Variability of Prion Protein (PrP) Gene and its Association with Productive Performance in Barki Lambs

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Abstract: The aims of the present study were to detect the allelic and genotypic polymorphisms in a coding region of the ovine prion protein (PrP) gene and to test their association with productive performance of Barki lambs. Fifty four male lambs of Barki sheep were genotyped for the PrP gene using the polymerase chain reaction-restricted fragment length polymorphism (PCR-RFLP) tool. The associations of the PrP genotype, the presence/ absence of each allele in animal genotype and the number of allele copies present in animal genotype with growth traits, body measurements, conformation indices and carcass characteristics were evaluated using general linear mixed models (GLMMs). The RFLP analysis detected two alleles R and C with frequencies of 0.843 and 0.157, respectively, and three genotypes RR, RC and CC with frequencies of 0.741, 0.204 and 0.055, respectively. The PrP genotype showed significant ($P < 0.05$) associations with slaughtering weight, thigh circumference and hot carcass weight; and high significant ($P < 0.01$) associations with weaning weight, pre-weaning daily gain and skeletal muscle index. The presence of allele R in the genotype significantly ($P < 0.05$) affected hot carcass weight and dressing percentage; and high significantly ($P < 0.01$) affected weaning weight, pre-weaning daily gain, slaughtering weight, thigh circumference and skeletal muscle index. The presence of one or two copies of allele R in animal genotype was significantly associated with heavier weaning, slaughtering and hot carcass weights; and also with higher pre-weaning daily gain, thigh circumference and skeletal muscle index. In view of our results, the variation in PrP gene affects a wide range of growth and carcass characteristics in Barki sheep and applying the marker assisted selection using the PrP gene is warranted to increase these traits will be of considerable economic value to sheep producers.
[A. H. M. Ibrahim. **Variability of Prion Protein (PrP) Gene and its Association with Productive Performance in Barki Lambs.** *J Am Sci* 2015;11(2):89-96]. (ISSN: 1545-1003). http://www.jofamericanscience.org. 11

Key words: Prion protein, growth, body conformation, carcass characteristics, PCR-RFLP, Barki sheep.

1. Introduction

Growth traits of sheep are great of economic importance for both breeders and industry due to their association with meat production. Fast growing lambs need less feed for their maintenance requirements because they reach their market weights faster than the slower lambs. Therefore these traits are traditionally included in selection criteria of sheep breeding programs.

Body conformation traits are also could be equally important because they are related to feed intake, body weight and fat and muscle percentages (Atta and Elkhidir, 2004; Afolayan et al., 2006; Otoikhian et al., 2008; Cam et al., 2010; Musa et al., 2012; Tariq et al., 2012; Younas et al., 2013). Body conformation are relevant to establish a morphological based standard with visual conformation appraisal which is most likely the oldest method of information collection for the purpose of selection in many sheep breeding association (Janssen and Vandepitte, 2004).

Carcass characteristics of lambs are economically important for both breeders and consumers, but it is difficult to be measured until slaughtering animals which makes the genetic improvement for this kind of traits is very slow and expensive. Therefore, to estimate carcass characteristics of selective live lambs, using a suitable technique to accomplish that goal is necessarily.

The previous traits are quantitative and the genetic improvement for them have been achieved by selection based on phenotype or on estimated breeding value derived from phenotype without knowledge of the number of genes that affect the trait (Naqvi, 2007). Over the last two decades, advances in molecular genetics have introduced a new generation of molecular markers for the genetic improvement of economically important traits in livestock (Teneva, 2009). The use of molecular markers offers a way to select animal for a wide range of traits at early age and to enhance reliability in predicting the mature phenotype of the individual (Naqvi (2007).

There are two approaches to identify the molecular marker associated with the trait of interest: the genome-wide scanning and candidate gene approach. The candidate gene approach allows focusing the analysis on particular gene(s) involved in key metabolic pathways or physiological processes which are probable to be involved in the trait(s) of interest (Sevane et al., 2014).

