JARQ 60 (1), 73-83 (2026) https://www.jircas.go.jp

Evaluation of Fat Characteristics of Water Buffalo Fattened on Napier Grass and Concentrate Feed in Comparison with Cattle in the Philippines

Tomomi BAN-TOKUDA[1]*, Momoka YAMAGUCHI[1], Madoka FUJII[2], Rosalina M. LAPITAN[3], Jesus Rommel V. HERRERA[3], Arnel N. del BARRIO[3], Thelma S. SALUDES[3], Makoto KONDO[2], Toshihiro NADE[4], Hiroki MATSUI[1] and Tsutomu FUJIHARA[5]

[1] Laboratory of Animal Production, Department of Sustainable Resource Science, Faculty of Bioresources, Mie University, Tsu, Japan
[2] Laboratory of Grassland and Animal Feed Production, Department of Sustainable Resource Science, Faculty of Bioresources, Mie University, Tsu, Japan
[3] Philippine Carabao Center at University of the Philippines, Los Baños, Philippines
[4] Department of Life and Food Sciences, Faculty of Animal Production Program, Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Japan
[5] Laboratory of Animal Science, Shimane University, Matsue, Japan

Abstract

Buffalo meat is a nutritious alternative to beef, offering the advantages of lower fat and cholesterol levels. This study compared the fat characteristics of five crossbred water buffalo and five crossbred cattle. The ten growing animals averaged 22 months of age and were fed a diet of 50% Napier grass and 50% commercial concentrate, administered in two equal portions at 7:00 and 16:00 hours. During a 16-week fattening period, the total plasma cholesterol concentrations in water buffalo were significantly lower ($P < 0.05$) than in cattle. Additionally, the ether extract and cholesterol content in muscle tissue were significantly lower in water buffalo ($P < 0.05$). However, there were no significant differences between the species in relative leptin mRNA levels in fat tissue ($P > 0.05$) or adipocyte diameter ($P > 0.05$). In terms of fatty acid composition, monounsaturated fatty acid levels were similar ($P > 0.05$), but water buffalo exhibited higher levels of polyunsaturated fatty acids than cattle ($P < 0.05$). Overall, buffalo meat presents lower fat, cholesterol content, and higher essential fatty acids than beef, making it a potentially healthier choice for health-conscious consumers.

Discipline: Animal Science
Additional key words: cholesterol, fat metabolism, leptin, polyunsaturated fatty acids

Introduction

Water buffalo (*Bubalus bubalis* Linn.) are a vital source of draft power, meat, and milk in the Philippines. They are generally more robust and easier to maintain than cattle in tropical and subtropical Asia. While buffalo milk boasts a high protein and fat content, the average yield per lactation is lower than that of dairy cattle (Rosati et al. 2002). Buffalo meat is reported to be comparable to beef in tenderness while also providing the benefit of lower cholesterol levels (Paleari et al. 1997). Furthermore, Naveena & Kiran (2014) found that buffalo meat matches beef in composition, quality, and organoleptic characteristics yet features reduced fat, cholesterol, and calorie content. Nutritionally, buffalo meat offers significant advantages, containing 40% less cholesterol, 55% fewer calories, 11% more protein, and 10% more minerals than beef (Nanda & Nakao 2003).

A variety of factors influences the fatty acid composition of beef. De Smet et al. (2004) found that dietary factors significantly impact beef's fatty acid profile more than genetic factors. While breed differences

*Corresponding author: tomomi@bio.mie-u.ac.jp
Received 10 June 2024; accepted 21 March 2025; J-STAGE Advanced Epub 20 October 2025.
https://doi.org/10.6090/jarq.24J08

in fatty acid composition tend to be minor, they reflect variations in gene expression and the enzyme activity related to fatty acid synthesis (Scollan et al. 2014). A higher percentage of unsaturated fatty acids (UFAs) results in a lower melting point of fat (Yang et al. 1999), which contributes to the softness of fat in cattle and may enhance the flavor of beef (Melton et al. 1982). Additionally, Giuffrida-Mendoza et al. (2015) noted that certain individual fatty acids vary between Brahman cattle and water buffalo in savanna conditions; however, the cholesterol and fat content of lean meat showed no significant differences. Their findings regarding cholesterol and fat content contrast with those of other studies (Ban-Tokuda et al. 2007, Kandeepan et al. 2013, Naveena & Kiran 2014).

Leptin regulates lipid reserves via changes in food intake and energy expenditure. Leptin mRNA secretion and plasma concentration correlate with total fat mass in humans, rodents (Hamilton et al. 1995, Maffei et al. 1995), and ruminants (Chilliard et al. 2005, Ban-Tokuda et al. 2008). Hamilton et al. (1995) isolated large and small adipocytes from the omental fat in humans and found that large adipocytes have higher leptin mRNA expression than small ones. Cattle also showed fat deposit differences in leptin mRNA expression because of differences in adipocyte size (Yang et al. 2003). Our previous plasma data (Ban-Tokuda et al. 2007) showed that leptin, insulin, and total cholesterol concentrations increase with fattening in both species and are significantly higher in cattle than in buffalo. The adipocyte size of cattle and water buffalo may also differ, but this has not been investigated.

