Fatty acid profile of zebu beef cattle from the Central African sub-region

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Abstract

This study analysed the meat fatty acid (FA) composition of three zebu breeds, Gudali (GU), White Fulani (WF) and Red Mbororo (RM), raised on savannah pasture and monitored in the commercial context of the Yaoundé abattoir. Samples of *m. longissimus thoracis* from 60 bulls belonging to the GU, WF and RM breeds were collected and analysed for fat and FA composition. The fat content of the meat was low, but similar across breeds (1.34 ± 0.912 g/100 g muscle, mean ± SD). Meat from the GU breed had higher C18:3*n*-3 and C22:5*n*-3 proportions and lower C18:0 and total saturated FA proportions than WF meat. Red Mbororo meat had an intermediate FA composition compared with the other breeds. The elongase and Δ9 desaturase indices were comparable among breeds. In summary, the results indicate that there are minimal differences in beef FA composition of the three breeds from the Central African sub-region. Additionally, based on the polyunsaturated FA (PUFA) proportion, 13.9% of the total lipids and *n*-6/*n*-3 PUFA ratio, 1.95, consumption of beef from these breeds could be beneficial to human health. This is possibly owing to the pasture feeding and low fat content of the beef.

Keywords: Intramuscular fat, fatty acid composition, natural pasture
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Introduction

The Central African sub-region is the smallest beef market in Africa. In the near future, this region, together with the Western African region, will have the largest increase in beef consumption in Africa (Livestock Data Innovation in Africa Project, 2013). The importance of meat as a source of high biological value proteins and micronutrients (vitamins A, B_6, B_{12}, D and E, and iron, zinc and selenium) is well recognized (Biesalski, 2005; Muchenje *et al*., 2009a). However, beef fat has a relatively high ratio of saturated to unsaturated fatty acids (SFA/UFA) in comparison with the meat from monogastric species. This is a risk factor in the development of vascular and coronary diseases (Calder, 2004).

Breed, together with age and nutrition of animals, is the most important factor influencing the content and composition of meat fat (Smith *et al*., 2009; Mapiye *et al.*, 2012). In the Central African sub-region, beef is produced from zebu cattle, the main breeds being Red Mbororo and White Fulani. Both breeds belong to the Fulani group, but present distinct characteristics that justify their separate breed status (Ibeagha-Awemu & Erhardt, 2006). However, in Cameroon, which is the main producer of zebu cattle in the Central African sub-region, the Gudali is the predominant beef cattle breed (Pamo, 2008). To the knowledge of the researchers, there is limited information on the fatty acid (FA) composition of African zebu breeds (Muchenje *et al*., 2009b). Therefore, the aim of this study was to compare the FA composition of Gudali (GU), White Fulani (WF) and Red Mbororo (RM) bulls raised on savannah pasture.

Materials and Methods

The study complies with the current laws of Cameroon (Decree No. 76/420, and No. 86/755). Approximately 2000 cattle were processed individually at the Livestock Development Corporation (SODEPA)

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Yaoundé abattoir between January 2009 and March 2012. The animals were then slaughtered, and the carcass weight recorded. As reported by Nfor *et al.* (2014), 99.2% of the slaughtered cattle were zebu belonging to the GU, WF and RM breeds, and 60% were bulls. The majority (75%) of cattle processed at the facility was raised under the transhumant pastoral system, characterized by the organized displacement of cattle herds during the dry season. To represent the animals slaughtered in terms of cattle category, breed, age and carcass weight within breed, 60 zebu bulls belonging to the GU (n = 19), WF (n = 20) and RM (n = 21) breeds were selected. The age at slaughter was similar for the breeds (median = 4; min. = 3; max. = 5 years). The GU breed (174.6 kg) had a higher average carcass weight than the WF (153.7 kg) and RM (153.2 kg) breeds. The experimental bulls were previously raised on Guinea savannah pasture, which is a mixture of trees and grass species such as *Hyparrhenia*, *Panicum* and *Setaria* spp. (Deffo *et al.*, 2011; Pamo, 2008). The diet consisted mostly of herbage, grazed in the dry and rainy seasons.

After chilling at 4 °C for 24 hours, a sample of approximately 400 g of *m*. *longissimus thoracis* was taken from the left side of the carcass by cutting a three-centimetre thick steak from the section dividing the thoracic and lumbar parts of the muscle (i.e. between the 12th and 13th ribs). The sample was then vacuum-packed, frozen rapidly and stored at −20 °C until FA analysis.

