STUDY ON THE MEAT QUALITY AND DEPOSITION MECHANISM OF INTRAMUSCULAR FAT IN GRAZING YAKS AT DIFFERENT AGES

Qin Bai[1], Jiuqiang Guan[1], Tianwu An[1], Hongwen Zhao[1], Xiaolin Luo[1,*] and Xiangfei Zhang[1,*]

[1]Institute of Plateau Animals, Sichuan Academy of Grassland Sciences, P. R. China

*Corresponding author email: Luoxl2004@sina.com, zxfsicau@foxmail.com

I. INTRODUCTION

Intramuscular fat (IMF) is a crucial component affecting meat quality, and represents the amount of fat deposited between muscle fibers or inside muscle cells [1]. The positive correlations between IMF and juiciness, tenderness, palatability of beef have been demonstrated in previous study [2]. The IMF deposition results from dynamic change of lipogenesis and lipolysis processes in intramuscular adipocytes, in which several transcriptional factors and lipid metabolic enzymes are involved [3]. The yak (*Bos grunniens*) is predominant livestock on the Qinghai-Tibet Plateau. Whereas, owing to the poor meat quality under traditional grazing feeding pattern, the metabolic feature and quality improvement of yak meat become the critical demands of yak industry. Therefore, the aim of this study was to evaluate the impact of age on meat quality, deposition and metabolic mechanism of IMF in grazing yaks.

II. MATERIALS AND METHODS

The Institutional Animal Care and Use Committee of the Sichuan Academy of Grassland Sciences approved all procedures in the study. A total of 30 healthy male yaks with different ages (0.5, 1.5, 2.5, 3.5, and 4.5 years old, 6 yaks per age group) were selected from the herd grazing on the same natural pasture. Body weight and size were measured before morning grazing, subsequently, all thirty yaks were slaughtered following standard procedure. Samples of *Longissimus dorsi* were collected for the analysis of meat quality (Shear force, cooked meat percentage, pH) and nutrients composition (IMF and fatty acids composition) using gas chromatography. Gene expressions of transcriptional factors and enzymes related to lipid metabolism were detected by Real-time PCR. The One-way ANOVA procedure of SAS was used for data analysis.

III. RESULTS AND DISCUSSION

From 0.5 to 4.5 years old, there were significant increases of the body weight and size of yaks ($P<0.05$). The shear force of Longissimus dorsi increased with age, with significantly higher value in 4.5 years old group than in 0.5 and 1.5 years old groups ($P<0.05$).

Table 1. Meat quality of yaks at different ages

Items	Age					SEM	P-value
	0.5	1.5	2.5	3.5	4.5		
Shear force, kg[1]	5.16^{c}	6.24^{bc}	6.72^{ab}	7.50^{ab}	8.19^{a}	0.41	0.001
Cooked meat percentage, %	76.9	76.3	71.9	69.6	69.2	2.32	0.125
$pH_{1\ h}$	6.51	6.85	6.76	6.77	6.51	0.08	0.045
$pH_{24\ h}$	5.49^{b}	5.69^{ab}	5.58^{ab}	5.89^{a}	5.85^{a}	0.09	0.022
Intramuscular fat content, %	0.99^{d}	1.18^{c}	1.55^{b}	1.71^{ab}	1.80^{a}	0.054	<0.001

[1]Values in the same row with different letter superscripts differed significantly ($P<0.05$).

The IMF content increased significantly with age($P<0.05$). Yaks of 4.5 years old group had a significantly higher IMF compared with those of 0.5-2.5 years old groups ($P<0.05$), and the IMF in 2.5 and 3.5 years old groups were significantly greater than the 0.5 and 1.5 years old groups ($P<0.05$). Whereas, no effect of age on the fatty acid composition of IMF including SFA, MUFA and PUFA was observed.

