

The Effects of Crossbreeding on Meat Fatty Acids Profile in Qazvinian Native Goats

Research Article

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Received on: 21 Jan 2019

Revised on: 2 Jun 2019

Accepted on: 15 Jun 2019

Online Published on: Mar 2020

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Online version is available on: www.ijas.ir

ABSTRACT

The study was conducted to investigate the fatty acid profile of intramuscular fat in longissimus lumborum (LL) of three genotypic groups: Qazvinian native (Q, n=10), crossbred Qazvinian native × Saanen breed (QS, n=10) and backcrossed Qazvinian native × Saanen breed (QSS, n=9) male kids. All of kids were weaned at 75-days-old and then fed with a diet consisted of concentrate (70%) and alfalfa hay (30%). The kids were slaughtered with an average age of 130 days and immediately samples of LL muscle were collected. Data were analyzed through one-way ANOVA using the generalized linear model (GLM) procedure. The total differences among genotypic groups were evaluated by a canonical discriminant analysis (CDA). The concentration of intramuscular fat (g/100g meat, Q=0.94, QS=2.01 and QSS=1.05) and saturated fatty acids (SFA; Q=40.87, QS=43.25 and QSS=36.9), polyunsaturated fatty acids (PUFA; Q=12.99, QS=13.89 and QSS=22.41), total conjugated linoleic acids (CLA, Q=2.1, QS=2.32 and QSS=1.02) and desirable fatty acids (Q=73.63, QS=67.18 and QSS=74.87) as g/100 g total fatty acids between genotypic groups were significant (P<0.05). Furthermore, the PUFA:SFA and linoleic (C18:2 n-6):alpha-linolenic acids (C18:3 n-3) ratio in genotypic groups were significant (P<0.05). The genotypic groups were separated by CDA, based on their meat fatty acids profile. Results demonstrated that crossbreeding could significantly change the intramuscular fatty acids profile. Therefore, it can be concluded that the fatty acids profile in crossbred kids are better than that of native Qazvinian kids. In these experimental conditions, results of the present study demonstrated that crossbreeding could be a suitable strategy for producing meat with higher concentration of unsaturated fatty acids with beneficial properties for health of consumers.

KEY WORDS crossbreeding, fatty acids profile, meat, Qazvinian goat, Saanen goat.

INTRODUCTION

The native goats of Qazvin province in Iran are often kept in high and mountainous regions and mainly reared for producing meat and milk. The goats have a medium body size with an average live weight 40-45 kg in female and 55-65 kg in male. Main source of income for the producers is sale of kids and milk production is of secondary importance. Qazvinian native goats are able to deal with severe environmental conditions. The goats are reared in an extensive

traditional system based mainly on natural feed resources and have low levels of milk production.

Taking into consideration the lower performance of native goats and the longer time needed to achieve genetic progress (Goetsch *et al.* 2011), crossbreeding of local goats with improved breeds was recommended. It is a fast method of improving on efficiency in the goat breeding industry. Saanen goat breed as a dairy breed has often been used to improve the milk production in native breeds that mostly reared for meat production (Stanišić *et al.* 2012).

Fatty acids (FAs) profile is an important factor affecting the meat quality and nutritional value (Horcada *et al.* 2012). Breed of goats and genetic group of animal are the factors influencing the meat quality and FAs profile. However, crossbreeding may be changing the meat FAs profile in crossbred goat kids, in compare to that of native goats. Currently, crossbreeding by Sannen breed is one of the livestock breeding strategies in Iran for increase in goat milk production.

In other hand, 50 percent of produced offspring is male that used for meat production. Thus, the evaluation of quantitative and qualitative changes in meat traits of crossbred kids are very important in goat husbandry. Therefore, the objective of this study was evaluation of qualitative meat production in Qazvinian native and Qazvinian × Saanen goats crossbred.

MATERIALS AND METHODS

Animals and feeding

The present study was carried out in the Fakhr-e-Iranian goat farm in Qazvin province of Iran. Animals used in this study included three genotypic groups: Qazvinian native goat kids (Q, n=10), crossbred goat kids from mating Q doe and Saanen (S) buck (QS, n=10) and backcrossed goat kids from mating QS doe and Saanen (S) buck (QSS, n=9). All goat kids in three genotypic groups were kept in the stall from birth to about 75-days-old with their dams and fed a starter feed in this period. Then, goat kids were weaned and separated from their mothers. In this period, all goat kids were fed a ration containing alfalfa hay (30%) and concentrate (70%).