Extraction of total lipids was performed according to the procedure of Folch *et al*. (1957). A total of 15 mg of nonadecanoic acid (C19:0) was added to a 1.5 g sample of minced meat and homogenised in 30 mL of a chloroform-methanol mixture (2:1 v/v) using an Ultra-Turrax homogeniser (T 25 basic; Ika-Werke, Staufen, Germany). The sample was subsequently filtered under vacuum through a Whatman No. 1820-047 filter paper. The extract was washed with 8.5 mL of 0.88% (w/v) KCl, mixed vigorously for 60 s, and then left overnight at room temperature. The organic phase was separated, and the solvents were evaporated under vacuum at 40 °C. Fatty acid methyl esters (FAME) were prepared using methanolic HCl (Sukhija & Palmquist, 1988). Lipid samples were mixed with 2 mL of hexane and 3 mL of methanolic HCl in 20 mL glass tubes with Teflon-lined caps. The mixture was heated at 70 °C for 2 hours, and then cooled to room temperature. The FAME was extracted in 2 mL of hexane after the addition of 5 mL of 6% (w/v) K_2CO_3 and Na_2SO_4 anhydrous. Samples stayed for 30 min prior to centrifugation at 1 006 x *g* for 10 min at 20 °C. The upper hexane layer was removed, concentrated under N_2 and diluted in hexane. The FAME was separated with a Carlo Erba gas chromatograph (GC) (HRGC 5300 mega-series; Rodano, Milan, Italy) fitted with an automatic sampler (model A200S; Rodano, Milan, Italy) and a flame ionisation detector (FID). A 1 µL sample was injected in 1 : 30 split mode. The GC was equipped with a 60 m SP-2380 fused silica capillary column (0.25 mm i.d., film thickness 0.25 µm; Supelco Inc., Bellafonte, PA), and the oven temperature was increased from 160 to 180 °C at 1 °C/min, from 180 to 260 °C at 5 °C/min and then held at 260 °C for 5 min. Helium was used as the carrier gas at the rate of 1.2 mL/min, and FAME were identified using external standards (Supelco 37-component FAME mix, including conjugated linoleic acids; Sigma-Aldrich, Milan, Italy). The FAME were quantified using C19:0 as the internal standard and were expressed as the percentage of the total lipids that were identified. The ∆9 desaturase, elongase and atherogenic indices were calculated according to Bartoň *et al*. (2010), Pitchford *et al*. (2002) and Ulbricht & Southgate (1991), respectively, as follows:

$$\Delta 9 \text{ desaturase index} = 100 \times (C14{:}1n\text{-}9c + C16{:}1n\text{-}9c + C18{:}1n\text{-}9c + CLA) / (C14{:}1n\text{-}9c + C16{:}1n\text{-}9c + C18{:}1n\text{-}9c + CLA + C14{:}0 + C16{:}0 + C18{:}0 + C18{:}1t);$$

$$\text{elongase index} = 100 \times [(C18{:}0 + C18{:}1n\text{-}9c) / (C16{:}0 + C16{:}1n\text{-}9c + C18{:}0 + C18{:}1n\text{-}9c)];$$

$$\text{atherogenic index} = [C12{:}0 + 4(C14{:}0) + C16{:}0] / (SFA+PUFA);$$

where C14:1*n*-9c, C16:1*n*-9c, C18:1*n*-9c, CLA, C14:0, C16:0, C18:0, C18:1t, C12:0, SFA and PUFA are myristoleic acid, palmitoleic acid, oleic acid, sum of CLA isomers, myristic acid, palmitic acid, stearic acid, trans-C18:1 acids, lauric acid, saturated fatty acids and polyunsaturated fatty acids, respectively.

The statistical analyses were performed with the free software R version 2.15.2. The normality of the data distribution and homogeneity of variance were tested with the Shapiro-Wilk and Levene tests, respectively. Data were subjected to one-way analysis of variance (ANOVA) with breed as the fixed effect. The Tukey-Kramer test for unequal sample size was used as a post-hoc test. If the ANOVA assumptions were not verified, multiple comparisons were performed according to the Herberich *et al*. (2010) procedure. Pearson coefficients were used to determine associations between FAs and intramuscular fat content (chloroform–methanol extractable fat) of *m. longissimus thoracis*. A probability level of $P \leq 0.05$ was established for statistical significance.

