Replacement of oat grass with highland barley straw: effects on lipid profiles, FA composition and lipogenetic genes expression in Tibetan sheep

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ABSTRACT

Studies associated with regional roughage utilisation in Tibetan sheep have been limited. This study focussed on the mechanism of lipid metabolism and deposition in Tibetan sheep fed local roughage sources. Twenty-four Tibetan sheep weighing 16.1 ± 1.76 kg were randomly assigned to two mixed diets containing the same concentrate mixed with oat grass (OG) or highland barley straw (HBS). The ME and CP of OG diet were 7.16 MJ/kg DM and 5.94%, respectively, while in HBS diet were 7.13 MJ/kg DM and 7.39%. Lipid profiles in the plasma and liver, fatty acid (FA) composition and lipogenetic genes expression in the muscle and adipose tissue were determined. No difference was observed in DMI, total cholesterol, triglyceride, low-density lipoprotein and high-density lipoprotein levels in the plasma and liver of sheep between two groups. Plasma leptin and liver non-esterified fatty acid (NEFA) content in HBS group tended to be greater than that in OG group (p < .01). Sheep in HBS group had greater C18:2, C20:4, PUFA and SFA ratio in the longissimus dorsi muscle (p < .05) and lower C17:0 (p < .05) and C20:1 (p < .01) in the perirenal adipose fat. Perirenal C18:0, C20:3 and C20:4 contents in HBS group tended to increase (p < .01). HBS stimulated the mRNA expression of SCD, C/EBP, and SREBF1 in the muscle and FASN in the perirenal adipose fat (p < .01), but inhibited HSL, LPL, C/EBP, and PPAR expression in the perirenal adipose fat. These results indicated that replacement of OG by HBS promotes PUFA deposition in the muscle and long-chain FAs in the adipose fat of Tibetan sheep. Lipid deposition-related genes (SCD, FASN, HSL and LPL) and lipid metabolism regulators (C/EBP, SREBF1 and PPAR) are involved in the transcriptional regulation.

Introduction

Tibetan sheep is one of the most important domestic animal species grazing on the Qinghai-Tibetan Plateau and plays critical roles in enhancing the regional rural economic development. However, the shortage of roughage resources is frequently happened in this region, especially in the long cold season (October to May) (Feng et al. 2013). Tibetan sheep have to suffer from inadequate nutrient supply under grazing and even housing feeding conditions, resulting in body weight loss and low productivity (Long et al. 2005; Sun et al. 2015). Hence, the importance has been recognised to improve Tibetan sheep productivity by developing local roughage resources during the cold season.

Simultaneously, highland barley and oat are two main annual crops and have a unique ability to adapt to the cold season in Qinghai-Tibetan Plateau. The planting barley accounts for about 43% of grain crop area and serves as an important food type for the Tibetan people (Dai et al. 2012; Wang et al. 2013; Zhao et al. 2015). Previous research evaluates the utilisation of barley or oat straws in ruminant production, although the results are ragged. Castells et al. (2012) suggested that offering chopped oat hay or barley...
straw ad libitum to young calves from 2 week of life to weaning promoted the starter feed intake and growth performance. Cows receiving oats in complete diet produced more milk and milk fat and owned greater OM digestibility than that fed rolled barley (Moran 1986). Oat replacing 42% barley in dairy total mixed rations could increase yield of milk fat and fat corrected milk (Yu et al. 2010). Nevertheless, replacing barley by oats led to the decline of daily live weight gain and feed conversion in growing dairy bulls (Huuskonen 2009) and crossbred steers (Arya and McKinnon 2011). In addition, no differences in animal performance and feed efficiency have been observed in steers receiving rolled barley and oats (Dion and Seoane 1992). DMI, ruminal fermentation characteristics and DE were also not affected in the beef cattle fed whole-crop oat and barley forage harvested at the hard dough and ripe stages compared to the late milk stage (Rosser et al. 2016). From the above, the feed efficiency, growth and lactating performances of cattle fed barley or oat have been described well, whether the meat quality and lipid metabolism are influenced by barley straw and oat grass (OG) is still unknown.

