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Identification of the Suitable Milk Recording Protocol for Small-scale Dairy Production

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ABSTRACT

The study was conducted to identify a suitable milk-recording protocol for small-scale dairy production. Data from Holstein-Friesian×Local and Sahiwal×Local crossbred cows on 2 selected farms in Chittagong metropolitan area of Bangladesh form 2010 to 2011 was used to compare and evaluate the co-efficients of 3 different mathematical models of lactation curve for daily and test-day milk yield. The estimated model co-efficients and the 210 days predicted lactation milk yields varied significantly between crossbreds. The models were evaluated with 3 fit statistic values (Coefficient of Determination (R^2), Root Mean Square Error (RMSE) and Coefficient of Variation (COV)). The highest lactation milk yield was found for Friesian×Local on Farm 1. The average daily milk yield of Friesian×Local was higher than Sahiwal crossbreds in both the farms. The Wood model was found to be suitable to transform test-day milk yield into a 210-days predicted milk yield for all crossbreds based on higher R^2 and COV and lower RMSE values. The test-day milk yield of 1 and 2 weeks interval was found to be best fitted with the actual 210-days milk yield by using Wood model for both crossbreds.

Key words: Crossbred, test-day milk yield record, lactation curve, fit-statistics

INTRODUCTION

In order to increase the productivity of the small-scale farmers, proper management practice is needed and the most important management tool is proper record keeping (Silver, 2006). The purpose of a recording system is to improve the level of herd performance by running the farm more competently, or reducing the possibility of poor future performances. Studies have shown that, the efficiency of milk production can be increased through the use of a simple, precise, understandable and easy to maintain recording system (Chagunda *et al*., 2006).

In order to monitor and improve the production of cows, milk recording is necessary: in a way, the persistence of satisfactory milk production in low-to medium-input environments is a sign of acceptable sustainability (Duclos *et al*., 2008).

Mathematical models of lactation curve can be used to predict the total amount of milk yield for the entire milking period using daily or test-day recorded yields. Three parametric mathematical models of lactation yields were developed in the 1960s by Wood (1967) which defines the shape of the lactation curve. However, before Wood, other workers (Ganies, 1927; Nelder, 1966) estimated lactation yields with simple mathematical models but those did not define the shape of the lactation curve accurately.

For establishing the sustainable dairy industry it is necessary to develop and adapt a suitable milk-recording protocol/system for small-dairy herd to undertake future nutritional, management and genetic improvement program. Therefore, the current study was undertaken for small-scale dairying with the objectives: (1) To estimate the actual milk yield of different genotypes (2) To simplify the milk-recording protocol through comparing actual and predicted milk yield by using different lactation models and (3) To chose a suitable milk recording interval for small-holder dairy production.

MATERIALS AND METHODS

Data used in this study was 210 days daily milk yield records collected from November 2010 to June 2011 on 137 cows from two selected dairy farms in Chittagong metropolitan area of Bangladesh. The available genotypes were Holstein-Friesian×Local (86) and Sahiwal×Local (51) crossbreds and the cows were in third lactation.

Milk recording was performed by the appointed data collector. Milk recording data was collected on daily (24 h) basis in a standard record sheet. The daily milk yield was estimated by adding the morning (AM) and evening (PM) milk yield.

Actual milk yield: The actual 210 days milk yield per cow was calculated by adding all days recorded milk yield data. The mean and standard error for 210 days milk yield of Holstein-Friesian×Local and Sahiwal×Local crossbred cows under two farming conditions was analyzed using PROC GLM of SAS (2000). The mean differences were estimated using Least Significant Differences (LSD) test (Steel *et al.*, 1997).

Simplification of records by using different models: For the simplification of milk recording, the recording was simulated by putting the intervals between the milk recording (test-days (TDs)). The interval between 2 test-days (TDs) milk recording was gradually increased from 4 up to 7, 14 or 30 days, respectively. The schematic diagram for this sampling is presented in Fig. 1.

Models for the lactation curve: Following three lactation curve models were used to predict the 210 days milk yield from the different milk recording protocol:

- Quadratic polynomial model, $Y= a+ bx+cx^2$
- Wood (1967) model, $Y = ax^b e^{-cx}$
- Wilmink (1987) model, $Y = a+bx+ce^{-dx}$

where, Y is milk yield (kg day^{-1}), x is the days in milk and a, b, c and d are co-efficient that define the shape of the lactation curve.

