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Genetic Contribution of Myogenicfactor 5 and Growth Hormone Genes for Live Body Measurements, Carcass Traits and Meat Quality of Dromedary Camel

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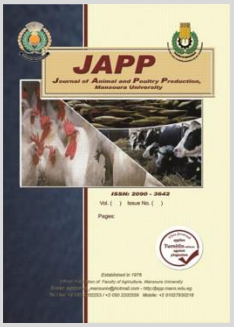

ABSTRACT

Eleven growing one-humped male camels with an average initial body weight of 251.36±6.97 kg were used. After finishing period of 5-month, camels were approximately 2.5 years of age with an average body weight of 359±1 kg. This study aimed to evaluate association analyses between identified SNPs in myogenic factor 5 (MYF5) and growth hormone (GH) genes and live body measurements, carcass merits and meat quality of one humped camel were performed. One region of MYF5 and two regions of GH (GH3UTR and GH5UTR) genes were tested to identify the SNPs in one humped camel. The results shown that detected SNPs in MYF5 and GH had a significant influence on several body measurements, carcass characteristic, histological traits, and chemical composition. The three regions were found to associate with several meat characteristics, and it is recommended that could be used as a candidate gene to characterize meat of dromedary camels. More researches are required to confirm the influence of MYF5 and GH genes on meat quantity and quality of camels.

Keywords: Dromedary, meat, growth hormone gene, myogenicfactor 5

INTRODUCTION

Quantitative trait loci (QTL) of growth parameters and carcass merits have been identified in animals with limited genetic background. Isolate QTL in outbred populations from numerous breeds is being followed. Description of QTL variant in outbred populations will give the possibility to a combination of microsatellites and single nucleotide polymorphisms (SNP) (Kim *et al.*, 2003). On the other hand**,** Forsyth and Wallis (2002) found that the encoded of growth hormone (GH) in the most of mammals is a single gene. Since of its biological function, GH is considered a better candidate gene in the selection programs of livestock, in terms of growth and carcass merits (Daverio *et al*., 2012). In dairy cattle Grochowska *et al*. (2001) found that, GH was associated with carcass characteristics. In Korean native cattle Lee *et al.* (2013) noted that SNPs of the bovine GH gene was correlated with growth traits and carcass merits.

The T450C of GH gene SNP for Saudi Arabian camel breeds were linked with increased estimated body weight (Afifi *et al.* 2014), where the CC genotype in Saheli camels recorded the highest body weight compared to other the genotypes (TT and CT), thus SNP could be used as a marker in the selection program of camels. Furthermore, Abdel-Aziem *et al*. (2015) mentioned that, the marker assisted selection (MAS) of camels, allele C could be that, due to its relation with high growth rate. Differentiation of skeletal muscle is controlled by transcriptional mechanisms, where the myogenic regulatory factors (MRFs) perform a vital function in muscle progress as well as transcript factors and epigenetic effects as reported by Braun and Gautel, (2011). MRFs were categorized as regulators of skeletal myogenesis (Barth *et al.* 1998). In various livestock species, MYF5 was performed as a candidate gene for carcass structure and meat quality (Muroya *et al*., 2002; Bhuiyan *et al*., 2009; Lühken *et al*., 2009). In local Chinese cattle breeds, the myogenic factor 5 (A1142G SNP) was used as an effective genomic marker for quality traits of meat (Ujan *et al*., 2011). And there are a few studies in this field of research (Jirimutu *et al.*, 2012; Burger and Palmieri, 2014; Al- Swailem *et al.*, 2018). Therefore, discover the camel potential is needed through understand the genetic makeup (Al Abri and Faye, 2019). The main objectives of the current study were to 1) define the variations in exon 1 region of MYF 5 and two regions of GH genes (3 UTR and 5 UTR) of *dromedarius* camel and 2) study the association among the detected SNPs in these regions and live body measurements, carcass traits, carcass cuts, histological traits, and chemical composition of meat.