Results and Discussion

The total lipid weight and relative proportion of FA in *m. longissimus thoracis* according to breed are shown in Table 1. The intramuscular fat content of meat was low (mean ± SD, 1.34 ± 0.912 g/100 g muscle) and did not differ across breeds. This was possibly because of the lack of genetic selection of the animals (Deffo *et al.*, 2011). Intramuscular fat content in the current study is comparable with that reported by Salifu *et al*. (2013) in Fulani bulls. However, the IMF content of beef from Nguni and Bonsmara steers raised on natural pasture was lower in the study by Muchenje *et al*. (2009b). Savell & Cross (1988) suggested a minimum of 3% fat to ensure acceptable palatability of beef. Given that fat content from the present study was below this threshold, meat from the three breeds could be poorly palatable.

Overall, breed had a limited effect on the FA profile of meat in the current study. This is in agreement with the general conclusion of De Smet *et al*. (2004). In studies with Canchim and Canchim × Charolais (Do Prado *et al.*, 2009) and Nguni and Bonsmara cattle (Muchenje *et al.*, 2009b), breed was also reported to have a small effect on FA composition of meat. However, in the current study, the FA profile of beef of the GU tended to be similar to that of the RM breed, with the only exception being that C18:0 was lower in GU than in RM beef. Considering the linear odd-chain FAs, GU had higher tridecanoic acid (C13:0), lower pentadecanoic acid (C15:0), and tended to have lower margaric acid (C17:0) proportions (P = 0.08) relative to WF beef. These results could be explained by genetic differences between the breeds related to *de novo* C15:0 and C17:0 syntheses from propionate in adipose tissue (Vlaeminck *et al*., 2006). Bressan *et al*. (2011) have suggested that differences in gastrointestinal tract and rumen volume between breeds can influence the ruminal microbial ecosystem, which could also explain observations made in the current study. This appears to be confirmed by the different α-linolenic acid (C18:3*n*-3) and C18:0 proportions of GU compared with WF beef. Indeed, beef from GU had a higher C18:3*n*-3 proportion, and tended to have higher linoleic acid (C18:2*n*-6) (P = 0.10) and lower C18:0 proportions than WF beef. Considering that C18:3*n*-3 and C18:2*n*-6 FAs are exclusively of dietary origin, and C18:0 is an end-product of the bio-hydrogenation of dietary UFA, it could be speculated that ruminal bio-hydrogenation of dietary fat occurred to a lower extent in GU than in WF cattle. Meat docosapentaenoic acid (C22:5*n*-3), which is derived from C18:3*n*-3 FA, was higher in GU and RM than in WF beef. The proportions of total monounsaturated FA (MUFA) and *n*-6 PUFA were not affected by breed, whereas the SFA was lower in GU than in WF, and PUFA and *n*-3 PUFA were higher in GU and RM than in WF beef.

On average, total PUFA and *n*-3 PUFA were 13.9% and 4.6% of total lipids, respectively, which is consistent with the values reported by Salifou *et al*. (2013) for Fulani zebu (mixed breeds) from Benin. However, total PUFA and n-3 PUFA were higher in Nguni and Bonsmara steers from South Africa (Muchenje *et al*., 2009b), whereas they were lower in Nellore cattle and in Nellore crossings with Simmental and Santa Gertrudes from South America (Ruiz *et al.*, 2005; Padre *et al.*, 2006). Since cattle in all these studies were raised on natural pasture, the differences in total PUFA and n-3 PUFA could possibly be explained by differences in age of slaughter and levels of marbling (Mapiye *et al*., 2012). In the current study, *n*-6/*n*-3 PUFA and PUFA/SFA ratios were similar across breeds and the mean *n*-6/*n*-3 PUFA ratio was 1.95. From a human health perspective, the maximum recommended *n*-6/*n*-3 PUFA ratio to reduce the risk of coronary heart disease is 4.0 (English Department of Health, 1994). The natural pasture-based diet, characterized by a high proportion of linolenic acid (Webb & Erasmus, 2013), may explain the lack of differences between breeds and the low *n*-6/*n*-3 ratio of beef. The minimum PUFA/SFA ratio recommended for human health is 0.45 (Simopoulos, 2004), a value much higher than the mean value of 0.29 reported in this study. This inability to achieve the optimum PUFA/SFA ratio is well documented in both *Bos taurus* (Piasentier *et al*., 2009; Corazzin *et al*., 2012; Ripoll *et al*., 2014) and *Bos indicus* (Ruiz *et al*., 2005; Bressan *et al*., 2011) cattle owing to the extensive bio-hydrogenation of the dietary UFA by the rumen microorganisms. The atherogenic index, which is an indicator for the risk of cardiovascular disease, should be as low as possible. This index did not vary among the tested breeds. The CLA content of beef from the three breeds was similar, and the average value (0.28% of total lipids) falls within the range reported in literature for zebu and zebu-derived cattle (0.15% to 0.43% of total lipids) raised on natural pastures around the world (De Mendoza *et al*., 2005; Muchenje *et al.*, 2009b; Salifu *et al*., 2013). Based on FA composition in the current study, consumption of beef from the GU, WF and RM breeds could be beneficial to human health.

