Recent Technology of Genetic Selection Indices in Sheep Breeding

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ABSTRACT: In developed countries, selection indices is usually used in the genetic improvement of sheep. One of the most critical assumptions used in constructing multiple trait selection indices is that parameters such as genetic and phenotypic variances and covariances are known - without error. In practise, however, only estimates of these parameters are used, and these are subject to sampling error. The objective of the present paper is to calculate genetic selection indices in sheep breeding using the "bending" technique develoved by Gunawan (1986). In the final model, 11 production traits are used in the breeding objective and 10 characters in the index. The results show that the accuracy of selection ranged from about 0.62 to 0.80. The efficiencies of selection indices including all traits relative to single trait selection are also calculated. The results show that selection indices are always more efficient than single trait selection. The efficiency ranged from about 102% to 176%. The highest relative efficiency is for traits with low heritability (h^2=0.14-0.20), with efficiencies of 176% and 139% respectively. For traits with moderate heritability (h^2=0.21-0.40) the efficiencies ranged from 115% to 132%, and for traits with high heritability (h^2>0.40) efficiencies are between 102% and 107%. It is concluded that a selection index is very efficient if the trait has a low heritability but also relatively high correlations with characters of high heritability in the index.

Key Words : Selection Indices, Single Trait Selection, Genetic & Phenotypic Parameters, Bending Technique, Breeding Objective, Heritability.

Introduction

In Indonesia, genetic selection experiments in sheep have usually been carried out based on single trait selection, for example fertility trait such as litter size (Iniguez et.al., 1993). In fact other trait such as growth rate is also economically important and usually has a high heritability. Growth rate in local sheep is usually low with an average daily gain less than 100gr/day. Combining those two traits simultaneously in the genetic improvement program of local sheep is desirable. Gunawan (1988) calculated the rate of respones to two trait selection in local sheep combining the number of lamb weaned and growth rate in the breeding objective. If the genetic and phenotypic parameters are known, combining more than two traits simultaneously in a genetic selection program is possible to be carried out using appropriate genetic selection indices. The theory of selection indices was introduced by Smith (1936) in plants and Hazel (1943) for selection in animals. It was further elaborated by Cochran (1951) and Henderson (1963). One of the most critical assumptions used in constructing multiple trait selection indices is that parameters such as genetic and phenotypic variances and covariances are known without error. In practice, however, only estimates of these parameters are used, and these are subject to sampling error. Sampling problems become more acute as the number of traits increases, and even for large experiments Hill and Thompson (1978) showed that the probability that the sample estimate of the genetic covariance matrix would not be positive definite is very high. For two-trait selection, a parameter estimate which is out of bounds can easily be modified by setting it to the nearest bound (Harris 1964; Sales and Hill 1976a). However, with more than two traits, defective partial genetic correlations can occur, and setting estimates to their bounds simultaneously is not necessarily satisfactory. Gunawan (1986) suggested that the phenotypic covariances (**P**), genetic covariances (**G**) and the product of the inverse of the phenotypic with the genetic covariance matrix (**P^{-1}G**) should always be checked before genetic selection indices are calculated. If the estimates were

found to be inconsistent (non-positive definite), he used the "bending" technique before genetic selection indices were calculated. The aim of the present paper is to calculate the efficiency of the genetic selection indices in sheep breeding using the bending technique developed by Gunawan (1986).

Materials and Methods

As the genetic parameters for multi-trait selection in local sheep are not available, overseas data are used. However the application of calculating genetic selection indices is still valid for sheep breeding in Indonesia. The production traits used in this study are weaning weight (WW), yearling weight (YW), hogget weight (HW), greasy fleece weight (GFW), yield (YLD), clean fleece weight (CFW), staple length (SL), crimps per centimetre (CPC), colour (COL), character (CHR), handle (HDL) and face cover score (FCS). Yearling weights were taken at about 12 months and hogget weights at about 16 months of age. They were taken from Border Leicester-Merino synthetic populations and the phenotypic and genetic parameters were describred in Gunawan et.al. (1985).

Initially all 12 traits are included in both the breeding objective and the index. After various trials, HW and YLD are dropped from the index, and HW is dropped from the objective, so in the final model there are 11 traits in the objective and 10 characters in the index. Before calculating genetic selection indices, the consistency of $P^{-1}G$ is checked by calculating eigen values. The $P^{-1}G$ is inconsistent if any of the eigen values is negative. The bending factor is then used to bend $P^{-1}G$, so that after bending it becomes $(P^{-1}G)^* = (1-\tau) P^{-1}G + v I$ (Gunawan, 1986). As P is more accurately estimated, then

$$G^* = (1-\tau) G + v P.$$

where
G = genetic variance covariances before bending
G^* = genetic variance covariances after bending
P = phenotypic variance covariances
$1-\alpha$ = bending factor = $v/v-v_1$
v_1 = the smallest eigen value

