GENETIC AND PHENOTYPIC RELATIONSHIPS BETWEEN SUBPOPULATIONS OF THE BONSMARA CATTLE PE STRYDOM & A KOTZÉ

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Summary: Ninety bull calves of five Bonsmara strains, viz. Edelheer (E), T-49 (T), Wesselsvlei (W), Roodebos (R) and Belmont Red (BR), were fattened under intensive feeding conditions and serially slaughtered at 4 different slaughter masses. Phylogenetic relationship between strains were determined through blood typing techniques. Production and product quality characteristics were compared between strains. Determination of genetic distances among the group of animals confirmed the existence of five genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetically independent subpopulations (breeding lines) with a variation of genetical subpopulations (breeding lines) with a variation of genetical subpopulation of genetical subpopulations (breeding lines) with a variation of genetical subpopulation of genetical subpopulations (breeding lines) with a variation of genetical subpopulation of genetical subpopulations (breeding lines) with a variation of genetical subpopulations (breeding lines) with a variation of genetical subpopulation of genetical subpopulations (breeding lines) with a variation of genetical subpopulation of genetical subpopulations (breeding lines) with a variation of genetical subpopulation of genetical subpopulations (breeding lines) with a variation of genetical subpopulation of genetical subpopulations (breeding lines) subpopulations (breeding lines) with a variation in genetic distances among them. Comparisons of production and product characteristic were done on a common subcutaneous fatness level (%) by means of analyses of covariance. T gained mass faster and more efficiently both a live and carcass mass basis and had proportionally more meat in the high-priced cuts of the carcass than W. Muscle of the W line hugh the state of the W l 7a significantly higher (p<0.05) myofibrillar fragmentation (MFI) than T, resulting in higher tenderness scores for W. There may therefore be a negative relationship between production potential and meat/muscle quality, which can be related to muscle enzyme activity.

INTRODUCTION

The Bonsmara is an indigenous composite breed which originated in the early 1940's from a 5/8 : 3/8 combination of the Afrikant (indigenous Sanga) and Shorthorn/Hereford (exotic) through an initiative of the former Department of Agriculture of South Africa (Bonstin 1980). When it was detected that the genetic strengthere is a strengthere is a strengthere in the strengthere in the strengthere is a strengthere is a strengthere in the strengthere is a strengthere is a strengthere in the strengthere in the strengthere in the strengthere is a strengthere in the stre 1980). When it was detected that the genetic structure of the breed has narrowed dangerously by 1970, four individual strains or breeding lines were developed to ensure greater genetic flexibility within the breed (Bosman, 1988). The Edelheer (E) breeding line (progenitor, the bull Edelheer) can be regarded as the main static of the breed (Bosman, 1988). bull Edelheer) can be regarded as the main strain of the breed, since it dominated the AI industry of the Bonsmara prior to the development of the other stains. The Wesselsvlei (W) strain originated from the bull, Spanner, a 5/8 Afrikaner x 3/8 Red Poll bull, instead of the normal Afrikaner / Hereford/Shorthorn combination while the Depiction (P) Afrikaner/Hereford/Shorthorn combination, while the Roodebos (R) strain was developed from an unrelated group of animals kept of specific government farm. T-49 (T) is no formal strain but and the specific government farm. specific government farm. T-49 (T) is no formal strain, but was regarded in this study as an independent strain due to the large number of the formal strain due to the for animals within the E strain that were related to a certain bull, T-49. This bull achieved exceptional growth performance indices in the National Performance Scheme (Bosman, 1996, personal activity). National Performance Scheme (Bosman, 1996 - personal communication). The Belmont Red (BR) is an independent breed, developed a sub-Australia from 1/2 Afrikaner, 1/4 Shorthorn and 1/4 Hereford. It was imported into South Africa and was further developed as a independent strain. In this study the phylogenetic and physical developed as a independent strain. In this study the phylogenetic and phenotypic relationship of these five strains are described and compared.

