ESTIMATION OF HERITABILITY AND BREEDING VALUES FOR SOME WOOL TRAITS IN BARKI SHEEP, USING SINGLE AND MULTIPLE TRAITS ANIMAL MODELS IN COMPARISON WITH SIRE MODELS

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SUMMARY

The present study was undertaken to evaluate some wool traits using animal versus sire model as well as analyzing single trait versus multiple traits in order to obtain accurate estimates of genetic parameters in Barki sheep. This study utilized 937 Barki fleeces obtained from animals raised in three Barki sheep flocks located at the north western desert. Wool samples taken from these animals were used to assess kemp score, *KS*, handle grade, *HG*, lustre grade, *LG* and measure staple length, *STL*. Results indicated that Barki wool has slightly more than average kemp fibres and tend to be more than average softness and lustrous with an average staple length of 10.31 cm. Heritabilities obtained from single and multiple-traits analysis using animal and sire models were estimated for KS (ranged from 0.58 to 1.00), HG (ranged from 0.50 to 0.71), LG (ranged from 0.61 to 1.00) and STL (ranged from 0.62 to 0.80). Estimates of h^2 obtained from single trait analysis were consistently higher than those obtained from multiple traits analysis using animal model. Moreover, the standard errors for heritability estimates obtained from sire model were obviously lower than those obtained from animal model. The present study revealed that sire model, particularly with the multiple traits analysis, is probably more adequate than animal model for estimating h^2 of the studied traits. The range of estimated breeding values (EBV's) was wider when estimated from animal model and from multiple traits analysis compared with the corresponding values obtained from sire model and from single trait analysis, respectively. Using animal model, particularly with the multiple trait analysis, for estimating BV's showed higher genetic diversity compared with sire model which would lead to a rapid genetic gain in the future generations.

Keywords: heritability, breeding values, animal model, sire model, wool traits, Barki sheep.

INTRODUCTION

Barki sheep is one of the native breeds dominate in the north western desert and raised primarily for mutton, with wool and milk being of secondary importance. Wool fibers do not only protect the sheep from extremes of environmental conditions, they are also utilized by human beings for protection, comfort and processing into many woolen products. The value of any particular wool depends upon its properties which influence the processing as well as the end-product performance. Subjective assessments of wool are those obtained by sensory (visual and tactile) observations such as fineness, lustrous, colour,

etc. They are useful to get quick evaluation at the sale point and particularly when the apparatuses used for measuring these traits are not available (El-Gabbas, 1993 and 1994). These traits together with staple length, while affecting the quality of wool, are likely to be used for the industry considered as easy to asses and measure as selection criteria. Knowledge of genetic parameters for these traits is required to provide an indication of the relative importance of various wool characters and how rapidly they can be improved by breeding (Safari et al., 2007). On the other hand, use of high genetic merit animals would bring higher genetic progress when animals are evaluated by an

effective method of selection. Selection of animals is mainly based on breeding values, accordingly animals are ranked on the basis of its own production performance (in case of evaluating individual animals) or on the basis of the production performance of their progenies (in case of evaluating sires). Linear models such as animal and sire models are often used for estimating breeding values and other genetic parameters. While animal model predicts each animal's genetic merit from pedigree information available about known relationships among all animals in a population, sire model takes the relationship only between the sires into account (Banik and Ghadhi, 2006 and Kim et al., 2006). Moreover, it is reported that estimates of genetic parameters of the same data might vary whether the analysis performed as a single trait or as a multiple-traits (Satoh et al., 1997 and Okut et al. 1999). Searching for more accuracy of estimating breeding values, heritabilities and genetic correlations underlying these wool traits is important, therefore the present study was undertaken to evaluate such parameters using animal versus sire model as well as analyzing single trait versus multiple traits to enhance the efficiency of selection and help improving wool quality in Barki sheep.