The chemical composition and ingredients of diets fed to goats were presented in Table 1. Animals were cared according to the guidelines of the research policy of Department of Animal Science of the University of Kurdistan, Sanandaj, Iran.

Slaughter and sampling

At the age of about 130 days, after 15 hours of starvation goat kids were weighted and then slaughtered. The number of animals, age at slaughter and hot carcass weight are presented in Table 2. After slaughtering the carcass of each kid weighted. Then carcasses were chilled at 4 °C for 24 hours. After this time, muscle samples of longissimus lumborum (LL) from the left half-carcass were taken from the lumbar vertebrae (vertebrae of 1 to 5). The covering fat depots above LL muscles were removed and cut in pieces and blended. The muscle samples from each kid have divided in two parts, one part was used to measure fat percent and another part was frozen at a temperature of -24 °C until analysis of FA profile.

The dry matter and total fat content were obtained in the LL muscle of the left half-carcass according to the method described in AOAC (1990).

Fatty acid analysis

Fat content of LL muscles was extracted according to the method described by Folch *et al.* (1957). For determining the composition of FAs of LL, a samples of each carcass was placed in 5 mL screw-top test tube. To each of the test tubes, 2 mL of 2 N potassium hydroxide was added. After closing the test tubes, they were vigorously shaken for 2 minutes.

Then, 2 mL of hexane was added to the contents of the tube. After 5 seconds, the tubes were placed in an ultrasonic bath at 35 °C for 15 minutes. The upper fat layer was separated and passed through a filter (0.45 µm), containing sodium sulfate anhydrous. Then, 1 µL of the filtrate was injected into a gas chromatograph apparatus (GC, Youngling 6100, Korea) equipped with a J&W CP-Sill 88 fused silica capillary column (100 m×0.25 mm, and 0.25 µm film thickness, Agilent Technologies, USA). The temperature of the injector and detector was 270 °C and 300 °C, respectively.

The FAs composition was analyzed by the isotherm program. The temperature program was a 175 °C column for 60 minutes. To measure individual amounts and total FAs methyl esters (FAME), the internal standard of nonadecanoic acid (C19:0) was used. Identification of individual FAs in FAME was performed by a standard mixture of 37 component FAME (Sigma-Aldrich, Supelco-18919-1AMP, FAME Mix, C4-C24, USA) and 60 individual FAME standards (Sigma-Aldrich, USA). Conjugated linoleic acid (CLA) isomers were identified by co-injection with commercial standard mixtures (Sigma-Aldrich, USA). The different types of FAs were reported as g per 100 g of total identified FAs. Then, different groups of saturated FAs (SFA), monounsaturated FAs (MUFA), polyunsaturated FAs (PUFA) and total CLA were calculated based on the individual amount of the corresponding FAs.

Indices of fat quality

The indices used in this study were: The ratio of unsaturated FAs/saturated FAs (UFAs/SFAs), the ratio of polyunsaturated FAs/saturated FAs (PUFAs/SFAs), n-6PUFA/n-3PUFA (n-6/n-3), hypocholesterolaemic/hypercholesterolaemic ($[(C18:1n-9+C18:2n-6+C18:3n-3)/(C14:0+C16:0)]$), (C18:0+C18:1):C16:0, atherogenicity index ($AI=(C12:0+4\times C14:0+C16:0)/[(MUFA)+(n-6)+(n-3)]$), thrombogenicity index ($TI=(C14:0+C16:0+C18:0)/[(0.5\times MUFA+0.5\times(n-6)+3\times(n-3)+(n-3)/(n-6)]$) and desirable FAs (C18:0+MUFA+PUFA) (Emami *et al.* 2015; Quaesma *et al.* 2016).

Table 1 Ingredients and chemical composition of diet

Ingredient	% of dry matter
Alfalfa hay	30
Barley grain	42
Wheat bran	13
Soybean meal	5.2
Cottonseed meal	3.9
Canola meal	3.9
Urea	0.35
Salt	0.35
Mineral/vitamins premix	1.3
Chemical composition (%)	
Crude protein	16.7
Ether extract	2.6
Neutral detergent fiber	28
Acid detergent fiber	17
ME (MJ/kg DM)	2.6
NEg (Mcal/kg DM)	1.1

ME: metabolisable energy and NEg: net energy growth.

