The Haryana Veterinarian (March, 2024) **63(SI),** 126-130 ISSN 0033-4359 (P) **Short Communication**

MULTI-STAGE SELECTION STRATEGY FOR GENETIC IMPROVEMENT IN ORGANIZED FLOCK OF CHOKLA SHEEP OF RAJASTHAN

PRAKASH*, S.B.S. YADAV, URMILA PANNU, MANJU NEHARA, MANISHA MEHRA, ASHISH CHOPRA[1] and H.K. NARULA[1]
Department of Genetics and Animal Breeding, College of Veterinary and Animal Science,
Rajasthan University of Veterinary and Animal Sciences, Bikaner-334001, Rajasthan
[1]Arid region Campus, Central Sheep & Wool Research Institute, Bikaner-304501

Received: 14.06.2022; Accepted: 06.01.2023

SUMMARY

Data on 3714 Chokla sheep, maintained at ICAR-Central Sheep and Wool Research Institute (CSWRI), Avikanagar, Rajasthan, collected for a period of 18 years (1994 to 2011) were used in the study. Traits analyzed were body weights at birth (BWT), 3 months (3 WT), 6 months (6 WT), 9 months (9 WT), 12 months (12 WT) of age and first six monthly greasy fleece yield (GFY1). Three multi-stage selection indices were constructed by incorporating these traits in different combinations.

Single-stage indices were more accurate and expected to produce higher genetic gain than their corresponding multistage indices. However, considering the cost of rearing animals for a long period, it has been proposed that 2 stage selection strategies with 20% selection at 6 months, next 50% selection at 9 months and further 40% selection at 12 months would be more practical and economic with an acceptable rate of genetic improvement. The recommended selection indices at two stages selection indices, index MSI_{31} and MSI_{32} were found more efficient ($\Delta H = 2.5313$) than others.

Keywords: Chokla Sheep, Multi-stage Selection, Multi-trait index, Selection index

How to cite: Prakash, Yadav, S.B.S., Pannu, U., Nehara, M., Mehra, M., Chopra, A. and Narula, H.K. (2024). Multi-stage selection strategy for genetic improvement in organized flock of Chokla sheep of Rajasthan. *The Haryana Veterinarian* **63(SI)**: 126-130.

Chokla a fine carpet wool producing sheep is distributed in Churu, Jhunjhunu, Sikar and bordering areas of Bikaner, Jaipur and Nagaur districts of Rajasthan (Jain *et al.*, 2009). For continuous improvement in Chokla sheep flock maintained since 1990 at ICAR-CSWRI, Avikanagar, Rajasthan through modifying selection indices, an exercise was carried out to find out the best selection index in the present situation.

The aim of the present-day livestock breeders is to raise animals on commercial lines which are based on the principle of maximum gain from minimum input. Animals which will bring maximum economic returns are kept while the rest unwanted low profitable stock culled at an earliest to reduce pressure on space, resources and also to increase efficiency of management. For this selection and culling, a kind of yard stick is needed to discriminate the animals likely to bring maximum economic returns from those less profitable. To develop this type of discriminating yardstick, all economically important traits are taken into account and combined according to their relative weights into a net economic score for each animal to construct selection index. The relative weight of a trait depends upon its heritability, relative economic value and association with other traits. The animals which rank best on these scales are retained and others culled for maximum returns from a livestock enterprise among different methods of selection *viz*. Index selection, tandem selection and independent culling level, index selection is the most efficient for bringing overall improvement in the flock for maximum net economic returns (Hazel and Lush, 1942). Chokla breed one of the 44 distinguished sheep breeds of India. It is distributed in Churu, Jhunjhunu, Sikar and bordering areas of Bikaner, Jaipur and Nagaur districts of Rajasthan. Animals true to the breed type are found in Sikar and Churu districts of Rajasthan. Chokla is fine carpet wool producing Indian sheep and reared basically for its wool quality and suitability for migration. Maintained at Central Sheep & Wool Research Institute since 1990 and there is frequent need of modifying selection indices for continuous improvement of institute flock, an exercise was worked out to find out best selection index in present situation.

MATERIALS AND METHODS

Data on body weights at birth (BWT), 3 (3 WT), 6 (6 WT), 9 (9 WT) and 12 (12 WT) months of age and first six monthly greasy fleece yield (GFYI) for 3714 Chokla sheep maintained at ICAR-CSWRI, Avikanagar (Rajasthan) under Network Project on Sheep Improvement were recorded from 1994 to 2011 and were used. The data were classified according to period and, season of birth, dam's age at lambing and sex of lamb. The years of lambing were divided into six periods, each comprising 3 years and each year was further divided into 2 seasons, i.e. S-1 (May-October) and S-2 (November-April). Data were analyzed using a mixed model least-squares analysis by fitting

---

*Corresponding author: drprakashjangu@gmail.com

constants (Harvey, 1990) including all main effects.