MATERIALS AND METHODS

The present study utilized 937 fleeces to assess and measure some wool characters in Barki sheep. These fleeces were obtained from 937 animals descended from 74 sires and 869 ewes. These fleeces were collected from three Barki sheep flocks raised at Maryout research station of the Desert Research Centre (n=356) together with two commercial flocks at the north western desert; El-Nahda (n=330) and North Tahrir (n= 251). After the first shearing, each fleece was spread over a sorting table, and then a handful wool sample was collected randomly from different parts of the fleece to have a composite sample representing the entire fleece. These samples were kept in a plastic bag for further analysis. On the greasy state, samples were subjectively evaluated for kemp score, *KS*, handle grade, *HG*, lustre grade, *LG* and measured for staple length, *STL*.

Assessment of *KS*, *HG* and *LG* was based on the grading system of El-Gabbas (1994). While one experienced grader evaluated all of these traits, these grades were repeated two weeks later and the average of both grades was recorded for each sample. *KS* was evaluated on a four-score system in which score one has no kemp fibres whereas score 4 has dense mass of kemp fibers. The appraisal of *HG* and *LG* were done using a five-score system in which score one means the harshest and the least lustrous wool, while score five means the softest and extremely lustrous wool. Ten staples were sub sampled at random to measure *STL*. Average length of ten staples was taken at random from each sample to be measured against a millimeter ruler without stretching.

Statistical analysis

The GLM procedure of SAS program (version 9.1, 2003) was used to determine the fixed factors affecting the investigated traits according to the following model:

$Y_{ijk}=\mu+F_i+G_j+(F*G)_{ij}+e_{ijk}$ (Model 1)

Where, Y_{ijk} is the observation of the studied trait (KS, HG, LG or STL) of kth animal of ith flock and j^{th} gender; μ is the overall mean; F_i is the fixed effect of flock (1, 2 and 3); G_j is the fixed effect of gender (1 = male and 2 = female); $(F*G)_{ij}$ is the interaction between flock and gender and e_{ijk} is the random residual assuming to be NID $(0,\sigma^2e)$.

Single and multiple traits analyses using animal and sire models were fit to estimate heritability and breeding values using multiple traits animal model program (MTDFREML) proposed by Boldman et al. (1995). While using animal and sire model, single trait analysis was done for the concerned trait only while multiple trait analysis was performed for the four studied traits together. On the other hand, bivariate analysis was fit to estimate genetic and phenotypic correlation coefficients between each couple of studied traits. The linear animal model used for the studied traits was

$Y= X\beta + Z_aa+ e$ (Model 2)

Where:

Y = is a vector of observations for the studied traits,

X= is the incidence matrix for the fixed effects,

β = is the vector including the overall mean and the fixed effects,

Z_a = is the incidence matrix for random effects,

a = is the vector of direct genetic effect of animal where Var(a) = $A\sigma^2 a$ where A is the numerator of relationship matrix of animals, and

e = is a vector of random residuals normally and independently distributed with zero mean and variance I σ^2_e.

The linear sire model used for the studied traits was

$$Y= X\beta + Z_s s + e \quad \text{(Model 3)}$$

Where,

s = is the vector of direct genetic effect of sire, and other terms in the model are defined as in model 2.

The spearman's rank correlation coefficients were estimated to confirm the degree of similarity between the rankings of estimated breeding values, *EBV's,* resulted from single and multiple traits analysis using animal and sire model. SAS program (version 9.1, 2003) was used to obtain these rank correlation coefficients.

RESULTS AND DISCUSSION

Tables 1 and 2 show the analysis of variance and least square means of the studied traits in Barki sheep. Results indicated that Barki wool has slightly more than average kemp fibres and tend to be more than average softness and lustrous with an average staple length of 10.31 cm. Similar findings were obtained on Barki sheep (El-Gabbas, 1993). Flock effect was found to be significant (P<0.01) in all traits. Female had significantly softer and more lustrous wool than males since the effect of gender was found to be significant (P<0.01) only in HG and LG.