MATERIALS AND METHODS

Ninety bull calves of five Bonsmara strains were fattened under intensive feeding conditions and serially slaughtered at 4 difference at 4 dif slaughter masses. The phylogenetic relationships between the strains (subpopulations) were studied using the gene frequency value obtained from the electrophoretic analysis of 8 structural gene loci, that code for blood-soluble proteins, together with 23 blood group within the genetic differentiation within the structural gene loci, that code for blood-soluble proteins, together with 23 blood group within the structural gene loci, that code for blood-soluble proteins, together with 23 blood group within the structural gene loci, that code for blood-soluble proteins, together with 23 blood group within the structural gene loci, that code for blood-soluble proteins, together with 23 blood group within the structural gene loci, that code for blood-soluble proteins, together with 23 blood group within the structural gene loci, that code for blood-soluble proteins, together with 23 blood group within the structural gene loci, that code for blood-soluble proteins, together with 23 blood group within the structural gene loci, that code for blood-soluble proteins, together with 23 blood group within the structural gene loci, that code for blood-soluble proteins, together with 23 blood group within the structural gene loci, that code for blood-soluble proteins, together with 24 blood group within the structural gene loci, that code for blood-soluble proteins, together with 24 blood group within the structural gene loci. In addition, the genetic differentiation within the subpopulations was studied. Values of the genetic distances among populations, in phenograms and cladograms as well as the genetic distances among populations. phenograms and cladograms, as well as the goodness-of-fit statistics of those dendograms have been computed using the BIOSYS-program (Swofford & Selander, 1981). On reaching target measure are the bio program (Swofford & Selander, 1981). On reaching target masses per slaughter group, animals were slaughtered and dressed at a local research abattoir according to commercial practice and processed into 15 when the statistics of those dendograms have been computed using the BIOS of the statistics of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of those dendograms have been computed using the BIOS of the BI research abattoir according to commercial practice and processed into 15 wholesale cuts the following day. Carcass yield (dressing the two states are as a state of two states are percentage) as well as carcass composition and meat distribution over the carcass were determined by physical dissection of the subcutaneous fat (SCF), meat and hone and the province and bone and the province and the pro subcutaneous fat (SCF), meat and bone and the proximate analyses of the soft tissue of the primerib for percentage protein, moisture, and fat (A.O.A.C., 1985; Naudé, 1972) With regard to much a soft tissue of the primerib for percentage protein, moisture, and the protein and the protein and the protein analyses of the soft tissue of the primerib for percentage protein, moisture, and the protein and the protein and the protein and the protein analyses of the soft tissue of the primerib for percentage protein, moisture, and the protein analyses of the primerib for percentage protein and the protein analyses of the primerib for percentage protein and the protein analyses of the primerib for percentage protein and the protein analyses of the primerib for percentage protein and the protein analyses of the primerib for percentage protein and the protein analyses of the primerib for percentage protein analyses of the primerib for percentage protein and the protein analyses of the primerib for percentage protein and the protein analyses of the primerib for percentage protein and the protein analyses of the primerib for percentage protein analyses of the percentage perc and fat (A.O.A.C., 1985; Naudé, 1972). With regard to muscle quality, collagen content and solubility (Bergman & Loxley, 1963; Hill, 1966; Weber, 1973), myofibrillar fragmentation index (MEL Culler et al. 1970) 1966; Weber, 1973), myofibrillar fragmentation index (MFI; Culler *et al.*, 1978 as adapted by Heinze & Bruggemann., 1994) as well as sensory quality (aroma intensity, juiciness, overall tenderrors, provided by Heinze & Bruggemann., 1994) as well as sensory quality (aroma intensity, juiciness, overall tenderness, residual amount of connective tissue, overall flavour intensity) and sheat force resistance measurement were determined on samples of the Markov Ma force resistance measurement were determined on samples of the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the *Mm. longissimus thoracis et lumborum* (LT) aged for 7 days at 0-7 due to the longistic Muscle fibre type ratio and fibre area were determined by means of video image analysis on a sample of the LT removed directly all exsanguination and before electrical stimulation of the carcass. Sources of variation between strains were investigated by analysis of variance (ANOVA) or analysis of covariance (ANCOVA) with SOF variance (ANOVA) or analysis of covariance (ANCOVA), with SCF and starting mass as covariants. Mean separation was achieved by application of the Bonferroni Multiple Comparison Method at the 5 % test level.