Considering the regional resources and high altitude characteristics in the Qinghai-Tibetan Plateau, we attempted to compare the potential effects of highland barley straw (HBS) and OG on blood lipid profiles and lipid distribution of muscle and fat tissues for Tibetan sheep, and explore the related regulatory mechanism at transcriptional level. Hence, we determined the fat metabolism parameters in the blood and liver, fatty acid (FA) percentage, and mRNA expression of related genes involved in the lipogenic process in the *longissimus dorsi* muscle and perirenal fat. The relevant results would provide some valuable information for local roughage sources utilisation to improve the performance of Tibetan sheep at finishing stage.

**Materials and methods**

The experiment was approved by the Animal Care Committee, Institute of Subtropical Agriculture, the Chinese Academy of Sciences, Changsha, China. This experiment was conducted at the research farm of the Academy of Agricultural and Animal Husbandry Sciences in Lhasa, Tibet, China (altitude = 3658 m, latitude = N29°30’).

**Experimental design, animal management and diets**

Twenty-four growing Tibetan sheep (16.1 ± 1.76 kg) were randomly allocated into two dietary treatment groups, namely HBS diet and OG diet. Each group contained six male sheep and six ewes with three sheep housed in each pen. Sheep in HBS group (15.8 ± 2.01 kg, 1.61 ± 0.10 years old) and in OG group (16.4 ± 1.50 kg, 1.65 ± 0.07 years old) were fed HBS and OG as unique roughage source in the diets contained the same pelleted concentrate, respectively. The ratio of dietary forage to concentrate was 50:50.

The ingredients and chemical composition of formulated experimental diet are presented in Table 1. Sheep were adaptive to the experimental diets for seven days and then fed for three weeks. Diets were daily premixed before feeding, and offered in equal amount (up to 5% refusal) at approximately 08:00 and 18:00 h, respectively. The sheep were allowed access to fresh water freely.

**Sampling and collection**

HBS, OG and concentrate were sampled once a week and pooled on individual sheep. The intake of diets was recorded every day, and the remnant was also recorded and sampled daily and pooled on individual sheep. At the end of the feeding experiment, all the sheep were fasted overnight and slaughtered by electrically stunning and exsanguinating. Blood samples were collected via jugular vein puncture into tubes with heparin before slaughter, and the plasma was retained for determining total cholesterol (TC), triglyceride (TG), low-density lipoprotein (LDL), high-density lipoprotein (HDL), non-esterified fatty acids (NEFAs) and leptin. The *longissimus dorsi* muscle and perirenal fat were collected after slaughter for further analysis.

**Chemical analysis**

Chemical composition of HBS, OG, concentrate and the remnant was analysed by Wang et al. (2016). The plasma biochemical components (TC, TG, LDL and HDL) were detected by Mindray automatic biochemistry analyser (BS-190, Shenzhen Mindray Company, Shenzhen, China). Plasma NEFA and leptin were measured according to the procedures of Elisa kits (NEFA, EK-S90370, EK-Bioscience Biotechnology Co., Ltd, Shanghai, China; leptin, CSB-EL012870SH, Cusabio Biotech Co., Ltd, Wuhan, China). The TC, TG, LDL and HDL concentrations in the liver were analysed according to the instructions of kits purchased from Nanjing Jiancheng Bioengineering Institute.

The total lipids in the *longissimus dorsi* muscle and perirenal fat were extracted by equal volume of chloroform and methanol for 2h and concentrated by vacuum concentrator (Christ RVC2-25 CD plus,
Osterode, Germany) at 235°C for 4–6 h. Lipids were methyl esterified by 1% sulphuric acid–methanol solution according to Kou and Yu (2005). After methyl esterification, the samples were measured using gas chromatography equipped with a sp-2560 column (100 m × 0.25 mm × 0.2 μm, Applied Biosystems, Foster City, CA) and FID detector. The gas chromatograph programme temperature was as follows: initial column temperature held at 140°C for 5 min; increased at a rate of 3°C/min to 220°C; held for 40 min at 220°C. The injector and detector temperatures were set at 280°C. Hydrogen was used at a flow rate of 30 mL/min, air 400 mL/min, and carrier gas was N₂ at a rate of 0.8 mL/min. The split ratio was 20:1 and the injection volume was 1 μL. The individual FA peaks were identified by comparison of their retention times with those of the standards (Supelco® 37 Component FAME Mix, Sigma Chemicals, St. Louis, MO). Results are expressed as g/100 g of total identified FA.