While some previous studies (Kandeepan et al. 2009, Lambertz et al. 2014) have examined the fatty acid composition, fat content, and cholesterol levels in buffalo meat, research comparing cattle and buffalo raised on identical diets and under the same conditions is limited. Moreover, no studies address the differences in fat cell size between the two species, which is closely linked to body fat accumulation. This study compares the fat characteristics in muscle and adipose tissues between cattle and water buffalo that were fattened using Napier grass, which is often used as roughage in the Philippines, under the same dietary conditions. In earlier research (Lapitan et al. 2004, Ban-Tokuda et al. 2007), the diet comprised corn silage, brewers grain, and a concentrate mixture in a 5:3:2 ratio. In contrast, the current study utilized a diet of Napier grass and concentrate mixture in a 1:1 ratio.

Materials and methods

1. Animals and management

The animals used in this experiment were cared for per the guidelines of Mie University. Five crossbred male cattle (Philippine native cattle × Brahman) and five crossbred male water buffalo (Philippine native water buffalo × Murrah) with an average age of 22 months (18-24 months) were used. The animals were dewormed, injected with vitamins before the start of the experiment, and were randomly housed individually in roofed concrete pens. The temperature and humidity were not controlled. An adjustment period of four weeks allowed the animals to adapt to the new feed and housing. All animals were fed fresh Napier grass (*Pennisetum purpureum*) and a concentrate mixture at a ratio of 50:50 on a dry matter basis. The fresh Napier grass and concentrate diets were fed in two equal portions at 7:00 and 16:00 h. Table 1 shows the chemical compositions of the experimental feed. Animals were allowed free access to water. The feeding trial lasted for 16 weeks, and the monthly and final body weights of the animals were obtained from the average body weight for two consecutive days in the morning before feeding. The amounts of feed offered and refused were recorded daily, and the feed consumed was calculated as the difference. The digestion trial was performed on the eighth week for six consecutive days. Daily samples of the feed offered and refused during the digestion trial were collected for chemical analyses. The total fecal output over 24 hours was collected during the digestion trial. A representative fecal sample was collected from each defecation and pooled daily, and a composite sample was collected to determine apparent nutrient digestibility. The feed, feed refusal, and fecal samples were dried to a constant weight at 60°C for 48 hours in a forced air oven and allowed to equilibrate. The samples were ground using a Wiley mill to pass through a 1 mm screen. Dry matter (DM), organic matter (OM), crude protein (CP), and ether extract (EE) were analyzed following the AOAC (2000). Neutral detergent fiber (NDF), acid detergent fiber (ADF), and acid detergent lignin (ADL) were analyzed using the procedure described by Van Soest et al. (1991). Non-fiber carbohydrate (NFC) was estimated by subtracting CP, NDF, EE, and crude ash from 100. Total digestible nutrients (TDN) were calculated from the equation of Weiss et al. (1992). The results of the chemical analyses were used to calculate the apparent digestibility of nutrients.

2. Plasma sampling and analyses

Blood samples were collected every four weeks at 7:00 h before morning feeding during the experiment, placed in heparinized tubes, immediately centrifuged at 1,400 × g for 20 min, and then stored at –80°C until analysis. Plasma samples were analyzed for total plasma cholesterol, triglyceride, and glucose concentrations using commercial kits (Total Cholesterol E-Test Wako, Triglyceride E-Test Wako, Glucose CII-Test Wako, Wako Pure Chemical, Osaka, Japan).