The prion proteins (PrPs) are small glycoproteins, dominated by three alpha helices and normally found at the cell surface in vertebrates and mammals (Lucock, 2007). They are most abundant in

neuronal tissue but are also expressed in other tissues including lung, kidney, mammary glands, gastrointestinal mucosa, lymphoid cells and skeletal muscle (Smith et al., 2011). The functions of normal PrPs are correlated with energy production, calcium metabolism, protein degradation and DNA replication, however the abnormal prion convert normal proteins into infectious disease-producing proteins responsible for the ovine and caprine scrapie, the bovine spongiform encephalopathy and the human Creutzfeldt-Jakob diseases (Beringue et al., 2006; Sikorska and Liberski, 2012; Cassard et al., 2014).

In sheep, the PrPs are encoded by the ovine PrP gene which located at the chromosome 13 and consisted of 3 exons and 2 introns (Lee et al., 1998). Numerous studies concerned the variation in the PrP gene and its association with performance traits of sheep. Some of these studies proved that the PrP gene polymorphism is significantly associated with litter size in Commercial Western White-Faced and Suffolk sheep (Alexander et al., 2005) and Texel sheep (Brandsma et al., 2004); lamb survival in Shropshire sheep (Lipsky et al., 2006); fertility traits of rams in Lacaune sheep (Vitezica et al., 2004); birth weight in Dorest sheep (Tongue et al., 2006) and Scottish Blackface sheep (Sawalha et al., 2007); weaning weight in German Black-Headed Mutton sheep (DeVries et al., 2004), Swaledale sheep (Man et al., 2006) and Texel sheep (Brandsma et al., 2005); slaughter weight in Scottish Black Face sheep (Sawalha et al., 2007); conformation score in Suffolk sheep (DeVries et al., 2004) and muscle depth in German Black-Headed Mutton sheep (DeVries et al., 2004) and Suffolk sheep (Hanrahan et al., 2008).

The objectives of this study were to identify the polymerase chain reaction –restricted fragment length polymorphism (PCR-RFLP) in a coding region at the ovine PrP gene and to test its association with growth traits, body measurements, conformation indices and carcass characteristics of Barki lambs.

2. Materials and Methods

Animal and phenotypic data

Fifty four males of Barki lambs, reared at Maryout Research Station, Desert Research Center, were used to carry out this study. Lambs were weighed and ear-tagged at birth. The live weights were taken again at the time of weaning (3 months of age approximately) and slaughtering (9 months of age approximately). From these weights, pre- and post-weaning daily gains were calculated.

At time of slaughtering, five body measurements were taken for each animal: body length, heart girth, height at withers, height at hips and thigh circumference. Body length was considered as the distance between the point of shoulder and pinbone; heart girth was measured as the circumference of the chest of animal; height at wither was measured as the distance from the floor to the point between the shoulders; height at hips was measured as the distance from the floor to the back of the animal; thigh circumference was measured as the circumference of the hind leg as close as the abdominal of animal. From these body measurements, 4 conformational indices were calculated according to Salako (2006).

- Body mass index = (slaughtering weight × 100) / height at withers.
- Skeletal muscle index = (thigh circumference × 100) / height at withers.
- Body index = (body length × 100) / heart girth.
- Relative body index = (body length × 100) / height at withers.

Slaughtering was carried out by serving the carotid artery and jugular vein. After slaughtering and skinning, all the abdominal and thoracic offal's were removed to obtain the hot carcass weight. All carcasses were chilled at 4 ºC for 24 h to evaluate the chilled carcass weight. Each chilled carcass was dissected into seven parts (neck, shoulder, racks, loin, flanks, legs and tail) according to the norms of the Egyptian wholesale mutton cuts as described by Hamada (1976). The seven cuts were weighed to calculate the percentages of the chilled carcass cuts. Also, the 9-10-11 rib cut of each animal was separated into its physical components (lean, fat and bone) and weighed to be expressed as percentages of the weight of the whole rib cut.

