Selection in Fat-tailed Sheep Based on Two Traits of Fat-tail and Body Weight *versus* Single-trait Total Body Weight

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ABSTRACT

The objective of the present study was to compare several selection strategies and to find a method of selection permitting improvement in body weight with possible decrease or, if possible, slight increase in fat tail weight. Stochastic simulation was used to produce a flock of 10 breeding rams and 250 breeding ewes with four lambs per ewe. A total of 1000 lambs were produced for five consecutive non-overlapping generations. Data were simulated using a two trait model. Both single trait and two trait models were used under phenotypic and genetic selection. In two trait selection, economic weights were used to construct the selection indices. A range of covariance components were used for generating data and different sets of economic weights were applied to test the sensitivity of different selection strategies to these parameters. With low heritability for both traits, the least genetic trend was achieved for tail weight with phenotypic selection index. Highest aggregate genotype was obtained with two trait genetic method. With increased heritability for tail weight and under single trait selection, an increase in total body weight fully coincided with increased genetic trend in fat tail weight. The highest aggregate genotype and the lowest genetic trend in fat tail weight was obtained when negative economic weight was applied to fat tail weight. When high heritability was used for simulation, the two trait genetic selection model performed the best. However, when two trait genetic evaluation is not practical, the best alternative would be to use two trait phenotypic selection based on economic weights for the two traits.

Key Words: Selection; Fat-tail; Sheep; Aggregate genotype

INTRODUCTION

Mutton and lamb production is the major goal under many sheep production systems, which produce fat tailed breeds of sheep and other products like wool and hide are considered as secondary products. The climatic condition in the tropics as well as the requirements of the people forced the sheep producers in many tropical areas to select for higher fat tail weight across generations. A few major factors could have been the underlying reasons for sheep producers to select for higher fat tail size during of documentation in the tropics. Fat, having higher energy content in less volume, is useful for the people living under nomatic conditions. It was used to preserve cooked meat for longer periods of time and also a relative energy reserve during times of drought and famine. It can be argued that increased fat tail weight was not the result of natural selection because none of the wild ancestors of domestic sheep living in similar tropical conditions have fat tail.

Most factors in favor of larger fat tail have now lost their importance. Animal fat has lost much of its market demand and sheep producers have easy access to other forms of auxiliary feeding during times of drought when pasture quality is not capable of meeting the requirements of the animals. Auxiliary feeding during drought is more efficient compared to preserving energy in the form of body fat. High weight of fat tail is also a burdon imposed to animals during grazing and animals spend some energy for carrying its extra weight. With the modern food industry there is no need for fat as a food preservative either. While fat had, in the other times, as high value as lean meat its market value is new experiencing manyfold decrease. Another negative economic impact of higher body fat content is higher feed conversion ratio in producing fat compared to producing lean carcass. Growth rate and feed efficiency in young animals is more than that of older animals (Notter *et al.,* 1991). Increased body weight at a certain and usually, younger age is often used to select for animals growing faster. Fat tail is a component of total body weight, hence, positive phenotypic correlation exists between the two traits and any selection program aimed for higher body weight would lead to higher fat tail weight. This has been a major issue for many Iranian sheep farmers as all Iranian sheep breeds, except the Zel breed of the southern areas of Caspian Sea in northern Iran, have fat tail. In recent years many farmers who attempted to select for sheep with higher body weight are faced with the problem of increased fat tail weight. The size of the fat tail is variable both within and between breeds but in general it constitutes about 20% of the total carcass weight.

Positive phenotypic covariance exists between body weight and fat weight (Zamiri *et al.,* 1997). Many studies

show positive phenotypic and genetic correlations between ultrasonic fat measurements and carcass traits (Atkins *et al.,* 1991; Saatci *et al.,* 1998). Docking fat tail of sheep leads to increased abdominal subcutaneous and muscle fat deposition (Sefidbakht & Ghorban, 1972). Increased carcass quality with decreased fat tail weight was reported in progeny of fat tailed breeds of Baluchi and Mehraban sheep crossed with Targhee and Corriedal (Farid, 1991). The objective of this study was to find an optimum method of selection for body weight and fat tail weight.