Table 2 Mean and standard error of age at slaughter, live weight and hot carcass of slaughtered kids from different genotypic groups

Item	Genotypic group		
	Q	QS	QSS
Number (N)	10	10	9
Age at slaughter (days)	133.10±0.99	129.10±0.06	130.44±2.68
Live weight (kg)	16.92±1.04	18.29±0.89	20.41±1.22
Hot carcass weight (kg)	6.72±0.55	7.58±0.36	8.89±0.67

Q: Qazvinian native goat; QS: with 50% Saanen genes and QSS: with 75% of the Saanen genes.

Statistical analysis

Data were analyzed for effects of genotypic groups on fat and FA content under one-way ANOVA using the GLM procedure of SAS software (SAS, 2002). The statistical model for analysis of fat and FA content were:

$$y_{ij} = \mu + G_i + e_{ij}$$

Where:

y_{ij} : each of observation.

μ : overall mean.

G_i : effects of i^{th} genotypic groups in 3 classes (Q, QS and QSS).

e_{ij} : random error.

The effect of the fat content in the LL muscle was introduced as covariate variable for FA content, but this factor did not have significant effect on these traits ($P > 0.05$), thus, it was removed from the final model. Duncan's test was used for comparisons of means values with significant level of 5% (Duncan, 1955).

To evaluate the total differences between genotypic groups and determine the contribution of FAs to these differences, a canonical discriminant analysis (CDA) was performed based on the individual percentages of FAs and related ratios for the IMF. For discriminant analysis, a stepwise method (SAS, 2002) was used for selecting traits that have a major discriminant capacity.

The canonical analysis was performed using the Proc DISCRIM in SAS software.

RESULTS AND DISCUSSION

The mean values and standard errors for total fat contents and FAs compositions in LL muscle of goat kids according to genotypic groups given in Table 3. Differences in the total fat content (g/100 g meat) among the genotypic groups Q, QS and QSS were significant (0.94, 2.01 and 1.05, respectively, $P < 0.05$). IMF obtained from genotypic group QS displayed higher than the other groups.

The major FAs identified in the intramuscular fat (IMF) were C18:1, C16:0 and C18:0, with percentages of 35.27-41.06%, 18.3-25.58% and 11.62-15.09%, respectively, and C18:2,n-6, which consisted of 7.84-16.29% of total FAs.

Genotype had a clear impact on IMF FA composition. The percentages of margaric (Q, 1.16 and QSS, 1.21 vs. QS, 0.74) and stearic (Q, 15.09 vs. QS, 11.62) FAs were significantly higher in genotypic group Q than in the other groups, while pentadecylic (QS, 0.3 vs. Q, 0.04 and QSS, 0.09), palmitic (QS, 25.58 vs. Q, 18.98 and QSS, 18.3) and rumenic acid (QS, 1.89 vs. QSS, 0.93) in genotypic group QS, and linoleic (QSS, 16.29 vs. Q, 7.84 and QS, 10.43), alpha-linolenic (QSS, 2.43 vs. QS, 0.88) and α -eleostearic (QSS, 2.52 vs. QS, 0.07) FAs in genotypic group QSS had higher proportions (g/100 g total FAs, $P < 0.05$).

Table 3 Fatty acid composition (g/100 g total fatty acids) of longissimus lumborum from different genotypic groups

Item	Genotypic group			SEM
	Q	QS	QSS	
Fat%	0.94 ^b	2.01 ^a	1.05 ^b	0.128
Saturated fatty acids	40.87 ^{ab}	43.25 ^a	36.9 ^b	0.990
C12	0.19	0.14	0.09	0.075
C14	1.4	3.0	2.0	0.331
C15	0.04 ^b	0.3 ^a	0.09 ^b	0.039
C16	18.98 ^b	25.58 ^a	18.3 ^b	0.896
C17	1.16 ^a	0.74 ^b	1.21 ^a	0.082
C18	15.09 ^a	11.62 ^b	12.87 ^{ab}	0.571
C20	0.7	1.01	0.45	0.145
C22	1.87	0.86	1.39	0.334
C24	0.44	ND ²	0.49	0.168
Unsaturated fatty acids	58.54 ^{ab}	55.56 ^b	62.0 ^a	0.999
C14:1c	0.43	0.23	0.28	0.054
C16:1c	2.19	2.69	1.69	0.214
C17:1c	0.83	0.84	0.83	0.074
C17:2c	0.10	0.05	0.14	0.036
C18:1, n-9c	41.06	36.73	35.27	1.235
C18:1, n-11t	0.3	0.47	0.82	0.165
C18:1, n-12c	0.01	0.04	0.06	0.022
C18:2, 11t, 15c	0.02	0.09	ND	0.032
C18:2, n-6	7.84 ^b	10.43 ^b	16.29 ^a	1.064
C18:3, 9c, 12c, 15t	0.45	0.05	ND	0.119
C18:3, 9t, 12c, 15c	0.16	ND	ND	0.025
C18:3, n-3	1.79 ^{ab}	0.88 ^b	2.43 ^a	0.303
C18:3, 9c, 11t, 13c	0.53 ^{ab}	0.07 ^b	2.52 ^a	0.462
C18:2, 9c, 11t, CLA	1.76 ^{ab}	1.89 ^a	0.93 ^b	0.212
C18:2, 10t, 12c, CLA	0.34	0.43	0.09	0.084
Total CLA	2.10 ^{ab}	2.32 ^a	1.02 ^b	0.315
C20:1	0.73	0.67	0.64	0.137
MUFA	45.55	41.67	39.59	1.223
PUFA	12.99 ^b	13.89 ^b	22.41 ^a	1.330