DNA extraction and polymerase chain reaction

Before slaughtering, blood samples (5 ml) were obtained by jugular venipuncture using vacuum tubes treated with 0.25% of EDTA, and stored at – 80 ºC upon the DNA extraction. DNA was extracted using a genomic DNA extraction kit (Qiagen, Hilden, Germany). A 678 pb fragment located at exon 3 of the ovine PrP gene was amplified using a pair of specific primers as described by Thorgeirsdottir et al. (1999). The sequences of these primers were as follow: (F: 5`-CAGGTTAACGATGGTGAAAA-GCCACATAGG-3`) and (R: 5`- CTGGGATTCT-CTCTGGACTG-3`). The PCR mixture contained 50 ng of extracted DNA, 100 µM of dNTP, 0.5 µM of each primer, 1.5 mM of $MgCl_2$, and 1 U of Taq polymerase. The PCR amplification was performed in the T100^{TM} thermal cycler (Bio-Rad, USA) with an initial denaturation at 94ºC for 10 min, followed by 39 cycles of 1 min at 94ºC, 1.5 min at 58 ºC and 1.5 min at 72 ºC. The final extension step was at 72 ºC for 10 min.

Restriction fragment length polymorphism

Without purification, 8 µl of each PCR product was digested with 6 units of *AvaII* restriction enzyme (Ferments) at 37 ^{0} c for 5 h. Digested fragments were

loaded on 2% agarose gels containing ethidium bromide and the gels analyzed in the UV rays. Then, an image for each gel was shot using a digital camera.

Statistical analysis

Allelic and genotypic frequencies were calculated by counting. The Hardy-Weinberg equilibrium of the PrP genotypes was examined using the χ^2 test. The population would be considered to be in Hardy-Weinberg equilibrium if it failed the χ^2 test at the level of 0.05.

Statistical analyses testing the effects of variation in PrP gene on the studied traits were undertaken using SPSS software, version 19 (SPSS Science Inc., Chicago, IL, USA). Three different sets of modeling approaches were used to test these effects. The first set of general linear mixed models (GLMMs) was used to test the effect of PrP genotypes on the studied traits, the second set of GLMMs was used to assess the effect of the presence/absence of each PrP allele in the genotype on the studied traits and the third set of GLMMs was performed to explore the effect of the number of PrP allele copies present in the genotype on the studied traits. PrP genotype was fitted as a fixed effect while sire was fitted as a random effect in each model.

In the model assessing the genotype effect on weaning weight and pre-weaning daily gain, weaning age was included as a covariate. Also, slaughtering age was included as a covariate in the model testing the effect of genotype on the rest of traits. Where significant, these were further explored using pairwise comparison (Duncan test; $P \leq 0.05$).

The generalized statistical model that was used:

$$Y_{ijk} = \mu + G_i + S_j + \varepsilon_{ijK}$$

Where Y_{ijK} = trait value, μ = general mean, G_i = *the* fixed effect of PrP genotype in the first set of GLMMs, the presence/ absence of each PrP alleles in the second set of GLMMs or the number of PrP allele copies present in the third set of GLMMs, S_j is the random effect of sire and ε_{ijK} = the random error associated with each observation, assumed to be normally and independently distributed with zero mean and variance σ^2.

3. Results and Discussion

Allelic and genotypic frequencies

According to the PrP genotype, the digestion with *AvaII*, traditionally, produces 3 fragments (678, 447 and 231 pb) as shown in figure (1). The RR genotype shows two fragments (447 and 231 pb), the RC genotype shows three fragments (678, 447 and 231 pb) and the CC genotype shows only one fragment (678 pb). In this study, three genotypes CC, RC and RR with frequencies of 0.055, 0.204 and 0.741, respectively, were identified. The frequencies of C and R alleles were 0.157 and 0.843, respectively. The PrP genotypes were not found to be in Hardy-Weinberg equilibrium. The high frequency of the homozygous RR genotype and the low frequency for the homozygous CC genotype indicate to a high genetic homogeneity at this coding region of PrP gene in Barki sheep. This result is consistent to the result obtained by Pacheco et al. (2007).

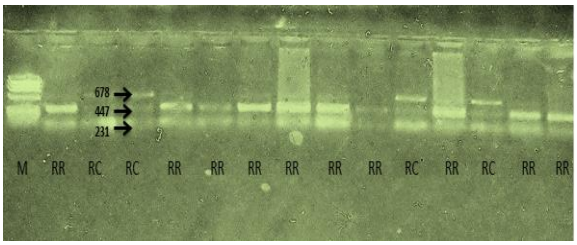

Figure (1). RFLP analysis for a coding region in the PrP gene in Egyptian Barki lambs.

