

The use of lactation and test day records for the genetic analyses of the performance of Philippine dairy buffaloes for milk production and persistency

ESTER B. FLORES

Doctor of Veterinary Medicine University of the Philippines
Master of Science in Agriculture University of Arkansas

A thesis submitted for the degree of Doctor of Philosophy of the
University of New England
December 2013

School of Environmental and Rural Science
Faculty of Arts and Science

Abstract

Milk production records of Philippine dairy buffaloes were analysed to be able to develop a method of yield calculation and genetic evaluation for milk production and lactation persistency. The method for yield calculation, a multiple trait procedure that utilizes the Wilmink's function (MTP-Wil) to describe the lactation curve of different cow-class categories as well as takes into consideration covariances between milk, fat and protein yields such that prediction of yields can be made with irregular and/or long intervals between test days with slight reduction in precision relative to a complete set of regularly spaced test day records. This method is particularly suitable for establishing a recording system for cows in the various dairy buffalo cooperatives in the Philippines as the yield calculation method may help minimize the cost of recording cow performance. Establishing a milk recording system for cows in the dairy cooperatives will increase the number of cows for genetic evaluation.

Test day and 305D lactation records can be obtained from the MTP-Wil method of yield calculation for use in genetic evaluation. Genetic parameters for milk, fat and protein yields were estimated from 305D lactation records and directly from test days in a repeatability test day model. Estimates of heritability were low to moderate with the use of either test days or 305D lactation records with the latter giving slightly higher estimates. Analysis of second parity milk records gave higher estimates compared with analysis of first parity records. Selection of yield traits will result in deterioration in Fat% and Prot% after long-term selection. The deterioration in fat and protein concentration was slightly greater with single-trait selection compared with multi-trait selection index.

Single and multi-trait random regression analysis of first parity test day records generally gave higher estimates of heritability especially at peak lactation period compared to those estimated using repeatability test day model. A three-parameter Wilmink's function was sufficient for fitting the additive genetic effects for milk, fat and protein yields as well as Fat% and Prot%. It was also

sufficient for fitting permanent environment effects for Fat% and Prot%. However, for milk, fat and protein yields, the Legendre polynomial was more appropriate to use for fitting permanent environment effects. Eigenvalue decomposition of the additive genetic covariance matrix for milk, fat and protein yields as well as Fat% and Prot% was done to extract independent variables for use in selection for milk production and lactation persistency. Applying varying weights to the second and third canonical variates from the eigenvalue decomposition of the genetic covariance matrix increased the response at the latter half of lactation compared to selection on total lactation and essentially would improve lactation persistency. Long-term selection on these two canonical variates would change the shape of the lactation curve. Optimization of the weight applied to the second and third canonical variates with respect to profit enabled maximum response to production traits without substantial deterioration in lactation persistency. Selection for persistency would increase lactation length but will also have an unfavourable correlation with calving interval. But as calving interval is more correlated with lactation length rather than peak yield, fertility traits that are measured early in lactation should be considered in the future for inclusion in the breeding program.

Declaration

I certify that the substance of this thesis has not been submitted previously for any degree and is not currently being submitted for any degree or qualification.

I also certify that any help received and all sources used in preparing this thesis have been acknowledged therein.

A solid black rectangular box used to redact the signature of the author.

ESTER B. FLORES

Acknowledgments

Acknowledgments are in order to many people both in Australia and the Philippines. First, I would like to thank my principal supervisor, Professor Julius van der Werf, for his never-ending patience, encouragement and support. Every discussion and consultation with Julius left me both enlightened and compelled to ask more with more questions. His guidance has undoubtedly enriched my knowledge and skills on the theoretical and applied aspects of animal breeding. Second, I would also like to thank Professor Brian Kinghorn for his valuable contribution to my thesis, supervision and encouragement. I would also like to extend my gratitude to Dr. Libertado Cruz for allowing me to pursue my doctoral program and making things possible.

I would also like to thank fellow scientists and students who have helped me with the thesis. Past and current “fish bowl” residents like Sam and Shalanee. Life indeed would have been boring in the “fish bowl” without Shalanee.