For the transcriptional regulatory factors related to IMF metabolism, PPARγ gene expression was significantly higher in the 4.5 years old group than in the 0.5 and 1.5 years old groups ($P<0.05$). FABP4 expressions in the 3.5 and 4.5 years old groups were significantly greater compared with the 0.5 and 1.5

years old groups (P<0.05). We also found significantly higher SREBP-1 expression in the 2.5-4.5 years old groups than in the 0.5 years old group (P<0.05). The C/EBPα gene expression of 3.5 years old yaks was significantly higher compared with those of 0.5 years old (P<0.05).

Table 2. Gene expression of transcriptional regulatory factors related to IMF metabolism in yaks at different ages

Items[1]	Age					SEM	P-value
	0.5	1.5	2.5	3.5	4.5		
PPARγ[2]	1.06^{b}	1.04^{b}	1.45^{ab}	1.35^{ab}	1.89^{a}	0.169	0.017
FABP4	1.03^{b}	1.22^{b}	1.51^{ab}	1.90^{a}	1.86^{a}	0.142	0.002
FoxO1	1.16	1.09	0.98	1.40	1.16	0.220	0.753
SREBP-1	1.02^{b}	1.41^{ab}	1.83^{a}	1.95^{a}	1.82^{a}	0.176	0.012
C/EBPα	1.01^{b}	1.45^{ab}	1.57^{ab}	1.90^{a}	1.57^{ab}	0.173	0.053

[1]PPARγ=Peroxisome proliferator-activated receptor gamma, FABP4= Fatty acid-binding protein 4, FoxO1=Forkhead box transcription factor O1, SREBP-1=Sterol regulatory element-binding protein 1, C/EBPα=CCAAT/enhancer binding protein α.
[2]Values in the same row with different letter superscripts differed significantly (P<0.05).

The expression of FAS gene, a key enzyme of lipogenesis, was significantly higher in the 3.5 and 4.5 years old groups than 0.5 and 1.5 years old groups (P<0.05). The DGAT1 gene expression of 2.5-4.5 years old yaks was significantly greater compared with those of 0.5 and 1.5 years old (P<0.05). In contrast, as a key enzyme of lipolysis, the HSL expression was reduced significantly at 2.5-4.5 years old in comparison with the 0.5 years old group (P<0.05).

Table 3. Gene expression of lipogenesis and lipolysis enzymes in IMF of yaks at different ages

Items[1]	Age					SEM	P-value
	0.5	1.5	2.5	3.5	4.5		
ACC[2]	1.03	1.38	1.54	1.70	1.60	0.161	0.061
FAS	1.02^{d}	1.20^{cd}	1.41^{bc}	1.67^{ab}	1.76^{a}	0.086	<0.001
DGAT1	1.03^{b}	1.12^{b}	1.55^{a}	1.69^{a}	1.63^{a}	0.127	0.003
SCD	1.07	1.14	1.01	1.11	1.04	0.121	0.947
LPL	1.02	1.19	1.33	1.34	1.51	0.156	0.349
HSL	1.03^{a}	0.95^{ab}	0.69^{b}	0.67^{b}	0.67^{b}	0.070	0.003
ACOX	1.06	1.01	0.87	1.08	0.98	0.133	0.877
CPT-I	1.33	1.30	1.18	1.35	1.29	0.265	0.995

[1]ACC=Acetyl-CoA carboxylase, FAS= Fatty acid synthase, DGAT1=Diacylglycerol acyl transferase-1, SCD=Stearoyl-CoA desaturase, LPL=Lipoprotein lipase, HSL=Hormone-sensitive lipase, ACOX=Acyl-coenzyme A oxidase, CPT-I=Carnitine palmitoyltransferase I.
[2]Values in the same row with different letter superscripts differed significantly (P<0.05).

IV. CONCLUSION

Our results suggest that the shear force and IMF content of yak meat increased with age. During the IMF deposition of yaks from 2.5 to 4.5 years old, the transcriptional factors PPARγ, FABP4, SREBP-1 and C/EBPα related to lipid metabolism were up-regulated and involved in the regulation of key enzymes. Subsequently, the increased gene expressions of lipogenesis enzymes FAS and DGAT1, as well as the decreased expression of lipolysis enzyme HSL, conduced to enhanced lipogenesis process.

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