EFFECT OF VARIATION IN THE ADRENERGIC RECEPTOR BETA 3 (*ADRβ3*) GENE ON WOOL TRAITS IN BARKI SHEEP

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Barki sheep is one of the three major Egyptian sheep breeds, raised for meat and less for coarse wool production and distributed mainly in the north-west coastal region. While wool produced from Barki sheep could contribute to the national textile industry, it is used for making carpets, blankets, tents and other handmade products in most Bedouins communities. Therefore increasing the quantity and quality of wool could improve the Bedouins textile handmade products which lead to increase income and improve the economic value of these raw materials.

Recently, there is a great interest to identify molecular markers controlling economically important traits of agriculture animals. Molecular markers are not affected by environmental factors and provide more accurate and reliable criteria to assess the true genetic merit of animals (Beuzen *et al.*, 2000). There are two commonly approaches used to identify the molecular markers: the genome scan approach and the candidate gene approach. In the genome scan approach, the whole genome is searched to identify where such gene(s) affecting the desired trait may lie. In the candidate gene approach, the purpose is to identify gene(s) that are thought to be responsible for the phenotype variance of the desired trait (Rothschild and Sölkner, 1997).

Although, wool traits can be measured easily and have moderate to high heritabilities, it is suggested that research into certain molecular markers affecting wool production and wool traits is still justified to improve target specific wool quality traits that are important for processing and to break antagonistic correlation which might be existed between some traits such as fleece weight and fiber diameter (Itenge-Mweza, 2012). The identification of molecular markers would allow sheep breeders to select lambs with improved wool traits at an early age and cull the non-desirable lambs. This would speed up the process of genetic selection and decrease the generation interval.

With the advent of genome scan approach, few studies localized the microsatellites associated with some wool traits in INRA 401 sheep and Sarda x Lacaune sheep, including OARAE101 on chromosome 6 and IDVGA088 on chromosome 25 for mean fiber diameter (Ponz *et al*., 2001); McM218 on chromosome 4

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for coefficient of variation of fiber diameter (Allain *et al.*, 1998 & 2006) and BMC1009 on chromosome 3, OARVH34 on chromosome 7 and ILST005 on chromosome 25 for mean staple length (Ponz *et al.*, 2001).

Previous reports, used the candidate gene approach, proved that the variation in many genes are associated with wool traits. Mean fiber diameter in Merino sheep was found to be associated with the variation in keratin associated protein (KAP) genes (Parsons *et al.*, 1994; Beh *et al.*, 2001), while mean staple strength in Romney sheep was associated with the variations in KAP1.1 and KAP1.3 genes (Rogers *et al.*, 1994). Also, the variation in adrenergic receptor β3 (*ADRβ3*) gene was associated with mean staple strength, brightness of wool and yield in New Zealand Merino sheep (Itenge-Mweza, 2007; Forrest *et al.*, 2009).

The *ADRβ3* is belongs to the superfamily of beta adrenergic receptors, located on the surface of white and brown adipose cells and plays a key role in the regulation of energy homeostasis through promoting lipolysis and thermogenesis under sympathetic neural control (Clément *et al.*, 1995). It is assumed that the energy homeostasis affecting most biological functions in the cells of various tissues and organs, including wool follicles that control wool growth and traits. Energy metabolism in Merino sheep was associated with the estimated breeding values for clean wool yield and mean fiber diameter (Adams *et al.*, 2006). Also, the estimated breeding values for wool growth and mean fiber diameter were affected by the energy expenditure in some Australian breeds of sheep (Li *et al.*, 2008). Therefore, the *ADRβ3* gene could be considered as a candidate gene affecting wool traits of sheep. The aim of this work was to investigate the association between the variation in the *ADRβ3* gene and some wool traits in Barki sheep.

MATERIALS AND METHODS

Animal resource and data collection

From Barki lambs that genotyped for the ADRβ3 gene in the previous study of Ibrahim (2014), 57 males were used to test the association between the variation in *ADRβ3* gene and some wool traits.

At shearing season, mid-side samples were collected, using a fine scissor, as close as possible to the skin surface forming a square of 10 x 10 cm. From each sample, the greasy wool was weighted and the greasy wool per unit area was calculated according to the method of El-Gabbas (1993). The greasy sample was used to estimate the clean wool yield according to the method of Chapman (1960) and the clean wool per unit area using the method suggested by El-Gabbas (1993).