MATERIALS AND METHODS

The base population consisting of 10 rams and 25 ewes per ram was simulated by sampling from a large population with bivariate normal distribution for two traits of fat tail weight and body weight. Four lambs with equal numbers of each sex were produced per ewe. Five discrete generations of selection were applied and the procedure was repeated 10 times to reduce sampling error.

Base population. The following model was used to simulate the base population:

$$\mathbf{p} = \boldsymbol{\mu} + \mathbf{g} + \mathbf{e}$$

Where, $\mathbf{p}$ is the vector of observation for the two traits of tail-free body weight and fat tail weight respectively; $\boldsymbol{\mu}$ is the vector of production mean for the two traits; $\mathbf{g} = \mathbf{z}_1 \mathbf{U}_1$ is the vector of additive genetic effect of the two traits; $\mathbf{e} = \mathbf{z}_2 \mathbf{U}_2$ is the vector of residual effect of the two traits; $\mathbf{z}_1$ and $\mathbf{z}_2$ are vectors of random deviates sampled from normal distribution of mean equal to zero and variance equal to one; $\mathbf{U}_1$ and $\mathbf{U}_2$ are lower triangular matrices obtained by Cholesky decomposition of the matrices of genetic ($\mathbf{G}$) and residual ($\mathbf{R}$) covariances among two traits. In constructing matrices $\mathbf{G}$ and $\mathbf{R}$ two sets of heritabilities for body weight (0.3 or 0.5) and fat tail weight (0.2 or 0.6) were used. Genetic and environmental correlations were set to 0.5. Both matrices $\mathbf{G}$ and $\mathbf{R}$ were checked to be positive definite.

Next generation. Depending on each of the four methods of selection, 25 males and 250 females were selected to produce 1000 progeny per generation. Selected parents were mated randomly and the following model was used to simulate each progeny generation:

$$\mathbf{p} = \boldsymbol{\mu} + 0.5\mathbf{g}_s + 0.5\mathbf{g}_d + \mathbf{m} + \mathbf{e}$$

Where $\mathbf{p}$, $\boldsymbol{\mu}$ and $\mathbf{e}$ are as before; $\mathbf{g}_s$ and $\mathbf{g}_d$ are the vectors of genetic values for sire and dam of each progeny, respectively and $\mathbf{m}$ is the vector of Mendelian sampling for the two traits. The vector m was simulated as:

$$\mathbf{m} = 0.5(2 - F_s - F_d)0.5\mathbf{z}\mathbf{U}_1$$

Where $\mathbf{z}$ and $\mathbf{U}_1$ are as before and F_s and F_d are coefficients of inbreeding of sire and dam of each progeny, respectively.

Methods of selection. From different selection strategies were used as follows:

(A). Single-trait phenotypic selection; in which weight of the fat tail was added to the body weight to give total body weight. Individuals were then ranked based on their total body weight within each sex and those with highest total body weight were selected to generate the next generation.

(B). Two-trait phenotypic selection; in which individuals were ranked based on an index of the two phenotypic observations of fat tail weight and body weight. Two sets of economic weights were assigned each of the two traits. An economic weight equal to 1 was assigned to tail-free body weight, while two arbitrary alternative weights of 0 and 1 were assigned to the un-desirable trait of fat tail weight to indicate different relative levels of economic importance. The economic weight were placed in the vector V of the following equation to derive vector of index weights, b:

$$b = P - 1 G v$$

Where P and G are matrices of phenotypic and genotypic covariences among two traits of fat weight and body weight, respectively. The index was then calculated as:

$$I = b' x$$

Where I is the index for selection and the vector x contains phenotypic values for the two traits (Gibson, 1995).

(C). Single-trait genetic selection; in which the phenotypic observations for total body weight were produced in the same way as method A. Phenotypic observations were then used in a single trait animal model to estimate the breeding values. Individuals were ranked based on their EBV's within each sex and those with highest EBV's for their total body weight were selected to generate the next generation.