Effect of sire on the studied traits

No associations were found between sire and all the studied traits.

Effect of PrP genotype on the studied traits

The effects of PrP genotype on the studied traits are presented in Table (1). High significant effects ($P < 0.01$) were observed for the PrP genotype on weaning weight, pre-weaning daily gain, and skeletal muscle index. In addition, significant effects ($P < 0.05$) were found for the PrP genotype on slaughtering weight, thigh circumference and hot carcass weight. The least square means showed that lambs with the homozygous genotype RR and the heterozygous genotype RC had higher birth weight, pre-weaning daily gain, slaughtering weight, thigh circumference, skeletal muscle index and hot carcass weight than lambs with the homozygous genotype CC.

Effect of the presence/ absence of PrP alleles in animal genotype on the studied traits

The association of the presence/ absence of the detected PrP alleles with the studied traits are shown in Table (2). The presence of allele R in animal genotype was significantly associated with heavier weaning and slaughtering weights ($P < 0.01$), increased thigh circumference ($P < 0.01$), higher skeletal muscle index ($P < 0.01$), heavier hot carcass weight ($P < 0.05$) and higher dressing percentage ($P < 0.05$). However, the presence of allele C significantly ($P < 0.05$) associated with lighter birth weight.

Table (1) Least Square means and standard errors for the studied traits according to the PrP genotypes in Barki lambs

Traits	LSM ± SE			P-value
	RR (n=40)	RC (n=11)	CC (n=3)	
Growth traits				
Birth weight (Kg)	3.68 ± 0.092	3.25 ± 0.175	3.33 ± 0.166	NS
Weaning weight (Kg)	**20.77 ± 0.567[a]**	**20.81 ± 0.932[a]**	**13.83 ± 2.488[b]**	**
Pre-weaning daily gain (gm/day)	**190.27 ± 7.157[a]**	**194.36 ± 11.111[a]**	**105.14 ± 22.214[b]**	**
Slaughtering weight (Kg)	**41.91 ± 1.446[a]**	**41.52 ± 2.707[a]**	**27.83 ± 0.440[b]**	*
Post-weaning daily gain (gm/day)	78.65 ± 4.680	76.98 ± 10.075	50.21 ± 10.674	NS
Body measurements				
Height at withers (cm)	71.11 ± 0.712	70.27 ± 1.395	74.00 ± 2.082	NS
Height at hip (cm)	69.68 ± 0.699	69.45 ± 1.351	73.00 ± 1.732	NS
Body length (cm)	71.09 ± 0.680	71.18 ± 1.976	75.33 ± 0.882	NS
Heart girth (cm)	90.35 ± 0.924	89.73 ± 1.810	98.00 ± 2.000	NS
Thigh circumference (cm)	**29.98 ± 0.466[a]**	**29.73 ± 0.787[a]**	**24.33 ± 0.667[b]**	*
Conformation indices				
Body mass index	59.42 ± 2.333	59.66 ± 4.568	47.69 ± 1.514	NS
Skeletal muscle index	**42.30 ± 0.771[a]**	**42.47 ± 1.421[a]**	**32.94 ± 1.476[b]**	**
Body index	78.86 ± 0.816	79.55 ± 2.466	76.89 ± 0.766	NS
Relative body index	100.25 ± 1.192	101.23 ± 1.645	101.90 ± 1.904	NS
Carcass characteristics				
Hot carcass weight (Kg)	**19.19 ± 0.819**	**19.07 ± 1.652**	**11.44 ± 0.662**	*
Dressing %	45.36 ± 0.498	45.41 ± 0.965	41.06 ± 1.766	NS
Neck%	7.34 ± 0.334	8.87 ± 1.116	7.86 ± 0.676	NS
Shoulder%	20.14 ± 0.262	19.79 ± 0.373	20.15 ± 0.263	NS
Rack%	24.10 ± 0.462	22.93 ± 1.653	24.52 ± 0.649	NS
Loin%	6.36 ± 0.191	6.85 ± 0.327	6.38 ± 1.298	NS
Flank%	4.71 ± 0.741	6.70 ± 2.854	4.01 ± 0.585	NS
Leg%	33.85 ± 0.829	31.55 ± 2.732	34.18 ± 0.656	NS
Tail%	3.45 ± 0.391	3.27 ± 0.503	2.88 ± 3.467	NS
9-10-11 rib weight (gm)	577.91 ± 25.133	517.70 ± 53.963	478.43 ± 27.839	NS
Lean meat %	45.65 ± 1.155	45.37 ± 3.214	47.45 ± 5.675	NS
Fat%	20.68 ± 0.937	20.59 ± 1.752	20.50 ± 4.340	NS
Bone%	29.68 ± 0.861	27.54 ± 2.640	30.21 ± 1.007	NS

