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Muscle cellular characteristics of male kids from Turkish indigenous goat breeds

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ABSTRACT

Indices of the transcriptional and translational capacity of muscle cells are directly related to growth in various livestock species. The main aim of this study was, therefore, to determine cellular characteristics and their relationship with metric measurements and muscle fibers number in longissimus-dorsi (LD) and semitendinosus (ST) skeletal muscles from male kids born to Angora, Hair, Honamli and Kilis breeds. Kilis kids had significant lower (except for Hair kids) muscle cross-sectional area (MSCA) in LD and ST muscles ($p<0.05$). Also depth and length (except for Angora kids) of ST muscle were significantly lower ($p<0.05$) in Kilis kids. Honamli kids had a significant higher ($p<0.05$) concentrations of DNA and RNA in both muscles, while Kilis kids had a significant lower ($p<0.05$) total protein in ST muscle. Protein:DNA and protein:RNA ratios of Angora kids in both muscles were significantly higher compared to other breeds ($p<0.05$). There were positive correlations between muscle depth (MD) and protein, MSCA and DNA, MSCA and RNA, MSCA and protein ($p<0.05$) in LD muscle. Similarly, positive correlations between MD and protein, muscle length (ML) and RNA, ML and protein, MSCA and protein ($p<0.05$) were observed in ST muscle. In conclusion, Turkish indigenous goat breeds have different transcriptional and translational capacity and these differences may be used to select more efficient breeds for fattening practices.

1. Introduction

Goat population in Turkey is about 11 million, makndes almost the half size of the EU's total goat population (%46) and ranking 22nd in the world (TurkStat, 2018; FAO, 2018). The most commonly raised goats in Turkey belong to indigenous pure breeds like Angora, Hair, Honamli and Kilis which constitute approximately 92 % of the total goat population in the Turkey (Daskiran and Koluman, 2014; Akbas and Saatci, 2016). Kid meat is one of the important sources of red meat in Turkey, however kid rearing is mainly based on pasture without any additional feeding and fattening is generally not practiced (Daskiran and Koluman, 2014; Akbas and Saatci, 2016; Sen et al., 2019). As a result limited information is available about the fattening potential of Turkish indigenous goat breeds.

Growth of animals is related to cellular characteristics such as indices of transcriptional and translational capacity of skeletal muscles (Greenwood et al., 2006). The concentrations of DNA, RNA and protein, and their ratio to each other reflect the transcriptional and translational capacity of cells from various tissues (Marguerat and Bähler, 2012). Although the genome content remains generally constant, larger cells produce and maintain higher concentrations of RNA and protein to maintain biomass and functions (Marguerat and Bähler, 2012). Additionally, the RNA:DNA and the protein:DNA ratios differ as a function of muscle cell size (Carpenter et al., 1996). Therefore, cellular characteristics of muscle tissue such as transcriptional and translational capacity have been used as an indicator of muscle fiber size, which is important for growth and development (Greenwood et al., 2006).

The muscle fiber characteristics are influenced by various factors including breed (Ryu et al., 2008; Sirin, 2018), maternal nutrition during gestation (Sen et al., 2016), gender (Ozawa et al., 2000), growth performance (Kim et al., 2013) and muscle location (Hwang et al., 2010). Skeletal muscle cells are multinucleated and therefore, their DNA concentration does not remain constant in relation to muscle fiber numbers (Eversole et al., 1981). Moreover, nuclear numbers of muscle fibers decrease postnatally with age. However, the ratio of protein:DNA (the so-called DNA unit) is an index of regulation of growth and volume of muscle (Cheek, 1985) and the variations in protein:DNA ratio reflect a change in muscle fiber size (Lorenzen et al., 2000; Greenwood et al.,

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2000). Therefore, quantitative analysis of DNA, RNA and proteins and their ratio to each other in the skeletal muscle tissue provide a means of estimating growth and development of animals (Greenwood et al., 2000). Additionally, Sirin (2018) reported that breed is an important factor affecting skeletal muscle fiber characteristics in goat and differences in muscle fiber characteristics may influence meat production and quality in kids.

The influence of maternal nutrition during gestation (Sen et al., 2016), birth weight and postnatal nutrition (Greenwood et al., 2000), and genetics (Carpenter et al., 1996; Greenwood et al., 2006) on cellular characteristics of muscles have been studied in various animal species and genotypes. Moreover, muscle fiber characteristics and their effects on meat quality of Turkish indigenous goat breeds (in Angora, Hair, Honamli and Kilis) have already been reported (Sirin, 2018). However, to our knowledge, there are no reports on the cellular characteristics of muscle cells which affect traits such as muscling, growth, and fatness in indigenous goat breeds of Turkey. Moreover, the relationship between muscle cellular characteristics, metric measurement and total fibers number of skeletal muscle mass remain to be determined in these breeds. The main objective of the present study was, therefore, to determine cellular characteristics like concentrations of DNA, RNA and protein and their relationship with metric measurement and total fibers number in longissimus-dorsi (LD) and semitendinosus (ST) skeletal muscles of male kids born to Angora, Hair, Honamli and Kilis breeds.