Table 1. Analysis of variance for kemp score (KS), handle grade (HG), lustre grade (LG) and staple length (STL) in Barki sheep

Sources of variation	df	Mean square			
		KS	HG	LG	STL
Flock	2	26.16**	49.21**	333.88**	1322.91**
Gender	1	0.11^{ns}	7.97**	009.49**	14.91 ^{ns}
Flock*Gender	2	4.38**	0.43 ^{ns}	1.12 ^{ns}	62.05**
Residual	931	0.81	0.69	0.93	4.42

KS=kemp score, HG= handle grade, LG= lustre grade and STL=staple length
** Significant at P<0.01 and ns = not significant at P< 0.05

Table 2. Number of observations (n) and least square means and their standard errors of wool traits in Barki sheep

Flock	Sex	n	KS	HG	LG	STL
Overall mean		**937**	**2.45±0.03**	**3.20±0.03**	**3.48±0.04**	**10.31±0.089**
Maryout	**Male**	96	2.30^{bc}±0.09	2.95^c±0.08	2.73^{bc}±0.10	11.76^a±0.21
	Female	260	2.11^c±0.06	3.06^c±0.05	2.90^b±0.06	11.59^a±0.13
	Overall	**356**	**2.20^c±0.05**	**3.00^c±0.05**	**2.81^b±0.06**	**11.67^c±0.13**
El Nahda	**Male**	236	2.83^a±0.06	3.56^b±0.05	4.67^a±0.06	10.63^b±0.14
	Female	94	2.78^a±0.09	3.80^a±0.09	4.78^a±0.10	12.02^a±0.22
	Overall	**330**	**2.80^a±0.05**	**3.68^a±0.05**	**4.72^a±0.06**	**11.32^a±0.13**
North Tahrir	**Male**	102	2.20^c±0.09	2.75^d±0.08	2.57^c±0.10	7.74^c±0.21
	Female	149	2.51^b±0.07	3.00^c±0.07	2.93^b±0.08	7.35^c±0.17
	Overall	**251**	**2.35^b±0.06**	**2.87^b±0.05**	**2.75^b±0.06**	**7.55^b±0.14**
Overall sex	**Male**	434	2.44^a±0.05	3.08^a±0.04	3.32^a±0.05	10.04^a±0.11
	Female	503	2.46^b±0.04	3.29^a±0.04	3.53^b±0.05	10.32^a±0.10

KS=kemp score, HG= handle grade, LG= lustre grade and STL=staple length
Means in the same column not followed by the same letter differ significantly at the 5% level

The interaction between flock and gender was significant (P<0.01) in KS and STL where the ranking of males and females was found to be different among flocks particularly in both traits.

Heritability estimates (h^2) obtained from single and multiple traits analysis are presented using animal (Table 3) and sire models (Table 4). Estimates of h^2 obtained from single trait analysis were consistently higher than those obtained from multiple traits analysis using animal model. On the other hand, the analysis of both single and multiple traits using sire model showed similar estimates of heritabilities for all studied traits. These results matched with Okut et al. (1999) who reported that estimates of heritability for fleece grade

obtained from multiple traits analysis are well agreed with those of single trait analysis. Moreover, the standard error for heritability estimates obtained from single and multiple traits analysis using sire model were obviously lower than those obtained from single and multiple traits analysis using animal model (Tables 3 and 4). These results might reveal that sire model, particularly the multiple traits analysis, is probably more appropriate than animal model for estimating h^2 of the studied traits. Furthermore, sire model was reported to have the benefit of increasing the information per animal which can help in a population with low pedigree information (Kim et al., 2006 and Dash et al., 2014).

Table 3. Estimates of heritability and their standard error obtained from single and multiple-traits analysis using animal model for the studied wool traits in Barki sheep

Trait	Single-trait analysis	Multiple-trait analysis
KS	1.00±0.15	0.66±0.11
HG	0.71±0.13	0.51±0.10
LG	1.00±0.14	0.75±0.12
STL	0.80±0.12	0.76±0.11

KS=kemp score, HG= handle grade, LG= lustre grade and STL=staple length

Table 4. Estimates of heritability and their standard error obtained from single and multiple-traits analysis using sire model for the studied wool traits in Barki sheep

Trait	Single-trait analysis	Multiple-trait analysis
KS	0.58±0.04	0.60±0.04
HG	0.50±0.04	0.51±0.04
LG	0.63±0.05	0.61±0.04
STL	0.62±0.05	0.62±0.04

KS=kemp score, HG= handle grade, LG= lustre grade and STL=staple length

The obtained heritability estimates from the analysis of sire model were found to be less for KS (0.73) and HG (0.62) and higher for LG (0.47) and STL (0.58) which were attained by EL-Gabbas and El-Wakil (2016) in Barki sheep. High heritability estimates resulted from the present study, for all investigated traits, appeared to be promising to attain higher genetic gain when included in a breeding program for improving wool quality in Barki sheep. As selection criteria, these traits are also considered to be easy assessed and measured.