3. Slaughter, sampling of tissue, and analyses

After the feeding trial at 16 weeks, the animals were fasted for 48 h and then slaughtered by stunning followed by exsanguination, as described by Ibarra et al. (1988). The slaughter by-products were separated, and the dressed carcasses were divided into quarters. The slaughter and hot-dressed carcasses were weighed. After slaughter, samples of subcutaneous, abdominal, and perirenal fat tissues were collected from the carcasses as soon as possible for mRNA expression analysis and adipocyte size measurements. The samples were immediately soaked in liquid nitrogen and stored at −80°C until analysis. The dressed carcasses were weighed after 24 hours of chilling at 4°C. The dressing percentage was calculated based on the hot and chilled carcass weights. The cold-dressed carcasses were separated following the procedure described by Ibarra (1988), and the weight of each cut part was recorded to estimate the carcass yield of crossbred cattle and crossbred buffalo. The longissimus thoracis (LT) muscle of the 9th to 11th ribs from the left side of the carcasses was utilized to determine the meat chemical composition, meat color, cholesterol content, fatty acid composition, and rib-eye area. The moisture, EE, and CP contents in the minced flesh (LT muscle) were measured following AOAC (2000). The color (grades of lightness, redness, and yellowness) on the surface of the rib eye was measured using a color meter (Model CR-200; Minolta, Osaka, Japan). The cholesterol content in the fat around the LT muscle was determined using a commercial kit (Cholesterol/Cholesteryl Ester Quantitation Kit, Bio Vision, USA). Samples were extracted for fatty acid composition analysis with chloroform and methanol (2:1, v:v; Folch et al. 1957). The lipids were saponified with potassium hydroxide (KOH) and methyl-esterified with a boron trifluoride-methanol complex methanol solution. The methyl esters of the fatty acids were dissolved in hexane and analyzed using gas chromatography (GC2010; Shimadzu Co., Kyoto, Japan) and capillary column (RT2560, 0.25 mm, 100 m; Shimadzu Co.). The integrator was a flame ionization detector, and the carrier gas was helium. The fatty acids lauric acid (C12:0), myristic acid (C14:0), myristoleic acid (C14:1), pentadecanoic acid (C15:0), palmitic acid (C16:0), palmitoleic acid (C16:1), heptadecanoic acid (C17:0), stearic acid (C18:0), oleic acid (C18:1), linoleic acid (C18:2), and linolenic acid (C18:3) were identified at each retention time. The saturated fatty acids (SFAs) were C12:0, C14:0, C15:0, C16:0, C17:0 and C18:0. The UFAs were C14:1, C16:1, C18:1, C18:2 and C18:3. The monounsaturated fatty acids (MUFAs) were C14:1, C16:1 and C18:1. The polyunsaturated fatty acids (PUFAs) are C18:2 and C18:3.

Table 1. Chemical composition of Napier grass and concentrates used

	Napier grass	Concentrates[1]
DM[2] (%FM[3])	14.8	87.8
OM[4] (%DM)	83.5	89.8
CP[5]	11.0	13.3
EE[6]	1.5	14.1
NDF[7]	63.7	30.9
ADF[8]	39.2	14.2
ADL[9]	4.7	2.9
NFC[10]	7.4	25.1
TDN[11]*	50.4	132.1

[1] Coconut meal (40.00%), hard wheat (21.24%), soft wheat (5.00%), wheat bran (20.00%), molasses (10.00%), calcium carbonate (2.50%), Dicalcium phosphate (0.20%), salt (1.00%), mineral and vitamin mix (0.06%, DM basis), [2] Dry matter, [3] fresh matter, [4] organic matter, [5] crude protein, [6] ether extract, [7] neutral detergent fiber, [8] acid detergent fiber, [9] acid detergent lignin, [10] non-fiber carbohydrate, [11] total digestible nutrients, *Calculated from the equation of Weiss et al. (1992)

4. Total RNA extraction and real-time PCR

Total RNA was extracted from adipose tissue samples using the RNeasy Lipid Tissue Mini Kit (QIAGEN Co., Ltd., Germany) following the manufacturer's instructions. The amount of RNA was determined by measuring absorbance at 260 and 280 nm using a spectrophotometer. The presence of the sample RNA was verified using agarose gel electrophoresis. Single-strand cDNA was reverse-transcribed from 1 μg total RNA using an ABI High-Capacity cDNA RT kit (Thermo Fisher Scientific Inc. Tokyo, Japan) per the manufacturer's instructions. Real-time PCR was performed using SYBR Premix Dimer Eraser (Takara Bio Inc., Shiga, Japan) following the manufacturer's instructions and run on StepOne Plus Real-Time PCR System (Thermo Fisher Scientific Inc.). The primer sequences were as follows: leptin,

5′-acatctcacacacgcagtcc- 3′ (forward) and 5′-ggatgaagtccaaaccagtga-3′ (reverse); stearoyl-CoA desaturase 1 (SCD1), 5′-cgacctaagagccgagaagc-3′ (forward) and 5′-gcagcactattcaccagccag-3′ (reverse); hypoxanthine phosphoribosyltransferase 1 (HPRT1), 5′-gtgattagcgatgatgaaccag-3′ (forward), 5′-ccatgaggaataaacaccttctc-3′ (reverse for cattle) and 5′-ccatgaggaataaacactttctc-3′ (reverse for buffalo). The quantitative real-time PCR thermal cycler program consisted of one cycle at 95°C for 30 s, followed by 40 cycles at 95°C for 15 s and 60°C for 60 s. The specificity of the PCR products was determined using melting curve analysis at the end of each run. The Ct value was normalized to the expression of the HPRT1 housekeeping gene. The results are expressed as estimates of mean normalized expression after subtracting the values of the housekeeping gene. Gene expression values were calculated for the targeted gene in the form of fold change calculated using the $2^{-\triangle\triangle CT}$ method (Livak & Schmittgen 2001).