**Real-time quantitative PCR**

Total RNA was isolated from the longissimus dorsi muscle and perirenal fat using the Trizol Reagent (Invitrogen, Carlsbad, CA). After genomic DNA was eliminated by digestion with DNase I (Thermo Scientific, Waltham, MA), the RNA quality and quantity was determined using NanoDrop 2000 (Thermo Scientific, Waltham, MA), all RNA samples showed an A260/A280 values within the range of 2.01–2.06 and A260/A230 values above 2.0. And the integrity of collected RNA was analysed with agarose gel electrophoresis. Afterwards, cDNA was synthesised using the Revert Aid First Strand cDNA synthesis kit (Applied Biosystems, Thermo Fisher Scientific, Waltham, MA). For relative quantification of gene expression, the ABI Prism 7900 HT Fast Real-Time PCR System (Applied Biosystems, Foster, CA) was used. Primers were designed using the Primer 3 plus programme, and sequences are listed in Table 2. The reaction system contained 5 μL SYBR® Premix Ex Taq™ (2×), 0.2 μL PCR forward primer (10 μM), 0.2 μL PCR reverse primer (10 μM), 0.2 μL ROX reference dye (50×), 1.0 μL cDNA and 3.4 μL sterilised ddH₂O. The thermal profile for all reactions was 30 s at 95°C, then 40 cycles of denaturation at 95°C for 5 s and annealing at 60°C for 30 s. Each reaction was completed with a melting curve analysis to ensure the specificity of the reaction. All the samples were analysed in duplicate, and the relative amount of each specific transcript was obtained after normalisation against the endogenous control β-actin (Drozdowski et al. 2010; Duan et al. 2016; Li et al. 2016). The relative amounts of target genes were quantified according to the 2^(-ΔΔCT) method (Livak and Schmittgen 2001).

**Statistical analysis**

Blood parameters, FA composition and quantitative PCR data were analysed by Proc GLM procedure of SAS 8.0 (SAS Institute, Inc., Cary, NC). The roughage source was the main effect. Mean values of each Table 1. Ingredients and chemical composition of the experimental diets (DM basis) and expected dry matter intake of Tibetan sheep.

| Item                        | Diet                | Forage |
|-----------------------------|---------------------|--------|
| Ingredients, g/kg DM        | HBS                 | OG     | HBS    | OG     | SEM    | p value |
| Corn                        | 470                 | 470    | 95.50  | 95.50  | 9.49   |         |
| Soya-bean meal              | 45                  | 45     | 5.94   | 1.42   | 4.34   |         |
| Wheat bran                  | 424                 | 424    | 2.18   | 7.09   | 5.97   |         |
| Palm oil                    | 9                   | 9      | 24.60  | 38.70  |        |         |
| Chemical compositionb, %    | Dry matter          | 96.70  | 95.50  |        |        | 9.49   |
| Crude protein               | 7.39                | 5.94   | 1.42   | 4.34   | 9.49   |         |
| Ether extraction            | 2.18                | 2.43   | 7.09   | 5.97   | 9.49   |         |
| Acid detergent fibre        | 30.00               | 26.40  | 45.80  | 38.70  |        |         |
| Neutral detergent fibre     | 53.90               | 48.30  | 70.90  | 59.70  |        |         |
| Metabolisable energyc, MJ/kg DM | 7.13   | 7.16   | 1.11   | 1.41   |        |         |
| DMId, g/d                   | 582                 | 609    | –      | –      | 13.3   | .32    |

HBS: highland barley straw; OG: oat grass.

aPremix contained per kg: Vitamin A 90,000 U, Vitamin D 20,000 U, MgSO₄·H₂O 340 g, FeSO₄·7H₂O 5 g, CuSO₄·5H₂O 2 g, MnSO₄·H₂O 6 g, ZnSO₄·H₂O 10 g, Na₂SeO₃ 0.03 g, KI 0.08 g, CoCl·6H₂O 0.06 g.

bDry matter, crude protein, ether extraction, acid detergent fibre, neutral detergent fibre, crude ash, calcium and inorganic phosphorus were determined values.

cMetabolisable energy was calculated according to Zhang and Zhang (1998).
group were compared by Duncan’s test. Statistical significance was declared at $p < .05$ and tendencies at $.05 < p < .10$.

