IMPROVING MILK PRODUCTION AND LACTATION PERSISTENCY OF PHILIPPINE DAIRY BUFFALOES USING RANDOM REGRESSIONS

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SUMMARY

Heritabilities and genetic correlations for milk production and lactation persistency were estimated from first parity test day records of 1,022 Philippine dairy buffalo cows using a random regression model. Varying orders of Legendre polynomials were combined with the Wilmink's function and were used in random regression models. Variance components for milk yield and various measures of lactation persistency were derived.

Heritabilities estimated by random regression for milk test day yields were moderate, ranging from 0.17 – 0.19 with a model that fitted a Wilmink's function for the random additive genetic and permanent environment effects. Two eigenvalues derived from the genetic covariance matrix explain 99% of the variation. The first eigenfunction was positive and constant while the second was negative at the beginning but increased and became positive halfway into the lactation. Selection emphasis on the second canonical variate can improve persistency. Optimal selection for increased milk yield and lactation persistency could be explored using the parameter estimates from a random regression model.

INTRODUCTION

Genetic evaluations for dairy cattle have shifted to the use of test day records directly rather than a single 305D lactation measure as test day yields can be adjusted for specific test day effects more accurately (Bilal and Khan 2009) and there is no need to adjust or standardize lactation yields to 305D. Schaeffer and Dekkers (1994) introduced a random regression test day model which involves the regression of merit on days in lactation to account for variation between cows in their performance across the lactation trajectory. This allows an individual cows' lactation curve to deviate from the average, making it possible to select for lactation persistency (Jamrozik *et al.* 1997). Functions frequently used in various studies to describe the shape of the lactation curve include among others, Woods's model, Legendre polynomials (Guo *et al.* 2002) and Wilmink's function (Schaeffer *et al.* 2000). Random regression models can also use higher order polynomial functions but these often have "end-of-range" problems resulting in erratic and extreme estimates of variance and genetic parameters (Meyer 2005).

Lactation persistency is defined as the rate of decline after peak lactation yield has been reached. With random regression models, estimated breeding values (EBV) can be calculated for any day within the lactation period. EBVs for lactation yields in the later part of lactation can be given more weight in selection thus; the shape of the lactation curve and persistency can be improved. A more persistent cow can be more profitable and may have less health and reproductive problems. Persistency could be especially useful in buffaloes that often suffer from too short lactations as well as negative energy balance in early lactation. Different measures of persistency have been proposed utilizing EBVs for daily yields or partial yields and these can be predicted from additive genetic effects estimated by the random regression test day model.

Information regarding the use of random regression models in dairy buffaloes is limited. Sesana *et al.* (2010) estimated genetic parameters for buffalo milk test days by random regression using Legendre polynomials and reported high genetic variance estimates at the beginning of lactation and negative genetic correlations between test days in early and mid to late lactations. The latter could be an indication of "end-of-range" problem which could be avoided with the use

of Wilmink's function. The objective of this study was to compare various random regression models for estimating genetic parameters for milk production traits in Philippine dairy buffaloes in terms of goodness of fit measures, genetic variance, genetic correlations between test days and heritabilities at different days in milk, and derive from such models breeding values for yield and persistency measure.

MATERIALS AND METHODS

Seven thousand eight hundred twenty five (7,825) test day records of 1,022 first parity Philippine dairy buffalo cows of 9 herds from 1997 to 2012 were used directly in a random regression (RR) model to estimate heritability at different days in milk (DIM) in a given lactation. The average test day milk, fat and protein yields as well as fat and protein concentration were 4.6 kg.±2.0, 0.34kg.±0.14, 0.20kg.±0.08, 7.22%±1.63 and 4.31%±0.61, respectively. The RR model is given as: $y_{ijkl} = HTD_i + \sum_{m=0}^{n} \beta_{km} z_{klm} + \sum_{m=0}^{n} \alpha_{jm} z_{jlm} + \sum_{m=0}^{n} pe_{jm} z_{jlm} + e_{ijkl}$ where y_{ijkl} is the test day record l of cow j made on DIM_{jl} of lactation; HTD_i is the fixed effect of herd-test date i; e_{ijkl} is random residual effect; β_{km}, α_{jm}, and pe_{jm} are regression coefficients on days in milk (DIM) within sub-class k age-season of calving, random additive genetic and permanent environment effects of mth order on days in milk, respectively. The Wilmink's function (Wil) and Legendre polynomial (Leg_m) of varying orders describe the shape of the lactation curve. For Wilmink's function, let $Z_{jl0} = 1, Z_{jl1} = DIM, Z_{jl2} = exp^{-0.05DIM}$ whereas for Legendre polynomial, let $Z_{jl0} = 0.7071, Z_{jl1} = 1.2247 * DIM, Z_{jl2} = 2.3717 * DIM^2 - 0.7906, Z_{jl3} = 4.6771 * DIM^3 - 2.8062 * DIM$ The order of the RR functions can vary between components and the days in milk (DIM5 – DIM329) were standardized from -1 to 1 for all Legendre polynomial functions. Residual variances were allowed to vary for each of the ten TD periods in a lactation but residual covariance between TD periods were assumed to be zero. Various combinations of Wilmink's function and Leg_m of varying *(m)* order of fit were used for the fixed and random regression coefficient estimation. For all models, the F_1/F_2 format describes the combination of functions for α (F_1) and pe (F_2) effect respectively. Average Information Residual Maximum Likelihood (ASREML) software (Gilmour *et al.* 2009) was used for variance component estimation. Random α and pe regression coefficients were used to build the covariance matrix for different days in milk along the lactation period (Jamrozik *et al.* 1997).