5. Cellularity of adipocytes

Samples of subcutaneous, abdominal, and perirenal adipose tissues were fixed in osmium tetroxide (Hirsch & Girllian 1968) and isolated in a urea solution following the method described by Etherton et al. (1977). Approximately 100 mg samples were sliced, rinsed with 0.9% NaCl solution, and then fixed with 50 mM collidine-HCl buffer (pH 7.1) containing 1.88% osmium tetroxide for 96 h at 37°C. The fixed samples were washed twice with 0.9% NaCl and then treated with 8 M urea in 0.9% NaCl for 48 h at room temperature for isolation. Fixed and urea-isolated adipocytes were placed in 0.01 Triton X-100 in 0.9% NaCl solution (pH 10). The diameter of the adipocytes was measured using Motic IMAGES Plus 2.0S (Shimadzu). More than 200 adipocytes were analyzed for each sample. The long and short diameters of the adipocytes were measured, and the average value was taken as the diameter of the cells.

6. Statistical analysis

Changes in total feed intake, body weight, daily weight gain, and plasma metabolite concentrations over 16 weeks were analyzed for each species using a one-way analysis of variance (ANOVA). When the one-way ANOVA was significant ($P < 0.05$), differences between weeks within each species were compared by a paired t-test. Additionally, differences between species for each week were analyzed using an unpaired t-test. Data on apparent digestibility, carcass weight, dressing yield, cut yield, rib-eye area, chemical composition, meat color, cholesterol content, and fatty acid composition in the LT muscle were compared between cattle and buffalo using an unpaired t-test. Data on adipocyte diameter and leptin and SCD mRNA expression were also compared using Fisher's least significant difference test. The correlation of the leptin mRNA level and the adipocyte diameter was determined by the correlation Z test. Statistical significance was set at $P < 0.05$. All calculations were performed using a commercially available computer program (Stat View; SAS Institute Inc. SAS campus Drive Cary, NC27513).

Results and discussion

The total feed intake (gDM/day/$BW^{0.75}$) was not significantly different ($P > 0.05$) between the cattle and buffalo. It was lower at 4-12 weeks than at 0-4 and 12-16 weeks in cattle ($P < 0.05$), while it was lower at 4-12 weeks than at 0-4 weeks ($P < 0.05$), and almost the same at 0-4 weeks and 12-16 weeks in buffalo ($P > 0.05$, Fig. 1). Body weight increased with fattening in both species ($P < 0.05$, Fig. 2), and was heavier in buffalo than in cattle at 0, 4, and 8 weeks ($P < 0.05$). The daily weight gain in cattle was higher at 4-8 weeks than at 0-4 and 8-12 weeks

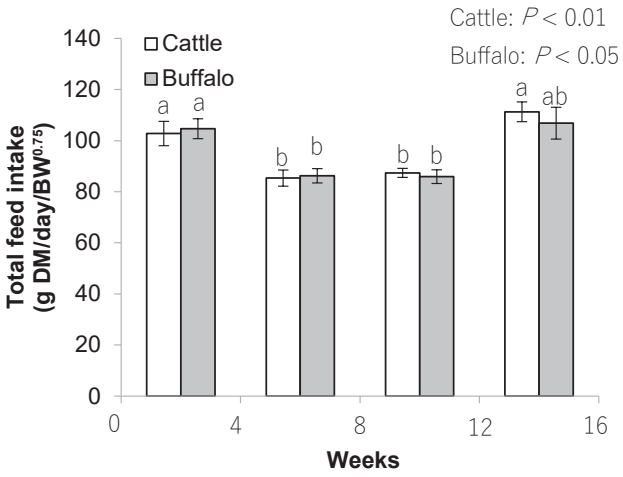

Fig. 1. Total feed intake of crossbred cattle and crossbred water buffalo

Data indicate the means (n= 5) and standard error. The *P* values for cattle and buffalo in the figure are the results of a one-way analysis of variance (ANOVA) of the time (weeks) for each animal. When the one-way ANOVA was significant ($P < 0.05$), differences between weeks within each species were compared by a paired t-test. [a, b] Different superscript letters within each species indicate a significant difference. Differences between species for each week were analyzed using an unpaired t-test. There was no significant difference between cattle and buffalo ($P > 0.05$).

($P < 0.05$), whereas in buffalo, it initially decreased from 0 to 12 weeks and then increased over 12-16 weeks ($P < 0.05$). Daily weight gain was significantly higher in cattle than in buffalo at 4-12 weeks ($P < 0.05$), although both species had the same daily gain of 0.75 ± 0.03 kg/day throughout the experiment. Feed intake was lower, and weight gain was slower in both species than in the previous study, which used corn silage as roughage (Ban-Tokuda et al. 2007). This is likely due to the lower feed intake and lower energy content of Napier grass used as roughage in this study. Additionally, no significant differences between cattle and buffalo were observed in the apparent digestibility of DM, OM, CP, EE, NDF, ADF, and NFC ($P > 0.05$, Table 2). There was no difference in total feed intake or digestibility between the two groups, which is likely why no difference was observed in daily weight gain during the experiment.