**Results**

The initial body weight of sheep in HBS group and OG group was 15.8 kg and 16.4 kg ($p = .43$), respectively. At the end of the experiment, final weight of sheep in two groups was 20.8 kg and 20.7 kg ($p = .90$), respectively. No significant difference was observed in the average daily gain (ADG, 177 g/d for HBS diet and 153 g/d for OG diet), dry matter intake (DMI, Table 1), weight of lean mass (7.38 kg for HBS diet and 7.21 kg for OG diet) and dressing percentage (35.5% for HBS diet and 34.8% for OG diet) of the sheep fed HBS diet compared to that fed OG diet ($p > .05$).

As illustrated by Table 3, TC, TG, LDL, HDL and NEFA levels in the plasma were not affected ($p > .05$) by HBS or OG. Plasma leptin concentration in HBS group tended to be increased ($p < .1$) twofold compared to that in OG group. There were no differences ($p > .05$) in the liver TC and TG concentrations between HBS and OG groups. The liver LDL and NEFA concentrations in sheep fed OG tended to be lower ($p < .1$) than those of sheep fed HBS.

The FA composition of *longissimus dorsi* muscle and perirenal adipose, expressed as mg/g of fat, is presented in Tables 4 and 5, respectively. In the *longissimus dorsi* muscle, sheep in HBS group had more

| Gene | GenBank accession | Forward Primer | Length (bp) |
|------|-------------------|----------------|-------------|
| FASN | XM_012186804.1    | GCAACCGTCTCTCTTCCTTT | 121         |
|      |                   | GCCACGCCTCTCTTGTTGAGT | 169         |
| HSL  | NM_001128154.1    | GAGTTAAGGCTCGTGAGACT | 115         |
| SCD  | NM_001009254.1    | TTTGCACCTCTCTCCGTTA | 123         |
| GLUT4| XM_012185632.1    | CCTCTCTCTGTCTTTGATG | 121         |
|      |                   | CCTGCTCTCTCTTTTACCTCT | 123         |
|      |                   | CGGGTTTACCTCTCTGCTC | 121         |
| PPARγ| NM_001009921.1    | TTTGCACCTCTCTCCGTTA | 109         |
| LPL  | NM_001009394.1    | GCCACGCCTCTCTTGTTGAGT | 113         |
| ACACA| NM_001009256.1    | CGGGTTTACCTCTCTGCTC | 121         |
| SREBF1| XM_015098336.1   | GCCACGCCTCTCTTGTTGAGT | 121         |
| C/EBPα| NM_004006020.2  | GCCACGCCTCTCTTGTTGAGT | 121         |
| C/EBPβ| XM_012190135.1 | GCCACGCCTCTCTTGTTGAGT | 121         |
| β-ACTIN| NM_001009784.2 | GCCACGCCTCTCTTGTTGAGT | 121         |

FASN: fatty acid synthase; HSL: hormone sensitive lipase; SCD: stearoyl-CoA desaturase; GLUT4: glucose transporter 4; PPARγ: peroxisome proliferator-activated receptor gamma; LPL: lipoprotein lipase; ACACA: acetyl-CoA carboxylase; SREBF1: sterol regulatory element binding protein 1; C/EBPα: CCAAT-enhancer binding protein zeta; C/EBPβ: CCAAT-enhancer binding protein beta; C/EBPγ: CCAAT-enhancer binding protein gamma.