Five staples were randomly taken from each greasy sample and used to measure the mean staple length, the mean staple crimp and the mean staple strength. Staple length was taken for the distance between the broad base and the end of dense region at the longest fiber without

stretching. The number of crimps along with each unscratched staple was counted per one centimeter. Staple strength was measured to estimate the force required to break the staple in Newton (Newton in Kilotex, N/Ktex) divided by the thickness of the staple using the Agritest Staple Breaker (Caffin, 1980). The length of the top and the base of each staple broken in the strength test were measured and added together. The increase in length as a proportion of the original staple length before testing was used to calculate the elongation percentage according to El-Gabbas *et al.* (1999). The length of the top as a percentage from the length of both the top and the base was recorded as the point of break for each sample (El-Gabbas *et al.*, 1999).

From each sample, the diameters of 500 fibers were measured using Axio Imager (Carl Zeiss Micro Imaging, Gottingen, Germany) with (A-plan 10 X/ 0.25 ∞ / -). The medullation percentage was estimated by counting the number of medullated fibers occurring in the sample used for measuring the fiber diameter (El-Gabbas, 1998). Prickle factor (coarse edge) was also estimated from the fiber diameter distribution of each sample as the percentage of fibers with diameter exceeding 30 micrometers from the total number of fibers (Naylor, 1992).

Polymerase chain reaction

Blood samples were collected from the jugular vein of the phenotyped animals, placed into 5 ml of heparinized tubes and stored at -80°C upon extracting the genomic DNA using a commercial kit (Qiagen, Hilden, Germany).

A highly variable fragment (263 pb) from the single intron of the ovine *ADRβ3* gene was amplified using a pair of specific primers suggested by Byun *et al.* (2008). The primer sequences were as follow: (F: 5`-CTAGCTCAGTTCT-TTCTCTGC-3` and R: 5`-CCCAACTCCAACCCGACC-3`). The polymerase chain reaction (PCR) mixture contained 50 ng of genomic DNA, 0.25 µM of each primer, 150 µM dNTPs (Eppendorf, Hamburg, Germany), 1x polymerase buffer (including 1.5 µM $MgCl_2$), 0.5 U Taq DNA polymerase (Qiagen, Hilden, Germany) and some deionized water up to final volume of 20 µl. The thermal cycling was carried out using a Bio-Rad C 1000 touch thermal cycler (Bio-Rad, USA). The program conditions were 94°C for 2 min, followed by 35 cycles of 94°C for 30s, 60°C for 30s and 72°C for 30s. The final step prolonged 5 min at 72°C.

Single strand conformational polymorphism

PCR products were resolved by the single strand conformational polymorphism (SSCP) analysis. Amount of 2 µl from each PCR product was mixed with 8 µl from a loading dye solution (98% formamide, 0.025% bromophenol blue, 0.025% xylene cyanol, 10 mM EDTA (Eppendorf, Hamburg, Germany), denatured at 105°C for 6 min, rapidly chilled on wet ice and loaded on 16 × 18 cm; 12% acrylamide: bisacrylamide (37.5: 1; Bio-

Rad, USA) gels. PCR products representative of the first eight known ADRβ3 alleles (A, B, C, D, E, F, G and H) which were detected by Byun *et al.* (2008) were included in the polyacrylamide gels (well numbers 13 and 14 in the gel a), and their banding patterns were used as standards for determining the alleles present in individual Barki sheep. The electrophoresis was run in 0.5 x TBE buffer for 18 h at 200 V and 25°C, using a Protean II xi cells electrophoresis apparatus (Bio-Rad, USA). Gels were silver stained using the method of Sanguinette *et al.* (1994).

Statistical analysis

Data were analyzed by general linear mixed effect models (GLMMs) using the software of SPSS, version 19 (SPSS, 2010). The statistical analysis was divided into two sets of analyses; the first set was to test the effect of ADRβ3 genotype on wool traits and the second set was to explore the effect of the presence/absence of each ADRβ3 allele in the genotype on the studied wool traits.

ADRβ3 genotype (in the first set) or the presence/ absence of each ADRβ3 allele in the genotype (in the second set), was fitted as a fixed effect while sire was fitted as a random effect in each model. Age of lamb at shearing was included in the model as a co-variate. Where significant, these were further explored using pairwise comparison (Duncan test; $P \leq 0.05$).

The generalized statistical model used to test the genotype effect was (without the added covariates) as follows:

$$Y_{ijk} = \mu + t_i + \beta_j + \epsilon_{ijk}$$

Where Y_{ijk} = traits (mean fiber diameter, mean staple length, mean staple strength, etc); μ = the overall mean for each trait; t_i = the fixed effect of i^{th} genotype (animal genotype in the first set or the presence/ absence of each allele in the second set); β_j = the random effect of j^{th} sire and ϵ_{ijk} = the random error for *ijk* observation; assumed N.I.D. $(0, \sigma^2, e)$.

