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Using random regression models to optimize selection for yield, persistency and calving interval in Philippine dairy buffaloes

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ABSTRACT: Eigenvalue (EV) decomposition of the genetic coefficient matrix from random regression analysis of milk test day yields in Philippine dairy buffaloes provided independent variables for use in selection. The 1st, 2nd and 3rd EVs explain 80.3%, 18.8% and 0.2% of the total genetic variance, respectively. Selection on the 2nd eigenvalue resulted in higher response in the latter half of lactation, thus better persistency. There was a 5% reduction in milk yield (MY), 5.6% higher net economic gain and improvement in persistency from 0.62 to 0.79 with an optimal index relative to selection on total lactation. There was also a high genetic correlation between calving interval (CI) and the 2nd EV for MY. As CI is mostly correlated with MY in late lactation, this suggests CI is mainly associated with lactation length and may not be a true measure of fertility.

Keywords: Philippine dairy buffaloes; Lactation persistency; Random regressions

Introduction

Lactation persistency is defined as the rate of decline after peak lactation yield has been reached. Persistent cows have flatter lactation curves and relatively lower peak that occurs at a later date, thus, require less energy at the beginning of lactation. This might lead to less health and reproductive problems (Harder et al. (2006)). By reducing the rate of decline after peak, lactation length could also be improved. It has been shown that lactation persistency can be included in routine genetic evaluation (Cole & Null (2009); Verbyla & Verbyla (2009)). However, selection for lactation persistency tends to reduce milk production in varying degrees (Togashi & Lin (2004)). With random regression models (RRM), the variation in lactation curve could be modeled and cows can be selected simultaneously for milk yield and lactation persistency based on estimated breeding values (EBV) of daily yields (Togashi & Lin (2004)) using the eigenvectors of the genetic coefficient matrix. Selection on the first eigenvalue produces a similar response throughout the lactation trajectory and was responsible for scaling the lactation curve without changing the shape while the second and third eigenvalues account for the shape of the lactation curve (Togashi & Lin (2006)). This change in shape can be quantified using economic values for milk yield on a daily basis.

In dairy buffaloes, studies regarding lactation persistency measures and their relationship with other traits have been limited. Geetha et al. (2006) used random regression to estimate EBVs for daily yields and used these EBVs to derive several persistency measures. The first measure was expressed as the sum of the deviation of EBVs on days after peak from EBV on peak day while the other set of measures were expressed as genetic yield gained/lost from day of peak to EBV on day 90, 120, 180, 210, 240, 270 and 305 relative to an average buffalo having the same yield on day 65 (Geetha et al. (2006)). Aspilcueta-Borquis et al. (2012)) reported two latent factors (principal components) from the phenotypic correlation matrix of test day milk records, one related to peak yield and one to lactation persistency. In both studies, optimizing response to selection for milk and persistency was not reported. Selection for persistency may be appropriate for the Philippine buffaloes because 1) low to medium-input management systems used by farmers may not be able to sustain the energy requirement for high yielding cows that peak high and early in lactation; 2) Buffalo cows, on average, have less than optimum fertility rates, and selection for increased milk yield (concomitant with high peak) may exacerbate the decline in reproductive performance; 3) buffalo cows on the average have short lactation period, reducing the rate of decline after peak through selection for persistency may extend the lactation period. The objective of this study is to determine the effect of varying selection weights for persistency and to optimize response to selection on persistency and milk yield using parameters from a random regression model for milk yield. We also consider a correlated response in calving interval.

Materials and Methods

Data. Test day records of 1,022 first parity buffalo cows from nine herds were available for univariate and bivariate analysis of milk yield (MY) and calving interval (CI). The additive genetic coefficient matrix was estimated from random regression analysis from a previous study (Flores & van der Werf (2013)).

Eigenvalue decomposition. Random regression coefficients of the additive genetic effects were used to build the **G** matrix at different days in milk (DIM) in the lactation period (Jamrozik et al. (1997)). The matrix **G** is given as: $\boldsymbol{G} = \Phi K_{\alpha} \Phi'$ where $\mathbf{K}_{\boldsymbol{\alpha}}$ is a 3 x 3 matrix containing the $\mathbf{k}_{\mathbf{ij}}$ (co)variance elements for the random genetic regression coefficients $\boldsymbol{\alpha}$ (α_0, α_1, α_2) and $\Phi = t \times k$ design matrix of Wilmink's function evaluated for t different DIM. Following van der Werf et al. (1998), the matrix $\boldsymbol{G}$ was decomposed to $\boldsymbol{G} = \Phi E' D E \Phi'$ which is $\boldsymbol{G} = QDQ'$ where **D** and **E** are the eigenvalues (EV) and eigenvectors (Evec) of $\mathbf{K}_{\boldsymbol{\alpha}}$ and $\mathbf{Q} = \Phi E'$ represent the set of eigenfunctions (Kirkpatrick et al. (1990)). Eigenfunctions (EF) can be used to analyze patterns of variation across the lactation period and from this, to infer the variation in lactation persistency. Rather than selecting on solutions for the additive genetic effects from RRM, we can consider an index based on the vector ***z*** with ***k*** canonical variates: I = $b_{z'}\mathbf{z}$; var(z) = **D** and if ***z*** represent true additive genetic values, response would be: $R_z = \frac{b_z' D}{\sqrt{b_z' D b_z}}$. The index has equivalence in the observable scale I = b'α because $b_i = (Q^{-1})bz$. Response to selection on canonical variates was optimized with respect to profit where the economic value for milk yield was calculated for milk yield on a day to day basis based on a previous study (Flores et al. (2011)). The economic value of the genetic gain from selection on canonical variates to change the shape of the lactation curve relative to selection on total lactation were calculated for each day of the trajectory based on milk returns and feed requirements. The response in genetic and economic gain using the persistency index with optimized weights applied to canonical variates (MY2) was compared with selection on total lactation (MY305D), equal weight applied to Z_1, Z_2 and Z_3 (MY1) as well as applying greater weight to Z_2 only relative to Z_1 and Z_3 (MY3).