Significance level * refers to significance at ($P < 0.05$) and ** refers to significance at ($P < 0.01$)

Effect of the number of PrP allele copies present in animal genotype on the studied traits

The results of testing the association between the number of PrP allele copies present in animal genotype and the studied traits are presented in Table (3). These results showed that, lambs carrying one or two copies of allele R had a superior performance for weaning weight, pre-weaning daily gain, slaughtering weight, thigh circumference, skeletal muscle index and hot carcass weight, in compare to lambs with two copies of allele C. These results suggest a dominance effect for allele R.

In this study, the potential associations of the PrP genotypes with growth traits, body measurements, conformation indices and carcass characteristics of lambs were tested 3 times. Association analysis between PrP genotypes and growth and carcass characteristics showed significant effects for the PrP genotype on slaughtering weight and hot carcass weight. These traits are the most important traits in sheep industry, where the value of lamb is based on both of them at harvest and the buyer and seller do not have to estimate any other traits. Results from the previous studies concerned the effects of the PrP genotypes on growth and carcass characteristics of lambs are highly variable and generally inconsistent among the different breeds. However many studies approved the significant associations between the variation in PrP genotypes and growth and carcass characteristics. This variation was found to be associated with weaning weight and daily live weight gain in German Black Headed Mutton and Texel sheep (Brandsma et al., 2004; DeVries et al., 2004; Man et al., 2006), and also with slaughtering weight in Scottish Blackface sheep (Sawalha et al., 2007).

Table (2) Least Square means and standard errors for the studied traits according to the presence/ absence of PrP alleles in Barki lambs

