

Communication N° 11-36

CHARACTERISATION OF CARCASSES OF BRAHMAN, BRAFORD AND AFRICANDER F₁ STEERS IN DIFFERENT ENVIRONMENTS. A. Rehman, H. Hearnshaw, B.J. Crook, P.F. Arthur and M. Ahmad. Livestock Production Research Institute, Bahadurnagar, Okara, Pakistan.

Carcass data on 185 steers in the three environments (locations) of NSW, Australia were used to characterise carcasses of Brahman x Hereford (BH), Braford x Hereford (BfH) and Africander x Hereford (AfH). Generally, the first canonical variate was the measure of size and second canonical variate was the function of eye muscle area and fat distribution among the depots. At Mallangane and Nevertire, the first canonical variate distinguished AfH from BH and the second canonical variate separated BfH from the other 2 genotypes. At Grafton, however, the first canonical variate separated BH from BfH and the second canonical variate discriminated AfH from the other two genotypes. The discriminant functions indicate that the carcass attributes of the genotypes are dependent on the environment.

Communication N° 11-37

EVIDENCE OF NON-ADDITIVE GENETIC EFFECTS ON PREDICTED CARCASS COMPOSITION. R.A. Afolayan, C.D.K. Bottema and W.S. Pitchford. Livestock Systems Alliance, Adelaide University, Roseworthy, SA 5371 Australia.

The importance of direct, maternal, heterosis and epistatic effects were examined on predicted carcass products using live-animal measurements at 600-day postpartum. Prediction equations were developed from measurements at slaughter and boned out data of large biological type genotypes before adaptation on five combinations of two pure breeds (Jersey, JJ and Limousin, LL), F₁ (LJ) and two backcrosses (XJ and XL). Direct genetic effects were large ($P < 0.001$) for kilogram carcass products. There were positive Jersey maternal effects only on bone and fat yields, an indication of high milk supply from this breed. Also, there were large heterotic and epistatic effects relative to direct effects on carcass yield percentage showing that the non-additive gene action due to these effects could be exploited using live measurement in crossbreeding programs.

Communication N° 11-38

DEVELOPMENT OF RIBEYE AREA AND FAT THICKNESS EVALUATED BY ULTRASOUND. L. Sugisawa, H.N. Oliveira, W. Mattos, A.C. Silveira and M.D.B. Arrigoni. Department of Animal Production, ESALQ/USP, Piracicaba, SP, Brazil.

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 to evaluate muscle development and back fat thickness by ultrasound in feedlot. Body weight and ultrasound measurements were taken each 28 days. The animals were slaughtered at approximately 120 days of feeding period and a minimum of 3 mm backfat thickness (BFT) as estimated by ultrasound. Overall there were significant differences ($P < 0.05$) for ribeye area (RA), BFT and body weight among genetic groups, measurements and genetic group x measurement interaction, suggesting those parameters showed different behavior among genetic make up. 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.

Communication N° 11-39

NEW ALLELE FOR PIT 1 LOCUS IN NELLORE CATTLE BREED (*Bos indicus*). F.H. Biase, L. Martelli, A.J.M. Rosa, F.M.F. Nunes, A. del V. Garnerio, R.J. Gunski, L.A.F. Bezerra and R.B. Lôbo. FMRP-USP - Depto. de Genética - Bl. C - Av Bandeirantes, 3900 - Ribeirão Preto-SP CEP14040-030, Brazil.

Pituitary-Specific Transcription Factor (PIT 1) is important in somatotropin synthesis once it regulates the growth hormone liberation. We described a new allele for PIT 1 in Nellore cattle breed (*Bos indicus*) and analyzed if the genotypes have influenced the weight at 210 and 450 days (W210, W450) and scrotal circumference at 365 and 450 days (SC365, 450). In 241 typed animals the frequencies of alleles were 0.00825, 0.7841 and 0.2072 for A, B and C, respectively. They are not in Hardy Weinberg equilibrium ($P = 0.05$). There was no influence of genotypes BB and BC on the following Expected Progeny Differences (EPD's): W210, W450, SC 365 and SC 450 at level of $P = 0.05$.

Communication N° 11-40

ESTIMATION OF VARIANCE COMPONENTS AND GENETIC PARAMETERS FOR VISUAL SCORES IN A NELLORE ZEBU CATTLE POPULATION. W.K. Filho, J.B.S. Ferraz, J.P. Eler and N. Pineda. GMA/FZEA, Universidade de São Paulo, C.P. 23, 16635-900 Pirassununga, SP, Brazil.

Variance components and genetic parameters of visual scores evaluations of a Nelore beef herd raised in Brazil, were estimated, so that the information could be used as auxiliary tool in breeding programs and create scientific knowledge about the criteria applied in cattle shows and exhibitions. A dataset of 2,146 visual scores of conformation (C), precocity (P) and muscularity (M) of a Nelore herd raised in Southeastern Brazil, out of a total of 4,867 animals in pedigree, was analyzed and the estimates of heritability obtained were 0.41 for carcass conformation, 0.48 for precocity of finishing and 0.34 for muscle score. The genetic correlations with weaning weight were 0.89, 0.77 and 0.74 and 0.69, 0.80 and 0.33 with yearling weight, indicating that such can be used as auxiliary selection criteria.

Communication N° 11-41

CANDIDATE GENES FOR GROWTH TRAITS IN BEEF CATTLE CROSSES *Bos taurus* X *Bos indicus*. D.D. Tambasco, C.C.P. Paz, M. Tambasco-Studart, A.P. Pereira, M.M. Alencar, A.R. Freitas, L.L. Coutinho, I.U. Packer and L.C.A. Regitano. Federal University of São Carlos, P. Box. 678, 13565-905, São Carlos, SP, Brazil.

Candidate gene strategy has been proposed to direct the search for QTLs, and many polymorphisms at these loci have been associated with several production traits in bovine. A total of 211 animals resulting from crosses between Nelore females with sires from either Aberdeen Angus, Canchim and Simmental breeds were analyzed using the RFLPs in the κ-casein, β-lactoglobulin and growth hormone genes. Average daily gain from birth to weaning (ADGbw) and from weaning to yearling (ADGwy) were analyzed based on a statistical model comprising GH and LGB genotypes and their interaction effects. Significant effects ($p < 0.05$) of GH and the interaction LGB*GH were verified for the ADGwy variation. Animals with LL genotypes for GH had higher ADGbw than LV animals but lower ADGwy ($p < 0.05$).