

## DEVELOPMENT OF RIBEYE AREA AND FAT THICKNESS EVALUATED BY ULTRASOUND

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### INTRODUCTION

Brazil has the world's largest commercial beef cattle herd, and despite the growing domestic market and the country's increasing share in the world market, a carcass classification and meat quality grading systems are still incipient. Pasture-fed *Bos indicus* (mostly Nellore - a zebu breed) and an inappreciable number of their crosses with British and Continental breeds make up for nearly 70% of the nation's herd. Slaughtered animals are older than 36 months, and this affects negatively carcass and meat quality. Therefore an increase in the use of *Bos taurus* sires and feedlot systems can rapidly decrease age at slaughter and improve meat quality. Differences in adipose tissue accretion and muscle development among genetic groups affect meat quality and retail yield. Large frame size animals begin adipose tissue accretion later than small frame size ones and therefore require longer feeding time to be slaughtered at the same finishing conditions (Owens *et al.*, 1993).

Ultrasound technology provides a fast, easy, non-invasive and non-destructive method for estimation of back fat thickness (BFT) and ribeye area (RA) in live animals. The repeatability of these measurements by ultrasound is high whether they are made by a single or several technicians. Thus this technique can be used as a reliable tool to predict carcass composition in live animals (Perkins *et al.*, 1992b ; Herring *et al.*, 1994b ; Bergen *et al.*, 1997 ; Hassen *et al.*, 1998).

### OBJECTIVES

The objectives of this work were to evaluate muscle development and back fat thickness using ultrasound in bullocks of four genetic groups under the same management and nutritional conditions in feedlot.

### MATERIAL AND METHODS

The experiment was done in the beef cattle research center at the Universidade Estadual Paulista (UNESP) in Botucatu, Sao Paulo. Yearling bullocks with 329 kg initial average weight from four genetic groups (30 ½ Angus x Nellore; 30 ½ Canchim x Nellore; 30 ½ Simmental x Nellore and 25 straight Nellore) were used in a feedlot system. Five animals were randomly assigned per pen according to their genetic make up. The ration offered was formulated to have 16% crude protein (CP) and 74% of total digestible nutrients (TDN) and to achieve an energy-allowable average daily gain of 1.35 kg (NRC, 1996). The dry matter basis forage concentrate ratio was 21 79%.