Traits	Allele being assessed	LSM ± SE				P-value
		Allele absent	n	Allele present	n	
Growth traits						
Birth weight (Kg)	**C**	**3.68 ± 0.092**	**40**	**3.26 ± 0.139**	**14**	*
	R	3.33 ± 0.166	3	3.59 ± 0.084	51	NS
Weaning weight (Kg)	C	20.77 ± 0.567	40	19.32 ± 1.166	14	NS
	R	**13.83 ± 2.488**	**3**	**20.78 ± 0.484**	**51**	**
Pre-weaning daily gain (gm/day)	C	190.27 ± 7.157	40	175.24 ± 13.928	14	NS
	R	**105.14 ± 22.214**	**3**	**191.15 ± 6.060**	**51**	**
Slaughtering weight (Kg)	C	41.91 ± 1.446	40	38.59 ± 2.620	14	NS
	R	**27.83 ± 0.440**	**3**	**41.83 ± 1.263**	**51**	**
Post-weaning daily gain (gm/day)	C	78.65 ± 4.680	40	71.24 ± 8.625	14	NS
	R	50.21 ± 10.674	3	78.29 ± 4.218	51	NS
Body measurements						
Height at withers (cm)	C	71.11 ± 0.712	40	71.07 ± 1.225	14	NS
	R	74.00 ± 2.082	3	70.93 ± 0.630	51	NS
Height at hip (cm)	C	69.68 ± 0.699	40	70.21 ± 1.168	14	NS
	R	73.00 ± 1.732	3	69.63 ± 0.615	51	NS
Body length (cm)	C	71.09 ± 0.680	40	72.07 ± 1.615	14	NS
	R	75.33 ± 0.882	3	71.11 ± 0.672	51	NS
Heart girth (cm)	C	90.35 ± 0.924	40	91.50 ± 1.731	14	NS
	R	98.00 ± 2.000	3	93.22 ± 0.815	51	NS
Thigh circumference (cm)	C	29.98 ± 0.466	40	28.57 ± 0.875	14	NS
	R	**24.33 ± 0.667**	**3**	**29.92 ± 0.400**	**51**	**
Conformation indices						
Body mass index	C	59.420 ± 2.333	40	54.95 ± 4.352	14	NS
	R	47.69 ± 1.514	3	59.47 ± 2.057	51	NS
Skeletal muscle index	C	42.30 ± 0.771	40	40.43 ± 1.571	14	NS
	R	**32.949 ± 1.476**	**3**	**42.34 ± 0.671**	**51**	**
Body index	C	78.86 ± 0.816	40	78.98 ± 1.945	14	NS
	R	76.89 ± 0.766	3	79.01 ± 0.819	51	NS
Relative body index	C	100.25 ± 1.192	40	101.37 ± 1.327	14	NS
	R	101.90 ± 1.904	3	100.46 ± 0.995	51	NS
Carcass characteristics						
Hot carcass weight (Kg)	C	19.19 ± 0.819	40	17.43 ± 1.555	14	NS
	R	**11.44 ± 0.662**	**3**	**19.17 ± 0.726**	**51**	*
Dressing %	C	45.36 ± .498	40	44.47 ± 0.954	14	NS
	R	**41.06 ± 1.766**	**3**	**45.37 ± 0.438**	**51**	*
Neck%	C	7.34 ± 0.334	40	8.65 ± 0.883	14	NS
	R	7.86 ± 0.676	3	7.67 ± 0.360	51	NS
Shoulder%	C	20.14 ± 0.262	40	19.87 ± 0.297	14	NS
	R	20.15 ± 0.263	3	20.06 ± 0.220	51	NS
Rack%	C	24.10 ± 0.462	40	23.27 ± 1.303	14	NS
	R	24.52 ± 0.649	3	23.85 ± 0.503	51	NS
Loin%	C	6.36 ± 0.191	40	6.75 ± 0.350	14	NS
	R	6.38 ± 1.298	3	6.47 ± 0.167	51	NS
Flank%	C	4.71 ± 0.741	40	6.13 ± 2.242	14	NS
	R	4.010 ± 0.585	3	5.14 ± 0.837	51	NS
Leg%	C	33.85 ± 0.829	40	32.11 ± 2.148	14	NS
	R	34.18 ± 0.656	3	33.35 ± 0.872	51	NS
Tail%	C	3.15 ± 0.239	40	2.79 ± 0.847	14	NS
	R	2.88 ± 0.467	3	2.91 ± 0.43	51	NS
9-10-11 rib weight (gm)	C	577.91 ± 25.133	40	509.29 ± 42.491	14	NS
	R	478.43 ± 27.839	3	564.93 ± 22.898	51	NS
Lean meat %	C	45.657 ± 1.155	40	45.82 ± 2.713	14	NS
	R	47.45 ± 5.67	3	45.59 ± 1.124	51	NS
Fat%	C	20.68 ± 0.937	40	20.57 ± 1.573	14	NS
	R	20.50 ± 4.340	3	20.66 ± 0.818	51	NS
Bone%	C	29.68 ± 0.861	40	28.11 ± 2.083	14	NS
	R	30.21 ± 1.007	3	29.21 ± 0.877	51	NS

Significance level * refers to significance at ($P < 0.05$) and ** refers to significance at ($P < 0.01$)

Table (3) Least Square means and standard errors for the studied traits according to the number of PrP allele copies present in Barki lambs