RESULTS AND DISCUSSION

Allelic and genotypic frequencies

In animal samples that phenotyped for wool traits, 10 ADRβ3 genotypes represented 6 alleles (A, B, C, D, E and H) were detected as shown in Figure (1). The allelic and genotypic frequencies were presented in Table (1).

Association of ADRβ3 genotype with the studied wool traits

The results of association analysis between the ADRβ3 genotype and the studied wool traits were shown in Table (2). The ADRβ3 genotype significantly ($P < 0.05$) affected clean wool yield, mean staple strength and prickle factor value. Least square means showed that, animals with the CC genotype had much higher ($P < 0.05$) clean wool yield than other genotypes. Mean staple strength was higher ($P < 0.05$) in animals with genotype CD than animals of other genotypes. Also, AA

animals had the highest value ($P < 0.05$) and BB and BH animals had the lowest value for prickle factor.

There was no effect for the ADRβ3 genotype on the rest of the studied traits that includes greasy wool per unit area, clean wool per unit area, mean fiber diameter, medullation percentage, mean staple crimp, mean staple length, elongation percentage and point of break

Association of the presence/ absence of ADRβ3 alleles in animal genotype with the studied wool traits

The effects of the presence/ absence of the ADRβ3 alleles in animal genotype on the studied wool traits are presented in Table (3). The presence of allele A was significantly ($P < 0.05$) associated with decreased clean wool yield and increased value of prickle factor and high significantly ($P < 0.01$) associated with decreased mean staple strength. In contrast, the presence of allele C was significantly ($P < 0.05$) associated with increased clean wool yield and increased mean staple strength. These results are in agreement with the results obtained by Forrest *et al.* (2009).

No association were found between the presence/ absence of the ADRβ3 alleles in animal genotype and each greasy wool per unit area, clean wool per unit area, mean fiber diameter, medullation percentage, mean staple crimp, mean staple length, elongation percentage and point of break

Mean staple strength, clean wool yield and prickle factor value that were affected by the variation in *ADRβ3* gene are of important in wool production and processing. Mean staple strength is one of the key raw wool characteristics in the prediction equation of estimating Hauteur of tops, and critically determining the price of raw wool (Schlink *et al.*, 2001). The prickle factor is known to cause problems in the perceived comfort of wool fabrics worn against the skin and resulted in unpleasant sensation of prickle and prolonged irritation and being associated with skin inflammation (Lupton *et al.*, 2001). Clean wool yield is a quantitative term to describe the proportion of clean yield in a given quantity of raw wool. It is a very important trait, since the wool is usually sold on a clean wool bases that have benefits to both wool manufactures and sheep breeders.

The effect of variation in *ADRβ3* gene on those three important wool traits means that the ADRβ3 has a biological function causing a variation in the phenotype of these wool traits. Few studies indicated that, fiber growth is markedly hormone dependent and experimental manipulation of hormone or enzyme status causes large changes in the rate of wool growth (Khan *et al.*, 2012). ADRβ3 was found to mediate the action of adrenaline and noradrenaline hormones. Addition of adrenaline and noradrenaline to cultured sheep skin reduced DNA synthesis, while injection of these two hormones into live animals significantly decreased the rate of cell division in the wool follicles and

hence reduced wool growth (Scobie *et al.*, 1994). Similarly, these two hormones were found to increase the secretion of glucocorticoids which cause the depression or complete cessation of wool growth (Khan *et al.*, 2012). These cited references indicate that the adrenaline and noradrenaline hormones which mediated by ADRβ3 can rapidly lower the rate of proliferative events in the wool follicle and may therefore play an important role in the regulation of wool growth. Also, beta adrenergic receptors were found to induce the activation of adenylate cyclase through the action of G protein. In the wool follicle cells, adenylate cyclase serves as an effector enzyme that acting to catalyze the adenosine triphosphate (ATP) into cyclic adenosine monophosphate (cAMP) to release energy that affect wool follicle (Lafontan and Berlan, 1993; Garland and Biaggioni, 2001).

CONCLUSION

This study suggests significant association for the variation in ADRβ3 with the most important wool traits. This genetic variation could be used as a molecular marker for the selection of animals with optimizing clean wool yield, mean staple strength and minimizing the prickle factor value. Moreover, further studies are needed in a large population of Barki sheep or other breeds of sheep to confirm the association we found.