Estimation of genetic and phenotypic correlation: Bivariate analysis under the (wombat) Animal model 1 was used to estimate genetic and phenotypic correlation between the traits with starting values derived from single traits analysis.

Relative economic value: Relative economic value (a) was estimated by simple regression method. 12 months body weight was taken as dependent variable and change in 12 months body weight by unit change in birth, 3, 6 and 9 months and clip I body weight was worked out. Relative economic values for body weights at birth, 3, 6, 9, 12 months of age and clip I were estimated as 2.1327, 0.8643, 0.8708, 1.0390,1 and 4.62, respectively.

Selection Index: Selection index was constructed as per Hazel's (1943) procedure. The aggregate genetic value (H) of an individual defined as follows:

$$H = a_1G_1 + a_2G_2 + \ldots \ldots\ldots + a_nG_n$$

In matrix notation

$$H = a'G$$

Where,

H= Aggregate genetic or breeding value,

a'= Row vector of economic values of traits,

G= Column vector of additive genetic values of traits included in the aggregate genotype.

Since H is not directly observable characteristic, hence improvement inH is then brought about by selection on an index:

$$I = b'X$$

Where,

I = Net score of an individual,

b' = Row vector of unknown regression coefficients (weighing factor) maximizing the correlation between index and aggregate breeding value,

X = Column vector of phenotypic values for traits included in the index.

The weighting factors (b) in index was obtained by solving the equation-

$$[P]\,b = [G]a$$

$$b = [P]^{-1}\,[G]a$$

Where,

[P] = Phenotypic variance-covariance matrix,

[G] = Genotypic variance-covariance matrix,

a = Vector of relative economic values of traits.

Reliability of the index:

The reliability of the index was measured by multiple correlations between the index and aggregate genotype:

$$\sigma_{HI} = Cov_{(HI)} / (\sigma_H \times \sigma_I)$$

Where,

σ^2_I = b'[P]b = Variance of the index,

σ^2_H = a'[G]a = Variance of the aggregate genotype,

σ_{HI} = b'[G]a = Covariance of the index and aggregate genotype.

Expected genetic gain: The aggregate gain achieved through use of index (es) constructed was computed as follows:

$$\Delta H = b_{HI}(\overline{Is} - \overline{I\mu})$$

$$= b_{HI}.i.\ \sigma_I$$

$$= r_{HI}.\ i\ .\sigma_H$$

Where,

ΔH = Genetic gain in aggregate breeding value,

b_{HI} = Regression of I on H

$(\overline{Is} - \overline{I\mu})$ = Selection differential,

i = Selection intensity,

σ_H, σ_I= Standard deviation

Genetic gain in the component traits of index were calculated as follow:

$$\partial = [G]\,b\,(i / \sigma_I)$$

Where,

∂ = Column vector of genetic gain corresponding to each trait of the index,

[G] = Genetic variance-covariance matrix,

b = Vector of weighting factors.

Multi-stage selection index: Multi-stage selection index programme was developed using the method of Cunningham (1975).

For constructing a two-stage selection index, the following notation was used:

X_1 = Phenotypic values of traits available at stage 1 (1……p)

X_2 = Phenotypic values of traits available at stage 2 (1……q)

$[P_1]$ p×p, $[P_2]$ q×q = Phenotypic variance-covariance matrices of traits available at stage 1 and stage 2, respectively.

$[P_{12}]$ p×q = Matrix of phenotypic co-variances between X_1 traits of stage 1 and X_2 traits of stage 2

$[G_1]$ p×p, $[G_2]$ q×q = Genotypic variance-covariance matrices of traits available at stage 1 and stage 2, respectively

$[G_{12}]$ p×q = Matrix of genotypic co-variances between X_1 traits of stage 1 and X_2 traits of stage 2

a_1, a_2 = Vector of relative economic values of traits available at stage1 and stage 2, respectively.