2. Material and Methods

A total of 24 male kids of Angora (n = 6), Hair (n = 6), Honamli (n = 6) and Kilis (n = 6) breeds were used as experimental animals. Kids were obtained from the National Sheep and Goat Breeding Project carried out in Ankara (Angora), Tokat (Hair), Antalya (Homanlı) and Kilis (Kilis) provinces of Turkey. The experimental animals belonged to different regions of Turkey, and were raised under similar feeding and management and practices until weaning. The management system is semi-extensive and all kids were born at the same breeding season. After birth all the kids were kept with their dams until weaning (90 days). Starting from day 15 of kidding, all does were allowed to graze during day time and to suckle their kids over the nights in the house until weaning. The grazing areas are a natural grassland dominant with *Anndropogon ischoemum, Festuca arundinacea, Medicago sativa, Trifolium pratense, Bromus cappadocicus, Cynodon dactylon, Astragalus sp., Capsella bursa, Hordeum murinum, Amaranthus sp*, and *Circium sp*. species. Moreover, kids were also fed to their appetite meadow grass hay starting from 15 days of age until weaning.

At the age of 90 days all the kids were transported to a slaughterhouse in their region. None of the kids were fed overnight (approximately 16 h) before slaughtering for determination of fasting live weight the next morning. Slaughter weight (SW) was measured before standard commercial slaughter procedure was carried out. Following slaughter, a cross-section from the mid-belly of the LD and ST muscles from the right side of the carcasses were taken on a drawing paper. Muscle cross-sectional area (MCSA) of all muscles was determined by a direct grid reading (Sen et al., 2011), and muscle depth (MD) and length (ML) were determined by a digital caliper. Immediately after slaughter, approximately 50−75 g muscle samples from the central part of the mid-section of the whole LD and ST muscles were excised from the right side of the carcasses. Muscle samples were quickly trimmed off subcutaneous fat and fascia. After that muscle samples were wrapped in aluminum foil, frozen in liquid nitrogen and stored at −80 °C until DNA, RNA and total protein analysis.

DNA and RNA of muscle samples were isolated by a commercial DNA (PureLink™, DNA Mini Kit Invitrogen™, K182001) and RNA (PureLink™, RNA Mini Kit, Invitrogen™, 12183018A) purification kit as suggested by the manufacturer. The purity and quantity of isolated DNA and RNA were measured by using NanoDrop™ 2000/2000c spectrophotometers (Thermo Fisher Scientific), and 1 % w/v agarose gel was used to check the DNA (Fig. 1) and RNA (Fig. 2) quality. Total protein of muscle samples was isolated by radioimmunoprecipitation assay (RIPA) with some modifications (Valkova et al., 2005). Total protein in the extracts was determined in triplicate in suitable dilutions of both fractions by the method of Bradford (1976) using bovine serum albumin as a standard. The quality of proteins was checked in 12 % w/v SDS-PAGE gel electrophoresis (Fig. 3).

Total muscle fibers composition in LD and ST muscles was determined using ATPase staining at pH 4.2 as defined by Broke and Keiser (1970) and Sen et al. (2016). The total muscle fibers number (TMFN) per mm^2 were counted according to Sirin (2018), using a microscope at × 200 magnification with a digital camera linked to image analysis software (Laica Q Win V3.4 Processing-Analysis Software). Average muscle fibers diameter (MFD) per mm^2 was determined according to Sirin (2018).

Using completely randomized design for different traits statistical analyses were performed using SPSS 17.0 (2008) package program (SPSS Inc., 2008, 17.0.1, Wacker Drive, Chicago, Illinois 60606, USA). The optimum sample size was determined by a simple randomized sampling method, and results showed that six repeats in each group were enough for the trait, which had the maximum variance. The observed power of the test was obtained as 92.07 %, which shows that the used sample size was adequate to get reliable results. Significant differences between means were tested by Duncan's multiple comparison tests. To estimate the optimum models curve estimation procedure was used and the results of the best models were interpreted. Multiple Cubic and Logarithmic regression analysis were used to determine the effect of muscles metric and cellular characteristics on the numbers of muscle fibers per mm^2. Relationships between variable traits for data were determined with the Pearson correlation analysis at the 95 % confidence interval. Results were computed as mean ± SE and statistical significance was determined at the level of $p < 0.05$.

3. Results

Metric measurements in LD and ST muscles are presented in Table 1. There were no significant differences among breeds in terms of the MD and ML measurements of LD muscle, but Kilis kids had significant ($p < 0.05$) lower MCSA compared to Hair and Honamli kids. Similarly, the MD, ML and MCSA of ST muscle in Kilis kids were significantly lower than those of Hair and Honamli indigenous Turkish breeds ($p < 0.05$).

The concentrations of DNA, RNA and protein, and ratios to each other in LD and ST muscles are presented in Tables 2 and 3, respectively. Honamli kids had significantly higher ($p < 0.05$) DNA concentration in LD and ST muscles than Angora, Hair and Kilis kids (Table 2). Similarly, the RNA concentration in both muscles of Honamli kids were significantly higher than those of other breeds ($p < 0.05$). There were no significant differences among breeds in terms of total protein in LD muscle, but Kilis kids had significantly lower total protein in ST muscle than those of other breeds ($p < 0.05$). There were no significant differences among breeds in terms of RNA:DNA ratio, but protein:DNA and protein:RNA ratios of Agora kids in LD and ST muscles were significantly higher ($p < 0.05$) than those of Hair, Honamli and Kilis indigenous Turkish breeds (Table 3).

The analysis of Pearson correlation coefficients on the pooled data for all the breeds showed that there were positive correlations ($p < 0.05$) between MD and protein, MSCA and DNA, MSCA and RNA, MSCA and protein in LD muscle (Table 4). Similarly, positive correlations ($p < 0.05$) between MD and protein, ML and RNA, ML and protein, MSCA and protein were observed in ST muscle. A negative correlation ($p < 0.05$) was calculated between ML and RNA:DNA in LD muscle (Table 4).