(D). Two-trait genetic selection, in which the two separate phenotypic observations for each individual were used in a two-trait animal model to estimate the breeding values. Estimated breeding values were multiplied by the relative economic weights to produce estimated aggregate phenotypes. Individuals were ranked based on their estimated aggregate genotypes within each sex and those with highest estimated aggregate genotypes were selected to generate the next generation.

Genetic evaluation. In both single-trait and two-trait method of genetic evaluation the following standard mixed linear model was used:

$$y = I\mu + Zg + e$$

Where y is the vector of phenotypic observations of the trait (s) of interest. The same covariance matrices of G and R as before were used in setting up the mixed model equations. The inverse of numerator relationship matrix was computed following Meuwissen and Luo (1992).

RESULTS

Table I to IV present the results with combinations of two different heritability levels for each of the two traits. Aggregate genotypes presented in the last column are inner products of the two vectors of true breeding values with the relative economic weights of the two traits. Although, in practice aggregate genotypes should be used to compare different selection methods but cumulative genetic trend in units of standard deviations of breeding values are also presented to indicate genetic trend in each of the two traits under different selection methods. Proper economic weights should be given to the traits of importance to achieve economic gain. Two sets of relative economic weights used in this study are arbitrary and do not represent any real economic value. Therefore, presenting separate genetic trends in two traits would help better understanding of genetic response of each trait to different selection methods.

DISCUSSION

Although results obtained for four different combinations of heritability for the two traits are reported here but heritability values used in Table IV are better representative of the two traits under study. Results obtained here may be used to evaluate the behavior of each selection method under different senarios (Table I, II & III). Comparison of aggregate genotypes in Table II with those in Table I indicated that increased heritability of fat tail weight does not lead to much economic gain. Similar conclusion was drawn when comparing Table IV and III. In both cases positive genetic trend was observed for the fat tail weight. However, due to use of zero or negative economic weight for fat tail weight, increase in fat tail weight did not lead to increase economic gain. In real life, when the actual relative economic value of fat tail is zero or negative, this increase in fat tail weight would only lead to increased cost of production without increasing revenue. Comparing Table III and V with Table I and II revealed that increased genetic trend of the desirable trait was due to increased heritability, which led to higher economic gain.

Multitrait genetic selection increases economic gain by increasing accuracy of selection, especially for traits with lower heritability (Pollak *et al.,* 1984; Vanvleck *et al.,* 1987; Falconer & Mackay, 1996). Genetic gain in traits of lower heritability may be increased through response to selection for correlated traits with higher hertability (Simm, 1998). Table IV shows that two-trait methods of selection have been slightly superior to single-trait methods but no superiority of genetic selection over phenotypic selection was observed in terms of economic gain. Therefore, with higher heritabilities for the traits of interest phenotypic records may be effectively used in combination with proper economic weights to construct selection indices. However, in both single-trait and two-trait model, genetic selection kept the economic gain with lower fat tail gain. If we also consider extra cost of increased fat tail weight, it is obvious

Table I. Genetic trend in two traits of fat tail weight and body weight (in units of s.d.) and aggregate genotype after five generations of selection (heritability of 0.3 for body weight and 0.2 for fat tail weight)

REW*	MS**	BW	FTW	AG
	A	3.39 (0.14)	0.69 (0.15)	10.99 (0.47)
	B	3.45 (0.13)	0.12 (0.14)	11.31 (0.43)
-1	C	3.78 (0.16)	0.60 (0.15)	12.33 (0.36)
	D	3.79 (0.11)	0.34 (0.17)	12.36 (0.52)
	A	3.34 (0.15)	0.59 (0.11)	10.97 (0.47)
	B	3.46 (0.15)	0.36 (0.13)	12.36 (0.48)
0	C	3.71 (0.17)	0.39 (0.20)	12.20 (0.55)
	D	3.88 (0.17)	0.32 (0.18)	12.75 (0.57)