The live weight of buffalo before slaughter was significantly higher than that of cattle ($P < 0.05$, Table 3). However, the hot and chilled carcass weights did not differ significantly between them. The dressing yields based on the hot and chilled carcass weights were significantly higher in cattle than in buffalo ($P < 0.05$) because buffalo have large, heavily bonded heads. In a related study, Rodas-González & Huerta-Leidenz (2023) found that, although buffalo tend to be heavier than cattle, their dressing yield is lower due to a larger proportion of non-carcass components, particularly the hide and head. The cut yield percentage in the brisket was significantly higher in cattle than in buffalo, but no differences were observed in the other cut yield percentages ($P > 0.05$).

The moisture and CP contents in the LT muscle did not differ between cattle and buffalo ($P > 0.05$), but the EE content was significantly lower in buffalo ($P < 0.05$, Table 4). Additionally, the cholesterol content in the LT muscle was significantly lower in buffalo than in cattle ($P < 0.05$). However, the fat surrounding the LT muscle showed considerable variation and did not differ significantly between the two species ($P > 0.05$). In our previous study (Ban-Tokuda et al. 2007), we did not examine the cholesterol content in muscle, but the results of this study were similar to other papers (Kandeepan et al. 2013, Naveena & Kiran 2014).

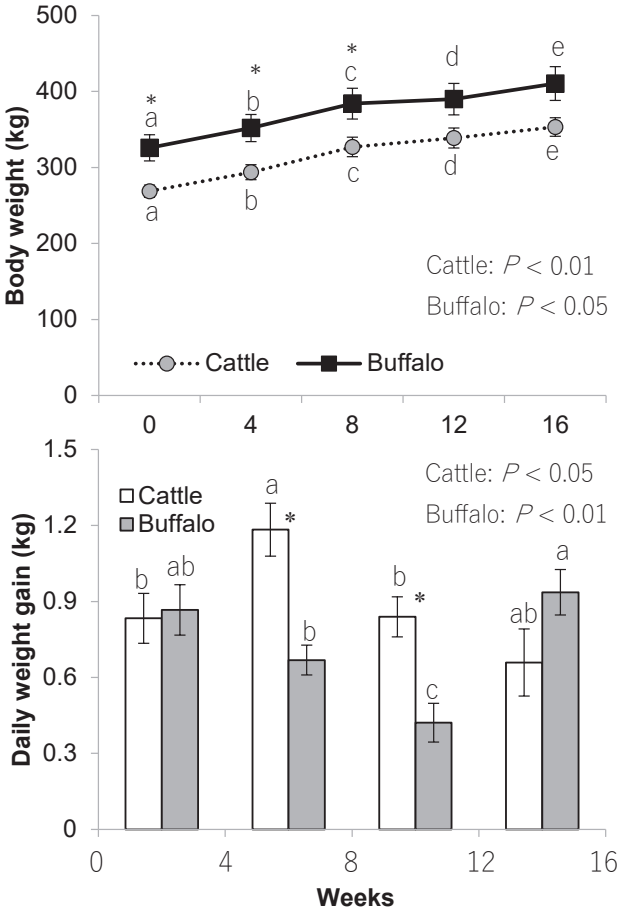

Fig. 2. Body weight and daily weight gain of crossbred cattle and crossbred water buffalo

Data show means (n= 5) and standard error. The *P* values for cattle and buffalo in the figure are the results of a one-way analysis of variance (ANOVA) of the time (weeks) for each animal. When the one-way ANOVA was significant ($P < 0.05$), differences between weeks within each species were compared by paired t-test. [a, b, c, d, e] Different superscript letters within each species indicate a significant difference. Differences between species for each week were analyzed using an unpaired t-test. *Significant difference ($P < 0.05$) between cattle and water buffalo.

Table 2. Apparent digestibility of the diet for crossbred cattle and crossbred buffalo

DM[1] (%)	Species		SEM[8]
	Cattle	Water buffalo	
DM[1]	58.2	61.8	1.4
OM[2]	61.8	65.4	1.3
CP[3]	61.2	65.1	1.3
EE[4]	91.7	92.9	0.4
NDF[5]	49.4	54.1	1.7
ADF[6]	63.0	65.7	1.4
NFC[7]	79.6	78.6	0.8

[1] Dry matter, [2] organic matter, [3] crude protein, [4] ether extract, [5] neutral detergent fiber, [6] acid detergent fiber, [7] non-fiber carbohydrate, [8] standard error of the mean. n= 5

No significant differences were found among species ($P > 0.05$).