RESULTS AND DISCUSSION

Phylogenetic relationships: The genetic variability showed heterozygosity levels varying between 0.31 and 0.43. The lowest level we observed in T, which is in accordance with the development of this strain, being the most inbred. The highest heterozygosity level with the development of this strain, being the most inbred. The highest heterozygosity level with observed in E and R, which represent the largest portion of the Bonsmara population. According to the dendogram (Figure 1), the formation of 2 large clusters were observed; the W strain and one cluster formation that the strain and one cluster formation is the strain and one cluster formation. of 2 large clusters were observed: the W strain and one cluster formed by the rest of the population, except the BR which separated from the hypothetical trunk very early. Within the second cluster R and R hypothetical trunk very early. Within the second cluster, E and T showed a higher relationship, perfectly differentiating from R. $E_{and}^{and} R$ were more related than E and W. The cladogram was topologically similar to the phenogram, which corroborates the stability of the classification.

Phenotypic relationships: The W strain of the Bonsmara gained mass at a higher rate and more efficiently on both a live mass and carcass mass basis than the other strains, but in particular T and R. Differences between T/R and W of more than 30 % for carcass g_{inter}^{about} rate (P<0.05) and 20 % for efficiency of carcass gain (P<0.05) were recorded. Furthermore, both T and R showed a tendency towards high total carcass fat yield and subsequent lower muscle yield compared to W (adjusted for carcass SCF; Table 1). In addition, T and E half higher distribution of total carcass mass (2.3 %) and meat (1.9 %) in the high-priced cuts, with an accordingly lower distribution to the high-priced cuts, with an accordingly lower distribution difference of the carcass compared to W and BP. (Table 2). But M ventral cuts of the carcass, compared to W and BR (Table 3). Both Kempster *et al.* (1976) and De Bruyn (1991) reported similar finding for breeds of different maturity types, suggesting that W is an earlier maturing strain than T and R. However, according to Table 1, and T and R. However, according to Table 1, and T and R. However, according to Table 1, and T a significant difference in final carcass mass (maturity type) existed between the two strains.

Regarding meat quality attributes, sensory panel scores (P<0.05), as well as shear force resistance values (P>0.05), showed a $17^{\frac{1}{10}}$ advantage in meat tenderness for W compared to T. These differences coincided with a 17 % difference in MFI in favour of W. Culler (1978) reported that MFI accounted for 50 % of the variation in Line with a 17 % difference in MFI in favour of W. (1978) reported that MFI accounted for 50 % of the variation in loin steak tenderness and regarded myofibrillar fragmentation as a more length or college of the variation of th important effector of tenderness than sarcomere length or collagen solubility. In addition, Crouse *et al.* (1991) and Seideman *et al.* (1987) reported correlation coefficients of 0.53 and 0.60 between MEL and sonore tenderness than sarcomere length or collagen solubility. reported correlation coefficients of 0.53 and 0.60 between MFI and sensory tenderness, which compared reasonably well with the 0.47 found in the current trial. Despite differences in other muscle absorbed elements is a sensory tenderness. in the current trial. Despite differences in other muscle characteristics, none of them seemed to correspond to differences in sensor tenderness or shear force between the strains.

