional dependence on mother's milk and were largely dependent on lower nutritional value food sources. When considering the kilograms of milk per lactation required by each genetic group to produce 1 kg WW, it appears that the calves of C and GC cows made more efficient use of available milk (average= 22.5 and 27.3 kg milk/kg WW, respectively) than did the calves of G and CG cows (average= 30.9 and 37.3 kg, respectively). The 10 kg gap between the calves of GC and CG cows in this parameter is important to consider when developing recommendations for the use of these genetic groups in cow-calf systems(11).

As a complement to the above study of milk production, an analysis was done of milk composition and its relationship to WW. When compared between the four genetic groups, no differences were observed in the percentages of milk fat (MF), lactose (ML) and non-fat solids (NFS) contents, nor in the weight of milk fat (MFK) and protein (MPK). In contrast, milk from C, GC and CG cows had a higher ($P<0.05$) protein content (MP) than that of G cows. Milk from G, GC and CG cows contained more ($P<0.05$) kilograms of lactose (MLK) and non-fat solids (NFSK) than that of C cows (Table 1). Guzaret (G) cows gave birth to heavier calves ($P<0.05$) than C, GC and CG cows, while G, GC and CG cows weaned heavier calves ($P<0.05$) than did C cows (Table 1). The fact that calves from crossbred cows weighed less at birth than those from G cows, and that G, GC and CG cows produced calves with similar WW was attributed to better productive performance during the birth-weaning period of crossbred cows and their calves. Of the non-additive genetic effects, h_i did not influence milk component percentages, but did influence ($P<0.05$) milk components in terms of weight. Maternal heterosis (h_m) was found to influence ($P<0.05$) expression of BW and WW. Its effects were significant ($P<0.05$) and favorable when BW decreased (h_m= -1.3 kg) and WW increased (h_m= 12.7 kg) (Table 2). In terms of additive genetic effects, no differences between g_m were significant for any milk composition variable. Differences ($P<0.05$) between the g_i values for ST were favorable to C by 0.20 percentage points. For the variables of milk components by weight, the differences ($P<0.05$) between the g_i values favored G for lactose (11.1 kg) and non-fat solids (17.0 kg); G was also favored by the differences ($P<0.05$) between g_i values for BW (3.8 kg) and WW (37.6 kg) (Table 2). The correlations between WW and milk component percentages were not significant, except for ST (r= -0.18; $P<0.05$), which suggests that milk quality had little influence on WW. However, for milk components in kilograms, correlations ($P<0.05$) were observed of WW with MFK (r= 0.16), MLK (r= 0.21) and NFSK (r= 0.19), with no correlation of WW with MPK (r= 0.13)(12).

Feedlot performance and carcass characteristics

In a study evaluating feedlot performance and carcass characteristics, initial weight, yearling weight and final weight were lower ($P<0.10$) in C cows than in G, GC and CG cows; indeed, the calves of G cows were up to 80 kg heavier. However, daily weight gain and feed efficiency (FE) of C cow progeny did not differ ($P>0.05$) from those of G, GC and CG cow progeny (Table 1). The progeny of G and GC cows had a larger ($P<0.10$) rib-eye area (REA) and hot carcass weight (HCW) than CG and C cow progeny. The progeny of C cows also had the lowest dressing percentage ($P<0.10$) of the four genetic groups, but fat thickness did not differ among them (Table 1). When compared to the calves of C cows, the calves of G and CG cows had higher ($P<0.10$) values for yield grade, cutability and retail yield, while the calves of GC cows had intermediate values. Kidney and pelvis fat (KPF) did not differ between the calves of G and C cows (Table 1). Daughters of C cows produced calves with higher ($P<0.10$) FE (0.01 kg) than daughters of G cows. In a similar way, the grandchildren of C grandmas had higher ($P<0.10$) REA (2.2 inches^2) and HCW (39.0 kg) than the grandchildren of G grandmas. Overall, most differences tended to favor the grandchildren of C grandmas, although the only significant differences ($P<0.10$) were for FE, REA and HCW. Finally, the h_m estimator was not significant ($P>0.10$) for any of the feedlot traits, but it was ($P<0.10$) for REA (1.18 inches^2) and KPF (-3.88 kg) (Table 2)(8).

Another study evaluated the fatty acid profile of meat from young C bulls fed different dietary energy levels (EL) (EL1 = 2.2; EL2 = 2.4; EL3 = 2.2 + 2.4; EL4 = 2.4 + 2.6 Mcal ME/kg DM). The EL4 diet had the highest ($P<0.05$) polyunsaturated fatty acids (PUFA) content and the lowest ($P<0.05$) saturated fatty acids (SFA) content, but a higher ($P<0.05$) content of unidentified fatty acids (Table 3)(13). Palmitic acid C16.0 and stearic acid C18.0 contents declined ($P<0.05$) as dietary energy level increased. Monounsaturated fatty acid (MUFA) content increased ($P<0.05$) beginning in EL2, although palmitoleic acid C16:1cis-9 decreased and oleic acid C18:1cis-9 content did not vary (Table 3). Linoleic acid C18:2cis-9, 12 (C18:2ω-6) and linolenic acid C18:3cis-9, 12, 15 (C18: 3ω-3) contents also varied ($P<0.05$) with dietary energy level, but inconsistently. The PUFA/SFA, (MUFA+PUFA)/SFA and C18:2ω-6/C18:3ω-3 ratios improved ($P<0.05$) as diet energy level increased (Table 3). Meat fatty acid profile is important in human health since the omega-6:omega-3 ratio can reach up to 17:1 in some Western diets(14).