| Item     | OG      | HBS     | SEM    | $p$ value |
|----------|---------|---------|--------|-----------|
| Plasma TC, mmol/L | 1.29   | 1.31   | 0.01   | .57       |
| TG, mmol/L    | 0.24   | 0.23   | 0.05   | .74       |
| LDL, mmol/L   | 0.21   | 0.22   | 0.04   | .78       |
| HDL, mmol/L   | 0.87   | 0.94   | 0.01   | .42       |
| Leptin, ng/mL | 6.82   | 14.20  | 2.60   | .07       |
| NEFA, μmol/L  | 225.20 | 245.99 | 29.98  | .64       |
| Liver TC, mmol/gprot | 0.08   | 0.09   | 0.01   | .52       |
| TG, mmol/gprot | 0.12   | 0.14   | 0.03   | .37       |
| LDL, mmol/gprot | 16.58  | 27.07  | 3.53   | .05       |
| HDL, mmol/L   | --     | --     | --     | --        |
| NEFA, μmol/gprot | 15.36  | 21.70  | 1.95   | .08       |

OG: oat grass; HBS: highland barley straw.

| Item     | OG       | HBS      | SEM     | $p$ value |
|----------|----------|----------|---------|-----------|
| C14:0    | 1.53     | 1.19     | 0.12    | .07       |
| C16:0    | 25.69    | 25.41    | 0.57    | .73       |
| C17:0    | 1.60     | 1.47     | 0.05    | .13       |
| C18:0    | 19.64    | 20.83    | 0.55    | .14       |
| C18:1    | 0.16     | 0.12     | 0.01    | .13       |
| C18:1    | 48.60    | 49.04    | 1.05    | .77       |
| C16:1 n-7| 1.85     | 1.70     | 0.08    | .24       |
| C18:1 n-9c| 33.24    | 31.12    | 0.67    | .04       |
| C18:1 n-9t| 1.37     | 1.52     | 0.05    | .07       |
| C20:1 n-9| 0.47     | 0.56     | 0.03    | .10       |
| ΣMUFA    | 36.96    | 32.57    | 1.74    | .09       |
| C18:2 n-6c| 8.97     | 11.46    | 0.66    | .02       |
| C18:3 n-6| 0.11     | 0.11     | 0.01    | .87       |
| C20:3 n-6| 0.46     | 0.56     | 0.04    | .06       |
| C20:4 n-6| 4.47     | 5.82     | 0.37    | .02       |
| C22:6 n-3| 0.45     | 0.50     | 0.03    | .28       |
| ΣPUFA    | 14.44    | 18.38    | 1.03    | .01       |

OG: oat grass; HBS: highland barley straw.
Our data on liver lipids change were not completely consistent with previous researches in which barley and oat or their byproducts are usually used as dietary ingredients. Oda et al. (1994) have ever reported that dietary oat gum addition can suppress the elevation of liver TC and TG concentrations in diet-induced hypertriglyceridaemic rats, but barley gum had no effect on the liver TC concentration. Jackson et al. (1994) have also stated that liver TC is lower in rats fed oat bran than in that fed barley or malted barley. Additionally, Delaney et al. (2003) have found that there are no differences in the liver TC between oat and barley consumption for hamsters. It has been suggested that the different lipid-lowering effects of oat and barley or their byproducts would be due to differences in species with different protein and lipids composition (Guo et al. 2014), growing and processing conditions.

### Table 5. Fat acid percentage in the perirenal adipose fat.

| Item | OG    | HBS   | SEM  | p value |
|------|-------|-------|------|---------|
| C14:0| 2.65  | 2.57  | 0.08 | .53     |
| C16:0| 22.35 | 22.00 | 0.45 | .58     |
| C17:0| 2.49  | 2.25  | 0.08 | .05     |
| C18:0| 31.02 | 32.73 | 0.68 | .09     |
| C20:0| 0.40  | 0.36  | 0.02 | .27     |
| ΣSFA | 58.89 | 59.91 | 1.01 | .49     |
| C16:1n-7| 2.32 | 2.35  | 0.06 | .76     |
| C18:1n-9c| 31.40 | 32.70 | 0.83 | .17     |
| C20:1n-9c| 4.35 | 5.00  | 0.27 | .10     |
| ΣMUFA| 38.34 | 37.28 | 0.95 | .44     |
| C18:2n-6c| 2.69 | 2.60  | 0.12 | .99     |
| C18:3n-6 | 0.04 | 0.05  | 0.00 | .65     |
| C20:3n-6c| 0.02 | 0.03  | 0.00 | .07     |
| C20:4n-6c| 0.10 | 0.13  | 0.01 | .05     |
| C22:6n-3| 2.76 | 2.81  | 0.13 | .80     |
| PUFA/SFA| 0.05 | 0.05  | 0.00 | .98     |

OG: oat grass; HBS: highland barley straw.

