

457. Response to index selection for temperate dairy cattle breeds in tropical Sri Lanka

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Abstract

This study aimed to predict selection responses for breeding objective traits based on large-scale dairy farms rearing temperate dairy breeds in Sri Lanka. Responses were predicted selecting 10% of bulls at 4 and 9 years of age assuming the availability of progeny records for the selection of older bulls. When economic weights were expressed relative to the trait genetic standard deviation, milk yield (MY, 74%) had the highest relative emphasis on selection. Favourable responses were only observed for MY and calving interval reflecting the high selection emphasis on MY to counteract with other traits. Predicted responses relative to the current mean varied from -0.67% (protein yield) to 0.40% (MY). Progeny selection increased the accuracy at the expense of higher generation interval. Predicted increase in profit due to genetic improvement was slightly higher under progeny testing compared to family selection (2,624 vs 2,506 rupees or 14.1 vs 13.5 USD per cow per year).

Introduction

Selection of dairy cattle based on estimated breeding values is currently not practiced in Sri Lanka. However, the need for development of dairy cattle breeding programmes has been highlighted. Therefore, as a precondition for establishment of a breeding programme in Sri Lanka, genetic parameters for the main traits of interest in a breeding objective for temperate dairy cattle in Sri Lanka were recently estimated, and economic values (EVs) were derived (Samaraweera 2020). Prediction of annual genetic response of traits in the breeding objective is a key criterion in evaluating the selection decisions and understanding the direction and magnitude of individual trait responses. Therefore, the objective of this study was to predict response to multi-trait selection for breeding objective traits in large-scale dairy farms in Sri Lanka.

Materials & methods

The breeding objective traits of the large-scale dairy farms rearing temperate dairy breeds were annual milk yield (MY, kg/cow/year), annual fat yield (FY, kg/cow/year), annual protein yield (PY, kg/cow/year), age at first calving (AFC, days/cow), number of services per conception (NSC, counts/cow/conception), calving interval (CI, days/cow), and number of episodes of mastitis (MS, counts/cow/lactation). Please see Samaraweera *et al.* (in press) for trait definitions and EVs.

Economic weights. The EVs were transformed into economic weights (EWs) by multiplying them by discounted genetic expression (DGE) coefficients to account for the different frequency and timing of expressions of the traits (McClintock and Cunningham 1974). Since AFC is expressed once per cow and early in the cow's lifetime, the DGE coefficient for AFC was equal to one, and EWs were expressed per cow at first calving. All other traits were expressed once per lactation. Therefore, DGE coefficients for MY, FY, PY, NSC, CI, and MS were calculated as the sum of all timings and the frequency of expressions over five lactations as follow:

$$DGE = \sum_{Lc=1}^{Lc=5} \frac{\rho}{(1+r)^{Lc}} \quad (1)$$

Where ρ = a vector with each element being the proportion of cows surviving in each lactation relative to the total number of surviving cows, weighted by lactation number, r = the annual interest rate of 5%, and L_c = lactation number reflecting lactations 1 to 5. Survival rate from one lactation to the next lactation was assumed to be 90%. The EVs and calculated economic weights are given in Table 1. When expressed relative to the trait genetic standard deviation, MY (74%) had the highest relative emphasis followed by FY (11%), CI (7%), and AFC (4%) (Table 1).

Selection index. Response to selection per year was predicted for two scenarios, i.e. (1) where bulls were selected at 4 years of age based on information from their dam and paternal half sibs (scenario 1); and (2) selection at 9 years of age based on progeny test (scenario 2). The breeding programme was based on a government nucleus farm with 2,000 cows, and 10% of male calves were selected as suitable to become breeding bulls in the nucleus. Therefore, selection intensity was 1.75 in both scenarios. Higher number of dam, half-sib, and progeny records were assumed for scenario 2 than scenario 1 (2, 5, and 10 vs 1, 2, and 0). The number of half-sib and progeny information were based on the assumption of limited matings per sire in Sri Lanka. Response to selection was predicted using a multi-trait selection index programme, MTINDEX (Van der Werf 2018) which expresses selection response for each trait per standard deviation of the index. To obtain the response per year, these values were multiplied by the intensity of selection and divided by the appropriate generation interval. The genetic parameters that were used to predict response to multiple trait selection are given in Table 2.

Results

Trait accuracies were higher from progeny testing (scenario 1) compared to selection based on dam and paternal half sib information (scenario 2) (Table 3). After selection, scenario 2 had the highest response for all traits except CI and MS. Favourable (in \$ terms) responses were observed only for MY and CI in both scenarios. Even though EWs were negative for FY and PY, response was positive and therefore unfavourable for FY and PY mainly due to the positive correlations between these traits with MY. The predicted increase in profit due to genetic improvement per year was slightly higher in scenario 2 than scenario 1 (2,624 vs 2,506 rupees or 14.1 vs 13.5 USD per cow per year). Predicted genetic response to selection relative to the current mean (% change, Table 3) varied from -0.67% (PY) to 0.40% (MY).