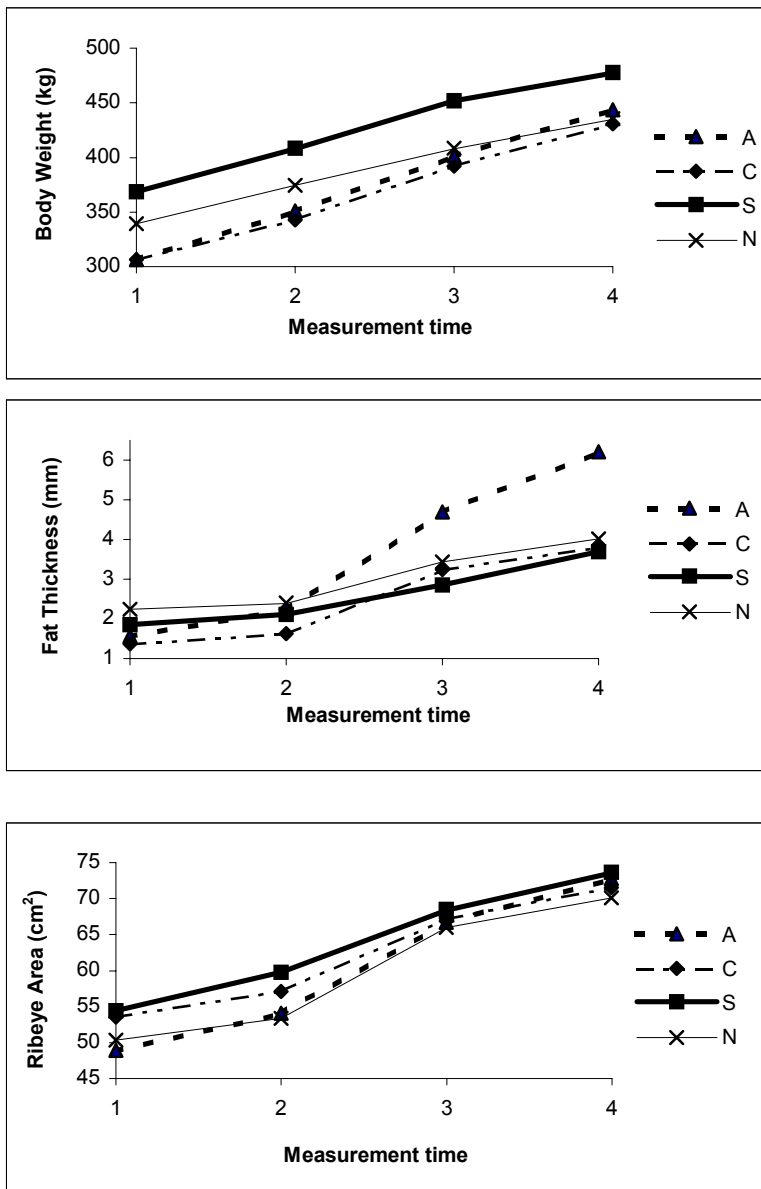


Figure 1. Body Weight, Ribeye Area and Fat Thickness, according to measurement time, on Nellore (N), Nellore X Angus (A), Nellore X Canchim (C) and Nellore X Simmental (S) cattle

Live body weight and ultrasound measurements were taken each 28 days, after 12-hour fast as proposed by Herring *et al.* (1994). The equipment used was a PIEMEDICAL Scanner 200 VET, with an 18 cm linear 3.5 MHz transducer. Animals were slaughtered after approximately 120 days of feeding and a minimum of 3 mm BFT as estimated by ultrasound.

The experimental design was completely randomized, with 30 replicates for Angus, Canchim and Simmental crosses and 25 for straight Nellore, with treatments in a split-plot arrangement. Genetic groups were allocated to plots and measurement time to subplots. Multiple comparisons were made by the Student-Neuman-Kleus multiple range test (SNK) when the F-test was significant. When the genetic group x time interaction was significant (5% level), traits were compared within each measurement time. All analyses were performed using the GLM procedure of SAS (SAS, 1987).

## RESULTS AND DISCUSSION

Overall, there were differences ( $P<0.05$ ) for RA, BFT and body weight among genetic groups, measurements and genetic group x measurement interaction, indicating those parameters showed different behavior among genetic make up. Straight Nellore and Angus crosses showed lower ( $P<0.05$ ) RA compared to the other two breeds in the first two measurements. In the second measurement, Simmental crosses showed a higher RA ( $P<0.05$ ) than that of Canchim crosses. The third and fourth measurements showed no differences among genetic groups (figure 1). The Simmental crosses had the highest weight ( $P<0.05$ ) during the whole feeding period. On the other hand, Angus and Canchim crosses showed a lower body weight ( $P<0.05$ ) at the first two measurements and similar values at the two last ones as compared to straight Nellore. At the beginning of the feeding period, straight Nellore animals were heavier but with smaller RA than Canchim crosses ( $P<0.05$ ). Angus and Canchim crosses showed a similar trend in body weight gain throughout the feeding period (figure 1).

Nellore animals had higher BFT ( $P<0.05$ ) compared to the Simmental and Angus crosses ; in the first ultrasound measurement the Canchim crosses showed a lower BFT ( $P<0.05$ ) than the two latter genetic groups. In the third and fourth measurements the Angus crosses had the largest ( $P<0.05$ ) BFT (figure 1) showing the largest and the fastest growing BFT of all genetic groups. This was expected since Angus crosses begin adipose tissue accretion earlier than the other breeds (Bergen *et al.*, 1996 ; Bergen *et al.*, 1997). The results on body weight gain and RA growth showed Angus crosses continued growing after the third measurement, that is, there was a simultaneous increase in fat and muscle accretion. This contrasts with the findings of Owens *et al.* (1993). However, one should emphasize the fact that as animals increase their body weight, the precision of the RA values predicted by ultrasound decreases, as suggested by some authors (Houghton and Turlington, 1992 ; Herring *et al.*, 1994).

## CONCLUSION

The Angus crosses showed a fast rate of growth as observed by the body weight gain, RA and BFT values. These results suggest Angus crosses are the most appropriate genetic group to be used in a feedlot young cattle production system.

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