Traits	Allele being assessed	LSM ± SE						P-value
		Allele absent	n	Allele 1 copy	n	Allele 2 copies	n	
Growth traits								
Birth weight (Kg)	C	3.68 ± 0.092	40	3.25 ± 0.175	11	3.33 ± 0.166	3	NS
	R	3.33 ± 0.166	3	3.25 ± 0.175	11	3.68 ± 0.092	40	NS
Weaning weight (Kg)	**C**	**20.77 ± 0.567[a]**	**40**	**20.81 ± 0.932[a]**	**11**	**13.83 ± 2.488[b]**	**3**	**
	R	**13.83 ± 2.488[b]**	**3**	**20.81 ± 0.932[a]**	**11**	**20.77 ± 0.567[a]**	**40**	**
Pre-weaning daily gain (gm/day)	**C**	**190.27 ± 7.157[a]**	**40**	**194.36 ± 11.111[a]**	**11**	**105.14 ± 22.214[b]**	**3**	**
	R	**105.14 ± 22.214[b]**	**3**	**194.36 ± 11.111[a]**	**11**	**190.27 ± 7.157[a]**	**40**	**
Slaughtering weight (Kg)	**C**	**41.91 ± 1.446[a]**	**40**	**41.52 ± 2.707[a]**	**11**	**27.83 ± 0.440[b]**	**3**	*
	R	**27.83 ± 0.440[b]**	**3**	**41.52 ± 2.707[a]**	**11**	**41.91 ± 1.446[a]**	**40**	*
Post-weaning daily gain (gm/day)	C	78.65 ± 4.680	40	76.98 ± 10.075	11	50.21 ± 10.674	3	NS
	R	50.21 ± 10.674	3	76.98 ± 10.075	11	78.65 ± 4.680	40	NS
Body measurements								
Height at withers (cm)	C	71.11 ± 0.712	40	70.27 ± 1.395	11	74.00 ± 2.082	3	NS
	R	74.00 ± 2.082	3	70.27 ± 1.395	11	71.11 ± 0.712	40	NS
Height at hip (cm)	C	69.68 ± 0.699	40	69.45 ± 1.351	11	73.00 ± 1.732	3	NS
	R	73.00 ± 1.732	3	69.45 ± 1.351	11	69.68 ± 0.699	40	NS
Body length (cm)	C	71.09 ± 0.680	40	71.18 ± 1.976	11	75.33 ± 0.882	3	NS
	R	75.33 ± 0.882	3	71.18 ± 1.976	11	71.09 ± 0.680	40	NS
Heart girth (cm)	C	90.35 ± 0.924	40	89.73 ± 1.810	11	98.00 ± 2.000	3	NS
	R	98.00 ± 2.000	3	89.73 ± 1.810	11	90.35 ± 0.924	40	NS
Thigh circumference (cm)	**C**	**29.98 ± 0.466[a]**	**40**	**29.73 ± 0.787[a]**	**11**	**24.33 ± 0.667[b]**	**3**	**
	R	**24.33 ± 0.667[b]**	**3**	**29.73 ± 0.787[a]**	**11**	**29.98 ± 0.466[a]**	**40**	**
Conformation indices								
Body mass index	C	59.42 ± 2.333	40	59.66 ± 4.568	11	47.69 ± 1.514	3	NS
	R	47.69 ± 1.514	3	59.66 ± 4.568	11	59.42 ± 2.333	40	NS
Skeletal muscle index	**C**	**42.30 ± 0.771[a]**	**40**	**42.47 ± 1.421[a]**	**11**	**32.94 ± 1.476[b]**	**3**	**
	R	**32.94 ± 1.476[b]**	**3**	**42.47 ± 1.421[a]**	**11**	**42.30 ± 0.771[a]**	**40**	**
Body index	C	78.86 ± 0.816	40	79.55 ± 2.466	11	76.89 ± 0.766	3	NS
	R	76.89 ± 0.766	3	79.55 ± 2.466	11	78.86 ± 0.816	40	NS
Relative body index	C	100.25 ± 1.192	40	101.23 ± 1.645	11	101.90 ± 1.904	3	NS
	R	101.90 ± 1.904	3	101.23 ± 1.645	11	100.25 ± 1.192	40	NS
Carcass characteristics								
Hot carcass weight (Kg)	**C**	**19.19 ± 0.819[a]**	**40**	**19.07 ± 1.652[a]**	**11**	**11.44 ± 0.662[b]**	**3**	*
	R	**11.44 ± 0.662[b]**	**3**	**19.07 ± 1.652[a]**	**11**	**19.19 ± 0.819[a]**	**40**	*
Dressing %	C	45.36 ± 0.498	40	45.41 ± 0.965	11	41.06 ± 1.766	3	NS
	R	41.06 ± 1.766	3	45.41 ± 0.965	11	45.36 ± 0.498	40	NS
Neck%	C	7.34 ± 0.334	40	8.87 ± 1.116	11	7.86 ± 0.676	3	NS
	R	7.86 ± 0.676	3	8.87 ± 1.116	11	7.34 ± 0.334	40	NS
Shoulder%	C	20.14 ± 0.262	40	19.79 ± 0.373	11	20.15 ± 0.263	3	NS
	R	20.15 ± 0.263	3	19.79 ± 0.373	11	20.14 ± 0.262	40	NS
Rack%	C	24.10 ± 0.462	40	22.93 ± 1.653	11	24.52 ± 0.649	3	NS
	R	24.52 ± 0.649	3	22.93 ± 1.653	11	24.10 ± 0.462	40	NS
Loin%	C	6.36 ± 0.191	40	6.85 ± 0.327	11	6.38 ± 1.298	3	NS
	R	6.38 ± 1.298	3	6.85 ± 0.327	11	6.36 ± 0.191	40	NS
Flank%	C	4.71 ± 0.741	40	6.70 ± 2.854	11	4.01 ± 0.585	3	NS
	R	4.010 ± 0.585	3	6.70 ± 2.85	11	4.71 ± 0.741	40	NS
Leg%	C	33.85 ± 0.829	40	31.55 ± 2.732	11	34.18 ± 0.656	3	NS
	R	34.18 ± 0.656	3	31.55 ± 2.732	11	33.85 ± 0.829	40	NS
Tail%	C	3.15 ± 0.239	40	3.11 ± 0.803	11	2.88 ± 0.467	3	NS
	R	2.88 ± 0.467	3	3.11 ± 0.803	11	3.05 ± 0.396	40	NS
9-10-11 rib weight (gm)	C	577.91 ± 25.13	40	517.70 ± 53.963	11	478.43 ± 27.839	3	NS
	R	478.43 ± 27.839	3	517.70 ± 53.963	11	577.91 ± 25.133	40	NS
Lean meat %	C	45.65 ± 1.155	40	45.37 ± 3.214	11	47.45 ± 5.675	3	NS
	R	47.45 ± 5.675	3	45.37 ± 3.214	11	45.65 ± 1.155	40	NS
Fat%	C	20.68 ± 0.937	40	20.59 ± 1.752	11	20.50 ± 4.340	3	NS
	R	20.50 ± 4.340	3	20.59 ± 1.752	11	20.68 ± 0.937	40	NS
Bone%	C	29.68 ± 0.861	40	27.54 ± 2.640	11	30.21 ± 1.007	3	NS
	R	30.21 ± 1.007	3	27.54 ± 2.640	11	29.68 ± 0.861	40	NS