SUMMARY

The adrenergic receptor β3 (*ADRβ3*) gene encodes for ADRβ3 which is mainly expressed in white and brown adipose tissues of mammals and plays a crucial role in energy homeostasis that affect the various tissues and organs including wool follicle that controls wool growth and traits. The objective of this study was to test the association between the variation in *ADRβ3* gene and some wool traits (greasy wool per unit area, clean wool per unit area, clean wool yield, mean fiber diameter, medullation percentage, mean staple crimp, mean staple length, mean staple strength, prickle factor value, elongation percentage and point of break in 57 males of Barki lambs using the polymerase chain reaction-single strand conformational polymorphism (PCR-SSCP) tool. General linear mixed effect models were used to test the effect of ADRβ3 genotype or the presence/ absence of ADRβ3 alleles in animal genotype on the studied wool traits. The genotype of ADRβ3 had significant effect ($P < 0.05$) on clean wool yield, mean staple strength and prickle factor value. The presence of allele C and the absence of allele A in animal genotype were significantly associated with increased clean wool yield, increased mean staple strength and decreased prickle factor value. The results presented here give valuable information to select for allele C and against allele A to improve some of the most important wool traits in Barki sheep.

REFERENCES

Adams, N. R., J. R. Briegel, J. C. Greeff and E. N. Bermingham (2006). Feed intake, body composition, and

plasma metabolic hormones in Merino sheep that differ genetically in fleece weight or fibre diameter. Australian Journal of Agricultural Research, 57: 27-32.

Allain, D., I. Lantier, J. M. Elsen, D. François, J. C. Brunel, J. L. Weisbecker, L. Schibler, D. Vaiman, E. P. Cribiu, A. Gautier, P. Berthon and F. Lantier (1998). A design aiming at detecting QTL controlling wool traits and other traits in the Inra401 sheep line. Proceedings 6th World Congress Genetics Applied to Livestock Production, Armidale, NSW, Australia, 24: 51-54.

Allain, D., L. Schibler, L. Mura, F. Barillet, T. Sechi, R. Rupp, S. Casu, E. P. Cribiu and A. Carta. (2006). A QTL detection with DNA markers for wool traits in a sheep backcross Sarda X Lacaune resource population. 8th World Congress on Genetics Applied to Livestock Production, Belo Horizonte, MG, Brasil. p. 5-7.

Beh, K. J., M. J. Callaghan, Z. Leish, D. J. Hulme, I. Lenane and J. F. Maddox (2001). A genome scan for QTL affecting fleece and wool traits in Merino sheep. Wool Technology and Sheep Breeding, 49: 88-89.

Beuzen, N. D., M. J. Stear and K. C. Chang (2000). Molecular markers and their use in animal breeding - review. The Veterinary Journal, 160: 42-52.

Byun, S., Q. Fang, H. Zhou and J. H. G. Hickford (2008). Rapid genotyping of the ovine *ADRB3* gene by polymerase chain reaction-single-strand conformation polymorphism (PCR-SSCP). Molecular and Cellular Probes, 22: 69-70.

Caffin, R. N. (1980). The CSIRO staple strength/length system. I. Design and performance. The Journal of the Textile Institute, 70: 65-70.

Chapman, R. E. (1960). In The Biology of the Fleece, edited by A. S. Fraser, and B. F. Short, Animal Research Laboratories Technical Paper No. 3. CSIRO, Australia.

Clément, K., C. Vaisse, B. Manning, A. Basdevant, B. Guy-Grand, J. Ruiz, K. D. Silver, A. R. Shuldiner, P. Froguel and A. D. Strosberg (1995). Genetic variation in the β3-adrenergic receptor and an increased capacity to gain weight in patients with morbid obesity. The New England Journal of Medicine, 333: 352-354.

El-Gabbas, H. M. (1993). Seasonal variation of wool productivity from various body positions in Barki sheep. Egyptian Journal of Animal Production, 30: 201-212.

El-Gabbas, H. M. (1998). Wool fiber diameter and its distribution in Barki

sheep with regard to the sampling positions and seasons. Egyptian Journal of Animal Production, 35: 123-141.

El-Gabbas, H. M., A. Helal and E. M. Al-Betar (1999). Wool tenacity in the coarse wool Barki fleeces. Alexandria Journal of Agricultural Research, 44: 67-83.

Forrest, R. H., T. O. Itenge-Mweza, G. W. McKenzie, H. Zhou, C. M. Frampton and J. H. G. Hickford (2009). Polymorphism of the ovine β3-adrenergic receptor gene (*ADRB3*) and its association with wool mean staple strength and yield. Animal Genetics, 40: 958-962.

Garland, E. M. and I. Biaggioni (2001). Genetic polymorphisms of adrenergic receptors. Clinical Autonomic Research, 11: 67-78.

Ibrahim, A. H. M. (2014). Single strand conformational polymorphism of *ADRB3* gene and its association with live performance traits in barki sheep. Egyptian Journal of Genetics and Cytology, 43: 287-299.