The variance-covariance matrix (phenotypic and genotypic) for full set of variates can be represented by the following super matrix:

$$M_1 = \begin{pmatrix} P : G \\ \ldots\ldots\ldots\ldots \\ G' : G \end{pmatrix}$$

In expand form, it can be written as:

$$M_1 = \begin{pmatrix} [P_1] & [P_{12}] & : & [G_1] & [G_{12}] \\ [P_{21}] & [P_2] & : & [G_{21}] & [G_2] \\ \ldots & \ldots & \ldots & \ldots & \ldots \\ [G_1] & [G_{12}] & : & [G_1] & [G_{12}] \\ [G_{21}] & [G_2] & : & [G_{21}] & [G_2] \end{pmatrix}$$

Selection at stage 1 was carried out using the information on X_1 traits. Weighing factors were calculated as follows:

$$b_1 = [P_1]^{-1} [G_1]\, a_1$$

$$I_1 = b_1' X_1$$

Variance of index I_1:

$$(\sigma^2_{I1}) = b_1'[P_1]\, b_1$$

Variance of aggregate breeding value of stage 1:

$$(\sigma^2_{H1}) = a_1'[G_1]\, a_1$$

Accuracy of selection at stage 1:

$$(\sigma_{H1I1}) = \sigma_{I1} / \sigma_{H1}$$

Selection at stage 2:

Selection at this stage can be done by two methods:

A. By using information on I_1 and X_2

B. By using information on X_1 and X_2 traits simultaneously

A. By using information on I_1 and X_2 traits

This was done by replacing X_1 in super matrix M_1 by I_1 and a new reduced super matrix M_2 was constructed as follows:

$$M_2 = \begin{pmatrix} \sigma^2_{I1} & b_1'\,[P_{12}] & b_1'[G_1] & b_1'[G_{12}] \\ [P_{21}]\,b_1 & [P_2] & [G_{21}] & [G_2] \\ & & & \\ [G_1]\,b_1 & [G_{12}] & [G_1] & [G_{12}] \\ [G_{21}]\,b_1 & [G_2] & [G_{21}] & [G_2] \end{pmatrix}$$

Whole super matrix (M_2) of variance and covariance was corrected for effects of selection a stage 1 as follows:

$$M_2^* = M_2 - T'T\,W$$

Where,

$$T = \sigma^2_{I1},\ b_1'[P_{12}],\ b_1'[G_1],\ b_1'[G_{12}]$$

$$W = S/\sigma^2_{I1}$$

$$S = i\,(i-t)$$

i = selection intensity, a function of animals selected at stage 1.

t = point of truncation on standard normal distribution

M* could then be represented as:

$$M_2^* = \begin{pmatrix} P^* : G^* \\ \ldots\ldots\ldots\ldots \\ G'^* : G^{**} \end{pmatrix}$$

Weighing factors for selection at stage 2 were calculated as follows:

$$b^* = [P^*]^{-1}\ [G^*]\, a$$

B. By using information on X_1 and X_2 traits simultaneously

In this process super matrix (M_1) was corrected for effects of selection at stage 1 as follows:

$$M_1^* = M_1 - T'T\,W$$

Where,

$$T = b_1'[P_1],\ b_1'[P_{12}],\ b_1'[G_1],\ b_1'[G_{12}]$$

$$W = S/\sigma^2_{I1}$$

$$S = i\,(i-t)$$

M* could then be represented as:

$$M_1^* = \begin{pmatrix} P^* : G^* \\ \ldots\ldots\ldots\ldots \\ G'^* : G^{**} \end{pmatrix}$$

Weighing factors for selection at stage 2 were calculated as follows:

$$b^* = [P^*]^{-1}\ [G^*]\, a$$

RESULT AND DISCUSSION

For single stage selection, 20% (i=1.4) animals are selected. To get the same selection intensity in two stage selection, 50% (i = 0.798) animals were selected in first stage and 40% (i = 0.996) out of first stage animals, selected on the basis of second stage index. For a given combination of traits at single stage and two stages two types of indices were constructed. In first approach the second stage index was having the first stage index as such besides traits available at second stage. These were MSI_{11}, MSI_{21} and MSI_{31}. In second approach the second stage index had all the traits i.e. traits of first stage as well as

Table 1. Estimates of genetic variance (on diagonal), phenotypic variance (on diagonal in brikets), genetic covariance (above diagonal) and phenotypic covariance (below diagonal) among body weights (kg) and greasy fleece weight (kg) at different ages in Chokla sheep

Traits	BWT	3WT	6WT	9WT	12WT	CLIP1
BWT	0.056 (0.223)	0.0563	0.195	0.010	0.025	0.001
3WT	0.388	0.985 (6.735)	0.865	0.510	0.782	0.073
6WT	0.500	6.849	0.965 (12.043)	0.872	0.523	0.090
9WT	0.402	5.137	9.449	2.044 (11.110)	2.514	0.047
12WT	0.475	5.821	10.485	11.543	2.880 (16.362)	0.062
CLIP1	0.028	0.433	0.102	0.475	0.469	0.0132 (0.101)