Table 3. Carcass weight, cut yield, and rib-eye area in crossbred cattle and crossbred water buffalo

	Species		SEM[1]
	Cattle	Water buffalo	
Live weight (kg)	329.4	393.9*	15.0
Hot carcass weight (kg)	177.2	196.9	7.3
Chilled carcass weight (kg)	172.3	191.9	7.2
Dressing yield (%)			
Based on hot carcass weight	53.8*	49.9	0.8
Based on chilled carcass weight	52.3*	48.6	0.7
Cut yield (% of chilled carcass weight)			
Chuck	30.0	34.8	2.2
Brisket	4.8*	3.5	0.2
Rib	9.4	9.0	0.3
Plate	5.5	6.0	0.2
Foreshank	0.7	0.8	0.02
Round	27.3	27.9	0.3
Loin	14.0	14.2	0.1
Flank	3.6	4.3	0.2
Rib-eye area (cm^2)	41.5	50.2	2.3

*Significantly different between cattle and water buffalo ($P < 0.05$).
[1] Standard error of the mean. n= 5

Table 4. Chemical composition, cholesterol content, and meat color of the Longissimus thoracis muscle in crossbred cattle and crossbred water buffalo

	Species		SEM[1]
	Cattle	Water buffalo	
Chemical composition (%FM[2])			
Moisture	74.33	75.40	0.31
CP[3]	20.91	20.74	0.25
EE[4]	2.71*	0.98	0.34
Cholesterol contents (mg/100g, FM)			
in muscle	52.76*	42.06	2.37
in fat around the muscle[5]	567.60	331.50	71.03
Meat color			
Lightness	30.0*	25.8	1.0
Redness	18.9	18.9	0.7
Yellowness	10.5	8.7	0.8

*Significantly different between cattle and water buffalo ($P < 0.05$).
[1] Standard error of the mean, [2] fresh matter, [3] crude protein, [4] ether extract, [5] fat around the longissimus thoracis muscle
The longissimus thoracis muscle of the 9th to the 11th rib from the left side of the carcass was utilized to determine the chemical compositions of meat, cholesterol contents, and meat color. n= 5

The LT muscle was lighter in color ($P < 0.05$, Table 4) in cattle than in buffalo, but the redness and yellowness of meat color in the muscle were not different ($P > 0.05$). Dosi et al. (2006) reported that buffalo meat was darker than beef because it contains twice as much myoglobin. However, this study showed only that the meat lightness differed between species.

The diameters of the subcutaneous, abdominal, and perirenal adipocytes in cattle and buffalo were not significantly different ($P > 0.05$, Table 5). Additionally,

Table 5. Diameter of adipocyte in crossbred cattle and crossbred water buffalo

	Cattle	Water buffalo	SEM[1]
Subcutaneous adipocyte (μm)	149.5[b]	168.1[b]	6.5
Abdominal adipocyte	174.3[a]	173.4[ab]	4.2
Perirenal adipocyte	172.6[a]	181.7[a]	4.4

[a, b] Values within a column with different superscripts differ significantly in each species ($P < 0.05$). There was no significant difference between cattle and buffalo ($P > 0.05$).
[1] Standard error of the mean. n= 5

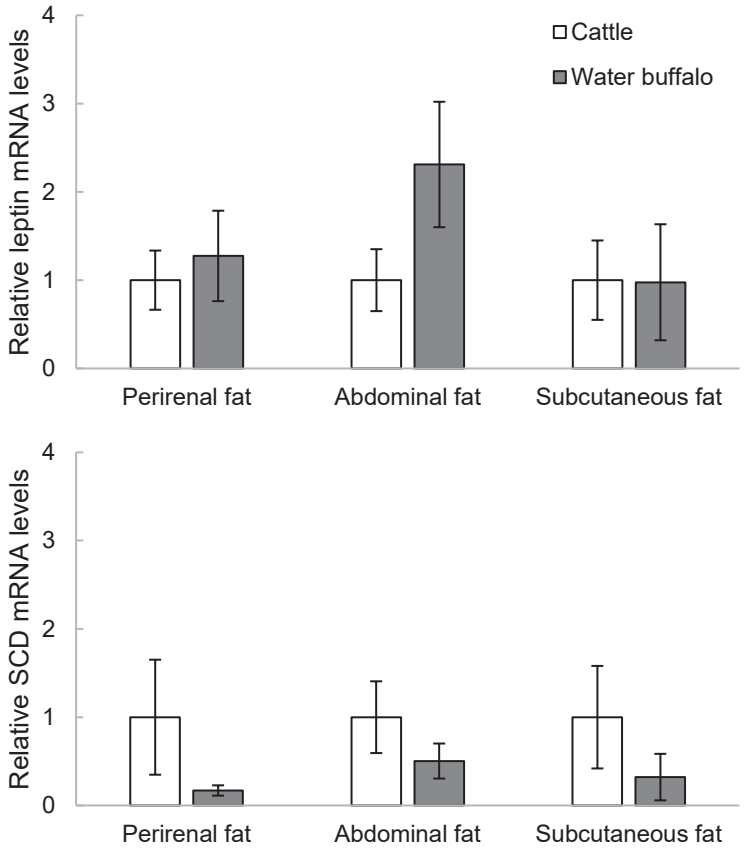

Fig. 3. Leptin and stearoyl-CoA desaturase (SCD) gene expression in subcutaneous, perirenal, and abdominal fat of crossbred cattle and crossbred water buffalo
HPRT1 mRNA was used as an internal control. The expression in crossbred cattle in each adipose tissue was set to 1. Data show means (n= 5) and standard error. There was no significant difference between cattle and buffalo ($P > 0.05$).