MATERIALS AND METHODS

A total number of eleven males of One-humped camel in growing stage were used with an average initial body weight of 251 ±7 kg. The studied camels were raised for five months and fed on the same diet. At the end of this period, camels were weighed, slaughtered and applied measurements on carcass, the average slaughter weight was 359±10 kg. Carcass characterises were recorded. Meat samples from best ribs (11th and 12th ribs) of each camel were collected and analysed to estimate meat quality parameters. Histological measurements were conducted according to the technique explained by Kiernan (1999).

DNA extraction and PCR reaction

Blood samples were used to isolate the DNA by Gene JET Kit. PCR was completed in a reaction volume of 25 µl containing 100 ng of DNA, 0.2 mM of each primer, 1X PCR buffer, 2.5 mM MgCl2, 0.2 mM of each dNTP and 0.5 units of Green Dream Taq DNA polymerase. The PCR steps were conducted according to Zayed (2016) (Table 1). Afterward, previous literature on llama were used to the primers design

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that used in the amplification of the GH gene (5 and 3 UTR), also the conditions of PCR cycles were adjusted to work on DNA of dromedary camel according to Zayed (2016).

Statistical analysis

Association analysis was performed between phenotypes and genotypes using the least squares means (GLM) using SAS (2004). The following statistical model was performed: $Y_{ij} = \mu + CG_i + e_{ij}$, Where: Y_{ij} = the observation, μ = the overall mean of the trait under study, CG_i= gene i, where i : 1 = Myogenic factor 5 gene (MYF5) and 2= Growth hormone gene (GH), e_{ij} = the random error

Table 1. PCR primers, annealing temperature (Ta) and amplicon size of the genes under study.

Gene name	Amplified part	Primer sequence	Ta °C	Amplification size	reference
MYF 5	Exon 1	TGCCAGTTCTCGCCCTCTGAGT TATAGTAGTTTTCCACCTGTTCC	56	400	Shah *et al.*, 2007
GH	3 UTR	TCCTCAGGCAAACCTACGAC TGATGCAACCTCATTTTATTAGA	50	230	Daverio *et al.*, 2012
GH	5 UTR	GAAAATAAGTGGGGGCAGAG AGTTTCCTCCCATTATGCAG	56	640	Daverio *et al.*, 2012

RESULTS AND DISCUSSION

The current results in Table (2) show the variations in the MYF5 and GH, there were significant contributions to the live body measurements. The effect of MYF5 on the fore shank height, height at wither, height at pelvic, circumference at pelvic, chest girth, leg circumference and leg length was significant (P<0.05). These findings were also indicated that the effects of GH on height at wither, circumference at pelvic, body conformation fore shank height, height at pelvic, chest girth, leg circumference and leg length were significant (P<0.05), that agree with the study of Gao *et al.* (2007), SNPs of hircine MYF5 and MYF6 genes in goat. They indicated that genotypes of the MYF5 locus were associated (P<0.05) with hucklebone width and hucklebone width index in goat. In in Sudani camels, the SNPs of GH gene were correlated with body measurements (Ishag *et al* 2010).

Table 2. Contribution of myogenicfactor 5 and growth hormone genes on live body measurements of dromedary camel.

Body measurements	MYF5	GH
Foreshank height	.0123*	.0040**
Height at wither	.0496*	.0416*
Height at pelvic	.0105*	.0033**
Circumference at pelvic	.0352*	.0234*
Chest girth	.0043**	.0028**
Leg circumference	.0031**	.0040**
Leg length	.0073**	.0029**
Body conformation	—	.0374*

*** Significant (P<0.05). ** Highly significant (P<0.01).**

The present results in Table 3 reveal that MYF5 and GH genes had a significant effect on camel carcass traits. The influence of MYF5 and GH genes was significant (P<0.05) on pre-slaughter weight, dressing percentage, dressing percentage with hump, and dressing percentage with edible parts. The influence on carcass weight, left fore quarter weight, left hind quarter weight, four quarters weight, edible parts weight, and carcass with hump weight was also highly significant (P<0.01). In this respect, Lee *et al.* (2013) found a relationship among, growth, carcass merits, and bovine GH gene, and ten SNPs in GH gene were genotyped for 242 Hanwoo steers.