Regression coefficients of SW, muscle fiber characteristics and muscle metric measurements on the concentrations of DNA, RNA and protein, and their ratios to each other in LD and ST muscles are presented in Tables 5 and 6, respectively. The TMFN was positively ($p < 0.05$) associated with the concentrations of DNA and RNA in both

Fig. 1. DNA image in 1 % w/v agarose gel.

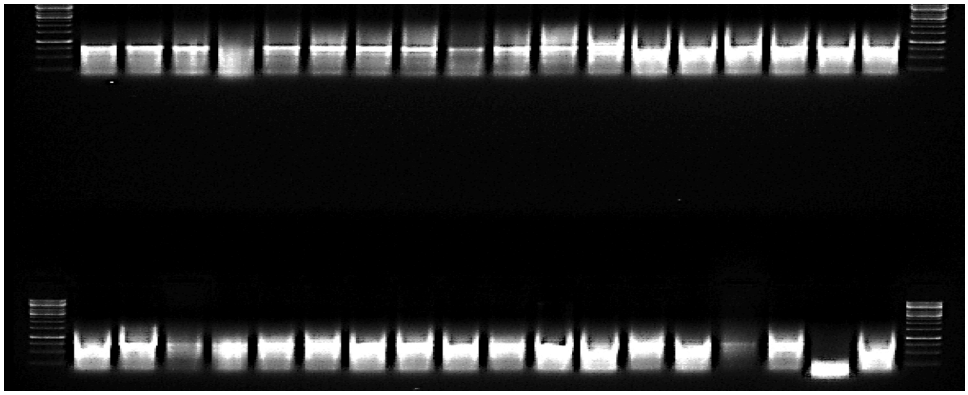

Fig. 2. RNA image in 1 % w/v agarose gel.

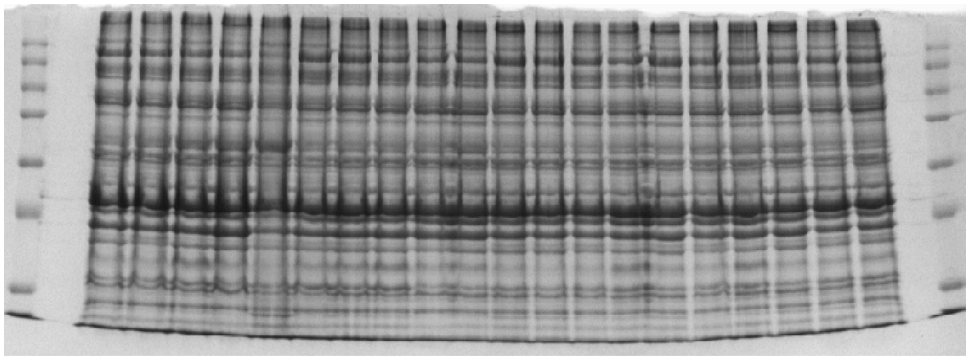

Fig. 3. Proteins image in 12 % w/v SDS-PAGE gel.

muscles, but it was inversely ($p < 0.05$) associated with total protein in LD muscle. There was a positive association of MSCA with total protein in both muscles, and also a positive relationship was observed between MFD and RNA concentration in LD muscle ($p < 0.05$). Additionally, MD and ML were related positively ($p < 0.05$) to total protein in ST muscle. Weaning SW was positively ($p < 0.05$) related to protein: RNA ratio, but a negative ($p < 0.05$) relation was observed between MFD and protein: RNA ratio in both muscles. Similarly, SW was positively ($p < 0.05$) related to protein: DNA ratio, but a negative ($p < 0.05$) relation was observed between MFD and protein:DNA ratio in LD muscle. TMFN and ML were inversely ($p < 0.05$) associated with RNA:DNA ratio in LD muscle, but a positive ($p < 0.05$) relation was observed between MD and RNA:DNA ratio.

SW of Angora, Hair, Honamli and Kilis male kids at 90 days of weaning age are presented in Fig. 4. Hair (18.24 ± 1.68 kg) and Honamli (20.40 ± 1.03 kg) kids had significantly higher ($p < 0.05$) SW than those of Angora (13.03 ± 0.26 kg) and Kilis (14.20 ± 0.21 kg) kids.

Regression graphs of DNA concentration on the total muscle fiber number in LD and ST muscles and the MCSA measurement on TMFN in LD muscle are presented in Figs. 5 and 6, respectively. Regression of the DNA concentration on TMFN was performed by cubic and logarithmic (base 10) regressions for LD and ST muscles, respectively. In the regression analysis, significant relationships were observed between the DNA concentration and numbers of total muscle fibers in both the muscles. In these models statistically significant coefficients of (R^2) were found as .598 ($p < 0.01$) and .278 ($p < 0.05$) for LD and ST muscles, respectively. The resulting regression models were $TMFN = 679.077 + 19334.544*DNA - 37042.048*\ DNA^2 + 50150.911*\ DNA^3$ for LD muscle and $TMFN = 2626.064 + 340.349*(DNA)$ for ST muscle (Fig. 4). Regression of MCSA on TMFN was performed by cubic regression. In the

Table 1
Metric measurements in longissimus-dorsi (LD) and semitendinosus (ST) muscles.