Q: Qazvinian native goat; QS: with 50% Saanen genes and QSS: with 75% of the Saanen genes.

CLA: conjugated linoleic acid; MUFA: monounsaturated fatty acids and PUFA: polyunsaturated fatty acids.

ND: not detected.

The means within the same row with at least one common letter, do not have significant difference ($P>0.05$).

SEM: standard error of the means.

The proportion of SFA ranged within 36.9-43.25% of IMF content. The proportion of SFA in genotypic group QS with 50% of Saanen genes was 6.35 and 2.38 (g/100 g total FAs) higher than genotypic group QSS with 75% of Saanen genes ($P<0.05$) and Qazvinian native goat kids ($P>0.05$), respectively. The difference was mainly related to the proportion of palmitic acid (C16:0) in IMF content as an individual SFA. The proportion of UFA FAs (MUFA+PUFA) was higher than that of the SFA.

The MUFA was the most predominant group in IMF in all of kids (embracing 39.59-45.55 g/100 g total FAs) and the oleic acid (18:1 cis-9) was the major individual MUFA, ranging between 35.27 and 41.06 g/100 g total FAs. The MUFA level was not significantly affected by genotype effects. The genotypic group Q had a non significantly higher MUFA percentage (mainly represented by C18:1n-9 cis) than other groups ($P>0.05$).

The results of the current study show that the PUFA, mainly the linoleic acid (C18:2, n-6) level in the LL muscle

was significantly different between genotypic groups ($P<0.05$).

Meat from kids of QSS had a higher ($P<0.05$) PUFA than the Q and QS (22.41 vs. 12.99 and 13.89 g/100 g total FAs, respectively).

CLA accounted for 1.02–2.32 g/100 g total FAs, while cis-9, trans-11 CLA contribute to 81–91% of total CLA (0.093–1.89) followed by trans-10, cis-12 CLA isomer (0.09-0.43). The proportion of cis-9, trans-11 CLA in IMF was significantly affected by the genotype of goat kids. The genotypic group QSS showed lower concentration of cis-9, trans-11 CLA ($P<0.05$) than the goat kids of Q and QS (0.93 vs. 1.76 and 1.89 g/100 g total FAs, respectively).

A comparison of FAs ratio and indexes of kids IMF in relation to human health is reported in Table 4. The genotype effects differed significantly in the UFA:SFA, PUFA:SFA, n-6:n-3, h:H and (C18:0+C18:1):C16:0 ratios, atherogenicity and thrombogenicity indexes and the proportion of DFA ($P<0.05$).

Table 4 Partial sums of fatty acids (g/100 g total FA) and nutritional ratios of longissimus lumborum from different genotypic groups

Item	Genotypic group			SEM
	Q	QS	QSS	
UFA:SFA	1.47 ^{ab}	1.30 ^b	1.73 ^a	0.062
PUFA:SFA	0.33 ^b	0.32 ^b	0.64 ^a	0.044
n-6:n-3	4.42 ^b	11.67 ^a	6.56 ^{ab}	1.208
DFA	73.63 ^a	67.18 ^b	74.87 ^a	0.908
h:H	2.57 ^a	1.70 ^b	2.72 ^a	0.118
(C18:0+C18:1):C16:0	3.19 ^a	1.93 ^b	2.67 ^a	0.168
AI	0.46 ^b	0.72 ^a	0.46 ^b	0.034
TI	1.14 ^b	1.41 ^a	0.96 ^b	0.062

Q: Qazvinian native goat; QS: with 50% Saanen genes and QSS: with 75% of the Saanen genes.