Heritabilities for a particular DIM i in lactation were calculated by dividing the estimated genetic variance by the sum of genetic, permanent environment and appropriate residual variances for that particular DIM. Different models were compared based on heritability, log likelihood, Akaike's Information Criterion (AIC) and Schwarz' Bayesian Information Criterion (BIC). The lower value for both AIC and BIC indicates a better fitting model. Eigenfunctions related to eigenvalues of the genetic covariance matrix were estimated based on the method of Kirkpatrick *et al.* (1990) to analyze the pattern of variation across the trajectory and from this, to infer the variation in persistency. Transformation of the RR model to canonical scale was done according to the method of van der Werf *et al.* (1998). Response to selection from varying weights applied to canonical variates Z_1 and Z_2 was determined and plotted across the lactation period.

RESULTS AND DISCUSSION

Goodness of fit values of various RR models is shown in Table 1. Generally, given the same function for the random effects, models with Wil function (e.g. Leg_2/Leg_2, Leg_1/Leg_3, Wil/Wil) in fixed regression have better goodness of fit values compared to models with Leg_m (e.g. M3, M5, M6) functions. Top models based on AIC and BIC values were those with more than 12 random parameters. But the top models either have relatively high genetic variance in early lactation (Wil/Leg_3) or low variance in mid-lactation (Leg_2/Leg_3) except for Leg_1/Leg_3 (Fig. 1). The high

genetic variance in early lactation by Wil/Leg$_3$ resulted in relatively high heritabilities (Fig.2) that might not be realistic whereas the low genetic variance in mid-lactation by Leg$_2$/Leg$_3$ resulted in low estimates of heritability at that period. Heritability estimates by Wil/Wil and Leg$_1$/Leg$_3$ models were closer to those of the repeated measures TD model at 0.15 as reported by Flores *et al.* (2013). The Leg$_1$/Leg$_3$ model has slightly lower estimates of genetic variance and heritability in early lactation compared with the Wil/Wil model (Fig. 1 & 2). This might be an indication of inadequate fit to the random additive genetic effect for models with Leg$_1$ functions at that period.

Table 1. Measures of goodness of fit for various random regression models applied to first parity milk yield test day records of Philippine dairy buffalo cows

Model	Regression function			No. of random parameters	Log Likelihood	AIC	BIC	Rank
	α	*pe*	Fixed effect					
M3	Leg$_2$	Leg$_2$	Leg$_2$	12	-6327.3	12679	12701	9
M5	Leg$_1$	Leg$_3$	Leg$_3$	13	-6196.5	12419	12443	8
M6	Wil	Wil	Leg$_3$	12	-6145.3	12315	12337	7
Leg$_1$ / Wil	Leg$_1$	Wil	Wil	9	-6027.8	12074	12090	5
Leg$_2$ / Leg$_2$	Leg$_2$	Leg$_2$	Wil	12	-6027.1	12078	12100	6
Leg$_2$ / Leg$_3$	Leg$_2$	Leg$_3$	Wil	16	-6006.6	12045	12074	3
Leg$_1$ / Leg$_3$	Leg$_1$	Leg$_3$	Wil	13	-6000.8	12028	12051	2
Wil / Wil	Wil	Wil	Wil	12	-6023.7	12072	12093	4
Wil / Leg$_3$	Wil	Leg$_3$	Wil	16	-5994.2	12020	12050	1

Leg$_1$ – first order Legendre polynomial; Leg$_2$ – 2nd order Legendre polynomial; Leg$_3$ – 3rd order Legendre polynomial; Wilmink – Wilmink's function. For all models described, the regression function used were always in the order α / pe effects. AIC – Akaike's information criterion; BIC – Bayesian information criterion