Variable	Muscles	Breeds			
		Angora	Hair	Honamli	Kilis
MD (mm)	LD	19.70 ± 0.66	21.20 ± 1.63	22.50 ± 1.19	19.20 ± 1.02
	ST	36.90 ± 1.72[a]	30.30 ± 2.21[a]	33.700 ± 0.70[a]	25.64 ± 1.52[b]
ML (mm)	LD	38.90 ± 1.08	38.70 ± 2.23	40.10 ± 0.93	34.60 ± 2.74
	ST	65.00 ± 6.17[ab]	73.50 ± 3.90[a]	82.40 ± 3.28[a]	52.20 ± 4.07[b]
MCSA (mm^2)	LD	65.20 ± 4.05[ab]	74.39 ± 2.05[a]	83.44 ± 5.19[a]	57.43 ± 5.14[b]
	ST	217.6 ± 11.90[a]	167.6 ± 29.60[ab]	237.7 ± 14.50[a]	95.89 ± 8.72[b]

[a,b]Mean values with different superscripts in the same row indicate a significant difference ($p \leq 0.05$).
MCSA = muscle cross-sectional area, MD = muscle depth, ML = muscle length.

Table 2
The concentrations of DNA, RNA and protein in longissimus-dorsi (LD) and semitendinosus (ST) muscles.

Variable	Muscles	Breeds			
		Angora	Hair	Honamli	Kilis
DNA (μg/g)	LD	440.9 ± 76.1[c]	943.6 ± 229.3[b]	2259.6 ± 949.5[a]	1251.8 ± 262.7[b]
	ST	413.4 ± 90.2[c]	1080.1 ± 349.5[b]	1799.8 ± 299.6[a]	587.3 ± 129.7[c]
RNA (μg/g)	LD	1560.4 ± 110.4[b]	2568.8 ± 230.3[b]	2910.3 ± 389.6[a]	2020.4 ± 140.1[b]
	ST	1600.3 ± 209.8[c]	2729.6 ± 160.4[b]	3060.1 ± 220.2[a]	1980.2 ± 249.5[bc]
Protein (mg/g)	LD	164.6 ± 9.3	157.3 ± 4.1	169.4 ± 4.1	149.1 ± 5.0
	ST	166.6 ± 9.3[a]	161.9 ± 5.0[a]	173.3 ± 3.9[a]	143.9 ± 3.5[b]

[a,b,c]Mean values with different superscripts in the same row indicate a significant difference ($p \leq 0.05$).

regression analysis, a significant relation was observed, and this model was found as statistically significant with coefficient determination of determination (R^2) as .350 ($p < 0.05$). The obtained regression model for LD muscle was TMFN = -2880.414 + 87.393* MCSA– 0.003* $MCSA^3$ (Fig. 5).

4. Discussion

The results of this study show that the characteristics of muscle cells differ between kids from indigenous Turkish breeds. Such differences in the characteristics of muscle cells could be explained on the basis of different growth patterns of kids until weaning age. As all the kids were raised under similar feeding and management regimens, these differences in the characteristics of muscle cells may reflect breed differences.

The concentrations of protein, DNA and RNA and their relationships between themselves are considered as good indicators of cellular activity in any tissue (Marguerat and Bähler, 2012; Moretti et al., 2014). Our findings about the concentrations of DNA and RNA in LD and ST in pure breed kids' muscles show similarities to the findings of Moretti et al. (2014), who reported that the concentrations of total protein, DNA and RNA and the ratios of these variables showed differences in the muscle of goat kids. On the other hand, there is a limited number of studies regarding differences of indices of muscle cellularity in different skeletal muscles conducted on different species such as sheep (Greenwood et al., 2006), cattle (Eversole et al., 1981) and pigs (Lösel et al., 2009).

Table 3
Ratios of DNA, RNA and total protein in longissimus-dorsi (LD) and semitendinosus (ST) muscles.

Variable	Muscles	Breeds			
		Angora	Hair	Honamli	Kilis
RNA:DNA	LD	3.8 ± 0.4	3.4 ± 0.7	2.8 ± 0.6	3.8 ± 0.9
	ST	4.5 ± 0.9	3.5 ± 0.9	2.1 ± 0.6	4.3 ± 1.2
Protein: DNA	LD	420.9 ± 52.1[a]	205.8 ± 45.4[b]	166.2 ± 46.1[b]	268.7 ± 91.1[b]
	ST	500.1 ± 119.0[a]	217.4 ± 64.3[b]	121.9 ± 38.9[b]	299.8 ± 63.7[b]
Protein: RNA	LD	111.0 ± 8.1[a]	62.90 ± 4.9[b]	60.1 ± 7.3[b]	74.4 ± 4.4[b]
	ST	108.1 ± 8.9[a]	59.6 ± 3.5[b]	58.8 ± 4.42[b]	77.3 ± 9.4[b]

[a,b]Mean values with different superscripts in the same row indicate a significant difference ($p \leq 0.05$).

Growth may be defined as either increase in the size of cells (hypertrophy) or increase in the number of cells (hyperplasia) and is a part of an ongoing process throughout the life of the organism (Falkner and Tanner, 1986). There is a strong relationship between weight of muscle and DNA concentration (Tulloh et al., 1986) and that reflects the growth capacity of the muscle. Koohmaraie et al. (1995) reported that callipyge-induced muscle hypertrophy is related to a greater the concentration of DNA in LD and ST muscles. In the present study, using pooled data of kids, positive correlations were noted between MD and total protein (in LD and ST muscles), MSCA and DNA (in LD muscle), MSCA and RNA (in LD muscle), MSCA and total protein (in LD and ST muscles). These results indicated that as the muscle depth and cross-sectional area increases, the cellular translation capacity also increases in kids from Turkish indigenous goat breeds. These observations are consistent with the findings of previous studies (Ezekwe and Martin, 1975; Harbison et al., 1976), which have found an increased translational capacity in muscle of breeds of animals selected for increased muscling. Additionally, the study of Greenwood et al. (2006) demonstrates that increasing skeletal muscle mass in lambs based on muscle metric measurement (such as muscle depth) has effect on muscle cell characteristics.