Table 3: Fatty acids profile (fatty acids g/100 g fat) in the meat of young Criollo Coreño bulls fed different energy levels

Variable	EL1	EL2	EL3	EL4
Palmitic acid C16.0	27.0^{a}	24.2^{c}	26.6^{a}	20.5^{b}
Palmitoleic acid C16:1cis-9	3.2^{a}	3.3^{a}	3.4^{a}	2.7^{b}
Stearic acid C18.0	20.7^{a}	17.6^{b}	16.9^{b}	17.0^{b}
Oleic acid C18:1cis-9	37.0^{a}	38.9^{a}	39.5^{a}	37.5^{a}
Linoleic acid C18:2 cis-9, 12	3.0^{a}	4.0^{bc}	3.6^{ac}	3.8^{ac}
Linolenic acid C18:3 cis-9, 12, 15	1.07^{a}	0.71^{a}	0.68^{a}	1.90^{b}
Saturated fatty acids	45.0^{a}	42.8^{a}	45.0^{a}	35.0^{b}
Monounsaturated fatty acids	39.7^{ac}	42.4^{bc}	42.6^{b}	41.2^{bc}
Polyunsaturated fatty acids	4.1^{b}	4.6^{b}	4.6^{b}	5.5^{a}
PUFA/SFA	0.08^{a}	0.12^{b}	0.11^{b}	0.15^{c}
Unidentified fatty acids	8.7^{b}	6.6^{b}	6.4^{b}	17.6^{a}
(PUFA+MUFA)/SFA	0.98^{a}	1.13^{b}	1.09^{b}	1.33^{c}
Linoleic/Linolenic	0.37^{b}	0.26^{b}	0.10^{b}	0.82^{a}

EL1= 2.2 Mcal ME/kg DM throughout assay; EL2= 2.4 Mcal ME/kg DM throughout assay; EL3= 2.2 Mcal ME/kg DM start to 300 kg body weight, then 2.4 Mcal ME/kg DM to end of assay; EL4= 2.4 Mcal ME/kg DM start to 300 kg body weight, then 2.6 Mcal ME/kg DM to end of assay.

PUFA= Polyunsaturated fatty acids; MUFA= monunsaturated fatty acids; SFA= saturated fatty acids.

^{a,b,c} Different letter superscripts in the same row indicate significant difference ($P<0.05$).

Source: Bustamante *et al*(13).

A study evaluating carcass characteristics in young bulls fed the same diets as in the above study(9), found that dressing percentage was higher ($P<0.05$) in EL4 (53.1 %) than in EL2 (51.2 %), but that EL1 (52.0 %) and EL3 (51.9 %) did not differ ($P>0.05$) from either of these two treatments. For the variables of REA, kidney, pelvic and heart fat, and lean cut yield, EL4 (12.3 in^2, 3.05 % and 50.1 %, respectively) was higher ($P<0.05$) than EL1 (11.2 in^2, 3.95 % and 49.2 %, respectively), but did not differ ($P>0.05$) from EL2 (11.6 in^2, 3.37 % and 48.1 %, respectively) and EL3 (11.4 in^2, 3.45 % and 48.9 %, respectively) (Table 4). In terms of fat thickness, EL3 had higher ($P<0.05$) values (0.31 in) than EL4 (0.22 in), although EL1 and 2 did not differ ($P>0.05$) from either. In contrast, yield grade was clearly higher ($P<0.05$) in EL2 (2.4 units) than in EL4 (1.6 units), but these did not differ ($P>0.05$) from EL1 and 3 (Table 4). In EL4 primary cuts (53.1 %) and total cuts (81.2 %) yields were higher than in EL2 (51.2 % and 77.4 %, respectively), but these did not differ ($P>0.05$) from EL1 and 3 (Table 4). In summary, the study showed that young C bulls in the feedlot produced carcasses with remarkable yield and quality characteristics in response to the high-energy diets commonly used in commercial finishing of beef cattle.