Table 2. Weighing factors (bi values) for traits selected in single and two stages

Strategy		Traits	bi values
	Single Stage	BWT 3WT 6WT	1.1758 0.1631 0.0248
MSI$_{11}$	Two stage		
	Stage1	BWT 3WT	0.5580 0.1120
	Stage2	I1 6WT	1.8597 0.0047
MSI$_{12}$	Stage1	BWT 3WT	0.5588 0.1120
	Stage2	BWT 3WT 6WT	1.1758 0.1631 0.0248
	Single Stage	BWT 3WT 6WT CLIP I	1.0098 -0.0128 0.1523 1.6465
MSI$_{21}$	Two stage		
	Stage1	BWT 3WT 6WT	1.1758 0.1631 0.0248
	Stage2	I1 CLIP I	0.9470 1.0310
MSI$_{22}$	Stage1	BWT 3WT 6WT	1.1758 0.1631 0.0248
	Stage2	BWT 3WT 6WT CLIP I	1.0099 -0.0128 0.1523 1.6465
	Single Stage	BWT 3WT 6WT 9WT 12WT	0.8553 0.4194 -0.7113 0.7143 0.1859
MSI$_{31}$	Two stage		
	Stage1	BWT 3WT 6WT	1.1758 0.1631 0.0248
	Stage2	I1 9WT 12WT	0.3320 0.2738 0.1992
MSI$_{32}$	Stage1	BWT 3WT 6WT	1.1758 0.1631 0.0248
	Stage2	BWT 3WT 6WT 9WT 12WT	0.8553 0.4194 -0.7113 0.7143 0.1859

second stage but the parameters of first stage traits were adjusted for selection at previous stage. These were MSI$_{12}$, MSI$_{22}$ and MSI$_{32}$.

BWT, 3WT, 6WT, 9WT, 12WT are the body weights at birth, 3, 6, 9 and12 months of ages, respectively. CLIP I is greasy fleece weight for Clip I.

The component traits of indices and their corresponding weighing factor (b value) are given in Table 2 and accuracy of indices (r_{IH} value), expected aggregate genetic gain (ΔH), overall gain in aggregate breeding value and relative gain are given in Table 3.

Among two approaches used for two stage selection index construction, based on accuracy of selection index and absolute genetic gain in aggregate genotype, the second approach using X_1 traits at first stage and X_1, X_2 traits at second stage was found better than the first approach using X_1 traits at first stage and I_1, X_2 traits at second stage. Similar results were obtained by Cunningham (1975). Among two stage selection indices, the selection index using five traits (BWT, 3WT, 6WT, 9WT, 12WT, CLIP1) was more efficient than the other indices in terms of genetic gain in aggregate genotype. The comparison of the two stage selection indices with their corresponding single stage indices revealed that the latter were more efficient in terms of absolute genetic gain. These results are in conformity with the findings of Cunningham (1975), Ganai *et al.* (2000) and Sharma (1995).

Though, single stage selection indices were more efficient in terms of aggregate genetic gain, the multi-stage indices have an edge over them, as far as economics of sheep farming is concerned. These sequential selection programmes ensure better utilization of feed and other resources that are overloaded on sheep to be ultimately culled.

BWT, 3WT, 6WT, 9WT, 12WT are body weights of lambs at birth, 3, 6, 9 and 12 months of age, respectively. CLIP I is greasy fleece weight clip I, Values within parentheses ( ) are the weighing factors (bi values) for the index at previous stage, MSI$_{11}$, MSI$_{21}$, MSI$_{31}$, are two stage selection index constructed by using X_1 traits at first stage and I_1, X_2 traits at second stage and MSI$_{12}$, MSI$_{22}$, MSI$_{32}$ are two stage selection index constructed by using X_1 traits at first stage and X_1, X_2 traits at second stage.