Previous studies have indicated that increase in the concentration of muscle DNA along with rise in the concentration of RNA and increased myonuclei number results in greater cellular transcriptional and translational efficiency and/or capacity (Koohmaraie et al., 1995; Greenwood et al., 2006). Additionally Koohmaraie et al. (1995) reported that Callipyge lambs with hypertrophied muscles had higher concentration of RNA, resulting in an increased RNA:DNA ratio and a decreased protein:RNA ratio compared to non-Callipyge lambs at similar carcass weights. It has been suggested that the number of myonuclei in a muscle

Table 4
Pearson correlation coefficients between cellular characteristics and muscle metric measurements for the pooled data.

Variable	DNA	RNA	Protein	RNA: DNA	Protein: DNA	Protein: RNA
LD						
MD	−.020	.324	.414*	.206	.025	−.227
ML	.255	.062	.225	−.406*	−.249	.073
MSCA	.454*	.485*	.507*	−.162	−.267	−.305
ST						
MD	.025	.108	.656*	.060	.169	.133
ML	.387	.518*	.541*	−.197	−.154	−.310
MSCA	.298	.271	.513*	−.081	.046	−.011

LD = longissimus-dorsi muscle, ST = semitendinosus muscle, MD = muscle depth, ML = muscle length MCSA = muscle cross-sectional area.
* $p \leq 0.05$.

Table 5
Regression coefficients ± s.e. of SW, muscle fiber characteristics (TMFN and MFD) and muscle metric measurements (MD, ML and MCSA) on concentration of DNA, RNA, and protein in LD and ST muscles.

Dependent variables	Independent variables	LD	ST
DNA (μg/g)	Intercept	0.033 ± 0.086	−0.023 ± 0.138
	SW	−2.45E-6 ± 0.000	8.96E-7 ± 0.000
	TMFN	4.46E-5 ± 0.000*	6.89E-5 ± 0.000*
	MFD	0.001 ± 0.001	0.003 ± 0.002
	MD	−0.006 ± 0.004	−0.006 ± 0.004
	ML	0.002 ± 0.002	4.95E-5 ± 0.002
	MCSA	0.001 ± 0.001	0.4E-3 ± 0.000
RNA (μg/g)	Intercept	−0.016 ± 0.138	−0.057 ± 0.124
	SW	1.16E-6 ± 0.000	4.43E-6 ± 0.000
	TMFN	5.08E-5 ± 0.000*	7.47E-5 ± 0.000*
	MFD	0.003 ± 0.001*	0.002 ± 0.001
	MD	0.006 ± 0.006	0.4E-3 ± 0.004
	ML	−0.004 ± 0.004	0.5E-3 ± 0.001
	MCSA	0.001 ± 0.002	−4.09E-5 ± 0.000
Protein (mg/g)	Intercept	11.927 ± 2.776*	4.844 ± 2.354*
	SW	0.1E-4 ± 0.000	0.1E-3 ± 0.000
	TMFN	−0.001 ± 0.000*	0.001 ± 0.001
	MFD	0.022 ± 0.026	0.04 ± 0.028
	MD	0.018 ± 0.118	0.248 ± 0.076*
	ML	−0.049 ± 0.07	0.075 ± 0.028*
	MCSA	0.116 ± 0.033*	−0.013 ± 0.007*

LD = longissimus-dorsi, ST = semitendinosus, SW = slaughter weight, TMFN = total muscle fibers number, MFD = muscle fiber diameter, MD = muscle depth, ML = muscle length, MCSA = muscle cross-sectional area.
* $p \leq 0.05$.

Table 6
Regression coefficients ± s.e. of SW, muscle fiber characteristics (TMFN and MFD) and muscle metric measurements (MD, ML and MCSA) on ratios of DNA, RNA, and protein in LD and ST muscles.

Dependent variables	Independent variables	LD	ST
RNA:DNA	Intercept	9.071 ± 3.749*	6.196 ± 4.667
	SW	−4.66E-5 ± 0.000	−4.07E-5 ± 0.000
	TMFN	−0.001 ± 0.001*	−0.002 ± 0.001
	MFD	−0.039 ± 0.036	−0.056 ± 0.056
	MD	0.34 ± 0.159*	0.081 ± 0.150
	ML	−0.273 ± 0.095*	0.008 ± 0.055
	MCSA	0.027 ± 0.045	−0.003 ± 0.013
Protein:DNA	Intercept	9.071 ± 3.749*	6.196 ± 4.667
	SW	782.908 ± 294.086*	638.928 ± 399.682
	TMFN	−0.011 ± 0.009	−0.022 ± 0.016
	MFD	−0.141 ± 0.04*	−0.191 ± 0.107
	MD	−4.049 ± 2.793	−4.567 ± 4.791
	ML	10.101 ± 12.452	5.102 ± 12.832
	MCSA	−11.723 ± 7.448	4.228 ± 4.728
Protein:RNA	Intercept	4.548 ± 3.534	0.099 ± 1.155
	SW	111.419 ± 48.958*	139.753 ± 45.53*
	TMFN	−0.002 ± 0.002	−0.003 ± 0.002
	MFD	−0.019 ± 0.007*	−0.022 ± 0.012*
	MD	−0.287 ± 0.465	−0.431 ± 0.546
	ML	−2.553 ± 2.073	0.348 ± 1.462
	MCSA	1.664 ± 1.24	0.179 ± 0.539