Table 4: Carcass characteristics in young Criollo Coreño bulls fed different energy levels

Characteristics	EL 1	EL 2	EL 3	EL 4
Dressing percentage, %	52.0^{ab}	51.2^{b}	51.9^{ab}	53.1^{a}
Rib-eye area, inches^2	11.2^{b}	11.6^{ab}	11.4^{ab}	12.3^{a}
Fat thickness, inches	0.26^{ab}	0.25^{ab}	0.31^{a}	0.22^{b}
Kidney, pelvic and heart fat, %	3.95^{b}	3.37^{ab}	3.45^{ab}	3.05^{a}
Yield grade, units	2.0^{ab}	2.4^{a}	2.1^{ab}	1.6^{b}
Primary cuts, %	52.0^{ab}	51.2^{a}	51.9^{ab}	53.1^{b}
Total cuts, %	79.4^{ab}	77.4^{b}	78.7^{ab}	81.2^{a}
Lean cuts, %	49.2^{b}	48.1^{ab}	48.9^{ab}	50.1^{a}

EL1= 2.2 Mcal ME/kg DM throughout assay; EL2= 2.4 Mcal ME/kg DM throughout assay; EL3= 2.2 Mcal ME/kg DM start to 300 kg body weight, then 2.4 Mcal ME/kg DM to end of assay; EL4= 2.4 Mcal ME/kg DM start to 300 kg body weight, then 2.6 Mcal ME/kg DM to end of assay.

^{a,b,c} Different letter superscripts in the same row indicate significant difference ($P<0.05$).

Source: Bustamante *et al*(9).

Molecular characterization

A study using nine microsatellites to evaluate autosomal diversity among seven cattle genetic groups (Criollos from the states of Chihuahua, Durango, Nayarit [Criollo Coreño] and Guerrero; Lidia; Central American Dairy Criollo; and Guzerat) identified considerable genetic differentiation among the Criollo cattle populations. No evidence of *Bos indicus* influence was found in the Criollo cattle of Nayarit, Chihuahua and Durango, but it was present in those from Guerrero(15).

High-density platform SNP markers were employed in an analysis of genetic diversity among C cattle from three locations in the state of Nayarit, Mexico: El Nayar (N), La Yesca (Y) and Santiago Ixcuintla (S). These populations were found to maintain moderate levels of observed average heterozygosity (from 0.29 to 0.34), and their estimated molecular co-ancestry values indicate that the N population differed from the S and Y populations, which can be considered portions of the same population(16). Copy number variation (CNV) analysis identified 2,170 CNV in 40 animals, located in 733 regions, with a coverage of 32.1 Mb of the autosomal genome. The functional analysis associated these CNVs with 131 genes mainly involved in inflammation and immune response, as well as 923 overlapping QTLs, classified into six different QTL-term categories: reproductive, productive, conformation, milk production, carcass, meat, and health. The group and principal component analyses showed that the animals were grouped by location of origin, although, the fact that they shared 75 of the 302 CNVs identified in more than two animals indicates they have a common genetic origin. The Y population was found to share 34 CNV with the N population and 30 CNV with the S. Between them, the N and S populations shared 56 CNV, suggesting that they are genetically closer, perhaps because the S population originated in part from animals brought from N 25 years ago. Total CNVs per population were 36 for N, 37 for Y and 34 for S, values which suggest the presence of genetic diversity among these populations(17).

Research challenges and outlook

Conserving diversity in animal genetic resources is vital to making livestock production systems sustainable. Genetic variation in livestock populations around the world is declining, both within and between breeds. But it is necessary for improving productivity and adapting to changing environmental conditions, such as climate and production or market conditions.

Research done at the INIFAP on Criollo Coreño cattle suggests that these cattle may play a prominent role as a maternal breed in commercial beef production. Short-term goals include continued systematic recording of economically interesting productive data in the experimental herd at EVSE, and identification of the most productive genotypes using high-density arrays. This will support the medium-term goals of using quantitative approaches to identify the genomic regions subject to natural selection and find evidence of artificial selection, and using homozygous runs to estimate genomic relationships between individuals and levels of consanguinity(18). No accurate data on risk is available for Criollo Coreño cattle, so another medium-term goal is to evaluate effective size and structure of the population every five years to effectively monitor trends in population size(19). In the long-term, research is needed to identify the genes associated with characteristics of present and future interest.

In other Mexican Criollo cattle populations, short-term genetic diversity studies are needed within and between groups using molecular genetic data. Over the medium-term, controlled herds should be integrated to allow systematic recording of productive and adaptive characteristics in different phenotypes. Long-term studies need to identify unique polymorphisms that distinguish these populations. Mexican Criollo cattle populations are small in size, suggesting that only small long-term financial gains can be expected from the application of genomic data(20). However, they can benefit from technological developments attained in other cattle breeds with larger populations, such as methods for optimizing genetic response and maintaining diversity, which are more easily applied in small populations(21).

Conclusions

Research done at the INIFAP over the last twenty years has found that h_i influences reproduction and milk production, and that h_m influences growth during offspring birth-weaning, which was reflected in higher productivity at weaning per cow exposed. Direct and maternal genetic effects did not affect the analyzed traits. Promising results include that young C bulls in feedlot fed high-energy diets produce meat with favorable fatty acid profiles and good carcass quality, and that reduced doses of FSH can be used for superovulation in C heifers without affecting their response to embryo production. Guzerat-Coreño (GC) cows are a better option than CG cows for growth calf production, and both are better producers than G or C cows. Finally, genetic diversity remains high in C populations. Future research in Mexican Criollo cattle populations needs to focus on genetic diversity studies using molecular genetic data, and integration of controlled herds to allow systematic recording of phenotypes, with their respective productivities and adaptabilities, to identify genes exclusive to these populations.

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