Statistical analyses: The Wood model was log linear transformed; then for the Wood model and quadratic polynomial regression equation, the test day milk yield was set as dependent variable and days in milk was set as independent variable for obtained the model co-efficient. The models were analyzed by using the SAS (2000). The Wilmink model was reduced to a 3-co-efficient linear model by setting the d exponent to a suitable fixed value. In the present study, d was assumed equal to 0.05 according to Khan (2009). Along with model co-efficient the fit statistics, R^2 (coefficient of determinant), COV (coefficient of variation) and RMSE (Root mean square error) were also obtained by SAS analysis. The predicted milk yields were obtained by using the model co-efficient with days in milk as independent variables. To obtain the mean value of different components (model co-efficient, fit statistics and predicted 210 days milk yields), the linear mixed procedure of SAS (2000) was used in the following model:

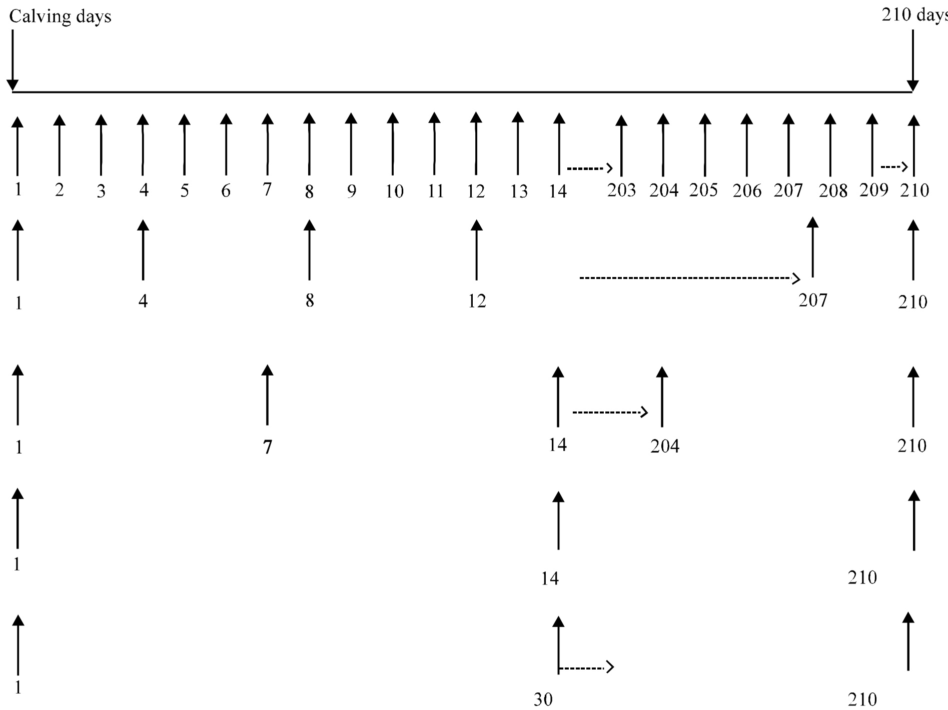

Fig. 1: Illustration of the recording procedure to simulate the simplification of milk-recording protocols

$$Y_{ijk} = \mu + B_i + F_j + e_{ijk}$$

where, Y_{ijk} represents the value of predicted milk yield, a, b, c, d, k and fit statistics:

μ = Mean of the data
B_i = Effect of the ith breed (Friesian×Local and Sahiwal×Local)
F_j = Effect of jth farm (Farm 1 and Farm 2)
e_{ijk} = Random residual effect distributed as N (0, σ^2)

The differences of model co-efficient, predicted milk yield and fit statistics were tested with the probability value of $p \leq 0.5$.

RESULTS

Actual and predicted lactation milk yield: The mean value along with their Standard Error (SE) of actual and predicted lactation milk yield of Friesian×Local and Sahiwal×Local in two different farms are presented in Table 1. From Table 1 it is seen that the 210 days actual milk yield was found to be higher (1689±11.74) for Holstein-Friesian×Local in farm 1 and lower (1553.08±20.75) for Sahiwal×Local genotype in farm 2.