LD = longissimus-dorsi, ST = semitendinosus, SW = slaughter weight, TMFN = total muscle fiber number, MFD = muscle fiber diameter, MD = muscle depth, ML = muscle length, MCSA = muscle cross-sectional area.
* $p \leq 0.05$.

fiber changes in proportion to the change in fiber size and number (Greenwood et al., 2000; Van der Meer et al., 2011; Sen et al., 2016). Moreover, the quantity of muscle fiber nuclei is extremely important for determination of DNA content (Greenwood et al., 2000; Shenkman et al., 2010). In the present study the concentrations of DNA and RNA in LD and ST muscles of Honamli kids were higher than those of other breeds. This suggests that the Honamli kids may have more myonuclei due to more the concentrations of DNA and RNA, which may result in greater transcriptional and translational capacity or efficiency for synthesis of muscle protein in Honamli kids. These observations are consistent with the findings of Sirin (2018), who reported that Honamli kids have higher total muscle fiber numbers compared to kids from Angora and Kilis breed. Therefore, Honamli kids may have more muscle growth capacity than kids born to other breeds. This view is also supported by the observation in the present study that Honamli kids had a relatively high the total protein in ST muscle.

Fraser and Nurse (1979) reported that small cells produce less RNA than large cells; suggesting that size of any cell is related to the transcription activity and that genome expression can be regulated by genetically triggered changes in cell size. In the present study, a high transcriptional and translational capacity was observed in relation to DNA, RNA and total protein in LD and ST muscles of Honamli kids. These results may indicate a greater increase in cellular activity in hypertrophied muscles and suggest that an increased capacity to synthesize

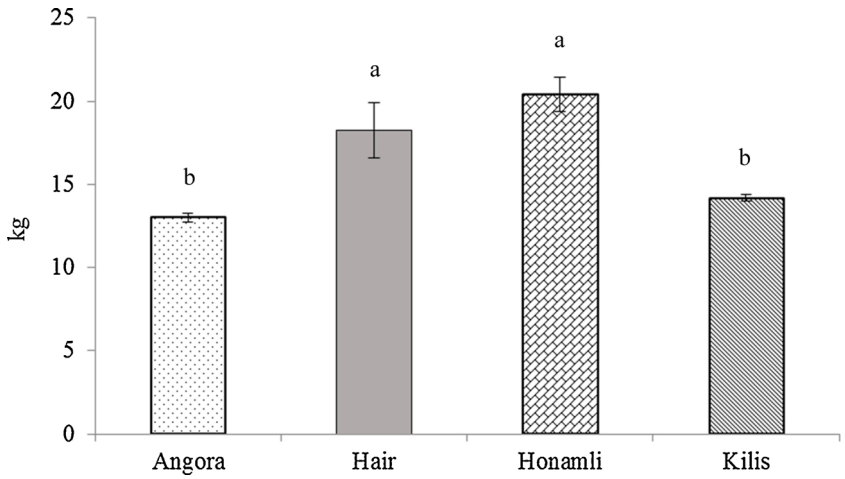

Fig. 4. Slaughter weights (kg) of Angora, Hair, Honamli and Kilis male kids at 90 days of weaning age. The error bars represent the standard error of the mean and bars with different letters are significantly different at $p < 0.05$.

and maintain protein may be associated with hypertrophy of skeletal muscle mass in Honamli kids.

During a period of nearly last 50 years the relationship between differentiated post-mitotic cells of varying size and their molecular properties have been examined (Margueratand Bähler, 2012). Observations of Schmidt and Schibler (1995) indicated that the total RNA concentration produced by a given genome can differ greatly in cells of different sizes. Especially, the differences in RNA:DNA ratio for a few genes analysed are caused by differences in mRNA synthesis (transcriptional efficiency) rather than by differences in mRNA turnover (Schmidt and Schibler, 1995). These findings indicate that cells of a given type can increase their RNA and protein production together with cell size while conserving their genome content. Accordingly, the RNA:DNA and the protein:DNA ratios differ as a function of cell size, revealing cellular tuning of gene expression at a global scale. In the present study, Angora kids had higher indices of muscle cells characteristics (protein:DNA and protein:RNA ratios) in skeletal muscles compared to other breeds. These results may indicate that Angora kids have higher potential for growth capacity compared to other breeds. Greenwood et al. (2006) reported that protein:DNA ratio, which is an index of cell size in syncytial tissues such as muscle, increase with increasing post-weaning muscle depth in the ST muscle of lamb. Additionally, protein:DNA ratio in the LD muscle was influenced positively, but RNA:DNA ratio negatively, and protein:RNA ratio were not affected by increasing post-weaning muscle depth (Greenwood et al., 2006). Considering the cellular muscle properties of kids, there were no relationships between RNA:DNA, protein:DNA and protein:RNA ratios and MD measurement in LD muscle, but negative relationships were observed between RNA:DNA ratio and MD and MSCA measurements in ST muscle in the present study.