W

CONCLUSION

Despite very definite phylogenetic differentiation between the strains of the Bonsmara, the only consistent differences relating to production (growth performance) as well as product quality characteristics (carcass and meat quality), were found between T and W. These different differences may be coupled to the specific origins of the strains as described in the introduction of this paper, and boils down to normal variations. What seems to Variation that occurs within breeds, except that for the Bonsmara breed, some of this variation is fixed within certain strains. What seems to be more important in terms of selection criteria, is the contrast found between growth performance and meat quality between T and W. This indication is the selection for increased net protein inding may suggest that selection for fast growing, more efficient animals in a breed, which, in effect, is a selection for increased net protein Rain a breed, which, in effect, is a selection for fast growing more efficient animals in a breed, which in effect, is a selection for increased net protein star, may be confounded by a retardation in the protein breakdown process in the muscle post mortem, resulting in conflicting production and product quality as found in the current trial. This process, although probably overemphasised, is clearly demonstrated by the effect of a growth. so the promoter such as β -agonists' positive effect on growth and detrimental effect on muscle tenderness through its inhibiting effect on myorkmyofibrillar protein breakdown by the proteolytic enzyme system.

and standa		E	Т	W	В	R	Cov.
Average daily gain: (kg/day) Feed conversion ratio: (kg feed /kg gain) Carcass mass (kg) Meat %	Line	1 35 (0.06)	1 47 (0 06)	1.28 (0.06)	1.35 (0.06)	1.51 (0.06)	NS
	Live	$0.87^{b}(0.03)$	$0.90^{b}(0.04)$	$0.69^{a}(0.05)$	0.89 ^b (0.04)	0.94 ^b (0.05)	*
	Ling	$6.71^{ab}(0.24)$	$6.21^{a}(0.24)$	$7.28^{b}(0.24)$	$6.75^{ab}(0.24)$	6.12 ^a (0.24)	NS
	Live	$10.11^{ab} (0.38)$	$9.29^{a}(0.38)$	$11.72^{b}(0.38)$	10.28 ^{ab} (0.38)	9.62 ^a (0.38)	NS
	Carcass	240.8 (2.3)	241 2 (2.2)	241.8 (2.9)	236.2 (2.3)	239.3 (3.4)	\$
		79 9 (0 3)	79.8 (0.3)	79.7 (0.3)	79.6 (0.3)	80.1 (0.4)	#
Auscle %		70.0 (0.7)	67.7 (0.7)	70.0 (0.7)	68.6 (0.7)	68.4 (0.7)	NS
Total carcass fat Bone % High-priced cuts:		15.0 (0.7)	17.4 (0.6)	14.8 (0.6)	16.3 (0.7)	16.6 (0.7)	#
		15.3 (0.3)	15.3 (0.3)	15.4 (0.3)	15.5 (0.3)	15.0 (0.4)	#
	Total vield	39.4 (0.3)	39.7 (0.2)	38.8 (0.2)	38.8 (0.2)	39.0 (0.3)	#
Sensory attributes: Shear force (N/2.5 cm (2))	Meat vield	42 2 (0 3)	42.3 (0.3)	41.6 (0.4)	41.6 (0.3)	41.9 (0.4)	\$
	Tenderness [@]	$50^{ab}(0.2)$	$4.6^{a}(0.2)$	$5.4^{b}(0.2)$	4.8 ^{ab} (0.2)	5.0 ^{ab} (0.2)	NS
	renderness	92.3 (4.0)	101.7 (4.0)	87.2 (4.0)	90.4 (4.0)	89.4 (4.0)	NS
Ayofibrillar fragmentation index:		1149 (6.6)	100.3 (6.6)	117.3 (6.6)	110.8 (6.6)	102.5 (6.6)	NS

\$ Both covariants, SCF and starting mass, were significant (P<0.05)

Only covariant, SCF, was significant

Only covariant, starting mass, was significant

NS Covariants non-significant

Eight-point Lydard scale; 8 measuring the most tender and 1 the least tender





mana broading lines

Figure 1: Dendogram obtained from Nei's distance (1978) for the different Bonsmara strains

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