Tables 5 and 6 show estimates of genetic and phenotypic correlations obtained from two-traits analysis using sire and animal models. Regarding the magnitude of genetic and phenotypic correlations, estimates obtained from both sire and animal models indicated almost the same trend in which these estimates were slightly higher using sire model compared with that of animal model. It is obvious that the lowest genetic and phenotypic correlations were found between STL and other traits in both sire and animal models.

Table 5. Estimated genetic (above diagonal) and phenotypic (below diagonal) correlations between the studied traits using bivariate animal model

Trait	KS	HG	LG	STL
KS	1.00	0.82(0.08)	0.96(0.04)	-0.12(0.13)
HG	0.32	1.00	0.95(0.03)	0.08(0.14)
LG	0.46	0.63	1.00	0.00(0.13)
STL	-0.01	0.09	0.02	1.00

KS=kemp score, HG= handle grade, LG= lustre grade and STL=staple length
Standard error in brackets

Table 6. Estimated genetic (above diagonal) and phenotypic (below diagonal) correlations between the studied traits using bivariate sire model

Trait	KS	HG	LG	STL
KS	1.00	0.87 (0.06)	0.97(0.03)	-0.23(0.14)
HG	0.35	1.00	0.97(0.03)	0.27(0.15)
LG	0.51	0.65	1.00	0.02(0.15)
STL	-0.04	0.12	0.03	1.00

KS=kemp score, HG= handle grade, LG= lustre grade and STL=staple length
Standard error in brackets

The range of estimated breeding values (EBV's) obtained from single and multiple traits analysis using sire and animal models were presented for all lambs (Table 7) and for sires only (Table 8). There is a trend for the range of EBV's obtained from the analysis of single and multiple traits using sire model to be obviously wider when estimated for sires only compared with the corresponding values estimated for all lambs. That trend was not clear when using animal model. Also, the range of EBV's obtained from multiple traits analysis using sire and animal models were generally higher than the corresponding values obtained from single trait analysis. It is reported that multiple traits analysis should be used instead of single trait analysis as a result of including correlated traits on estimates of breeding values of other traits (Hanford et al., 2005 and 2006). The range of EBV's obtained from single and multiple traits analysis, using animal model were consistently wider than those obtained from sire model for all studied traits. Moreover, higher range of EBV's obtained from Tables 7 and 8 for single and multiple traits analysis using animal model compared to those obtained from sire model suggesting greater differentiation of the animal model which matched also with Dash et al. (2014). That would reflect more genetic variation through the animal model and hence more chance of selecting the top sires and dams based on additive genetic value which might result in a rapid genetic gain in the future generations. Similar conclusion was reached by El-Bayoumi et al. (2015) and Radwan et al. (2017).

The wider range of EBV's observed for STL compared with other studied traits in Tables 7 and 8 probably attributed to the nature of STL as a continuous trait with more variation compared with the other categorical traits. The negative breeding values noticed in Tables 7 and 8 might be a result of using sires of low breeding values which agree with Sahin et al. (2014) and Radwan et al. (2017).

The accuracy in terms of Spearman's rank correlation coefficients calculated between breeding values obtained from single and multiple traits analysis using sire and animal models was presented for all lambs (Table 9) and for sires only (Table 10) for all studied traits. For all lambs, the spearman's rank correlation coefficients between breeding values, obtained from single and multiple traits analysis, tend to be significantly higher (P<0.01) within each of sire and animal models (ranged from 0.78 to 0.98) compared with those coefficients calculated between both animal and

sire models for all studied traits (ranged from 0.48 to 0.61).