PUFA:SFA: unsaturated fatty acids/saturated fatty acids; PUFA:SFA: polyunsaturated fatty acids/saturated fatty acids; n-6:n-3 = C18:2, n-6/ C18:3, n-3; DFA: desirable fatty acids = C18:0 + MUFA + PUFA; h:H: hypocholesterolaemic / hypercholesterolaemic ratio = [(C18:1n-9+C18:2n-6+C18:3n-3) / (C14:0+C16:0)]; AI: atherogenicity index = (C12:0+4×C14:0+C16:0) / [MUFA + (n-6) + (n-3)] and TI: thrombogenicity index = (C14:0+C16:0+C18:0) / [0.5 × MUFA + 0.5 × (n-6) + 3 × (n-3) + (n-3) / (n-6)].

The means within the same row with at least one common letter, do not have significant difference (P>0.05).

SEM: standard error of the means.

The values of those ratios, indexes and the proportion of DFA ranged from 1.3-1.73, 0.32-0.64, 4.42-11.67, 1.70-2.72, 1.93-3.19, 0.46-0.72, 0.96-1.41 and 67.18-74.87 g/100 g total FAs, respectively. Regarding the results presented in Table 4, for these characteristics, genotypic groups Q and QSS has meat with higher quality for human health rather than that of QS.

The results of discriminant analysis are presented in Figure 1. The function 1 and 2 explained 100% of the total variation in IMF FA composition. The function 1 accounted for 68% of the total variability and was mainly determined by C16:0, C17:0 and C18:2,11trans, 15cis (g/100 g total FAs) with emphasizing some of saturated FAs, while function 2 accounted for 32% of total variability and was mainly determined by C18: 1,12cis, C18: 3,9cis, 12cis, 15cis and C18: 3, 9trans, 12cis, 15cis FAs (g/100 g total FAs) with emphasizing some of unsaturated FA. As it can be observed in the Figure 1, the genotypic group Q was located on the left side of function 1 and on the upper part of function 2.

The Genotypic group QS was located in the right and middle and the genotypic group QSS was located in the left and bottom. In relation to IMF of the LL muscle, the genotypic groups Q, QS and QSS were clearly separated from each other in terms of their FAs profile.

Crossbreeding of the Qazvinian native goat with the Saanen breed had an effect on changes of total fat contents and FA compositions in LL muscle of kids (Table 3 and 4). The kids with 50% of Saanen genes had total fat contents twice of that in Qazvinian native kids, but this trend was not observed for kids with 75% of Saanen genes pool, similar to the result reported by Ding *et al.* (2010) for Boer × Guanzhong crossbred kids.

The range of IMF values found in this study were similar to results reported by Horcada *et al.* (2012) for seven Spanish breeds, and Quaresma *et al.* (2016) for Serrana, Bravia and Serrana × Bravia crossbred genotypes.

The results of the present study for IMF was higher than those of reported by Bonvillani *et al.* (2010) for Criollo Cordobes goat kids in Argentina, and lower than that of obtained in Italian Saanen kids (De Palo *et al.* 2015) and Balkan × Saanen crossbred kids from Serbia (Stanišić *et al.* 2012). Inconsistence results, are possibly due to breed effects, age at slaughter and consumed diets, as major factors affecting IMF content (Banskalieva *et al.* 2000; Bonvillani *et al.* 2010; Pena *et al.* 2007; Todaro *et al.* 2006).

Results demonstrated that main FAs of IMF from the Qazvinian native kids and Qazvinian native × Saanen crossbred kids were oleic followed by palmitic and stearic acids, which comprised more than 70% of the total FAs, which agreement to other literature values reported in Kacang crossbred male kids (Aghwan *et al.* 2014; Ebrahimi *et al.* 2012), Boer × Saanen crossbred kids (Maia *et al.* 2012) and Pateri kids (Talpur *et al.* 2008).

The proportion of C16:0 recorded in this study was lower than that of reported by the others (Cimmino *et al.* 2018; Talpur *et al.* 2008; Zurita-Herrera *et al.* 2013). Relative to the Qazvinian native kids, crossbreeding by Saanen goat resulted to a decrease in the proportion of C18:0, a final product of complete biohydrogenation of C18:2n-6 and C18:3n-3, and C18:1, n-9c. The major FA in goat meat is oleic acid (Banskalieva *et al.* 2000). Buccioni *et al.* (2012) reported that increasing UFA in the diet may increase the range of C18:2 and C18:3 biohydrogenation in rumen and this would consequently influence the proportion of C18:0 of IMF. While in the present study diet was similar for genetic groups, therefor it is appearing that crossbreeding resulted to these observations. Santos *et al.* (2007) reported that genotype was associated with differences in proportion of C18:0 of IMF for Serrana, Bravia and Serrana × Bravia crossbred goat kids. The C18:1 produced from C18:0 by a stearoyl-CoA desaturase namely Δ^9 desaturase enzyme, and have more abundance in neutral lipid (Jerónimo *et al.* 2011).