Table 1. Economic values (EV), the discounted genetic expression (DGE) coefficients, economic weights (EW), rupees per genetic standard deviation (SD), and relative emphasis (RE) of each trait.

Parameter	Traits ¹						
	MY	FY	PY	AFC	NSC	CI	MS
EV ² (rupees ³ /cow/year)	107	-162	-15	-59	-270	-84	-8,303
DGE	2.36	2.36	2.36	1.00	2.36	2.36	2.36
EW (rupees/cow/year)	253	-382	-35	-59	-637	-198	-19,595
rupees per genetic SD	50,496	-7,341	-730	-3,122	-1,126	-4,357	-305
RE (%)	74	11	1	4	2	7	1

¹ MY = annual milk yield (kg); FY = fat yield (g); PY = protein yield (g); AFC = age at first calving (days); NSC = number of services per conception; CI = calving interval (days); ME = number of episodes of clinical mastitis.

² EV: from Samaraweera *et al.* (in press).

³ USD = 186 rupees, May 2020.

Table 2. Phenotypic standard deviation (σ_p), heritability (diagonal), genetic (below the diagonal) and phenotypic (above the diagonal) correlations of the traits used in the multiple-trait selection index.

	op	MY	FY	PY	AFC	NSC	CI	MS
MY ^{1,2}	707 ⁵	0.08 ⁵	0.81 ⁹	0.81 ⁹	0.00	0.15 ¹⁰	0.23 ¹⁰	-0.13 ¹¹
FY	48 ¹⁴	0.63 ⁹	0.16 ¹⁴	0.88 ¹⁰	0.00	0.14 ¹⁰	0.20 ¹⁰	-0.11 ¹¹
PY	45 ⁹	0.63 ⁹	0.80 ¹⁰	0.21 ³	0.00	0.16 ¹⁰	0.22 ¹⁰	-0.11 ¹¹
AFC	100 ⁴	0.31 ⁷	0.00	0.00	0.28 ⁴	0.45 ¹²	-0.01 ¹²	0.00 ¹³
NSC	10.2 ⁵	0.25 ¹⁰	0.25 ¹⁰	0.21 ¹⁰	0.87 ¹²	0.03 ⁵	0.73 ¹⁰	0.00
CI	98.3 ⁵	0.11 ⁸	0.49 ⁶	0.44 ⁶	-0.52 ¹²	0.71 ¹⁰	0.05 ⁵	0.03 ¹³
MS	0.09 ¹¹	0.32 ¹¹	0.22 ¹¹	0.29 ¹¹	-0.18 ¹³	0.00	0.06 ¹³	0.03 ¹¹

¹ Traits and units are as given in Table 1.

² For reference 1 US dollar is equal to 186 rupees (May 2020).

References for the parameters are indicated by superscripts: ³Bang *et al.* (2019); ⁴Montaldo *et al.* (2010); ⁵Samaraweera *et al.* (2020); ⁶Adapted from Haile-Mariam *et al.* (2003); ⁷Salah Khattab *et al.* (2005); ⁸Samaraweera (2020); ⁹Adapted from Carabano *et al.* (1989); ¹⁰Kadarmideen *et al.* (2003); ¹¹Carlén *et al.* (2004); ¹²Eghbalsaied (2011); ¹³Pryce *et al.* (1997); ¹⁴Wahinya *et al.* (2020). Values without a reference are indicated as zero.

Table 3. The trait accuracy (Acc), annual response to multiple-trait selection in trait units (Tu) and rupee value (Rs), and percentage change of the traits in breeding objective relative to the current mean (% change) when sires are selected at 4 (Scenario 1) and 9 years of age (Scenario 2).

Trait ¹	Scenario 1				Scenario 2			
	Acc	Tu	Rs	% Change	Acc	Tu	Rs	% Change
MY	0.22	18.9	2,722	0.38	0.53	19.9	2,878	0.40
FY	0.30	0.6	-133	-0.22	0.66	0.8	-176	-0.34
PY	0.35	1.17	-23	-0.61	0.72	1.2	-25	-0.67
AFC	0.34	4.6	-156	-0.43	0.72	3.8	-127	-0.34
NSC	0.21	0.05	-20	-0.75	0.52	0.03	-11	-0.31
CI	0.29	-1.08	122	0.24	0.63	-0.81	92	0.18
MS	0.16	0.0005	-5.55	-0.17	0.40	0.0006	-6.84	-0.21
Total ²			2,506				2,624	

¹ Traits and units are as given in Table 1.

² Total: rupee value per cow per year.