This thesis would not have been possible without the loving and selfless understanding and patience of my family and friends. To my father, who did not give up trying to convince me to pursue my PhD program, my gratitude.

Lastly, I would like to acknowledge the financial support of the Philippine Carabao Center.

Table of Contents

Abstract	iii
Declaration	v
Acknowledgments	vii
Table of Contents	viii
List of Figures	x
List of Tables	xii
Chapter I General Introduction	1
1.1 Genetic evaluation system	1
1.2 The water buffaloes.....	4
1.3 Constraints in breeding program implementation for Philippine dairy buffaloes	5
1.4 The breeding objective in dairy buffaloes	6
1.5 Scope of the thesis.....	8
Chapter II Review of Literature	11
2.1 Dairy buffalo production in the Philippines.....	11
2.2 Calculation and prediction of lactation yield	18
2.3 Standardization of lactation yields.	32
2.4 Genetic evaluation models in dairy cattle and buffaloes	38
2.5 Selection Indices for multiple traits.....	50
2.6 Conclusions	55
Chapter III Predicting lactation yields in dairy buffaloes by interpolation and multiple trait prediction	57
3.1 Abstract.....	58
3.2 Introduction	59
3.3 Materials and Methods	61
3.4 Results.....	68
3.5 Discussion	76
3.6 Conclusion.....	78
3.7 Acknowledgement	79
Chapter IV The genetic analyses of milk yield and milk component traits using of test day and 305D lactation records of Philippine dairy buffaloes and the consequence of long term selection for milk yield on fat and protein percentage	83
4.1 Abstract.....	84
4.2 Introduction	85
4.3 Materials and Methods	86

4.4 Results.....	89
4.5 Discussion	95
4.6 Conclusion.....	97
4.7 Acknowledgement	98
Chapter V Random regression test day models to estimate genetic parameters for milk yield and milk components in Philippine dairy buffaloes	101
5.1 Abstract.....	102
5.2 Introduction	102
5.3 Materials and Methods	103
5.4 Results.....	106
5.5 Discussion	116
5.6 Conclusion.....	119
5.7 Acknowledgement	119
Chapter VI Optimizing response to selection on milk production and lactation persistency of first parity Philippine dairy buffaloes by random regression analysis	123
6.1 Abstract.....	124
6.2 Introduction	124
6.3 Materials and Methods	126
6.4 Results.....	131
6.5 Discussion	142
6.6 Conclusion.....	144
6.7 Acknowledgement	145
Chapter VII General Discussion and Conclusions.....	149
7.1 General Discussion.....	149
7.2 Summary and Conclusions.....	153
Chapter VIII Consolidated Reference List.....	157

List of Figures

Figure 2.1 Common buffalo breed groups in the Philippines	13
Figure 2.2 Current breeding structure of the dairy buffalo sector	15
Figure 3.1 Mean squared error between predicted and true 305D yield by five methods of yield prediction with increasing number of test day records using data set I	68
Figure 3.2 Mean squared error between predicted and true 305D yield by five methods of yield prediction for sampling plans with increasing intervals due to missing fat and protein tests using data set II	73
Figure 3.3 Effect of missing milk test day on the shape of the lactation curve by Wilmink's and Wood's function	74
Figure 5.1 Additive genetic and permanent environment variances estimated from first parity milk test day records of Philippine dairy buffaloes by random regression	109
Figure 5.2 Estimates of heritability and genetic correlation of different days in milk (DIM) with DIM5 for milk yield by various random regression models	110
Figure 5.3 Genetic and permanent environment variances for fat and protein yields across lactation estimated by random regression from test day records of first parity Philippine dairy buffaloes	113
Figure 5.4 Additive genetic and permanent environment variances for fat and protein concentration across lactation estimated by random regression from test day records of first parity Philippine dairy buffaloes	114
Figure 5.5 Additive genetic variances across lactation from running multi-variate analyses between milk and milk components by random regression	115
Figure 6.1 Economic values for daily milk and fat yields plotted across the lactation trajectory. Economic values for protein yields follow the same pattern but at a higher scale (not shown) .	130
Figure 6.2 Eigenfunctions related to the first three eigenvalues of the genetic covariance matrix from fitting univariate random regression test day model to milk, fat and protein yields of first parity Philippine dairy buffaloes	132
Figure 6.3 Response to selection on total 305D lactation and on various persistency indices with varying weight applied to the 2 nd and 3 rd canonical variates of the genetic coefficient matrix for milk, fat and protein yields analyzed by univariate random regression test day model.	133