When single stage selection indices were constructed

Table 3. Accuracy of index (r_{IH}), expected genetic gain in aggregate genotype (ΔH), absolute gain in breeding value of traits selected in single and two stages

Strategy		Proportion	r_{IH}	ΔH	Absolute gain
MSI$_{11}$	Single Stage	20%	0.4290	1.1948	1.1948
	Two stage				
	Stage1	50%	0.4114	0.3593	1.1028
	Stage2	40% of 50%	0.3934	0.7435	
MSI$_{12}$	Stage1	50%	0.4114	0.3593	1.1080
	Stage2	40% of 50%	0.4298	0.7487	
MSI$_{21}$	Single Stage	20%	0.4291	1.4172	1.4172
	Two stage				
	Stage1	50%	0.4291	0.6810	1.2991
	Stage2	40% of 50%	0.2859	0.6181	
MSI$_{22}$	Stage1	50%	0.4291	0.6810	1.3399
	Stage2	40% of 50%	0.4357	0.6599	
MSI$_{31}$	Single Stage	20%	0.4886	2.9953	2.9953
	Two stage				
	Stage1	50%	0.4291	0.6810	2.1673
	Stage2	40% of 50%	0.3600	1.4863	
MSI$_{32}$	Stage1	50%	0.4290	0.6810	2.5313
	Stage2	40% of 50%	0.5387	1.8503	

with BWT, 3WT and 6WT, the expected absolute gain was estimated to be 1.1948 and if BWT, 3WT, 6WT and CLIP I traits were taken, the gain was 1.1472. On taking BWT, 3WT, 6WT, 9WT and 12WT the gain was 2.9953. In first two stage selection strategy (MSI$_{11}$) BWT and 3WT were considered in first stage and 6WT were in second stage. The absolute gain expected by this two-stage index was 1.1028. In another two-stage selection strategy (MSI$_{12}$) BWT and 3WT were considered in first stage and BWT, 3WT and 6WT were considered in second stage the absolute gain was expected to be 1.1080.

In second two stage selection strategy (MSI$_{21}$) BWT, 3WT and 6WT were considered in first stage, and CLIP I were in second stage. The absolute gain expected by this two-stage index was 1.2991. In another two-stage selection strategy (MSI$_{22}$) BWT, 3WT and 6WT were considered in first stage, and BWT, 3WT, 6WT and CLIP I were considered in second stage the absolute gain was expected to be 1.3399.

In third two stage selection strategy (MSI$_{31}$) BWT, 3WT and 6WTwere considered in first stage, and 9WT, 12WT were in second stage. The absolute gain expected by this two-stage index was 2.1673. In another two-stage selection strategy (MSI$_{32}$) BWT, 3WT and 6WT were considered in first stage and BWT, 3WT, 6WT, 9WT and 12WT were considered in second stage the absolute gain was expected to be 2.5313. Among two stage selection indices, index MSI$_{32}$ {(first stage = 1.1758 BWT + 0.1631 3WT + 0.0248 6WT) + (second stage= 0.8553 BWT + 0.4194 3WT - 0.7113 6WT + 0.7143 9WT + 0.1859 12 WT)} found more efficient (ΔH = 2.5313) than the 3 two-stage selection. This strategy will result in overall gain of 2.5313 units which is higher than the multistage (MSI$_{12}$ & MSI$_{22}$) index. Though the multistage selection resulted in slower gain but reduced the cost of selection.

CONCLUSION

Though, single stage selection indices were more efficient in terms of aggregate genetic gain, the multi-stage indices have an edge over them, as far as economics of sheep farming is concerned. These sequential selection programmes ensure better utilization of feed and other resources that are overloaded on sheep to be ultimately culled.

REFERENCES

Cunningham, E.P. (1975). Multi-stage index selection. *Theor. Appl. Genet.* **46**: 55-61.

Ganai, N.A., Yadav, S.B.S., Kachwaha, R.N. and Singh, V.K. (2000). Multi-stage strategy for genetic improvement of Marwari sheep. *Indian J. Anim. Sci.* **70(9)**: 957-960.

Harvey, W.R. (1990). User's Guide for LSMLMW and MIXMDL PC-2 version. Mixed model least-squares and maximum likelihood computer program. Ohio State University, Columbus, Ohio, USA.

Hazel, L.N. (1943). The genetic basis for constructing selection indexes. *Genet.* **28**: 476-490.

Hazel, L.N. and Lush, J.L. (1942). The efficiency of three methods of selection. *J. Hered.* **33**: 393-399.

Jain, A., Singh, G. and Yadav, D.K. (2009). Chokla- an endangered sheep genetic resource. *Indian J. Anim. Sci.* **79**: 1071-107.

Meyer, K. (2007). WOMBAT- A tool for mixed model analyses in quantitative genetics by REML. *J. Zhejiang Univ. Sci.* **B8(11)**: 815-821.

Sharma, P.R. (1995). Selection indices for genetic improvement of Nali sheep. M.V.Sc. Thesis, Rajasthan Agricultural University, Bikaner.