### Table 7. Expression of genes related to fatty acid metabolism in the perirenal adipose fat.

| Item | OG    | HBS   | SEM  | p value |
|------|-------|-------|------|---------|
| FASN | 1.06  | 1.80  | 0.19 | .00     |
| HSL  | 1.06  | 0.70  | 0.06 | <.00    |
| SCD  | 1.05  | 1.46  | 0.13 | .06     |
| GLUT4| 1.08  | 0.85  | 0.07 | .06     |
| LPL  | 1.07  | 0.76  | 0.07 | .00     |
| ACACA| 1.06  | 1.07  | 0.10 | .94     |
| CEBPβ| 1.14  | 0.92  | 0.10 | .14     |
| CEBPγ| 0.98  | 0.66  | 0.09 | .02     |
| CEBPα| 1.16  | 0.88  | 0.10 | .05     |
| PPARγ| 1.07  | 0.63  | 0.07 | <.00    |
| SREBF1| 1.04  | 1.30  | 0.13 | .18     |

OG: oat grass; HBS: highland barley straw.

C18:2, C20:4, PUFA and PUFA:SFA ratio (p < .05) than those in OG group. C18:1n-9 c percentage was higher (p < .05) in sheep fed OG when compared to those in sheep fed HBS. C20:1 and C20:3 percentages in sheep fed HBS tended to be greater (p < .1) than those in sheep fed OG. In the perirenal adipose fat, C17:0 (p < .05) and C20:1 (p < .01) percentages of sheep fed HBS were declined in comparison with those of sheep fed OG. Percentages of C18:0, C20:3 and C20:4 of sheep fed HBS tended to be increased (p < .1) when compared with those of sheep fed OG.

The transcripts of genes involved in FA metabolism in the *longissimus dorsi* muscle and perirenal adipose are listed in Tables 6 and 7, respectively. In the *longissimus dorsi* muscle, the mRNA expression of stearoyl-CoA desaturase (*SCD*, p < .01), CCAAT/enhancer-binding protein gamma (*CEBPγ*), and sterol regulatory element binding protein 1 (*SREBF1*, p < .001) were upregulated by HBS feeding, and glucose transporter 4 (*GLUT4*, p < .001) expression tended to be increased (p < .1) by HBS. In the perirenal adipose, HBS feeding upregulated (p < .01) the mRNA expression of fatty acid synthase (*FASN*), but inhibited hormone sensitive lipase (*HSL*), lipoprotein lipase (*LPL*), *CEBPγ* and peroxisome proliferator-activated receptor gamma (*PPARγ*) expression. The *SCD* expression tended to be upregulated (p < .1) by HBS, however, *GLUT4* and CCAAT-enhancer binding protein zeta (*CEBPζ*) expression tended to be downregulated (p < .1) by HBS when compared to OG.

### Discussion

In the present study, replacement of OG with HBS did not affect the lipid profiles (TC, TG, LDL and HDL) in the plasma and liver. Considering the unchanged DMI between two groups, these results indicated that it was not a wise strategy for regulating lipid metabolism in the blood and liver of Tibetan sheep via simple roughage substitution. In previous studies, barley and oat or their byproducts are used as a part of rations for animal or human, some inconsistent results have been investigated. For example, TC-, TG- and LDL-lowering effects with increase in HDL by oat and barley bran have been observed in the blood of hypercholesterolaemic rats (El Rabey et al. 2013; Abulnaja and El Rabey 2015).
Furthermore, increasing tendency in the plasma leptin, and LDL and NEFA concentrations in the liver was observed in sheep fed HBS in this study. HBS promoted adipocytokines secretion to regulate the feed intake (HBS 582 g/d vs. OG 609 g/d) and blood pressure via its widely distributed receptors (Rondinone 2006), facilitates the mobilisation of liver fat to better adapt to the cold climate. OG is more beneficial to reduce the chance of LDL-induced fatty liver formation in sheep. Considering the increased PUFA in longissimus dorsi muscle and unchanged PUFA composition in perirenal adipose fat, we inferred that increase in the secretion of leptin by HBS-feeding might distribute fat deposition to the muscle rather than adipose tissue.