The major FAs in the current study were C16:0, C18:0, C18:1*n*-9c and C18:2*n*-6c. As reported in Table 2, C16:0 and C18:1*n*-9c were positively correlated, whereas C18:2*n*-6c was negatively correlated with the intramuscular fat content of the *m. longissimus thoracis*. No statistically significant correlation was found between C18:0 and the total fat content. Moreover, SFA and MUFA were positively correlated, whereas PUFA was negatively correlated with the intramuscular fat content. These results are in close agreement with the findings of Brugiapaglia *et al*. (2014) in *Bos taurus* breeds, and are caused by the decrease in the phospholipids/neutral lipids ratio that arises from the increase in the intramuscular fat, as shown by Itoh *et al*. (1999) in steers of *Bos taurus* breeds.

Table 1 Estimated marginal means of fatty acid total weight (g/100 g muscle) and proportion (percentage of total fatty acids) of *m*. *longissimus thoracis* depending on bull breed[1]

Fatty acids	Gudali (n = 19)	White Fulani (n = 20)	Red Mbororo (n = 21)	SEM
Total weight	1.38	1.58	1.09	0.118
C10:0	0.08	0.07	0.11	0.071
C12:0	0.12	0.10	0.13	0.005
C13:0	0.25[a]	0.11[b]	0.21[a]	0.018
C14:0	2.31	2.53	2.40	0.100
C14:1*n*-9c	0.27	0.30	0.28	0.017
C15:0	0.29[b]	0.37[a]	0.35[ab]	0.012
C15:1	0.17	0.18	0.18	0.013
C16:0	24.7	25.5	24.5	0.438
C16:1*n*-9t	0.57	0.45	0.48	0.051
C16:1*n*-9c	2.21	2.09	2.18	0.084
C17:0	1.03	1.15	1.13	0.022
C17:1	0.51	0.61	0.55	0.025
C18:0	18.0[b]	20.7[a]	19.8[a]	0.279
[2] *trans*-C18:1	1.98	2.09	1.85	0.083
C18:1*n*-9c	29.2	29.0	27.5	0.500
C18:1*n*-7	2.62	2.60	2.58	0.067
C18:2*n*-6t	0.16	0.15	0.17	0.017
C18:2*n*-6c	6.34	4.61	5.92	0.349
C18:3*n*-6	0.18[b]	0.36[a]	0.13[b]	0.046
C18:3*n*-3	2.34[a]	1.61[b]	2.16[ab]	0.124
CLAt7,c9/t8,c10/c9,t11	0.29	0.30	0.26	0.015
C20:3*n*-6	0.39	0.34	0.48	0.027
C20:3*n*-3	0.01	0.03	0.11	0.035
C20:4*n*-6	2.65	1.94	2.94	0.162
C20:5*n*-3	0.96[ab]	0.73[b]	1.18[a]	0.070
C22:5*n*-3	1.62[a]	1.17[b]	1.60[a]	0.077
C22:6*n*-3	0.12	0.15	0.13	0.011
C23:0	0.13	0.14	0.13	0.011
C24:0	0.13	0.16	0.15	0.011
C24:1*n*-9	0.11	0.20	0.19	0.019
SFA	47.2[b]	51.0[a]	49.1[ab]	0.546
MUFA	37.7	37. 6	35.8	0.538
PUFA	15.2[a]	11.4[b]	15.2[a]	0.750
Total *n*-6 PUFA	9.83	7.45	9.73	0.538
Total *n*-3 PUFA	5.05[a]	3.69[b]	5.18[a]	0.240
MUFA/SFA	0.803	0.743	0.733	0.014
PUFA/SFA	0.331	0.230	0.322	0.019
n-6/*n*-3	1.93	2.04	1.88	0.049
Atherogenic index	0.549	0.574	0.537	0.013
Elongase index	63.8	64.4	64.0	0.397
∆9 Desaturase Index	40.6	38.5	38.4	0.482