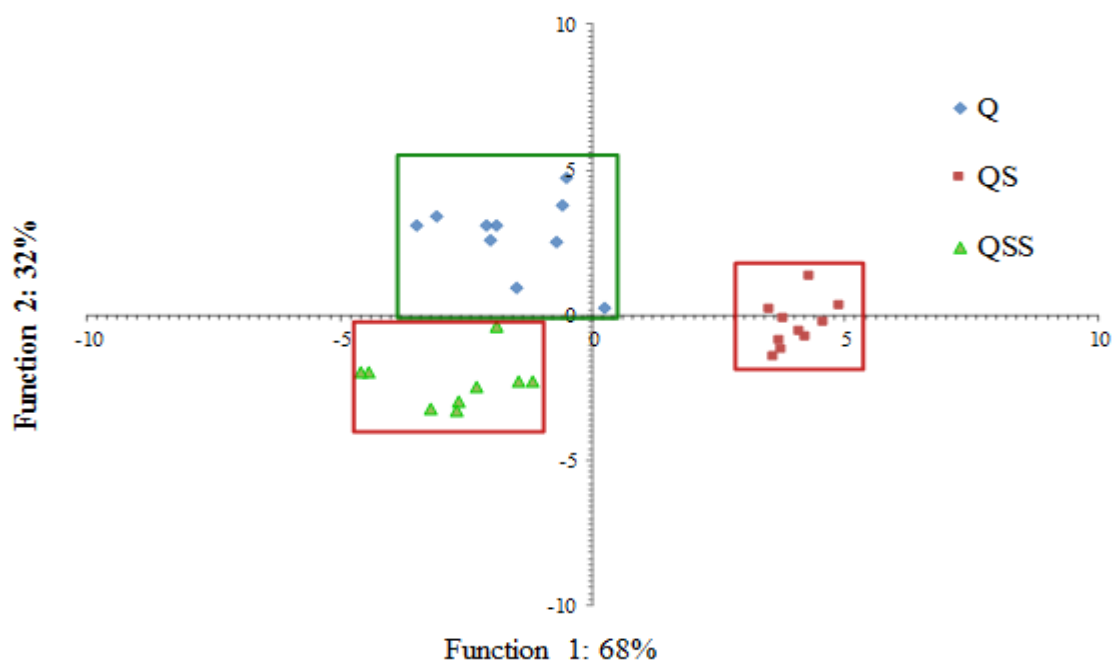


Figure 1 Discriminant functions of different genotypic groups (Q: Qazvinian native goat; QS: 50% of Saanen breed genes and QSS: 75% of the Saanen breed genes)

The findings of [Quaresma et al. \(2016\)](#) in Serrana, Bravia and Serrana \times Bravia crossbred genotypes and Saanen goat kids, concur with the present results for C18:1, n-9c content in LL muscle.

As IMF is usually not trimmable and hence not removed before consumption, it is highly necessary to determine FA composition in the muscles for consumer's health. Due to its lower lipid content and higher content of UFA (MUFA+PUFA), goat meat has been classified better than beef and mutton ([Banskalieva et al. 2000](#)). The results from the present study indicated a high proportion of UFA in goat muscle lipids and crossbreeding had a valuable effect on UFA proportion in IMF.

Major FA groups (SFA, MUFA and PUFA) from the Qazvinian native goat and Qazvinian native \times Saanen crossbred goat kids were close to the results reported in Saanen kid (38–44% of SFA, 45–49% of MUFA and 6–10% of PUFA; [De Palo et al. 2015](#)), and Criollo Cordobes and Anglo nubian goat (37–42% of SFA, 36–39% of MUFA and 21–23% PUFA; [Pena et al. 2009](#)), but differ from reported value for Brazilian native goats (52–54% of SFA, 36–38% of MUFA and 2–5% of PUFA; [Lopes et al. 2014](#)), and Sarda goats (52–54% of SFA, 32–35% of MUFA and 12–13% of PUFA; [Vacca et al. 2014](#)). This may be due to the different IMF concentration in the LL muscle of the animals (0.99–2.52 g/100 meat).