The Predicted Lactation Milk Yield (PLMY) for different models was varied between breeds within the model (Table 1). However, for Wood model, the actual lactation yields calculated from the raw data was close to that of the PLMY. The PLMY for various intervals fitting after Wood model were different between breed groups within the farm and also between breed groups within the intervals (Table 2). The PLMY for 4 and 30 day intervals were different with the actual milk

Table 1: Estimated model co-efficient, fit statistics and the predicted milk yield of various models for different genotypes in two farms

Models	Farm 1		Farm 2		
	HF×L	Sah×L	HF×L	Sah×L	Level of significance
Polynomial					
a	7.62±0.78[a]	7.66± 0.65[a]	8.54±0.84[b]	10.84±1.29[c]	**
b	-0.030±0.06	-0.048±0.01	-0.03±0.02	-0.02±0.01	NS
c	0.0004±0	0.0005±0.01	0.0002±0.01	0.0001±0.01	NS
R^2	0.019±0.01	0.02±0.01	0.023±0.01	0.02±0.02	NS
COV	16.63±1.91[a]	20.438±2.21[ab]	26.22±3.43[a]	18.32±0.02[a]	*
RMSE	1.23±0.23	1.51±0.25	2.02±0.22	1.92±0.32	*
Actual	1688.78±11	1672.95±23	1652.82±13	1553.08±21	NS
Predicted	1708.56±544[a]	2231.22[b]±227	1595.1±826[a]	2124.75±589[b]	*
Wilmink					
a	6.35±0.79[a]	6.11±0.54[a]	9.004±0.80[b]	11.04±1.16[c]	**
b	1.07±0.61[b]	1.57±0.38[b]	-0.39±0.59[a]	-0.57±0.64[a]	*
c	0.009±0.02	0.019±0.01	-0.04±0.02	-0.04±9 0.03	NS
R^2	0.026±0.01	0.02±0.02	0.021±0.001	0.024± 0.01	NS
COV	17.035±1.45[a]	20.43±2.21[b]	27.73±2.03[c]	21.67±2.72[b]	*
RMSE	1.202±0.16[a]	1.51±0.26[a]	2.23±0.19[b]	2.172±0.35[b]	*
Actual	1688.78±11.7	1672.95±22.2	1652.82±12.7	1553.08±20.7	NS
Predicted	1559.403±270[b]	1717.57±199[b]	1073.45±205[a]	1210.98±484[a]	*
Wood					
a	1.57±0.31	1.505±0.51	1.79±0.33	1.46±0.73	NS
b	0.3026±0.09[a]	0.707±0.14[b]	0.327±0.09[a]	0.332±0.20[a]	*
c	-0.0037±0.01[a]	-0.011±0.01[b]	-0.0056±0.02[a]	-0.006±0.01[a]	*
R^2	0.49±0.08[c]	0.689±0.12[b]	0.79±0.08[a]	0.836±0.17[a]	*
COV	5.75±0.53	6.11±0.88	5.91±0.56	3.98±1.24	NS
RMSE	0.117±0.02	0.118±0.018	0.118±0.02	0.089±0.03	NS
Actual	1689±11.7	1673±22.3	1653±12.7	1553±20.7	NS
Predicted	1504± 233.8[b]	1616±387.8[b]	1490±245.3[a]	1338±548.5[a]	*

a: Intercept, b: Shape of the curve, c: Placement of the curve, R^2: Coefficient of determinant, RMSE: Root Mean Square Error, COV: Coefficient Of Variation, HF×L: Friesian×Local, Sah×L: Sahiwal×Local, PMY: Predicted milk yield. Mean with different superscripts are different at $p<0.05$ between breeds within model. NS : Not significant, *,**Significant at 0.05 and 0.01 level, respectively

yield. But the PLMY for 7 and 14-days interval were similar with the actual milk yield except for Sahiwal×Local (1481.1±110.32) under farm 1.

Use of 3 different lactation models to the base data to predict the 210 days milk yield: The mean value of the estimated model co-efficients (a, intercept; b, shape of the curves and c, placement of the curve; fit statistics (R^2, RMSE and COV) and predicted lactation milk yield for three different models along with their standard error for different genotypes (Holstein-Friesian×Local and Sahiwal×Local) under two different farming conditions are shown in Table 1.

The model co-efficient a, b and c for different models were differed between breed groups within and between the models. In the Polynomial model, the a was different between breed groups and farm but the b and c was not differed between breed groups. The difference in a, b and c was observed between breed groups and farms using Wilmink model. But in case of Wood model, the a was varied between breed groups within the farm. However, the b and c was different between breed groups and within farm.