Genetic correlation of milk yield with calving interval. Bivariate analysis between MY and CI by random regression was done to estimate genetic correlations between the two traits following Veerkamp et al. (2001). The estimated additive genetic covariance matrix (**M**) combines the variance for CI (σ^2_{CI}), the matrix $\mathbf{K}_\alpha$ for MY containing (co)variances for ***n***=3 random regressions coefficients (var α = K_α), and the ***n*** covariances between α and CI ($\sigma_{CI,\alpha}$). We can use the same eigenvalue decomposition of K_α for MY as before and calculate the correlation between CI and Z_1, Z_2 and Z_3 as $E'\sigma_{CI,\alpha}$.

Results and Discussion

Eigenvalue decomposition. The first (EV_1), second (EV_2) and third (EV_3) eigenvalues from the RRM for milk yield explain 80.3%, 18.8% and 0.8% of the total genetic variance, respectively (Fig. 1A). However, based on a Chi-square test (van der Werf et al. (1998)), only the first two EVs were significantly different from zero ($P<0.05$). This implies that only two canonical variates corresponding to linear combinations of the three Wilmink function's regression coefficients would be sufficient to fit $\hat{\mathbf{G}}$. The EF related to EV_1 was positive and constant throughout the lactation period. The result suggests that most of the variation in the test day milk yield is explained by a genetic component acting constantly throughout the lactation period. The EF related to EV_2 was negative in the first half of lactation but became positive after DIM164. This eigenvalue may correspond to a genetic component for persistency and indicates that it may be possible to select for lactation persistency, especially so because the percentage of variance explained by EV_2 was slightly higher than those estimated from Brazilian dairy buffaloes (Sesana et al. (2010)) and from dairy cattle (Togashi & Lin (2006); van der Werf et al. (1998)).

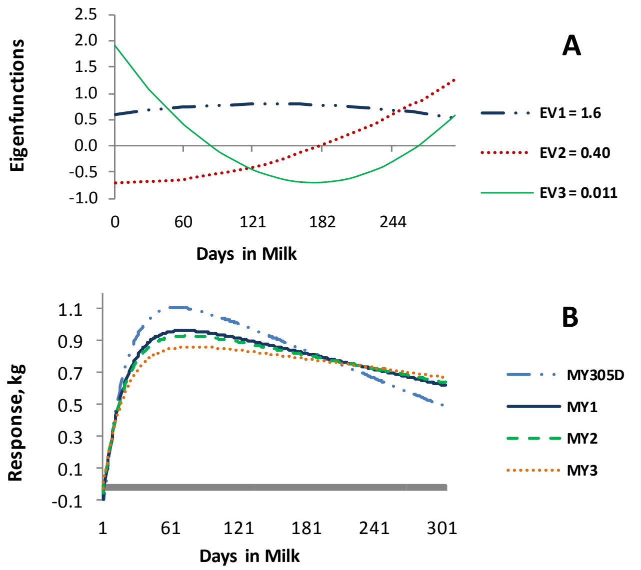

Figure 1. (A) Eigenfunctions related to the first three eigenvalues of the genetic covariance matrix for milk yield and (B) Response to selection on various indices with varying weights applied to Z_1, Z_2 and Z_2