Table 7. Minimum to maximum values (Min. to Max.) and range with the standard error (SE) of estimated breeding values for all lambs, estimated from animal and sire models using single and multiple traits analysis for the studied wool traits

Trait		Animal model		Sire model	
		Single trait	Multiple trait	Single trait	Multiple trait
KS	Min. to Max.	-1.82 to 1.84	-1.96 to 1.93	-0.49 to 0.63	-0.55 to 0.68
	Range±SE	3.67±0.029	3.89±0.024	1.11±0.006	1.22±0.007
HG	Min. to Max.	-1.55 to 1.61	-1.51 to 1.70	-0.35 to 0.39	-0.41 to 0.46
	Range±SE	3.15±0.019	3.21±0.019	0.74±0.005	0.88±0.005
LG	Min. to Max.	-2.32 to 2.27	-3.64 to 2.30	-.0.60 to 0.65	-0.60 to 0.65
	Range±SE	4.59±0.032	5.94±0.028	1.25±0.007	1.25±0.007
STL	Min. to Max.	-5.21 to 4.35	-5.38 to 4.44	-1.83 to 0.86	-1.83 to 0.78
	Range±SE	9.56±0.060	9.82±0.054	2.69±0.015	2.61±0.015

KS=kemp score, HG= handle grade, LG= lustre grade and STL=staple length

Table 8. Minimum to maximum values (Min. to Max.) and range with the standard error (SE) of estimated breeding values for sires only estimated from animal and sire models using single and multiple traits analysis for the studied wool traits

Traits		Animal model		Sire model	
		Single trait	Multiple trait	Single trait	Multiple trait
KS	Min. to Max.	-1.93 to 2.38	-1.97 to 2.52	-0.98 to 1.25	-1.09 to 1.35
	Range±se	4.31±0.096	4.49±0.093	2.23±0.048	2.44±0.052
HG	Min. to Max.	-1.37 to 1.50	-1.43 to 1.60	-0.71 to 0.78	-0.82 to 0.93
	Range±se	2.87±0.072	3.03±0.072	1.49±0.037	1.75±0.041
LG	Min. to Max.	-2.28 to 2.45	-2.21 to 2.62	-1.20 to 1.30	-1.20 to 1.42
	Range±se	4.73±0.109	4.83±0.105	2.50±0.057	2.62±0.057
STL	Min. to Max.	-6.68 to 2.92	-6.62 to 2.94	-3.66 to 1.71	-3.66 to 1.56
	Range±se	9.60±0.224	9.56±0.222	5.37±0.124	5.22±0.124

KS=kemp score, HG= handle grade, LG= lustre grade and STL=staple length

This means that the ranking of animals based on estimated BV's was much closer within either sire or animal model compared with that ranking between both models. On the other hand, ranking of sires was found to be almost similar in both models (sire and animal models) and both types of analysis (single and multiple traits analysis) for all studied traits. The Spearman's rank correlation coefficients between breeding values obtained from single and multiple traits analysis using sire and animal models were consistently higher in the analysis of sires only which ranged from 0.88 to 1.00 (Table 10) compared with the corresponding values estimated for all lambs (Table 9).

CONCLUSION

The present study revealed that sire model, particularly the multiple traits analysis, is probably more adequate than animal model for estimating h^2 of the studied traits. High heritability estimates obtained from the current study appeared to be promising to include the investigated traits in a breeding program for improving wool quality in Barki sheep. Using animal model for estimating breeding values showed higher genetic diversity compared with sire model which would lead to a rapid genetic gain in the future generations. Ranking of sires was found to be almost similar in both models (sire and animal models) and both types of analysis (single and multiple traits analysis) for

all studied traits when the current data was   analyzed for sires only or for all lambs.

Table 9. Spearman rank correlation coefficients between breeding values for all lambs obtained from single trait animal model (STAM), multiple traits animal model (MTAM), single trait sire model (STSM) and multiple traits sire model (MTSM) for the studied wool traits in Barki sheep

Trait	STAM & MTAM	STAM & MTSM	STSM & MTSM	STSM & MTAM	STAM & STSM	MTAM & MTSM
KS	0.83	0.51	0.92	0.50	0.53	0.52
HG	0.78	0.56	0.90	0.55	0.61	0.58
LG	0.82	0.50	0.86	0.49	0.54	0.53
STL	0.98	0.48	0.98	0.50	0.49	0.50

KS=kemp score, HG= handle grade, LG= lustre grade and STL=staple length
All correlation coefficients were significant (P<0.01).