Table 2: Estimated model co-efficients, fit statistics and the predicted milk yield of various intervals/test-day for different genotypes under two farming condition by using wood model

	Farm 1		Farm 2		
Intervals	HF×L	Sah×L	HF×L	Sah×L	Level of significance
4 days interval					
a	1.42±0.233	1.15±0.125	1.89±0.203	1.49±0.712	NS
b	0.31±0.073[a]	0.73±0.12[b]	0.43± 0.076[ab]	0.33±0.243[a]	*
c	-0.006±0.001	-0.012±0.002	-0.009±0.002	-0.006±0.002	NS
R^2	0.49±0.09[a]	0.72±0.04[b]	0.79±0.05[b]	0.84±0.05[bc]	*
COV	5.95±0.61[b]	5.92±0.60[b]	6.18±0.88[b]	4.073±0.38[a]	*
RMSE	0.13±0.02	0.12±0.015	0.13±0.015	0.093±0.016	NS
Actual	1689±11.7	1673±22.3	1653±12.7	1553±20.7	NS
Predicted	1093± 202.7[b]	1109±161.9[a]	1196±148.6[b]	1003±404.6[b]	*
7 days interval					
a	1.47±0.15	0.84±0.148	1.53±0.15	1.6±0.57	NS
b	0.45±0.06	0.55±0.09	0.49±0.08	0.49±0.19	NS
c	-0.004±0.001	-0.0003±0.0002	-0.008±0.0014	-0.007±0.002	NS
R^2	0.55±0.08[a]	0.69±0.04[a]	0.83±0.05[b]	0.83±0.04[b]	*
COV	5.99±0.89[b]	6.17±0.59 [b]	5.53±0.49[b]	4.12±0.37[a]	*
RMSE	0.12±0.01	0.12±0.01	0.12±0.01	0.094±0.02	NS
Actual	1689±11.7	1673±22.3	1653±12.7	1553±20.7	NS
Predicted	1427±133.6	1583±264.6	1295±248.1	1513±530.3	NS
14 days interval					
a	0.93±0.1	1.54±0.28	1.1003±0.094	1.32±0.356	NS
b	0.66±0.06[a]	0.82±0.18[b]	0.82±0.10[b]	0.56±0.05[a]	*
c	-0.001±0.001	-0.012±0.002	-0.005±0.002	-0.004±0.003	NS
R^2	0.59±0.07[a]	0.79±0.04[b]	0.75±0.09[b]	0.82±0.04[b]	*
COV	5.56±0.64[a]	5.505±0.50[a]	7.04±1.28[b]	4.56±0.09[a]	*
RMSE	0.12±0.01	0.108±0.01	0.15±0.03	0.103±0.005	NS
Actual	1688±11.7	1673±22.3	1653±12.7	1553±20.7	NS
Predicted	1505±46.6	1481±110.3	1538± 51.3	1456±99.5	NS

a: Intercept, b: Shape of the curve, c: Placement of the curve, R^2: Coefficient of determinant, RMSE: Root Mean Square Error, COV: Coefficient Of Variation, HF×L: Friesian×Local, Sah×L: Sahiwal×Local, PMY: Predicted milk yield. Mean with different superscripts are different at p<0.05 between breeds within model. NS : Not significant, *,**significant at 0.05 and 0.01 level, respectively

The values of three fit statistics differed between breed groups and also in between the farms. The R^2, COV and RMSE values for both Polynomial and Wilmink models indicated its inconvenience as fitness. In the case of Wood model, the smaller value of RMSE (0.117±0.02 and 0.118±0.02), for R^2 (0.49±0.08 and 0.79±0.08) and COV (5.75±0.529 and 5.91±0.555), the bigger values were observed which indicated the superiority of model in the Holstein-Friesian×Local crossbred in both farming conditions.

Use of wood models to the different test-day data to predict the milk yield: The Wood model was observed to be good fitted in all genotypes under both the farms therefore the Wood model was used to predict various test-days milk yield from the different milk recording protocols. The estimated model co-efficients (a, b and c), fit statistics (R^2, RMSE and COV) and predicted lactation milk yield for Wood model along with their standard error of Holstein-Friesian×Local and Sahiwal×Local crossbreds under two different farming conditions are shown in Table 2. Only 4, 7 and 14 days intervals values are shown in Table 2.

For 4 days intervals, the Predicted Milk Yield (PMY) varies between the genotypes and within the farms. On the other hand, for 7 days intervals, the PMY differed only in farm but not in breed groups. For 14 days intervals, the PMY differed slightly between the crossbreds and within the farms. While for 30 days interval, the PMY varied highly in between breed groups and also in between the farms.

The model co-efficients (a, b and c) for different interval (4, 7, 14 and 30 days) were differed between genotypes within the model and also between the farms. Among various intervals, values the 14 days intervals were uniformly fitted with the actual milk yield value. The fit statistics (R^2, COV and RMSPE) values were also varied between the breeds of different farms and within the breeds in same farm for various intervals.