[1] Fatty acids detected at <0.1% of total lipids are not reported.
SEM: standard error of the mean.
CLA: conjugated linoleic acid; SFA: saturated fatty acids; MUFA: monounsaturated fatty acids; PUFA: polyunsaturated fatty acids.
[a,b] Row means with different superscripts differ significantly at $P < 0.05$.
[2] *trans*-C18:1 corresponds to the sum of t6-8-, t9-, t10-, t11-, t12- and t13/14-18:1.

Indeed, C16:0, C18:1*n*-9c and total SFA are present mainly in the neutral fraction, whereas C18:2*n*-6c and total PUFA are present mainly in the phospholipids fraction. The elongase index was not correlated with

the total fat content (*P* = 0.12). Kazala *et al*. (1999) reported only a moderate negative correlation between the elongase index and the total lipid content (r = −0.31; *P* <0.10) of the *longissimus muscle* of crossbreed Wagyu cattle. No statistically significant correlation was found between the ∆9 desaturase index and total lipid content. These results are in agreement with the findings of Corazzin *et al*. (2013), which showed no differences in the ∆9 desaturase index when comparing animals with different subcutaneous fat deposits, but in contrast with the findings of Jiang *et al*. (2008), who reported a positive correlation between ∆9 desaturase activity and the marbling of beef.

Table 2 Correlation between fatty acid composition and intramuscular fat content of *m*. *longissimus thoracis*[1]

Fatty acids	r	Significance level
C10:0	−0.092	ns
C12:0	−0.233	*
C13:0	−0.450	***
C14:0	0.359	**
C14:1*n*-9c	0.261	*
C15:0	−0.004	ns
C15:1	−0.436	**
C16:0	0.497	***
C16:1*n*-9t	−0.142	ns
C16:1*n*-9c	0.285	*
C17:0	−0.144	ns
C17:1	−0.246	ns
C18:0	0.136	ns
[2] *trans*-C18:1	0.229	ns
C18:1*n*-9c	0.416	**
C18:1*n*-7	0.009	ns
C18:2*n*-6t	−0.293	*
C18:2*n*-6c	−0.608	***
C18:3*n*-6	−0.074	ns
C18:3*n*-3	−0.567	***
CLAt7,c9/t8,c10/c9,t11	0.396	**
C20:3*n*-6	−0.497	***
C20:3*n*-3	−0.046	ns
C20:4*n*-6	−0.551	***
C20:5*n*-3	−0.490	***
C22:5*n*-3	−0.647	***
C22:6*n*-3	−0.203	ns
C23:0	−0.348	**
C24:0	−0.367	**
C24:1*n*-9	−0.249	ns
SFA	0.471	***
MUFA	0.428	**
PUFA	−0.650	***
Total *n*-6 PUFA	−0.627	***
Total *n*-3 PUFA	−0.654	***
Atherogenic index	0.591	***
Elongase index	−0.198	ns
∆9 Desaturase index	0.062	ns

[1] Fatty acids detected at <0.1% of total lipids are not reported.
CLA: conjugated linoleic acid; SFA: saturated fatty acids; MUFA: monounsaturated fatty acids; PUFA: polyunsaturated fatty acids.
Level of significance:* *P* <0.05; ** *P* <0.01;***P* <0.001; ns: not significant.
[2] *trans*-C18:1 corresponds to the sum of t6-8-, t9-, t10-, t11-, t12- and t13/14-18:1.

Conclusions

Results from this study indicate that there are marginal differences in FA composition of beef from Gudali, White Fulani and Red Mbororo breeds reared in the transhumance system of the Central African sub-region. This could be attributed to the lack of genetic selection and the similar herbage foraged by cattle. Additionally, based on the polyunsaturated FA (PUFA) proportion and *n*-6/*n*-3 PUFA ratio, consumption of beef from these breeds could be beneficial to human health.

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