The HBS elevated C18:2, C20:4, PUFA and ratio of PUFA to SFA in the longissimus dorsi muscle of Tibetan sheep. Our results were not consistent with previous studies where oat and barley are applied as dietary components. Leiber et al. (2008) have found that percentages of C18:2, C20:4 and PUFA in the M. quadriceps of rabbits are not varied by dietary oats. Ponnampalam et al. (2002) have also failed to alter C18:2, C20:4 and PUFA percentages in the longissimus thoracis muscle of lambs fed barley diets. Meanwhile, OG increased the percentages of C17:0 (heptadecanoic acid) and C20:1 (cis-11-eicosenoic acid) in the perirenal adipose fat of Tibetan sheep. Leiber et al. (2008) have also reported similar result that oats supplementation can elevate C20:1 percentage in the perirenal adipose tissue of rabbits. The current results showed that intramuscular PUFA was easier to be regulated by roughage source than adipose fat, and HBS was superior to OG for the deposition of PUFA in the longissimus dorsi muscle. More PUFA content in the muscle of sheep indicated that the meat quality of Tibetan sheep had been improved by HBS and this kind of meat is more beneficial to human health. Greater C17:0 and C20:1 were deposited in the perirenal adipose fat implied that OG feeding promoted the storage of long-chain FA in adipose fat for further utilisation in cold seasons.

In the longissimus dorsi muscle of Tibetan sheep, SCD, C/EBPα and SREBF1 mRNA expression were upregulated by HBS, meanwhile GLUT4 expression tended to be increased. The SCD, also named Δ9-desaturase, involves in the desaturation of trans-vaccenic acid into conjugated linoleic acid (Corl et al. 2001; Schmid et al. 2006). It has been confirmed the association between the SCD gene and the FA profile of different fat deposits was developed in goats (Zidi et al. 2010; Crepaldi et al. 2013; Aviles et al. 2016). The C/EBPα is a member of the C/EBPs family that includes α, β, δ, ε and γ (Ramji and Foka 2002). The C/EBPα and C/EBPβ are known to directly influence adipocytes development (Rosen et al. 2002) and to regulate PPARγ expression during the differentiation of mouse fibroblasts into adipocytes (Park et al. 2004). The SREBF1 is a key transcription factor that regulates cellular lipogenesis in skeletal muscle and adipose tissue (Guillet-Deniau et al. 2002; Ferre and Foufelle 2007; Raghow et al. 2008). The upregulation of all above-mentioned genes coincides with increases in PUFA and PUFA to SFA ratio in the muscle (Table 4). Drozdowski et al. (2010) have found non-significant differences in rat intestinal SREBF1 mRNA expression between barley β-glucan and oat β-glucan extracts. The inconformity between our data and previous researches would ascribe to differences in species, target tissues and concentrate composition. Additionally, we found that FASN mRNA expression in the perirenal adipose fat was upregulated by HBS, other lipogenic genes HSL, LPL and C/EBPα and regulatory genes PPARγ were downregulated by HBS. Unfortunately, no similar researches could be compared for discussion. More concerns were needed to illustrate the possible mechanism of FA deposition in the adipose fat affected by HBS and OG.

Conclusions

In summary, HBS was relatively superior to OG in the PUFA deposition in the longissimus dorsi muscle by upregulating SCD, C/EBPα and SREBF1 transcription. Replacement of OG by HBS also promoted long-chain FAs deposition in the adipose fat by regulating the mRNA expression of FASN, HSL, LPL, C/EBPα and PPARγ. More local roughage species should be exploited to improve the productivity and meat quality of Tibetan sheep and the related mechanism must be illuminated. Our findings in Tibetan sheep will provide priceless knowledge of local roughage sources utilisation. The management of Tibetan sheep is very interesting and probably can be connected to Yak or other ruminants grazed in the Qinghai-Tibetan Plateau.

Disclosure statement

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