DISCUSSION

From the study it has been observed that the highest 210 days milk yield was found in Friesian×Local and lowest in Sahiwal×Local genotypes in both the farms. Al-Amin and Nahar (2007) found average lactation yield of Friesian×Local genotype was higher than other breeds groups. The lactation milk yield for both the genotypes was found to be higher in Farm 1 than in Farm 2. The variation is due to the effect of feeding and also due to the effect of different environment surrounding both the farms. The higher production could be due to the effect of Genotype×Environment interactions in that particular farm. Rehman *et al.* (2008) observed that total milk yield per lactation affected by the difference of herd. Similarly, milk production between breed groups, seasons and management systems were reported by other researchers (Val-Arreola *et al.*, 2004; Perochon *et al.*, 1996).

The model co-efficients a, b and c for different models were varied between breed groups within the model and also between the models. The differences of model co-efficients were differed due to the differences in breeds were previously reported by other workers (Khan *et al.*, 2012; Alam *et al.*, 2009; Perochon *et al.*, 1996).

The variation of fit of the models between breeds may have arisen from the differences in breeds, mathematical functions of the models and amount of records. The Polynomial and Wilmink models were not considered further due to their unsuitable model co-efficients and poor fit statistics values. In case of Wood model, the smaller value of RMSE (Val-Arreola *et al.*, 2004) was considered to be superior but for R^2 and COV, the bigger values indicated the superiority of Friesian×Local in both farming conditions. A similar finding was observed by Alam *et al.* (2009) for the Wood model. The differences of lactation curve traits can be differed with genetic group (Perochon *et al.*, 1996; Khan *et al.*, 2012) and also their fitting ability (Alam *et al.*, 2009).

There was a variation in predicted lactation milk yield among the different genotypes under both farming conditions. For Polynomial model, the lactation yield varied with in breed in between the two farms. In case of Wilmink model, lactation milk yield also varied between the breeds within the farms. However, for the Wood model, the predicted lactation yield was slightly varied between breed but a considerable variation occurred within the two farms. The total lactation milk yields calculated from the raw data for different genotypes under two farms were similar with the total lactation yields predicted by Wood model than the lactation yields predicted by Polynomial and Wilmink model. Finding of Alam *et al.* (2009) and Khan *et al.* (2012) were similar to the results of the study.

For 4 days intervals, the predicted lactation milk yield (PLMY) varies between the crossbreds and within the farm. On the other hand, for 7 days intervals, the PLMY differed only in farm but not in breeds. For 14 day intervals, the PLMY differed slightly between the breed and within the farms. While for 30 day interval, the PLMY varied highly in between breeds and also in between the farms. However it was seen that the total lactation yields predicted at 14 day interval by Wood model was similar for both genotypes, except for the Sahiwal×Local under farm 2. Duclos *et al.* (2008) investigated on simplified milk recording protocol at various test-day intervals and found similar result.

The model co-efficient a, b and c for different interval were varied between breed groups within the models and also between the farms. The b (shape of the curve) was significantly of Sahiwal×Local at 4 and 30 days intervals in both farms and Friesian×Local also higher in farm 2 at 14 days interval than other genotypes. Three fit statistics (R^2, COV and RMSPE) values were used to evaluate the model performance at various intervals. The values of fit statistics varied between the breeds of different farms and within the breeds in same farm for various intervals. The smaller value of RMSE was considered to be superior but for R^2 and COV, the bigger values. The fitness of the 3 fit-statistics value indicated that the 7-days interval was good but best for the interval at 14 days with the fitting of Wood model (Khan *et al.*, 2012) repeated the similar result.

The variation of fit of models between breeds may have arisen from differences of test-day yield, the amount of data, the number of test day records and the intervals between tests. The effects of the number of test day records and the intervals between tests on the estimation of fit statistics and also their fitting ability, was reported by Tekerli *et al.* (2000) and Wiggans *et al.* (2002).

This study indicated that the Wood model was the most suitable to transform test-day milk yields into a 210 days predicted milk yield for all crossbreds based on higher R^2 and COV and lower RMSE values. It was seen that one week (7 days) interval test-day milk recording was good fit with actual 210 days yield. However, two weeks (14 days) interval test-day milk recording was best fit with that of actual 210 days milk yield by using Wood model for both crossbreds based on the different fit statistics value. The Holstein-Friesian×Local genotypes fitted better than Sahiwal×Local for all models. Such study could be useful for the scientist to undertake further research on genetic improvement programme of dairy cattle under different management system where herd size is small. However, research is needed with more order polynomials and other non-linear and logistic models for the estimation of predicted total yield to confirm the results.

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