Table 10. Spearman rank correlation coefficients between breeding values for sires only obtained from single trait animal model (STAM), multiple traits animal model (MTAM), single trait sire model (STSM) and multiple traits sire model (MTSM) for the studied wool traits in Barki sheep

Trait	STAM & MTAM	STAM & MTSM	STSM & MTSM	STSM & MTAM	STAM & STSM	MTAM & MTSM
KS	0.93	0.93	0.93	0.93	1	0.99
HG	0.93	0.90	0.91	0.93	1	0.99
LG	0.90	0.88	0.89	0.91	0.99	0.99
STL	0.99	0.98	0.98	0.98	1	1

KS=kemp score, HG= handle grade, LG= lustre grade and STL=staple length
All correlation coefficients were significant (P<0.01).

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الملخص العربى

تقدير المكافيء الوراثى والقيم التربوية لبعض صفات الصوف في الأغنام البرقي باستخدام نموذج الحيوان للصفة الفردية وللصفات المتعددة مقارنة بنماذج الطلوقة.

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أجريت هذه الدراسة لتقييم استخدام نموذج الحيوان مقابل نموذج الطلوقة وكذلك تحليل الصفة منفردة مقابل تحليل الصفات المتعددة وذلك للحصول على تقديرات دقيقة للمعالم الوراثية لبعض صفات الصوف في الأغنام البرقي. استخدمت فى الدراسة 937 جزة من الأغنام البرقى المرباه في ثلاثة قطعان تقع في الصحراء الشمالية الغربية. استخدمت عينات الصوف المأخوذة من هذه الحيوانات فى تقييم درجة الكمب، درجة الملمس ، درجة اللمعان وكذلك فى قياس طول الخصلة. أوضحت النتائج أن صوف الأغنام البرقي يحتوي على ألياف من الكمب أكثر قليلا من المتوسط بينما كانت أكثر من المتوسط فى صفات النعومة واللمعان وكان متوسط طول الخصلة 10.31 سم. تم تقدير المكافئات الوراثية من تحليل الصفة منفردة وتحليل الصفات المتعددة باستخدام نموذج الحيوان ونموذج الطلوقة لكل من درجة الكمب (تراوحت من 0.58 إلى 1.00) ، درجة الملمس (تراوحت من 0.50 إلى 0.71) ، درجة اللمعان (تراوحت من 0.61 إلى 1.00) وطول الخصلة (تراوحت من 0.62 إلى 0.80). كانت تقديرات المكافئ الوراثى التي تم الحصول عليها من تحليل الصفة منفردة أعلى دائما من تلك التي تم الحصول عليها من تحليل الصفات المتعددة باستخدام نموذج الحيوان. الخطأ القياسى لتقديرات المكافيء الوراثى التي تم الحصول عليها من نموذج الطلوقة كان أقل من تلك التي تم الحصول عليها من نموذج الحيوان. أوضحت الدراسة أن نموذج الطلوقة خاصة مع تحليل الصفات المتعددة ربما يكون أكثر ملائمة من نموذج الحيوان لتقدير المكافئ الوراثى للصفات المدروسة. كان المدى للقيم التربوية المقدرة أوسع عندما تم تقديره من نموذج الحيوان وكذلك من تحليل الصفات المتعددة مقارنة مع القيم المقابلة التي تم الحصول عليها من نموذج الطلوقة ومن تحليل الصفة منفردة على التوالي. أظهر استخدام نموذج الحيوان خاصة مع تحليل الصفات المتعددة لتقدير القيم التربوية اختلافات وراثية أعلى مقارنةً بنموذج الطلوقة الذي قد يؤدي إلى عائد وراثى أسرع في الأجيال القادمة.

ESTIMATION OF HERITABILITY AND BREEDING VALUES FOR SOME WOOL TRAITS IN BARKI SHEEP, USING SINGLE AND MULTIPLE TRAITS ANIMAL MODELS IN COMPARISON WITH SIRE MODELS

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