Itenge-Mweza, T. O. (2007). Identification of genetic markers associated with wool quality traits in merino sheep. Ph. D. thesis, Lincoln University, Canterbury, New Zealand.

Itenge-Mweza, T. O. (2012). Identification of polymorphism in the keratin genes (*KAP3.2*, *KAP6.1*, *KAP7* and *KAP8*) and microsatellite BfMS in Merino sheep using polymerase chain reaction-single strand conformational polymorphism (PCR-SSCP) analysis. In the book "Electrophoresis" edited by Kiumars Ghowsi, InTech. Chapter 11: 193-220.

Khan, M. J., A. Abbas, M. Ayaz, M. Naeem, M. S. Akhter and M. H. Soomro (2012). Factors affecting wool quality and quantity in sheep. African Journal of Biotechnology, 11: 13761-13766.

Lafontan, M. and M. Berlan (1993). Fat cell adrenergic receptors and the control of white and brown fat cell function. Journal of Lipid Research, 34: 1057-1091.

Li, L., V. H. Oddy and J. V. Nolan (2008). Whole-body protein metabolism and energy expenditure in sheep selected for divergent wool production when fed above or below maintenance**.** Australian Journal of Experimental Agriculture, 48: 657-665.

Lupton, C. J., D. F. Waldron and F. A. Pfeiffer (2001). Prickle factor in fleeces of performance-tested Fine-wool rams. Sheep and Goat Research Journal, 17: 9-13.

Naylor, G. R. S. (1992). Precision of measurement of the coarse edge in the wool fiber diameter distribu-

tion. Wool Technology and Sheep Breeding, 40: 44-46.

Parsons, Y. M., D. W. Cooper and L. R. Piper (1994). Evidence of linkage between high glycine-tyrosine keratin gene loci and wool fibre diameter in a Merino half-sib family. Animal Genetics, 25: 105-108.

Ponz, R., C. Moreno, D. Allain, J. M. Elsen, F. Lantier, I. Lantier, J. C. Brunel and M. Pérez-Enciso (2001). Assessment of genetic variation explained by markers for wool traits in sheep *via* a segment mapping approach. Mammalian Genome, 12: 569-572.

Rogers, G. R., J. G. H. Hickford and R. Bickerstaffe (1994). A potential QTL for wool strength located on ovine chromosome 11. Proceedings of the 5th World Congress on Genetics Applied to Livestock Production: 7-12 August; Guelph, 21: 291-294.

Rothschild, M. and M. Sölkner (1997). Candidate gene analysis to detect genes controlling traits of economic importance in domestic livestock. Probe, 8: 13-20.

Sanguinetti, C. J., E. Dias Neto and A. J. G. Simpson (1994). Rapid silver staining and recovery of PCR products separated on polyacrylamide gels. Biotechniques, 17: 915-919.

Schlink, A. C., D. J. Brown and M. Longree (2001). Role of fibre length variation in staple strength of Merino wool. Wool Technology and Sheep Breeding, 49: 202-211.

Scobie, D. R., P. I. Hynd and B. P. Setchell (1994). Reduction of synthetic and mitotic activity in the wool follicle by catecholamines. Australian Journal of Agricultural Research, 45: 1159-1169.

SPSS (2010). IBM SPSS Statistics 19 Core System User's Guide, Science Inc., Chicago, IL, USA

Table (1): Allelic and genotypic frequencies for *ADRβ3* gene in Barki sheep.

Allele	Frequency	Genotype	No.	Frequency	Genotype	No.	Frequency
A	0.38	AA	10	0.18	BH	3	0.05
B	0.20	AB	9	0.16	CC	5	0.09
C	0.30	AC	11	0.19	CD	4	0.07
D	0.03	AE	3	0.05	CH	4	0.07
E	0.02	BB	3	0.05			
H	0.06	BC	5	0.09			

Table (2): Least Square means and standard errors of wool traits according to the ADRβ3 genotype effects in Barki sheep.