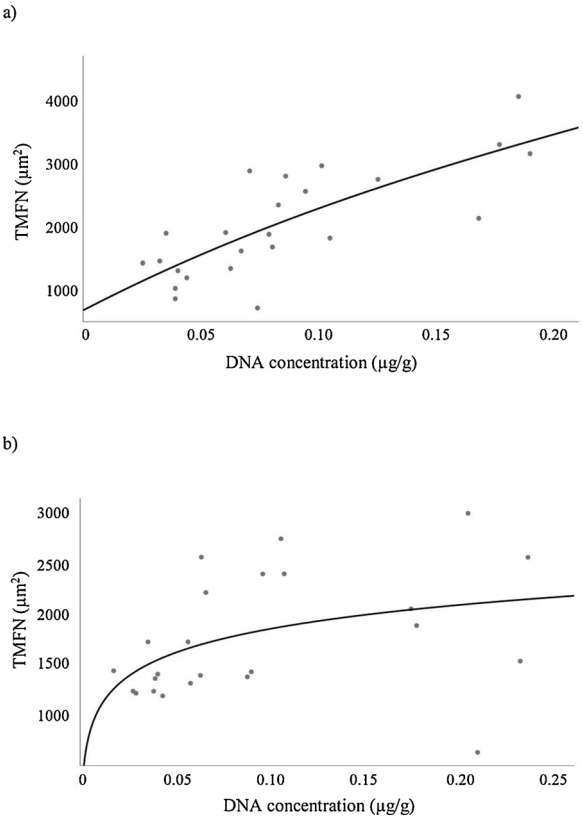

Fig. 5. Regression graphs of DNA concentration on the total muscle fiber number (TMFN) in longissimus-dorsi (a) and semitendinosus (b) muscles.

5. Conclusions

This study has shown that the cellular characteristics and metric measurements of skeletal muscle mass exhibited differences across the indigenous Turkish goat breeds. The results of present study indicated that Honamli and Angora breeds have a far better capacity for protein synthesis and muscle growth due to their cellular characteristics and more active metabolic rate. In other words, Honamli and Angora breeds are highly suggested for a more efficient fattening practice. Especially,

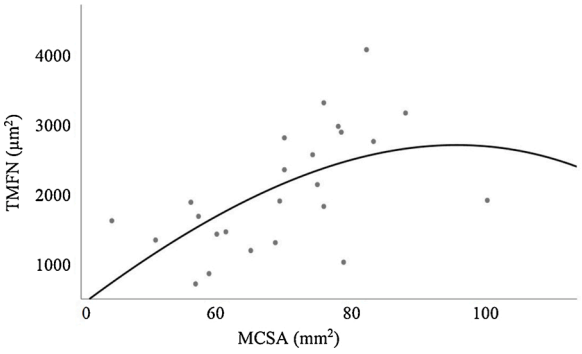

Fig. 6. Regression graph of the muscle cross-sectional area (MCSA) on the total muscle fiber number (TMFN) in longissimus-dorsi muscle.

Angora breed could be more suitable for short term fattening practices due to their higher muscle cellularity ratio which is responsible for faster growth rate while Honamli breed for long term fattening due to the higher concentration of DNA, RNA and protein in the muscle which provides more muscle mass volume.

The results of present study may help to determine the relationship between characteristics of muscle cells (such as transcriptional and translational capacity) and meat yield in Turkish indigenous goat breeds. Thus, potential fattening performances of native goat breeds at the molecular level have been revealed, and even important information has been obtained about which breeds can be used as fattening material for more meat production. Moreover, characteristics of muscle mass may use as molecular markers in future breeding studies on meat production characteristics of native breeds.

Animal welfare statement

The authors confirm that the ethical policies of the journal, as noted on the journal's author guidelines page, have been adhered to. The experimental procedures were approved by the Local Animal Care and Ethics Committee of Kırşehir Ahi Evran University, Kırşehir, Turkey (approval number; 021013.04.1), and ensuring compliance with EC Directive 86/609/EEC for animal experiments.

Declaration of Competing Interest

None of the authors of this paper has a financial or personal relationship with other people or organizations that could inappropriately influence or bias the content of the paper.