the relative leptin mRNA levels in the subcutaneous, perirenal, and abdominal fat did not differ between species ($P > 0.05$, Fig. 3). We predicted that the size of adipocytes and leptin mRNA level would be lower in buffalo than in cattle because the plasma leptin concentrations in buffalo were lower than in cattle in the previous study (Ban-Tokuda et al. 2007). However, the current study was unable to measure plasma leptin concentrations. In addition, no significant correlation was observed between leptin mRNA expression levels and adipocyte diameter in either species ($P > 0.05$). Further investigation is needed into the relationship between leptin mRNA expression level, plasma leptin concentration, and adipocyte size between species. The adipocytes of subcutaneous fat in cattle were smaller than those of abdominal and perirenal fat, while those in buffalo were significantly smaller than those of perirenal fat ($P < 0.05$). Yang et al. (2003) also found that adipocyte size was greater in the perirenal fat depot than in subcutaneous depots. This suggests that both species might store lipid droplets more in visceral fat.

The total plasma cholesterol concentration in each species did not change significantly during the experiment in either species ($P > 0.05$, Fig. 4). As with the cholesterol content in muscle, the plasma cholesterol concentration in buffalo was lower than that in cattle, and the concentration in cattle was about twice that of buffalo ($P < 0.05$), probably due to the lower cholesterol synthesis in buffalo (possibly due to differences in the secretion of enzymes). Changes in triglycerides in each species were almost stable during the 16-week fattening period ($P > 0.05$). Plasma glucose concentrations increased significantly ($P < 0.05$) at 4 and 16 weeks compared with 0 weeks in buffalo but remained almost unchanged in

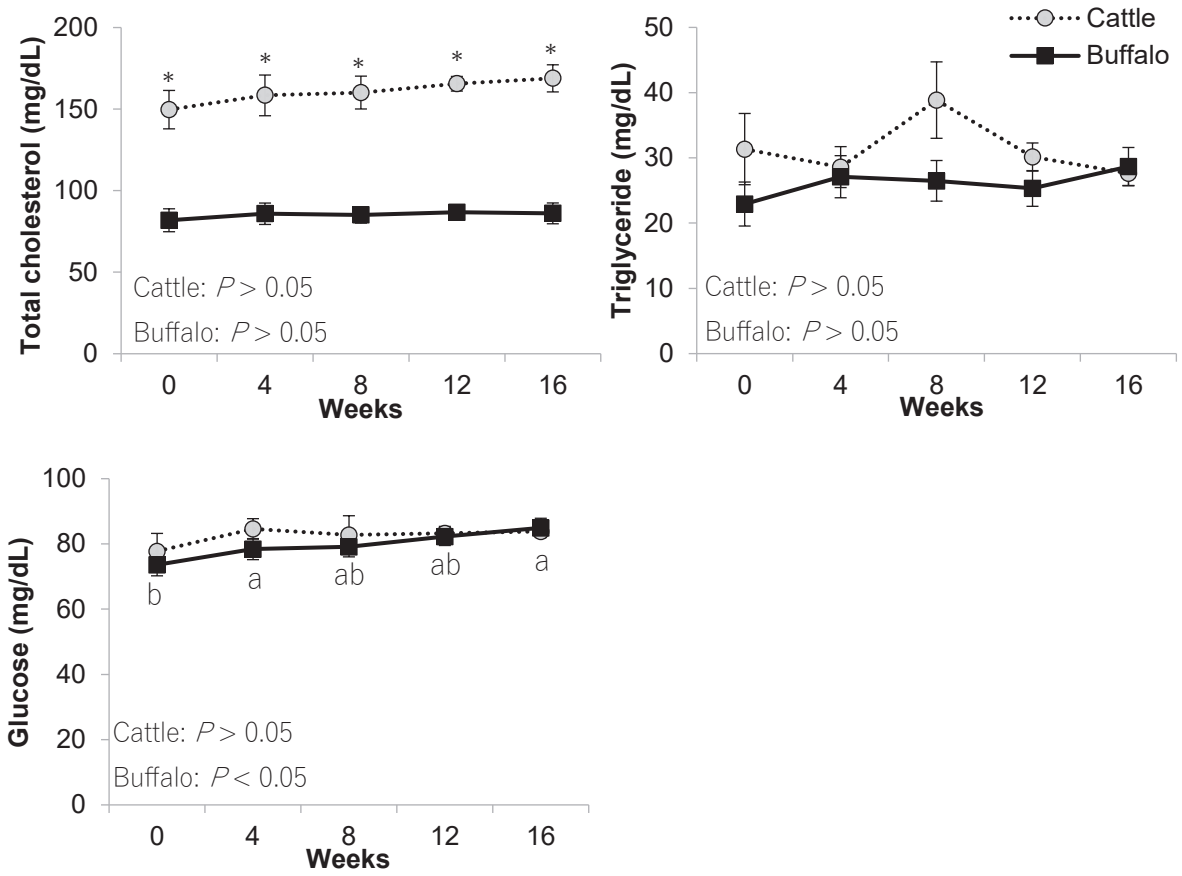

Fig. 4. Changes in plasma total cholesterol, triglyceride, and glucose concentrations in crossbred cattle and crossbred water buffalo