The genetic selection indices are calculated using the program SELIND (Cunningham and Mahon, 1977). So the procedure is always to check the covariances matrices before and after bending, before calculating selection indices. Since estimates

for reproductive traits are not available, a complete breeding objective is not specified, and indices to predict breeding values of individual traits are calculated. This is done by giving each trait an arbitrary economic weight (unity) in input to the computer program and using only the sub indexes, which give estimated breeding values for individual traits, and are independent of the economic weights. Efficiency of estimating breeding value of each trait by an index relative to use of the phenotype is calculated as r_{IH}/h, where r_{IH} is the correlation between breeding value (BV) of the trait in the objective and the index, and h is the square root of heritability of the trait, which is the correlation between BV of that trait and its phenotype.

Results and Discussion

For the 12 traits, none of the eigen values of P before bending are negative. For G and $P^{-1}G$ at least two of 12 eigen values are negative. However the P inverse has very large elements, because P is almost singular, i.e. has a determinant near zero. If the columns (or rows) of a square matrix are dependent, its determinant is zero and consequently it has no inverse (Searle and Hausman, 1970). It is therefore likely that an almost linear relationship among some rows of P and since YLB = CFW/GFW one would expect an approximate linear relation among these traits. Thus P matrix including these three traits would be nearly singular, and its inverse would be subject to substantial computational rounding errors.

In G there are very high genetic correlations between WW, YW and HW. WW and YW has negative genetic correlations with FCS, but HW has a positive one. When a partial genetic correlation is calculated between YW and FCS while holding HW constant, the value is less than -1, and this outside its bound. This is an indication that some parameters for HW has been badly estimated. Since YW and HW are very nearly the same character, little information is lost by omitting one of them.

For the reasons given above, HW is dropped from the objective, and HW and YLD are dropped from the index. As G and $P^{-1}G$ has still negative eigen values, the bending procedure is applied. After bending, none of the negative eigen values are found in P and G.

Heritabilities, phenotypic and genetic correlations for 11 traits after bending which are used to calculate selection indices are given in Table 1. They

Tabel 1. Genetic correlations (below diagonal) and phenotypiccorrelations (above diagonal) after bending

	WW	YW	GFW	YLD	CFW	SL	CPC	COL	CHR	HDL	FCS
WW	**0.20**	0.63	0.30	0.03	0.26	0.11	0.01	0.03	0.01	0.07	-0.06
YW	0.80	**0.46**	0.37	0.02	0.28	0.07	0.04	-0.04	0.03	0.08	-0.14
GFW	0.24	0.23	**0.58**	-0.06	0.80	0.24	-0.32	-0.22	0.23	0.10	0.06
YLD	-0.21	-0.08	-0.21	**0.44**	0.54	0.22	-0.37	0.09	0.13	-0.08	-0.02
CFW	0.03	0.09	0.75	0.42	**0.56**	0.33	-0.48	-0.12	0.27	0.05	0.02
SL	0.12	0.07	0.35	0.17	0.38	**0.53**	-0.43	0.10	0.08	0.22	-0.15
CPC	0.23	0.07	-0.58	-0.45	-0.70	-0.48	**0.37**	0.02	-0.18	0.01	-0.01
COL	-0.12	0.06	-0.36	0.39	-0.08	0.10	-0.23	**0.14**	-0.15	0.06	-0.00
CHR	-0.02	-0.03	0.51	0.10	0.50	0.19	-0.45	-0.60	**0.34**	0.19	-0.03
HDL	0.18	0.31	0.18	-0.51	-0.09	0.38	0.02	-0.16	0.32	**0.26**	0.00
FCS	-0.30	-0.25	0.10	-0.18	-0.18	-0.07	-0.14	0.22	-0.00	0.04	**0.48**

Tabel 2. Per cent reduction in rate of overall genetic gain if certain trait is omitted from the subindex and correlation between index and trait in breeding objective (r_{IH})