The kids with 75% of Saanen genes had the highest proportion of UFA and PUFA in IMF. This improvement was due to effects of Saanen gene pool. This could have related to the level of microbial biohydrogenation of the dietary unsaturated fat in the rumen and genotype differences in mammary Δ^9 desaturase enzyme ([Jerónimo et al. 2011](#)).

The relatively high percentage of PUFA may be due to increase of membranes in myocytes and adipocytes and concentrations of the n-6 and n-3 FA in cell membranes ([Ebrahimi et al. 2018](#)) of crossbred goats. These include C18:2n-6 (majority) and C18:3n-3. These essential FA can be anticarcinogenic and cannot be synthesized in the body and have to be obtained via diet ([Banskalieva et al. 2000](#)).

The PUFA:SFA and n-6:n-3 ratios determine how FAs affect human health. The PUFA:SFA balance to prevent of coronary heart disease is >0.45 , while for n-6:n-3, a value < 4 is recommended ([Enser et al. 1996](#); [Simopoulos, 2008](#); [Webb et al. 2005](#)). In all genotypes, the PUFA:SFA ratio ranged from 0.33 to 0.64. These results are better for human health than those of reported by [De Palo et al. \(2015\)](#) in Saanen kids, also, [Emami et al. \(2015\)](#) in Mahabadi kids, [Mandal et al. \(2014\)](#) in Black Bengal kids and close to those recorded by [Cimmino et al. \(2018\)](#) in Saanen kids, and [Yalcintan et al. \(2018\)](#) in Saanen, Gokceada and Maltese kids. Results obtain from this study showed that IMF in kids with 75% of Saanen genes had higher PUFA:SFA

ratio (0.64) than the other genotypes.

Yalcintan *et al.* (2018) reported that the differences between the PUFA:SFA ratios for genotypes Saanen, Gokceada and Maltese are significant which confirm results of this study.

The results of n-6:n-3 ratio for all genotypes were within the range of 4.42-11.67. These results are lower than the values (14-18) reported by Aghwan *et al.* (2014) and higher than the results reported by Turner *et al.* (2014).

The Qazvinian goat kids had lower n-6:n-3 ratio than that of goat kids with 50% of Saanen genes. It appears that crossbreeding panel in the present study resulted to change in n-6 and n-3 FA metabolism as observed the highest C18:2,n-6 concentration in IMF of kids LL increased with rising of Saanen genes (7.84, 10.43 and 16.29 g/100 g total FAs for Q, QS and QSS, respectively).

To assess the nutritional implications of IMF on human nutrition, the DFA were calculated (MUFA+PUFA+C18:0) according to Huerta-Leidenz *et al.* (1991). The average percentage of DFA of IMF in kids and lambs was greater than 68%. Values ranging from 67.18 to 74.87% of total FAs were obtained (Horcada *et al.* 2014). These values for kids with 75% of Saanen genes and Qazvinian native kids were higher than that of kids with 50% of Saanen genes (74.87 and 75.63 vs. 67.18, $P < 0.05$). Horcada *et al.* (2012) recorded DFA within the ranges of 66.16-72.27 in seven Spanish breeds and Madruga *et al.* (2009) reported in the ranges of 74.87–76.0% for Boer, Boer \times SPRD crossbred and Anglo Nubian \times SPRD crossbred goat. Horcada *et al.* (2012) reported the effect of genotype and indigenous production system on the DFA content that confirm our findings.

The three major FAs of muscle fat have different implications for consumer health, only C16:0 increases blood cholesterol, whereas C18:0 has no effect and C18:1 decreases blood cholesterol content. Therefore, the ratio (18:0+18:1) / C16:0 was suggested to describe the potential health effects of different types of lipids (Banskalieva *et al.* 2000).

In the present study, the values of this ratio (1.93-3.19), were similar to the values reported by Longobardi *et al.* (2012), ranged between 1.45 and 3.3, for Garganica goat kids slaughtered at 9.7 kg live weight, and close to the values reported by Pena *et al.* (2011), ranged between 2.14 and 2.32, for Criollo Cordobes Anglo Nubian goat kids slaughtered at 10.7 kg live weight, and Cimmino *et al.* (2018), ranged between 1.86 and 2.49, for Saanen goat kids slaughtered at 18.25 kg live weigh. In this study, because lower proportion of C18:0 and higher proportion of C16:0, kids with 50% of Saanen genes had the least value for the index.