Significance level * refers to significance at ($P < 0.05$) and ** refers to significance at ($P < 0.01$).

The results of the present study indicate that there are associations between the PrP genotypes and both thigh circumference and skeletal muscle index. These indices are important indicators for the muscularity of meat animals. Studies regarding the effect of PrP genotypes on body measurements and conformation indices are missing from the literature; however there is a rare study carried out by DeVries et al. (2004) and proved significant effects for the PrP genotype on both conformation score in Texel sheep and muscle mass score in German Black Headed Mutton sheep. These results suggest that the PrPs play an important role in the formation of muscles in meat animals.

The role of PrPs in muscles is not completely cleared. Stella et al. (2010) found that the PrPs control the release of TNF-α factor which involved in muscle differentiation and downstream signaling pathways that affect the longevity of cells in adult muscles in many species of mammals. Smith et al. (2011) cited that the low level of PrP is associated with decreased muscle mass of rat. Isler et al. (2006) proved a correlation between the variation in PrP genotypes and the longissimus muscle depth of Dorset × Romanov sheep.

4. Conclusion

The results obtained here show that the PrP gene is a polymorphic gene. While the misfolded PrPs cause lethal diseases in sheep, cattle and human, the identified polymorphisms that coding for the normal PrPs were found to be associated with the most important growth and carcass characteristics in Barki sheep. Genotyping lambs for the PrP gene and preferring RR animals and culling CC animals may lead to increase growth rate, marketing weight and muscularity of lambs that will increase the benefits of breeders. Further studies with large sample size from Barki sheep and other local breeds of sheep are needed to confirm these associations.

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2/1/2015