Breeding Objective	% reduction if the trait is omitted from subindex										r_{IH}
	WW	YW	GFW	CFW	SL	CPC	COL	CHR	HDL	FCS	
WW	2.8	11.3	2.4	4.1	1.0	0.6	0.1	0.0	0.0	2.1	0.6223
YW	0.6	37.7	0.2	1.1	0.0	0.3	0.1	0.1	1.1	0.5	0.7111
GFW	0.2	0.2	25.4	1.7	0.2	0.7	0.2	1.3	0.0	0.0	0.8052
YLD	0.9	0.6	33.9	37.8	0.0	0.1	0.4	0.1	3.5	0.4	0.7994
CFW	1.1	0.2	0.7	13.4	0.0	0.0	0.6	0.8	0.7	0.5	0.7925
SL	0.1	0.0	0.8	0.1	44.1	0.2	0.0	0.1	0.0	0.0	0.7403
CPC	2.3	0.0	2.0	0.5	0.6	9.2	3.0	1.4	0.5	0.7	0.7394
COL	1.8	6.4	13.8	4.8	0.1	3.2	7.2	10.3	0.0	4.7	0.6592
CHR	0.0	1.2	2.4	0.0	0.0	0.6	1.0	25.2	0.4	0.1	0.6692
HDL	0.5	3.6	4.8	11.2	6.7	0.0	0.4	2.0	17.3	0.9	0.6716
FCS	0.3	0.1	3.6	3.9	0.1	1.8	1.3	0.1	0.0	48.3	0.7440

may also be compared with the straight estimates given by Gunawan et.al. (1985).

The correlations between subindex and BV for each trait, and per cent reduction in overall genetic gain when a certain character is omitted from the index, are presented in Table 2. The table shows that the accuracy of selection (r_{IH}) ranged from about 0.62 to 0.80.

For WW, the most valuable correlated trait is YW, since omitting it from the index reduced efficiency by 11%, while omitting the trait itself efficiency dropped by only about 3%.

For YW and GFW, if the trait itself are not recorded, the efficiency dropped by about 38% and 25% respectively.

For YLD, information from GFW and CFW has had a profound effect on estimation of breeding value, as dropping each of the characters would reduce efficiency by 34% - 38%. As YLD itself is not included in the index because of the problem with the **P** inverse, the high value of r_{IH} confirms that GFW and CFW can together give a good estimate of BV for YLD. In addition, HDL contributes about 3.5% to efficiency of selecting for YLD.

For CFW, if the trait itself are not recorded, efficiency could drop by about 13%. For SL, recording the trait itself is sufficient, as dropping various other characters from the index has negligible effects on efficiency.

For CPC, COL, CHR, HDL and FCS, if the trait itself are not recorded, the efficiency would drop by about 9%, 7%, 25%, 17% and 48% respectively. From these results it is clear that when scored characters such as COL, CHR or HDL are included in indices for genetic improvement of an important economic trait (WW, YW, GFW or CFW), efficiency is increased by less than 1%. COL would increase the efficiency about 3% for CPC, and FCS increased the efficiency by about 2% for WW. Thus, the contributions of these subjectively scored traits to efficiency of selection for weight of meat or wool would not warrant their inclusion in a selection index.

The efficiencies of selection indices including all traits relative to single trait selection are given in Table 4. The table shows that selection indices are always more efficient than single trait selection. This agrees with the established theory that index selection is never less efficient than single trait selection and under certain conditions, it should be much more efficient (Hazel and Lush 1942; Young

1961).

The efficiency ranged from about 102% to 176%. The highest relative efficiency is for traits with low heritability such as COL ($h^2 = 0.14$) and WW ($h^2 = 0.20$), with efficiencies of 176% and 139% respectively. For traits with moderate heritability ($h^2 = 0.21$-0.40) the efficiencies ranged from 115% to 132%, and for traits with high heritability ($h^2 > 0.40$) efficiencies are between 102% and 107%, except for YLD with a relative efficiency of 120%. This high efficiency for YLD, compared with other traits of high heritability, although YLD itself is not included in the index, is no doubt due to its genetic relationship with CFW and GFW.

Although some traits have relatively higher accuracy of selection (r_{IH}), for example GFW and YLD where r_{IH} is about 0.80, versus WW and COL where r_{IH} is between 0.62 and 0.66 (Table 2), the efficiency of index selection relative to selection for the trait itself is higher with WW and COL as they have lower heritabilies (Table 3). Hence a selection index is very efficient if the trait has a low heritability but also relatively high correlations with characters of high heritability in the index.

Tabel 3. Efficiency of selection index relative to single trait selection

Trait in objective	h2	r_{IH}/h
WW	0.20	1.3915
YW	0.46	1.0485
GFW	0.58	1.0573
YLD	0.44	1.2051
CFW	0.56	1.0590
SL	0.53	1.0169
CPC	0.37	1.2156
COL	0.14	1.7618
CHR	0.34	1.1477
HDL	0.26	1.3171
FCS	0.48	1.0739

For two-trait selection, Sales and Hill (1976b) calculated about 40% extra improvement achieved for a trait with low heritability ($h^2 = 0.2$) by having additional information from another character included in the index. Without considering the effects of error in parameter estimates, Gjedrem

(1967) gave examples where the gain was up to 300% for an important trait of low heritability (h^2 = 0.1).