REW: relaive economic weight, MS: method of selection, BW: body weight, FTW: fat tail weight, AG: aggregate genotype. *Economic weight of 1 was assumed for body weight. With single-trait selection methods (A and B) economic weights were used to calculate aggregate genotypes in the last column. With two-trait selection methods (C and D) economic weights were used in constructing selection indices as well as calculating aggregate genotypes. **A: single-trait phenotypic, B: single-trait genetic, C: two-trait phenotypic and D: two-trait genetic

Table II. Genetic trend in two traits of fat tail weight and body weight (in units of s.d.) and aggregate genotype after five generations of selection. (heritability of 0.3 for body weight and 0.6 for fat tail weight)

REW*	MS**	BW	FTW	AG
	A	3.46 (0.18)	0.69 (0.13)	11.10 (0.60)
	B	3.41 (0.14)	0.99 (0.15)	10.52 (0.43)
-1	C	3.85 (0.18)	0.84 (0.18)	12.33 (0.58)
	D	3.87 (0.21)	0.65 (0.20)	12.47 (0.68)
	A	3.43 (0.18)	0.72 (0.17)	12.27 (0.59)
	B	3.45 (0.13)	1.62 (0.14)	11.34 (0.41)
0	C	3.76 (0.17)	0.98 (0.20)	12.36 (0.53)
	D	3.76 (0.16)	1.05 (0.15)	12.34 (0.57)

REW: relaive economic weight, MS: method of selection, BW: body weight, FTW: fat tail weight, AG: aggregate genotype. *Economic weight of 1 was assumed for body weight. With single-trait selection methods (A and B) economic weights were used to calculate aggregate genotypes in the last column. With two-trait selection methods (C and D) economic weights were used in constructing selection indices as well as calculating aggregate genotypes. **A: single-trait phenotypic, B: single-trait genetic, C: two-trait phenotypic and D: two-trait genetic

that genetic selection would lower the cost of production without lowering revenue. Belonsky and Kennedy (1988) used simulation to show advantage of genetic selection over phenotypic selection. Simm and Dingwall (1989) used negative economic weight for ultrasonic fat depth and positive economic weight for meat production and showed an increase in meat production, while decreasing fat depth. Lewis *et al.* (1996) obtained similar results in Suffolk sheep fed high-energy ration.

CONCLUSION

With positive genetic correlation between two traits of fat tail weight and body weight it is possible to select for faster increase in body weight and slower increase in fat tail weight. Applying more negative selection pressure on fat tail weight would make it possible to further reduce genetic gain in fat tail weight or even to decrease the size of fat tail with increased body weight and therefore increased economic gain.

Table III. Genetic trend in two traits of fat tail weight and body weight (in units of s.d.) and aggregate genotype after five generations of selection. (heritability of 0.5 for body weight and 0.2 for fat tail weight)

REW*	MS**	BW	FTW	AG
	A	4.19 (0.14)	0.68 (0.12)	17.62 (0.59)
	B	4.27 (0.12)	0.20 (0.15)	18.07 (0.50)
-1	C	4.59 (0.16)	0.67 (0.17)	19.01 (0.65)
	D	4.50 (0.12)	0.35 (0.21)	19.34 (0.34)
	A	4.28 (0.16)	0.79 (0.16)	18.16 (0.66)
	B	4.38 (0.14)	0.17 (0.13)	18.60 (0.58)
0	C	4.48 (0.13)	0.69 (0.19)	19.02 (0.57)
	D	4.57 (0.14)	0.46 (0.10)	19.39 (0.60)

REW: relaive economic weight, MS: method of selection, BW: body weight, FTW: fat tail weight, AG: aggregate genotype. *Economic weight of 1 was assumed for body weight. With single-trait selection methods (A and B) economic weights were used to calculate aggregate genotypes in the last column. With two-trait selection methods (C and D) economic weights were used in constructing selection indices as well as calculating aggregate genotypes. **A: single-trait phenotypic, B: single-trait genetic, C: two-trait phenotypic and D: two-trait genetic

Table IV. Genetic trend in two traits of fat tail weight and body weight (in units of s.d.) and aggregate genotype after five generations of selection. (heritability of 0.5 for body weight and 0.6 for fat tail weight)