Figure 6.4 Response to selection on total lactation EBV and on canonical variates Z_1 , Z_2 and Z_3 related to the corresponding three leading eigenvalues for milk, fat and protein yield derived from additive genetic coefficient matrix of a multi-trait random regression test day model . . .	138
Figure 6.5 (A) Genetic correlations between milk yield and calving interval at different days in lactation; (B) Genetic correlations between calving interval and with canonical variates Z_1 , Z_2 and Z_3 related to the eigenvalues of the genetic coefficient matrix for milk yield	140
Figure 6.6 Correlated response on calving interval and milk yield from selection on 2nd canonical variate (Z_2) related to the genetic covariance matrix of milk yield	141

List of Tables

Table 2.1 Volume and value of production, 2009	12
Table 2.2 Reported milk production and reproductive performance of dairy buffaloes from Philippines and various countries	16
Table 3.1 Average true 305D yield of buffalo cows per parity group	66
Table 3.2 Sampling scheme for missing milk, fat and protein tests	67
Table 3.3 Mean deviation and correlation between predicted and true 305D yield with increasing number of test day records used by five methods of yield prediction using data set II	70
Table 3.4 Mean squared error, mean deviation and correlation between predicted and true 305D yield by five methods of yield prediction for sampling plans with increasing intervals due to missing tests using data set II	72
Table 3.5 Predicted yield and standard error of prediction by MTP-Wil method of first and second parity cow for various sampling schemes	75
Table 4.1 Mean 305D and test day lactation record of Philippine dairy buffalo cows	87
Table 4.2 Heritability and permanent environment estimates for milk, fat and protein yields of Philippine dairy buffaloes by single trait analysis of 305D and test day lactation records per parity	90
Table 4.3 Estimates of heritability (diagonal), genetic (lower off diagonal) and phenotypic correlations (upper off diagonal) from running multi-variate analysis of first, second and third parity 305D lactation records for milk and milk components of Philippine dairy buffaloes	91
Table 4.4 Estimates of heritability (diagonal), genetic (lower off diagonal) and phenotypic (upper off diagonal) correlations from running multi-variate analysis of first and second parity test day records for milk and milk component of Philippine dairy buffaloes	92
Table 4.5 Estimates of heritability (diagonal), genetic (lower off diagonal) and phenotypic (upper off diagonal) correlations from running univariate and multivariate analysis of first parity test day and 305D records for milk yield, fat and protein percentage of Philippine dairy buffaloes	93
Table 4.6 Predicted response to using selection index based on economic weights for milk, fat and protein yield	94
Table 5.1 Average milk test day (TD) records of 1,022 first parity dairy Philippine dairy buffalo cows	105
Table 5.2 Comparison of Log likelihood values for models fitted with varying number of residual classes as well different regression functions for fixed effects	107

Table 5.3 Measures of goodness of fit for various random regression models applied to first parity milk yield test day records of Philippine dairy buffalo cows	105
Table 5.4 Measures of goodness of fit for various random regression models applied to first parity milk component test day records of Philippine dairy buffalo cows	111
Table 5.5 Estimates of heritability at different days in milk (DIM) and genetic correlation with DIM15 for milk component traits by various random regression models from first parity test day records of Philippine dairy buffalo cows	112
Table 5.6 Genetic correlations and heritabilities for milk yield and milk component traits at different days in milk estimated by multi-trait random regression model from first parity test day records of Philippine dairy buffaloes	115
Table 6.1 Response to selection on varying weights applied to canonical variates Z_1 , Z_2 and Z_3 relative to selection on total 305D milk, fat and protein yield	135
Table 6.2 Response to selection on canonical variates Z_1 , Z_2 and Z_3 related to the correlation matrix of the additive genetic coefficients for milk, fat and protein yields estimated by multi-trait random regression test day model	139