Figure 1. Additive genetic variance for milk yield trait estimated from first parity test day records by random regression.
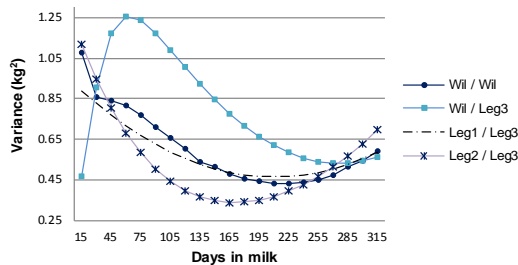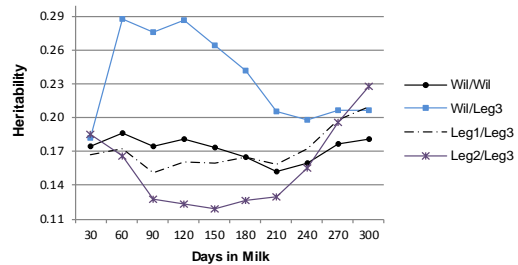
Figure 2. Estimates of heritability for milk yield trait estimated from first parity test day records by random regression.

*Wil - Wilmink's function; **Leg1 - first order Legendre polynomial; Leg2** - 2nd order Legendre polynomial; **Leg3** - 3rd order Legendre polynomial. For models described, the regression function used were alsways in the order α / pe effect*

Genetic correlation between DIM5 and DIM$_i$ showed positive but decreasing values as distance between days increased (Table 2). This is a pattern similar to dairy cattle but, correlations among adjacent test days were considerably lower for Wil/Leg$_3$ while they were unexpectedly high for Leg$_1$/Leg$_3$ and Leg$_2$/Leg$_3$ models. The Wil/Wil model had more realistic estimates for genetic correlation between test day periods. Overall, when considering formal test statistics, estimates of genetic variance and genetic correlations between test days, as well as model parsimony point of view, we conclude that the Wil/Wil is the preferred model.

Principal component analysis was done of the genetic covariance matrix from fitting the Wil/Wil model. The first and second principal components with eigenvalues EV$_1$ and EV$_2$ (Figure 3) were statistically significant (chi-square test, P<.0001) and explained 78% and 21% of the total genetic variance, respectively. The eigenfunction related to EV$_1$ was positive and constant

throughout the lactation. 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 eigenfunction related to EV_2 was negative in the first half of lactation but increased to positive values after DIM160. This eigenfunction may correspond to a genetic component for persistency (van der Werf *et al*. 1998) indicating it may be possible to select for lactation persistency.

Table 2. Genetic correlation between DIM5 and other days in milk estimated by different RR models

Model	Days in Milk									
	30	60	90	120	150	180	210	240	270	300
Wil / Wil	0.70	0.47	0.44	0.45	0.47	0.49	0.49	0.48	0.45	0.37
Wil / Leg$_3$	0.32	0.18	0.16	0.16	0.16	0.17	0.17	0.16	0.16	0.13
Leg$_1$ / Leg$_3$	1.00	0.99	0.97	0.93	0.88	0.70	0.70	0.59	0.47	0.25
Leg$_2$ / Leg$_3$	1.00	0.99	0.96	0.91	0.83	0.63	0.63	0.56	0.52	0.52

Figure 3. Eigenfunctions related to the three eigenvalues of the genetic covariance matrix from fitting Wil/Wil RR model to milk test day records of first parity Philippine dairy buffalo cows.
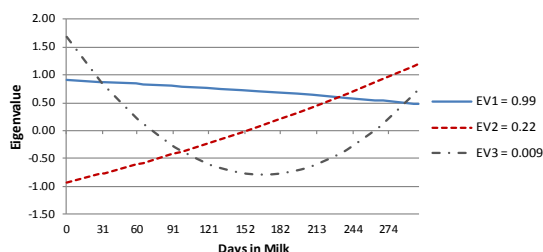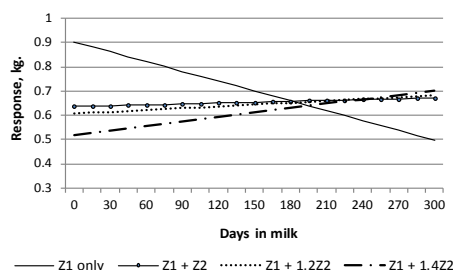

Figure 4. Response to selection on canonical variates Z$_1$ and Z$_2$ on milk yield trait

The transformation of the RR model to canonical scale with only the EV_1 and EV_2, enables selection on canonical varieties Z_1 and Z_2. Selection on Z_1 only will result to increase in milk yield mostly in the first trimester of lactation (Fig. 4). Equal weights applied to Z_1 and Z_2 will produce an even response across lactation but with a decrease in total milk yield. Increasing the weight applied to Z_2 further will increase milk production in the 3rd trimester of lactation. More emphasis on Z_2 results in a lower increase in total milk production but the increase rely less on a higher peak yield in first trimester of lactation. This may decrease stress to cows in this period. The relative economic weights of persistency and milk yield need to be known to optimally select for these traits simultaneously and genetic parameters from the RR model can be used for that purpose.

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