REW*	MS**	BW	FTW	AG
	A	4.33 (0.15)	0.92 (0.17)	18.03 (0.61)
	B	4.28 (0.12)	0.31 (0.16)	18.05 (0.50)
-1	C	4.54 (0.15)	0.76 (0.16)	18.99 (0.63)
	D	4.51 (0.14)	0.36 (0.15)	18.99 (0.57)
	A	4.36 (0.16)	0.85 (0.16)	18.03 (0.66)
	B	4.37 (0.13)	0.78 (0.14)	18.03 (0.57)
0	C	4.56 (0.13)	0.87 (0.18)	19.33 (0.53)
	D	4.64 (0.12)	0.80 (0.11)	19.68 (0.49)

REW: relaive economic weight, MS: method of selection, BW: body weight, FTW: fat tail weight, AG: aggregate genotype. *Economic weight of 1 was assumed for body weight. With single-trait selection methods (A and B) economic weights were used to calculate aggregate genotypes in the last column. With two-trait selection methods (C and D) economic weights were used in constructing selection indices as well as calculating aggregate genotypes. **A: single-trait phenotypic, B: single-trait genetic, C: two-trait phenotypic and D: two-trait genetic

REFERENCES

Atkins, K.D., J.J. Murray, A.R. Gilmour and A.L. Luff, 1991. Genetic variation of live weight and ultrasonic fat depth in Australian pool Dorset sheep. *Australian J. Agric. Res.,* 42: 629–40

Belonsky, G.M. and B.W. Kennedy, 1988. Selection on individual phenotype and best linear un-biased predictor of breeding value in a closed swine herd. *J. Anim. Sci.,* 66: 1124–31

Falconer, D.S. and F.C. Mackay, 1996. *Introduction to Quantitative Genetics,* 4th editions, p: 430. Longman Scientific & Technical

Farid, A., 1991. Slaughter and carcass characteristics of three fat-tailed sheep breed and their crosses with Corriedal and Targhee rams. *Small Rumin. Res.,* 5: 255–71

Gibson, J.P., 1995. *An Introduction to the Design and Economics of Animal Breeding Strategies,* p: 175. Course note: CGIL. Department of Animal breeding and Poultry Science, University of Guelph, Guelph, Ontario, Canada, N1G2W1

Lewis, R.M., G. Simm, W.S. Dingwall and S.W. Murphy, 1996. Selection for lean growth in terminal sire sheep to produce leaner crossbreed progeny. *Anim. Sci.,* 63: 133–42

Meuwissen, T. and Z. Luo, 1992. Computing inbreeding coefficients in large populations. *Genet. Sel. Evol.,* 24: 305–13

Notter, D., R. Kelly and F.S. McClaughety, 1991. Effects of ewe breeds and management system on efficiency of lamb production. *J. Anim. Sci.,* 69: 22–3

Pollak, E.J., J. Van Der Werf and R.I. Quaas, 1984. Selection bias and multiple trait evaluation. *J. Dairy Sci.,* 67: 1590–5

Saatci, M., I. Appewi, H.E. Jones and Z. Ulutas, 1998. Genetic parameter and estimated breeding value of live weight, fat and muscle depth in Welsh Mountain rams. *6th World Congress on Genetic Applied to Livestock Production,* 24: 238

Sefidbakht, N. and K. Ghorban, 1972. Changes arising from docking of fat-tailed sheep in feedlot performance. *Iranian J. Agric. Res.,* 1: 72–7

Simm, G. and W.S. Dingwall, 1989. Selection indices for lean meat production in sheep. *Livest. Prod. Sci.*, 21: 233–8

Simm, G., 1998. *Genetic Improvement of Cattle and Sheep*, p: 446. Farming Press. United Kingdom

Vanvleck, L.D., E.J. Polak and E.A.B. Oltenacu, 1987. *Genetics for Animal Science,* 2th edition, p: 390. W.H. freeman and Company

Zamiri, M.J. and G. Izadifard, 1997. Relationship of fat-tailed weight with fat-tailed measurement and carcass characteristics of Mehraban and Ghezel rams. *Small Rumin. Res.,* 26: 262–6