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References

Akbas, A.S., Saatci, M., 2016. Growth, slaughter, and carcass characteristics of Honamlı, Hair, and Honamlı × Hair F1 male goat kids bred under extensive conditions. Turk. J. Vet. Anim. Sci. 40, 459–467.
Bradford, M.M., 1976. A rapid and sensitive method for the quantitation of microgram quantities of protein utilizing the principle of protein–dye binding. Anal. Biochem. 72, 248–254.
Broke, M.M., Keiser, K., 1970. Muscle fiber type; how many and what kind? Arch. Neurol. 23, 369–370.
Carpenter, C.E., Owen, D.R., Cockett, N.E., Snowder, G.D., 1996. Histology and composition of muscles from normal and Callipyge lambs. J. Anim. Sci. 74, 388–393.
Cheek, D.B., 1985. The control of cell mass and replication. The DNA unit-A personal 20-year study. Early Hum. Dev. 12, 211–239.
Daskiran, I., Koluman, N., 2014. Goat breeds of Turkey and their specific characteristics. In: European Regional Conference on Goats ERCG 2014, Debrecen-Hungary. Oradea-Romania.
Eversole, D.E., Bergen, W.G., Merkel, R.A., Magee, W.T., Harpster, H.W., 1981. Growth and muscle development of feedlot cattle of different genetic back-grounds. J. Anim. Sci. 53, 91–101.
Ezekwe, M.O., Martin, R.J., 1975. Cellular characteristics of skeletal muscle in selected strains of pigs and mice and the unselected controls. Growth 39, 95–106.
Falkner, F.T., Tanner, J.M., 1986. Human Growth, a Comprehensive Treatise, 2nd ed. Plenum Press, New York.
FAO, 2018. Faostat, Live Animals Data. http//www.fao.org/faostat/en/#data/QA. (Accessed December 5, 2018).
Fraser, R.S., Nurse, P., 1979. Altered patterns of ribonucleic acid synthesis during the cell cycle, a mechanism compensating for variation in gene concentration. J. Cell. Sci. 35, 25–40.
Greenwood, P.L., Hunt, A.S., Hermanson, J.W., Bell, A.W., 2000. Effects of birth weight and postnatal nutrition on neonatal sheep, II. Skeletal muscle growth and development. J. Anim. Sci. 78, 50–61.
Greenwood, P.L., Gardner, G.E., Hegarty, R.S., 2006. Indices of cellular development in muscles of lambs are influenced by sire estimated breeding values and pastoral nutritional system. Aust. J. Agric. Res. 57, 651–659.
Harbison, S.A., Goll, D.E., Parish Jr., C., Wang, V., Kline, E.A., 1976. Muscle growth in two genetically different lines of swine. Growth 40, 253–283.
Hwang, Y.H., Kim, G.D., Jeong, J.Y., Hur, S.J., Joo, S.T., 2010. The relationship between muscle fiber characteristics and meat quality traits of highly marbled Hanwoo Korean native cattle steers. Meat Sci. 86, 456–461.
Kim, G.D., Jeong, J.Y., Jung, E.Y., Yang, H.S., Lim, H.T., Joo, S.T., 2013. The influence of fiber size distribution of type IIB on carcass traits and meat quality in pigs. Meat Sci. 94, 267–273.
Koohmaraie, M., Shackelford, S.D., Wheeler, T.L., Lonergan, S.M., Doumit, M.E., 1995. A muscle hypertrophy condition in lamb Callipyge, characterization of effects on muscle growth and meat quality traits. J. Anim. Sci. 73, 3596–3607.
Lorenzen, C.L., Koohmaraie, M., Shackelford, S.D., Jahoor, F., Freetly, H.C., Wheeler, T. L., Savell, J.W., Fiorotto, M.L., 2000. Protein kinetics in Callipyge lambs. J. Anim. Sci. 78, 78–87.
Lösel, D., Kalbe, C., Rehfeldt, C., 2009. L-Carnitine supplementation during suckling intensifies the early postnatal skeletal myofiber formation in piglets of low birth weight. J. Anim. Sci. 87, 2216–2226.
Marguerat, S., Bähler, J., 2012. Coordinating genome expression with cell size. Trends Genet. 28, 560–565.
Moretti, D.B., Nordi, W.M., Lima, A.L., Pauletti, P., Machado-Neto, R., 2014. Enteric, hepatic and muscle tissue development of goat kids fed with lyophilized bovine colostrum. J. Anim. Physiol. Anim. Nutr. 982, 201–218.
Ozawa, S., Mitsuhashi, T., Mitsumoto, M., Matsumoto, S., Itoh, N., Itagaki, K., 2000. The characteristics of muscle fiber types of longissimus thoracis muscle and their influences on the quantity and quality of meat from Japanese Black steers. Meat Sci. 54, 65–70.
Ryu, Y.C., Choi, Y.M., Lee, S.H., Shin, H.G., Choe, J.H., Kim, J.M., Hong, K.C., Kim, B.C., 2008. Comparing the histochemical characteristics and meat quality traits of different pig breeds. Meat Sci. 80, 363–369.
Schmidt, E.E., Schibler, U., 1995. Cell size regulation, a mechanism that controls cellular RNA accumulation, consequences on regulation of the ubiquitous transcription factors Oct1 and NF-Y and the liverenriched transcription factor DBP. J. Cell Biol. 128, 467–483.
Sen, U., Sirin, E., Ulutas, Z., Kuran, M., 2011. Fattening performance, slaughter, carcass and meat quality traits of Karayaka lambs. Trop. Anim. Health Prod. 432, 409–416.
Sen, U., Sirin, E., Aksoy, Y., Ensoy, U., Ulutas, Z., Kuran, M., 2016. The effect of maternal nutrition level during mid-gestation on post-natal muscle fiber composition and meat quality in lambs. Anim. Prod. Sci. 56, 834–843.
Sen, U., Sirin, E., Filik, A., 2019. Carcass traits of some Turkish native goat breeds. In: Prague, Czechia, 11–13 SeptemberInternational Congress on Domestic Animal Breeding, Genetics and Husbandry 2019 ICABGEH-19, 3, pp. 86–89.
Shenkman, B.S., Turtikova, O.V., Nemirovskaya, T.L., Grigoriev, A.I., 2010. Skeletal muscle activity and the fate of myonuclei. Acta Naturae 22, 59–66.
Sirin, E., 2018. Relationship between muscle fiber characteristics and meat quality parameters in Turkish native goat breeds. Indian J. Anim. Res. 52, 1526–1530.
Tulloh, N.M., Brimblecombe, H., Dennis, C., 1986. The effect of severe nutritional deprivation in early post-natal life on tissue and cellular responses during subsequent growth of lambs to the age of 4 months. J. Agric. Sci. 106, 341–350.
TurkStat, 2018. Turkish Statistical Institute, Livestock Statistics. http//www.turkstat.gov.tr (Accessed January 19, 2018).
Valkova, N., Yunis, R., Mak, S.K., Kang, K., Kültz, D., 2005. Nek8 mutation causes overexpression of galectin-1, sorcin, and vimentin and accumulation of the major urinary protein in renal cysts of jck mice. Mol. Cell. Proteom. 4, 1009–1018.
Van der Meer, S.F., Jaspers, R.T., Degens, H., 2011. Is the myonuclear domain size fixed? J. Musculoskelet. Neuronal Interact. 114, 286–297.