We have shown, at least in the data from Border Leicester-Merino synthetic populations, some of the problems of constructing multiple trait selection indices when there are errors in parameter estimates. For 10 and 12 traits, the **P** are always positive definite. Nevertheless, this does not guarantee that the **P** could be used straight forwardly in calculating selection indices. Our results show that including the three traits YLD, CFW and GFW made **P** very close to singular. Hence these results warn of the need to check the inverse of **P** as well as checking that it is positive definite.

For **G**, although the matrices for 10 or 12 traits do not include any estimates outside their bounds, they have one or two negative eigenvalues. This implied that, although no estimates are outside their bounds, some derived parameters would be, for example, partial genetic correlations outside the range -1 to +1.

Conclusion

The bending technique applied to **G** before genetic selection indices are calculated and give some reasonable results for accuracy of selection. However, the application of this technique needs to be tested further. The possibility of better methods for modifying estimates is not ruled out, as we changed only the eigenvalues and left the corresponding eigenvectors unchanged.

The bending procedures for multi-trait selection described in this study can be used in sheep breeding program for the genetic improvement of local sheep in Indonesia. For this purpose the estimation of phenotypic and genetic parameters of the production traits of the Indonesian local sheep are required. Although the data are used from overseas, the genetic principles of calculating genetic selection indices is valid and can be applied for sheep breeding in Indonesia. As the phenotypic and genetic parameters are not available, a more simple genetic approach such as ICL (Independent Culling Level) is usually practised, i.e. selecting single trait at a certain stage, for example litter size of the ewes, mortality and defects before weaning, growth rate after weaning and growth after postweaning etc. In fact if those traits are combined and selected simultaneously by giving appropriate economic weights, the genetic effects of ICL and selection indices are basically the same. Although by this method it may be possible to save considerable on costs of measurements, it is still a problem to find optimum independent level selection procedures. So it would be best to select at each stage on an index combining information on all traits measured up to that stage. We have shown from overseas parameters, that a sheep breeding program using index selection is always more efficient than single trait selection assuming the selection index is appropriately constructed.

Literature Cited

Cochran, W. G. (1951). Improvement by means of selection. Proc. 2nd Berkeley Symp. on Math. Stat. and Prob. (Ed. J. Neyman.) pp.449-70. (Univ. California Press: Berkeley.)

Cunningham, E. P., and Mahon, G. A. T. (1977). SELIND, a Fortran computer program for genetic selection indexes. User's Guide.

Gjedrem, T. (1967). Selection indexes compared with single trait selection. I. The efficiency of including correlated traits. Acta Agric. Scand. 17, 263.

Gunawan, B., James, J. W., and McGuirk, B. J. (1985). Genetic parameters for production traits in Border Leicester- Merino synthetic populations. Proc. 5th Conf. Aust. Assoc. Anim. Breed. Genet., Sydney, pp. 234-5.

Gunawan, B. (1986). Genetic studies of quantitative characters in synthetic population. Ph.D. thesis, University of New South Wales, Sydney, Australia.

Gunawan, B. (1988). Teknologi Pemuliabiakan Domba Lokal Indonesia. Proceedings Seminar Export Ternak Potong, Hotel Horison, Jakarta, 2-3 September 1988.

Harris, D. L. (1964). Expected and predicted progress from index selection involving estimates of population parameters. Biometrics 20, 46.

Hazel, L. H. (1943). The genetic basis for constructing selection indices. Genetics 28, 476.

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

Henderson, C. R. (1963). Selection index and expected genetic advance. In 'Statistical Genetics and Plant Breeding'. NAS-NRC 982.

Hill, W. G., and Thompson, R. (1978). Probabilities of nonpositive definite between group or genetic covariance matrices. Biometrics 34, 429.

Iniguesz, L., Pattie, W. A. and Gunawan, B. (1993). Aspects of Sheep Breeding with Particular Emphasis on Humid Tropical Environments. In : Small Ruminant Production in the Humid Tropics. pp. 80-143. Editors : M. Wodzicka- Tomaszewska, S. Gardiner, A. Djajanegara, I.M. Mastika and T.R. Wiradarya. Sebelas Maret University Press.

Sales, J., and Hill, W. G. (1976a). Effect of sampling errors on efficiency of selection indices. 1. Use of information from relatives for single trait improvement. Anim. Prod. 22, 1.

Sales, J., and Hill, W. G. (1976b). Effect of sampling errors on efficiency of selection indices. 2. Use of information on associated traits for improvement of a single important trait. Anim. Prod. 23, 1.

Searle, S. R., and Hausman, W. H. (1970). 'Matrix Algebra for Business and Economics.' (Wiley: New York.)

Smith, H. F. (1936). A discriminant function for plant selection. Ann. Eugen. 7, 240.

Young, S. S. Y. (1961). A further examination of the relative efficiency of three methods of selection for genetic gains under less restricted conditions. Genet. Res 2, 106.