Genotype	No.	GWA (g/cm^2)	CWA (g/cm^2)	YLD	MFD (μm)	M%	MCR/cm
AA	10	0.225 ± 0.009	0.090 ± 0.003	40.47 ± 1.503^{bb}	33.58 ± 0.783	10.12 ± 1.252	0.630 ± 0.040
AB	9	0.242 ± 0.024	0.096 ± 0.008	40.20 ± 1.115^{bb}	28.90 ± 1.254	6.91 ± 1.314	0.628 ± 0.053
AC	11	0.212 ± 0.022	0.090 ± 0.009	42.39 ± 1.216^{bb}	28.69 ± 0.985	7.83 ± 1.577	0.709 ± 0.035
AE	3	0.182 ± 0.009	0.075 ± 0.001	41.68 ± 1.728^{bb}	30.81 ± 3.537	8.86 ± 3.766	0.523 ± 0.080
BB	3	0.189 ± 0.051	0.078 ± 0.018	42.46 ± 2.174^{bb}	27.17 ± 2.539	4.60 ± 2.318	0.747 ± 0.047
BC	5	0.257 ± 0.027	0.111 ± 0.014	42.92 ± 2.005^{bb}	31.53 ± 1.886	9.64 ± 2.469	0.696 ± 0.053
BH	3	0.186 ± 0.005	0.079 ± 0.005	42.48 ± 3.419^{bb}	28.42 ± 1.224	7.13 ± 1.686	0.660 ± 0.073
CC	5	0.230 ± 0.025	0.112 ± 0.012	48.93 ± 1.355^{aa}	29.62 ± 2.073	9.36 ± 2.825	0.695 ± 0.052
CD	4	0.174 ± 0.027	0.077 ± 0.013	43.90 ± 1.989^{ab}	31.32 ± 3.214	12.20 ± 4.594	0.637 ± 0.114
CH	4	0.266 ± 0.043	0.108 ± 0.012	41.60 ± 1.726^{bb}	29.90 ± 1.526	5.80 ± 1.776	0.714 ± 0.027
P-value		NS	NS	*	NS	NS	NS

GWA: greasy wool per unit area; CWA: clean wool per unit area; YLD: clean wool yield; MFD: mean fiber diameter; M%: medulation percentage; MCR: mean staple crimp.

Genotype	No.	MSL (cm)	MSS (N/Ktex)	PF	EL%	POB
AA	10	8.73 ± 0.349	13.53 ± 0.947^{bb}	52.68 ± 2.258^{aa}	31.47 ± 1.515	46.42 ± 1.533
AB	9	8.85 ± 0.405	14.18 ± 1.084^{bb}	34.75 ± 4.896^{ab}	29.12 ± 1.195	46.58 ± 2.135
AC	11	8.20 ± 0.622	14.02 ± 1.195^{bb}	33.30 ± 3.961^{ab}	29.17 ± 2.848	49.66 ± 1.997
AE	3	8.13 ± 0.120	13.33 ± 2.965^{bb}	36.66 ± 10.859^{ab}	23.89 ± 2.558	45.93 ± 4.733
BB	3	7.73 ± 0.876	16.40 ± 1.732^{bb}	28.40 ± 8.680^{bb}	37.27 ± 5.503	47.72 ± 3.836
BC	5	8.74 ± 0.927	18.56 ± 4.150^{ab}	42.36 ± 5.486^{ab}	37.98 ± 3.964	46.79 ± 2.254
BH	3	8.46 ± 0.600	15.34 ± 2.853^{bb}	28.66 ± 4.370^{bb}	28.41 ± 2.744	46.94 ± 3.046
CC	5	8.88 ± 0.549	16.81 ± 2.528^{bb}	37.40 ± 8.042^{ab}	33.03 ± 4.972	46.67 ± 3.016
CD	4	7.12 ± 1.400	24.88 ± 4.387^{aa}	34.90 ± 4.373^{ab}	32.93 ± 6.212	51.18 ± 2.466
CH	4	9.12 ± 0.626	16.91 ± 1.255^{bb}	38.75 ± 5.168^{ab}	27.96 ± 3.623	46.94 ± 5.329
P-value		NS	*	*	NS	NS

MSL: mean staple length; MSS: mean staple strength; PF: prickle factor value; EL%: elongation percentage; POB: point of break; NS: no significance; *: refers to significance at ($P < 0.05$).

Table (3): Least Square means and standard errors of wool traits according to the presence/absence of ADRβ3 alleles in Barki sheep.