Data show means (n= 5) and standard error. The *P* values for cattle and buffalo in the figure are the results of a one-way analysis of variance (ANOVA) of the time (weeks) for each animal. When the one-way ANOVA was significant ($P < 0.05$), differences between weeks within each species were compared by paired t-test. [a, b]Different superscripts in plasma glucose indicate significant differences between weeks in buffalo. Differences between species for each week were analyzed using an unpaired t-test. *Significant difference ($P < 0.05$) between cattle and water buffalo.

cattle ($P > 0.05$). The plasma glucose and triglyceride concentrations did not significantly differ between the two species ($P > 0.05$). These results were similar to the findings of a previous study (Ban-Tokuda et al. 2007).

SFAs in muscle were higher ($P < 0.05$) in cattle than in buffalo, while UFAs and PUFAs in muscle were significantly higher in buffalo than in cattle ($P < 0.05$), as shown in Table 6. Some studies comparing the fatty acid composition of muscle from cattle and buffalo have found that SFAs are higher in buffalo, while PUFAs are either higher in cattle or unchanged (Giuffrida-Mendoza et al. 2015, Mello et al. 2018, Spanghero et al. 2004), which might be due to differences in the cattle breeds used for comparison. Generally, PUFAs are easily oxidized, but they are known to lower LDL cholesterol levels in the blood and prevent arteriosclerosis. The high PUFA content of buffalo meat might increase its value even further.

SCD is the enzyme responsible for converting SFAs into MUFAs in mammalian adipocytes, and SCD mRNA expression levels are related to the MUFA percentage (Taniguchi et al. 2004). MUFAs contents did not significantly differ ($P > 0.05$, Table 6). The relative SCD mRNA levels also did not differ ($P > 0.05$) between cattle and buffalo (Fig. 3). The MUFAs of Japanese Black cattle in studies by Zembayashi et al. (1995) and He et al. (2005) were much higher than those of the cattle and buffalo in this study. Therefore, the meat from the cattle and buffalo used in this study may be less tender and have less flavor than that of Japanese Black cattle.

Fat content and cholesterol levels in muscle and plasma were lower in buffalo than in cattle. Under the same conditions and diets, buffalo meat has a lower fat and cholesterol content. However, there was no difference in the adipocyte size between cattle and buffalo, suggesting that there could be more adipocytes in cattle than in buffalo. The high intake of high-fat meat can lead to cardiovascular disease, obesity, and high blood

Table 6. Fatty acid composition in Longissimus thoracis of crossbred cattle and crossbred water buffalo

	Cattle	Water buffalo	SEM[1]
Fatty acid composition (%)			
Lauric acid (C12:0)	0.59	0.42	0.10
Myristic acid (C14:0)	6.30*	3.71	0.30
Myristoleic acid (C14:1)	1.10*	0.25	0.15
Pentadecanoic acid (C15:0)	0.57*	0.38	0.01
Palmitic acid (C16:0)	30.25*	25.57	0.90
Palmitoleic acid (C16:1)	3.15	2.64	0.18
Heptadecanoic acid (C17:0)	1.23	1.42	0.21
Stearic acid (C18:0)	19.99	22.77	0.91
Oleic acid (C18:1)	33.71	36.15	1.04
Linoleic acid (C18:2)	2.81	5.98*	0.68
Linolenic acid (C18:3)	0.32	0.73*	0.09
Total	100	100	
SFA[2]	58.92*	54.26	1.15
UFA[3]	41.08	45.74*	1.15
MUFA[4]	37.95	39.03	1.41
PUFA[5]	3.13	6.71*	1.34
Ratio			
SFA /UFA	1.44*	1.19	0.06

*Significantly different between cattle and water buffalo ($P < 0.05$)
[1] Standard error of the mean
[2] Saturated fatty acid (C12:0+C14:0+C15:0+C16:0+C17:0+C18:0)
[3] Unsaturated fatty acid (C14:1+C16:1+C18:1+C18:2+C18:3)
[4] Monounsaturated fatty acid (C14:1+C16:1+C18:1)
[5] Polyunsaturated fatty acid (C18:2+C18:3)
n= 5

pressure. Since buffalo meat has low cholesterol and fat and high PUFA, it is healthier than beef. To fully leverage the benefits of buffalo meat and promote its consumption, it is essential to elucidate the mechanisms of lipid metabolism that contribute to its lower fat and cholesterol content. Such research could provide valuable insights for individuals with elevated blood cholesterol levels.

Acknowledgements

This work was supported by JSPS KAKENHI Grant Numbers JP20780207. We would like to thank Editage (www.editage.jp) for editing the English language manuscript.

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