The current results proved that MYF5 had a significant impact on carcass cuts (Table 4). The impact of MYF5 on neck weight, shoulder as a percentage, fore shank percentage, fore shank bone as a percentage, foreribs percentage, brisket weight, leg weight and loin weight were significant(P<0.05). The influence on carcass component weight, shoulder weight, filet weight and total carcass bone weight and percentage were even highly significant (P<0.01). The results also indicated that GH significantly contributed to the carcass cuts. The influence of GH on neck percentage, brisket weight and best ribs meat weight were significant, and the effects on carcass component weight, neck meat weight, shoulder weight and percentage, fore shank weight and leg weight were highly significant.

Table 3. Contribution of (P<0.05) myogenicfactor 5 and growth hormone genes on carcass traits of dromedary camel.

Carcass traits	MYF5	GH
Slaughter wt (kg)	.0467*	.0264*
Carcass wt (kg)	.0042*	.0017**
Left fore quarter wt (kg)	.0110*	.0049**
Left hind quarter wt (kg)	.0036**	.0030**
Quarters wt (kg)	.0049**	.0021**
Neck wt (kg)	.0147**	.0057**
Edible parts wt (kg)	.0063**	.0145*
Hump wt (kg)	.0232*	.0103*
Carcass with hump wt (kg)	.0026**	.0008**
Empty body wt (kg)	—	.0363*
Dressing percentage	.0340*	.0278*
Dressing percentage (with hump)	.0306*	.0250*
Dressing percentage (with Edible parts)	.0306*	.0223*
Chilled carcass wt (kg)	.0034*	.0013**

*** Significant (P<0.05). ** Highly significant (P<0.01).**

Table 4. Contribution of myogenicfactor 5 and growth hormone genes on carcass cuts of dromedary camel.

Carcass cuts	MYF5	GH
Carcass component wt (kg)	.0034**	.0013**
Neck wt (kg)	.0147**	.0057**
Neck percentage	—	.0335*
Neck bone	.0016**	.0010**
Neck meat	—	.0411*
Shoulder wt (kg)	.0075**	.0029**
Shoulder percentage	.0237*	.0462*
Shoulder meat wt (kg)	.0072**	.0031**
Foreshank wt (kg)	—	.0332*
Foreshank percentage	.0420*	.0019**
Foreshank bone wt (kg)	.0473*	—
Foreshank meat wt (kg)	—	.0435*
Foreribs percentage	.0368*	.0275*
Foreribs bone wt (kg)	.0045**	—
Brisket wt (kg)	—	.0455*
Brisket percentage	.0271*	.0126*
Brisket meat wt (kg)	.0406*	.0187*
Brisket bone wt (kg)	.0496*	.0393*
Best ribs meat wt (kg)	.0385*	.0175*
Flank wt (kg)	.0443*	—
Flank percentage	.0422*	—
Leg wt (kg)	.0151*	.0093**
Leg meat wt (kg)	.0306*	.0306*
Leg bone wt (kg)	.0101*	.0001**
Hindshank bone	.0268*	.0164*
Loin wt (kg)	.0404*	.0256*
Loin percentage	.0205*	.0161*
Loin meat wt (kg)	.0122*	.0087**
Loin bone wt (kg)	—	.0487*
Filet wt (kg)	.0027**	.0011**
Filet percentage	—	.0369*
Total carcass bone wt (kg)	.0030**	.0014**
Total carcass bone percentage	.0090**	.0451*

*** Significant (P<0.05). ** Highly significant (P<0.01).**

Additionally, there were a significant effect of MYF5 and GH on histological traits and chemical composition of camel carcasses (Table 5). The significant influence of MYF5 and GH on LD muscle area**,** protein and fat contents were observed**.** The significant impact of GH on cooking loss %, thickness of myofibers and bundle area were detected.