Trait	Allele being assessed	LSM ± SE				P-value
		Allele absent	No.	Allele present	No.	
GWA (g/cm^2)	A	0.222 ± 0.013	24	0.221 ± 0.010	33	NS
	B	0.217 ± 0.009	37	0.229 ± 0.015	20	NS
	C	0.218 ± 0.010	28	0.225 ± 0.013	29	NS
	D	0.225 ± 0.008	53	0.174 ± 0.027	4	NS
	E	0.223 ± 0.008	54	0.182 ± 0.009	3	NS
	H	0.218 ± 0.008	53	0.266 ± 0.043	4	NS
CWA (g/cm^2)	A	0.097 ± 0.006	24	0.090 ± 0.004	33	NS
	B	0.092 ± 0.004	37	0.094 ± 0.006	20	NS
	C	0.088 ± 0.003	28	0.098 ± 0.005	29	NS
	D	0.094 ± 0.003	53	0.077 ± 0.013	4	NS
	E	0.094 ± 0.003	54	0.075 ± 0.001	3	NS
	H	0.092 ± 0.003	53	0.108 ± 0.012	4	NS
YLD	A	44.00 ± 0.915	24	41.15 ± 0.691	33	*
	B	42.77 ± 0.757	37	41.56 ± 0.886	20	NS
	C	40.94 ± 0.757	28	43.71 ± 0.814	29	*
	D	42.23 ± 0.609	53	43.90 ± 1.983	4	NS
	E	42.39 ± 0.609	54	41.68 ± 1.723	3	NS
	H	42.41 ± 0.615	53	41.60 ± 1.728	4	NS
MFD (µm)	A	29.89 ± 0.859	24	30.42 ± 0.690	33	NS
	B	30.72 ± 0.678	37	29.23 ± 0.848	20	NS
	C	30.54 ± 0.775	28	29.87 ± 0.748	29	NS
	D	30.11 ± 0.534	53	31.32 ± 3.217	4	NS
	E	30.16 ± 0.541	54	30.81 ± 3.530	3	NS
	H	30.22 ± 0.567	53	29.90 ± 1.526	4	NS
M%	A	8.42 ± 1.178	24	8.37 ± 0.800	33	NS
	B	8.99 ± 0.891	37	7.28 ± 0.955	20	NS
	C	8.04 ± 0.809	28	8.73 ± 1.076	29	NS
	D	8.10 ± 0.639	53	12.20 ± 4.592	4	NS
	E	8.36 ± 0.688	54	8.86 ± 3.760	3	NS
	H	8.58 ± 0.706	53	5.80 ± 1.779	4	NS
MCR/cm	A	0.691 ± 0.025	24	0.646 ± 0.024	33	NS
	B	0.664 ± 0.022	37	0.668 ± 0.030	20	NS
	C	0.634 ± 0.026	28	0.695 ± 0.023	29	NS
	D	0.667 ± 0.017	53	0.637 ± 0.114	4	NS
	E	0.673 ± 0.017	54	0.523 ± 0.080	3	NS
	H	0.661 ± 0.019	53	0.714 ± 0.027	4	NS

GWA: greasy wool per unit area; CWA: clean wool per unit area; YLD: clean wool yield percentage; MFD: mean fiber diameter; M%: medullation percentage; MCR: mean staple crimp; NS: no significance; *: refers to significance at ($P < 0.05$).

Table (3): Continued.

Trait	Allele being assessed	LSM ± SE				P-value
		Allele absent	No.	Allele present	No.	
MSL (cm)	A	8.40 ± 0.356	24	8.53 ± 0.254	33	NS
	B	8.41 ± 0.273	37	8.60 ± 0.319	20	NS
	C	8.57 ± 0.210	28	8.38 ± 0.359	29	NS
	D	8.58 ± 0.197	53	7.125 ± 1.403	4	NS
	E	8.49 ± 0.219	54	8.13 ± 0.120	3	NS
	H	8.43 ± 0.219	53	9.12 ± 0.626	4	NS
MSS (N/Ktex)	A	18.30 ± 1.358	24	13.85 ± 0.598	33	**
	B	15.69 ± 0.913	37	15.78 ± 1.213	20	NS
	C	14.22 ± 0.640	28	17.18 ± 1.234	29	*
	D	15.04 ± 0.626	53	17.88 ± 4.387	4	NS
	E	15.86 ± 0.748	54	13.33 ± 2.965	3	NS
	H	15.64 ± 0.773	53	16.91 ± 1.255	4	NS
PF	A	36.02 ± 2.551	24	40.87 ± 2.574	33	*
	B	40.13 ± 2.294	37	34.79 ± 2.998	20	NS
	C	40.02 ± 2.849	28	36.54 ± 2.351	29	NS
	D	38.50 ± 1.954	53	34.90 ± 4.373	4	NS
	E	38.34 ± 1.877	54	36.66 ± 10.859	3	NS
	H	38.21 ± 1.949	53	38.75 ± 5.168	4	NS
EL %	A	33.15 ± 1.903	24	29.37 ± 1.141	33	NS
	B	30.16 ± 1.367	37	32.45 ± 1.634	20	NS
	C	30.20 ± 1.079	28	31.71 ± 1.809	29	NS
	D	30.82 ± 1.059	53	32.93 ± 6.212	4	NS
	E	31.36 ± 1.086	54	23.89 ± 2.558	3	NS
	H	31.19 ± 1.107	53	27.96 ± 3.623	4	NS
POB	A	47.65 ± 1.279	24	47.50 ± 1.062	33	NS
	B	47.95 ± 1.062	37	46.86 ± 1.232	20	NS
	C	46.61 ± 1.044	28	48.48 ± 1.226	29	NS
	D	47.29 ± 0.844	53	51.18 ± 2.466	4	NS
	E	47.66 ± 0.825	54	45.93 ± 4.733	3	NS
	H	47.61 ± 0.797	53	46.94 ± 5.329	4	NS

MSL: mean staple length; MSS: mean staple strength; PF: prickle factor value; EL%: elongation percentage; POB: point of break; NS: no significance; *: refers to significance at ($P < 0.05$); ** refers to significance at ($P < 0.01$).