Discussion

The two scenarios were compared to understand the response to selection from early selection with lower accuracy using family information versus selection based on more accurate progeny test information but with a longer generation interval. The accuracy of selection and slightly higher responses were obtained for all traits except CI and MS in scenario 2. However, the response in scenario 1 is likely overestimated since selection was based on family information, and genetic variance is reduced due to selection (Bulmer 1971). The genetic variance can be further reduced in family selection due to inbreeding. Despite the overestimated response in scenario 1, the family records can be used to achieve annual responses over a four-year period in a breeding programme until the progeny records become available.

Among the milk yield traits, the selection for FY and PY is not economically viable in both scenarios, even though, increased FY and PY in milk is favoured. Therefore, increased payment for FY and PY or reduced feed costs are recommended (Samaraweera, in press). A high relative emphasis on MY, FY, and PY (92%)

in the selection index is not beneficial for a tropical country like Sri Lanka where fertility, disease, and heat tolerance traits are equally important in the breeding objective for a more resilient dairy population. Therefore, inclusion of these functional traits in the breeding objective is recommended.

Genomic selection is advantageous in reducing the generation interval and increasing the genetic gain compared to conventional progeny testing. In Sri Lanka, genomic selection has not been evaluated so far, and a major problem for functional dairy cattle breeding programmes is the absence of reliable pedigree information. Genomic selection would benefit such systems given parentage can be traced using genetic markers. However, the cost of implementation and monetary benefits should be carefully considered before implementing genomic selection in developing countries.

In conclusion, progeny selection increased the accuracy of selection and response per year at the expense of higher generation interval. Favourable responses after selection were only predicted for MY and CI due to the very high selection emphasis on MY and its unfavourable genetic associations with other traits.

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References

- Bang N., Hayes B., Randhawa I., Lyons R., Gaughan J. et al. (2019) Proc. of the 23rd AAABG, Armidale, Australia.
- Bulmer M. (1971) *The American Naturalist* 105(943):201-211. <https://doi.org/10.1086/282718>
- Carabano M., Van Vleck L.D., Wiggans G., and Alenda R. (1989) *J. Dairy Sci.* 72(11):3013-3022. [https://doi.org/10.3168/jds.S0022-0302\(89\)79454-6](https://doi.org/10.3168/jds.S0022-0302(89)79454-6)
- Carlén E., Strandberg E., and Roth A. (2004) *J. Dairy Sci.* 87(9):3062-3070. [https://doi.org/10.3168/jds.S0022-0302\(04\)73439-6](https://doi.org/10.3168/jds.S0022-0302(04)73439-6)
- Eghbalsaied S. (2011) *Trop. Anim. Health Prod.* 43(4):811-816. <https://doi.org/10.1007/s11250-010-9767-z>
- Haile-Mariam M., Morton J., and Goddard M. (2003) Proc. of the 15th AAABG,
- Kadarmideen H.N., Thompson R., Coffey M.P., and Kossaibati M.A. (2003) *Livest. Prod. Sci.* 81(2):183-195. [https://doi.org/10.1016/S0301-6226\(02\)00274-9](https://doi.org/10.1016/S0301-6226(02)00274-9)
- McClintock A., and Cunningham E. (1974) *Anim. Sci.* 18(3):237-247. <https://doi.org/10.1017/S0003356100022418>
- Montaldo H., Castillo-Juárez H., Valencia-Posadas M., Cienfuegos-Rivas E., and Ruiz-López F. (2010) *J. Dairy Sci.* 93(5):2168-2175. <https://doi.org/10.3168/jds.2009-2050>
- Pryce J., Veerkamp R., Thompson R., Hill W., and Simm G. (1997) *Anim. Sci.* 65(03):353-360. <https://doi.org/10.1017/S1357729800008559>
- Salah Khattab A., Atil H., and Badawy L. (2005) *Arch. Anim. Breed.* 48(1):24-31. <https://doi.org/10.5194/aab-48-24-2005>
- Samaraweera A.M., van der Werf J.H.J., Boerner V., and Hermes S. (in press) *J. Anim. Breed. Genet.* <https://doi.org/10.1111/jbg.12667>
- Samaraweera A.M. (2020) Development of a temperate dairy cattle breeding programme in Sri Lanka using milk, fertility and udder health traits. PhD thesis. University of New England Armidale, Australia.
- Samaraweera A.M., Boerner V., Cyril H.W., van der Werf J., and Hermes S. (2020) *Asian Austral. J. Anim.* 33(11):1741-1754. <https://doi.org/10.5713/ajas.19.0798>
- van der Werf J.H.J. (2018) Software MTINDEX-multiple trait selection index 20 trait version. Available at <https://jvanderw.une.edu.au/software.htm>.
- Wahinya P.K., Jeyaruban G., Swan A., and Magothe T. (2020) *J. Anim. Breed. Genet.* 137:495-509. <https://doi.org/10.1111/jbg.12473>