Table 5. Contribution of myogenicfactor 5 and growth hormone genes on physical properties, chemical composition and histological traits of dromedary camel.

Meat quality traits	MYF5	GH
Physical properties		
Eye muscle area (cm^2)	.0342*	.0144*
Expressible fluid %	.0068**	.0025**
Longissimus dorsi area 10(cm^2)	.0292*	.0464*
Cocking loss %	—	.0455*
Chemical composition		
Protein	.0488*	.0409*
Fat	.0261*	.0383*
Color parameters		
L (lightness)	.0143*	.0387*
b (yellowness)	.0457*	—
Muscle structures		
Thickens of fibers (µm)	—	.0249*
Bundle area (μm^2)	.0151*	.0063**

*** Significant (P<0.05). ** Highly significant (P<0.01).**

CONCLUSION

The results indicated that there were polymorphisms in MYF5 and GH genes with significant influence on body measurements, carcass merits, and histological parameters and chemical contents of meat. Three regions in both MYF5 and GH genes were associated with carcass and meat quality traits, which considered as candidate genes for growth performance in one humped camel.

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المساهمة الجينية لجين هرمون النمو وجين معامل التخليق العضلى رقم 5 وعلاقتهما بمقاييس الجسم الحى وصفات الذبيحة وجودة اللحم للإبل وحيدة السنام

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الملخص

أجريت هذه الدراسة فى محطة بحوث مريوط التابعة لمركز بحوث الصحراء بالقرب من الإسكندرية. وقد أستخدم فى هذه الدراسة عدد 11من ذكور الإبل وحيدة السنام، وكان متوسط وزن البداية 251.36 ± 97. 6 كجم وبعد خمس شهور من إتباع نظام غذائى يحتوى على عليقة تجارية 12 % بروتين خام وعمر حوالى 30 شهر وصل متوسط الوزن النهائى إلى 359.09 ± 95. 9 كجم. استهدفت الدراسة إجراء دراسة أولية لمحاولة توصيف بعض المواقع الجينية (SNPs) لجين هرمون النمو وجين معامل التخليق العضلى رقم 5 وعلاقتهما بصفات جودة اللحم فى ذبائح الإبل فى محاولة للوصول إلى دليل إنتخابى مبكر يساعد فى برامج التربية الخاصة بقطعان الإبل. خلصت الدراسة إلى أن هناك مناطق جينية (SNPs) موجودة فى جزئين من جينوم الجمل وحيد السنام بمصر ، إحداها فى جين معامل التخليق العضلى رقم 5 و الاخرى فى جين هرمون النمو. تلك المناطق الجينية ارتبطت بالعديد من صفات إنتاج وجودة اللحم فى الإبل وحيد السنام، مثل مقاييس الجسم الحى، وكلا من الوزن عند الذبح، نسبة التصافى بينما كانت معنوي جدا مع كلا من وزن الذبيحة ، وزن الارباع المختلفة وايضا أشارت النتائج إلى وجود ارتباط بين جين هرمون النمو والقطعيات التجارية المختلفة لذبائح الإبل كما لوحظ من النتائج وجود ارتباط معنوى بين جين معامل التخليق العضلى رقم 5 وجين هرمون النمو وكلا من مساحة العضلة العينية و محتوى اللحم من البروتين والدهن. وكذلك كان هناك ارتباط معنوى جدا لجين هرمون النمومع نسبة الفقد بالطهى ، وسمك الليفة العضلية ومساحة الحزمة العضلية . وتوصى الدراسة بإمكانية إستخدامها كدليل إنتخابى مبكر يساعد فى برامج التربية الخاصة بقطعان الإبل.

الكلمات الدالة: الإبل وحيدة السنام ،خصائص اللحوم ، جين معامل التخليق العضلى رقم 5 و جين هرمون النمو.