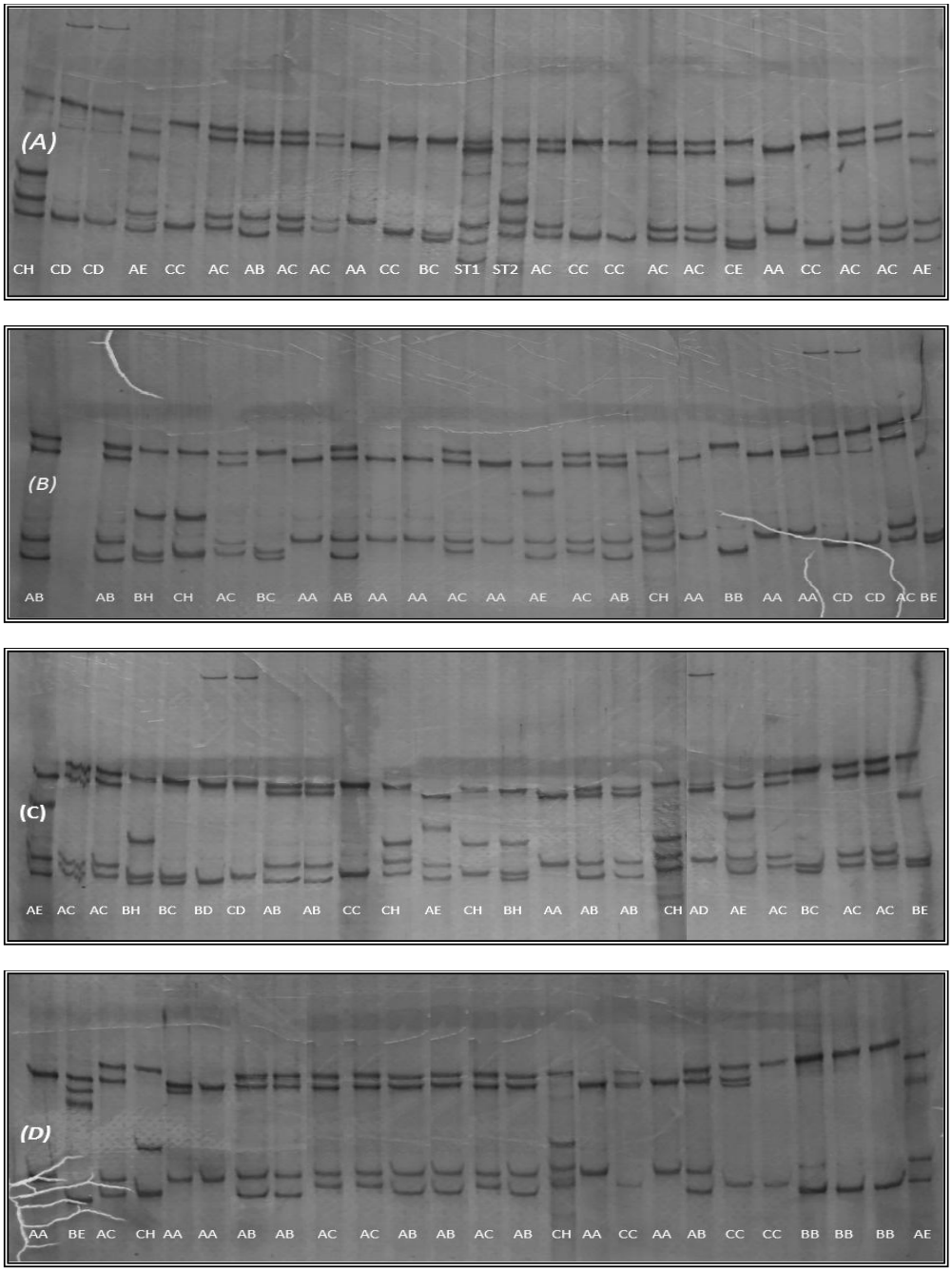

Fig. (1): Polymorphisms in the intron of *ADRβ3* gene in Barki sheep identified by SSCP analysis.