Response to selection on lactation persistency. Selection on total 305D yield (MY305D in Fig. 1B) will result in greatest increase in milk production, but the response comes mostly from the increased yield in the first 90 days of lactation. This is because selection for increased milk yield will also invariably increase peak yield as the two are highly correlated. Per observation of the Philippine dairy buffalo cows' performance, almost half of the total milk produced is in the first trimester of lactation only. Selection on total lactation will result in deterioration of lactation persistency. The transformation of the RR model to canonical scale enables selection on canonical variates Z_1, Z_2 and Z_3 that are related to the first three leading eigenvalues. As EV_2 explains a smaller proportion of the total genetic variance, more weight should be applied to Z_2 to achieve more response to selection on the latter half of the lactation period and decrease the response at peak. The reduction in response at peak and on total milk yield became greater with increasing weight applied to Z_2 (index MY3 in Table 1 and Fig. 1B). Economic optimization of the weights (b_z) applied to Z_2 and Z_3 resulted in index MY2 with a response intermediate between MY305D and MY3 for yield and persistency with a 5% decrease in total milk yield and 5.6% increase in overall economic gain (Table 1), relative to selection on total lactation. This is similar to the reports in dairy cattle (Togashi & Lin (2004)) where selection on persistency resulted in decrease in milk yield. However, besides an additional economic benefit, there is also a benefit in terms of health and fertility of the cow that could ensue with selection for persistency. As a measure of persistency, the ratio of the response at DIM240 over DIM90 from selection on MY1, MY2, MY3 indices and on total lactation was 0.76, 0.79, 0.85 and 0.62, respectively. There was a 27% improvement in persistency with selection on MY2 relative to selection on total lactation. Given a slight decrease in response to milk yield, a substantial improvement in persistency, and a better overall economic result, the MY2 index should be considered as a better alternative to selection on total lactation.

Table 1. Genetic and economic gain from selection on varying weights applied to canonical variates Z_1, Z_2 and Z_3 relative to selection on total lactation

Selection	Genetic gain		Economic gain[3]	
Index[1]	kg/Lact	%Change[2]	PhP	%Change
MY3	227	-8.4	255.7	5.2
MY2	236	-5.0	256.6	5.6
MY1	239	-3.7	256.2	5.4
MY305D	248	-	242.9	-

[1] **MY3** = $Z_1 + 1.3Z_2 + Z_3$, **MY2** = $Z_1 + 2.6Z_2 + 5.5Z_3$, **MY1** = $Z_1 + Z_2 + Z_3$, **MY305D** = selection on total lactation

[2] Percentage decrease in response from selection on the different indices relative to total lactation

[3] Economic gain from selection on different indices relative to total lactation. 1AUD = 41PhP

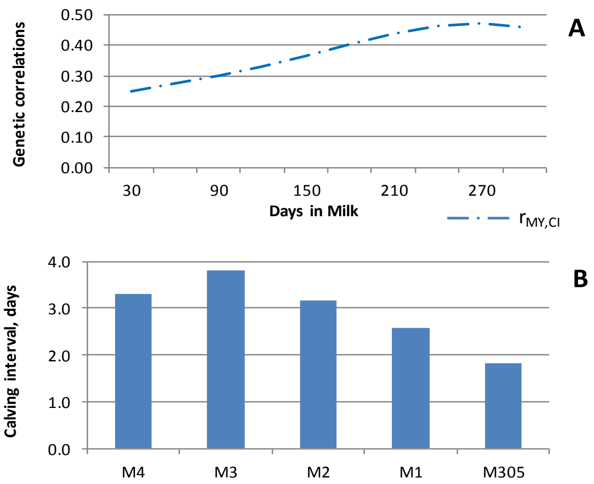

Figure 2. (A) Genetic correlations between milk yield and calving interval across the lactation period and (B) the correlated response on calving interval from selection on the various indices for canonical variates for milk yield.

Note: **M1** = $Z_1 + Z_2$, **M2** = $Z_1 + 1.1Z_2$, **M3** = $Z_1 + 1.2Z_2$, **M4** = $Z_1 + 0.72Z_2 - 0.64Z_3$, **M305** = selection on total lactation

Correlated response on calving interval. Persistent cows have a flatter curve and might have better reproductive performance. Does selection for higher MY yield increase calving interval? Genetic correlation between MY at specific test days and CI was positive, ranging from 0.25 to 0.47 (Figure 2A). Correlations were lowest at the beginning and increased steadily towards the end of lactation. In dairy cattle, heritability for CI was reported to be 0.04, while genetic correlation between MY and CI was 0.43, estimated from a two-step analysis for first parity cows (Haile-Mariam et al., 2003), i.e. very similar to the estimates obtained in this study. Based on the results, lactation length rather than high MY at peak lactation may be the main reason for long CI. Genetic correlations between CI and MY was stronger for cows with longer lactations. Furthermore, CI is highly correlated with EV_2, the principal component associated with persistency at 0.87 compared with -0.27 and -0.22 for EV_1 and EV_3, respectively. Selection on Z_2 showed that with increasing weight, there was a better persistency, reduction in MY, as well as an increase in CI (Figure 2B). This suggests that selection for persistency will also increase lactation length and indirectly, increase CI. As the genetic correlation of CI with MY at early and peak lactation period is low to moderate, it might be possible to consider other fertility traits measured early in lactation to be included in selection such days-to-first service to conception.

Conclusion

Selection on canonical variates was used to optimize response to selection on persistency and milk yield. There was a slight decrease in milk yield but accompanied by a substantial improvement in persistency and better overall economic merit. Results also indicated that selection for persistency will have an increase in calving interval due to calving interval being more correlated with MY in late lactation rather than peak yield. Selection for fertility traits that are measured before or during peak lactation period could be explored in the future.

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