One of the main objectives of research in ruminant animals is to produce healthy food. For example, one proposi-

tion is to reduce the SFA content (which are known to raise total and low density lipoprotein (LDL) cholesterol) and increase the UFA content of fatty deposits (Oliveira *et al.* 2015) because meat enriched with UFA reduces the risk of cardiovascular and metabolic diseases (Parodi, 2016; Silva *et al.* 2016). Atherogenic (AI), thrombogenic (TI) and h:H index take into account the different effects that single FA might have on human health and in particular on the probability of increasing the risk of cardiovascular disease (CVD). It is assumed that lower AI and TI, and higher h:H are beneficial for human health (Fehily *et al.* 1994; Livingstone *et al.* 2012; Ribeiro *et al.* 2018). In this work, the AI, TI and h:H were in the ranges of 1.7-3.19, 0.46-0.72 and 0.96-1.41, respectively. These results were within the ranges of the results obtained by other authors (1.19-2.09, 0.51-0.94 and 0.53-1.46, respectively) for goat kids at 1.5–2 months of age (De-la-Vega *et al.* 2013; De Palo *et al.* 2015; Horcada *et al.* 2014; Ripoll *et al.* 2012; Zurita-Herrera *et al.* 2013), and (3-3.47, 0.25-1.28 and 0.39-2.13, respectively) for goat kids at 5–6 months of age (Cimmino *et al.* 2018; Ribeiro *et al.* 2018; Yalcintan *et al.* 2018). According to the authors, these differences are mainly associated with genetic factors and management systems. The present study for these index s, Qazvinian native goat kids and goat kids with 75% of Saanen genes had better AI and TI indices than the goat kids with 50% of Saanen genes.

Conjugated linoleic acid (CLA) has a wide range of biologically beneficial activities such as decrease severity of atherosclerosis, reduction of adverse effects of immune stimulation, growth promotion, reduction of body fat, increase in lean body mass in several animal species and anti-carcinogenic (Benjamin *et al.* 2015; Park and Pariza, 2007).

It needs to be pointed out that naturally occurring CLA primarily consists of the cis-9, trans-11 isomer present in some animal sources food, such as meat, milk, and dairy products. This isomer originates from incomplete ruminal biohydrogenation of linoleic acid to stearic acid. The other main isomer of CLA, trans-10, cis-12, is present in food in lower amounts. In current study, CLA accounted for 1.02–2.32% of total FAs, while cis-9, trans-11 CLA contribute to 81–90% of total CLA (0.93–1.89%) followed by trans-10, cis-12 CLA isomer. The values are higher than the results reported by Ebrahimi *et al.* (2012) in Kacang goat kids, Mandal *et al.* (2014) in Black Bengal goats and Todaro *et al.* (2006) in Girgentana goats (0.25-1.2%) for IMF. The kids with 50% of Saanen genes had higher CLA than that of the kids with 75% of Saanen genes. These results show the influence of genotype on Δ^9 desaturase activity and CLA, since CLA cis-9, trans-11 isomers are naturally formed as intermediates during the incomplete biohydrogenation of linoleic to stearic acid in the rumen and mammary gland by the action of Δ^9 desaturase activity.

FA profiles in meat good markers of production system. Several authors have been successful in using the FA composition of beef and veal as discriminating tools to separate them into weaning classes, production systems, breeds, certification labels (Horcada *et al.* 2012; Moreno *et al.* 2006). Canonical discriminant analysis was applied to FA composition of IMF and it could clearly separate three genotypic groups (Figure 1). In the present study, the result would show the differences in the FA composition. This analysis separated the Qazvinian native kids and kids with 50% of Saanen genes based on UFA and SFA of their FAs profile, respectively. This methodology has been previously applied by Horcada *et al.* (2012) for the discrimination of FA profiles in suckling goat kids from seven Spanish breeds and Quaresma *et al.* (2016) in Serrana, Bravia and Serrana × Bravia crossbred genotypes.

CONCLUSION

The results indicated a high proportion of UFA in IMF for Qazvinian native kids and kids with 50% and 75% of Saanen genes. Based on the data presented in this study it can be concluded that meat from Qazvinian native kids and kids with 75% of Saanen genes had better quality than that from kids with 50% of Saanen genes. The crossing had a positive effect on PUFA content in kids with 75% of Saanen genes. Although further studies are required, take into account human health indexes, our results suggest that crossbreeding may be increase quality of meat from kids with 75% of Saanen genes relative Qazvinian native kids and kids with 50% of Saanen genes.

ACKNOWLEDGEMENT

We would like to thank the respected Management of Fakhr-Iranian farm for their assistance in conducting the present study.

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