

Do-it-yourself milk recording as a viable alternative to supervised milk recording in Ireland

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The objective of the current study was to determine the feasibility of do-it-yourself (DIY) milk recording in commercial Irish dairy herds as well as the accuracy of predicting 24-h milk production and somatic cell count from part-day samples. The data consisted of 3,850 testday records from 1,565 cows across 23 herds in southern Ireland. Observed part-day and 24-h milk yield and composition were in accordance with previously reported observations in Ireland. Accurate prediction of 24-h milk, fat and protein yield was achieved using either AM or PM samples incorporated within prediction equations. Prediction of daily somatic cell count (SCC) was less accurate although the sensitivity and specificity of predicted daily SCC at identifying true daily $\text{SCC} \geq 200,000$ was high. The accuracy of predicting 24-h fat and protein yield was augmented when two consecutive milk weights, simultaneous with one milk composition, were included in the prediction equation. Minimal effect on accuracy was observed when two milk weights were included in the prediction model for daily SCC. Thus, AM or PM SCC alone are as good, if not better, an indicator of daily SCC than predicted daily SCC using prediction equations. Milking interval defined as individual cow-testday interval measured in minutes fitted the data better than individual cow-testday interval rounded to the nearest half-hour, which was in turn superior to average herd-testday interval and average herd interval. Hence, results from this study suggest DIY milk recording is a viable alternative to supervised milk recording in Ireland.

Keywords: AM-PM; dairy; do-it-yourself; milk recording

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Introduction

The level of milk recording in Ireland is low relative to most other major milk producing countries (International Committee for Animal Recording, 2002). Such low participation hinders genetic progress in Ireland given the heavy reliance on progeny testing as a means of genetically evaluating young sires. Increasing pressure on profit margins in dairy herds, coupled with increased labour shortage, is strengthening farmer reluctance to enter or continue milk recording. The level of milk recording in Ireland decreased from 391,975 cows in 2000 to 365,128 cows in 2003 (Irish Cattle Breeding Federation, 2004); this corresponds to a decline of nearly 7% over four years. Such trends, if continued, may have a deleterious effect on genetic progress in Ireland, unless other systems of genetic evaluation of animals (e.g., within nucleus herd(s) or specific 'sire proving' herds) are adopted. Milk recording is also vital for everyday farm management, including management of somatic cell count (SCC), on an individual cow basis.

Do-it-yourself (DIY) milk recording, with or without reduced frequency milk composition sampling, may be viewed as a possible alternative system to entice farmers to enter, or remain in, milk recording. Schaeffer *et al.* (2000) observed that 24-h fat yield may be predicted with an accuracy of 0.89 from morning (AM) milking and 0.88 from evening (PM) milking. Their model adjusted for the herd average time interval between AM and PM milkings and estimated the prediction equations within subclasses of days in milk, parity and season of calving. However, the authors are unaware of any study that quantified the effect of definition of milking interval (e.g., defined at a cow or herd level) on the accuracy of predicting 24-h yields.

Berry *et al.* (2005), using data from research herds, corroborated results from Schaeffer *et al.* (2000), concluding that 24-h yield can be accurately predicted from part-day samples. However, preliminary analysis (Berry *et al.*, 2004) revealed that the previously derived prediction equations from research data (Berry *et al.*, 2005) unsatisfactorily predicted 24-h yield in a data set of DIY testday records when the time interval between AM and PM milking was > 10 h; the range in milking interval used to predict 24-h yield by Berry *et al.* (2005) was between 6 and 9 h. The unsatisfactory fit of the equations to the DIY data was attributed mainly to the uncertainty of extrapolation of milking interval beyond values originally available to derive the equations. Previous research (Berry *et al.*, 2004; Schaeffer *et al.*, 2000) also revealed poorer predictive capacity of equations when applied to data independent to that used to derive the prediction equations. All previous studies investigating the accuracy of predicting 24-h yield from part-day samples examined milk, fat and protein yield. The authors are unaware of any research investigating the accuracy of predicting daily SCC from part-day-samples.

The objective of the present study was to investigate the suitability of DIY milk recording in commercial Irish dairy herds as a means of reducing the cost and labour requirements of milk recording.

Materials and Methods

Data

Milk weights and milk samples were collected at four-weekly intervals across 23 herds participating in a pilot DIY milk recording study in southern Ireland, for both AM and PM milking separately.

Data from the herds were extracted from the Irish Cattle Breeding Federation database on the 12th August 2004. The initial, unedited data set comprised 7,945 part-day observations from 1,581 cows. In total, 68 herd-testdays were included in the data set; the number of part-day observations per herd-testday varied from 10 to 576. Days in milk varied from 1 to 535. Records were available from cows calving across all months of the year.

True 24-h testday yield was computed as the sum of the respective part-day yields. Twenty-four-hour SCC was calculated as the average of the part-day SCC weighted by their respective part-day milk yields. Days in milk were grouped into seven classes, 50 day intervals from 0 to 300 and a final class for ≥ 300 days. Parities greater than two were grouped together.

Only consecutive non-zero PM-AM (or AM-PM) samples per cow-testday were retained. Following editing 3,850 records (i.e., 7,700 part-day samples) from 1,565 cows were available for inclusion in the analysis. Milking interval was defined as the difference, in minutes, between morning and evening milking for each cow-testday. Alternative definitions were generated whereby milking interval was defined as individual testday milking interval rounded to the nearest half hour, average herd-testday milking interval, and average herd milking interval across the entire study period.

Analysis

The analysis procedures adopted in the present study were similar to those used by Berry *et al.* (2005). A linear multiple regression model, fitted in SAS (SAS, 2004) to predict true 24-h yield from AM and/or PM samples was as follows:

$$Y_{ik} = [b_0 + b_1 (MI) + b_2 (Milk)_i + b_3 (Fat)_i + b_4 (Protein)_i] k + e_{ik}$$

where:

Y_{ik} = 24-h milk yield, fat yield, protein yield or somatic cell count

MI = milking interval from AM to PM (milking interval from PM-AM is directly related so was not included in the model)

$(Milk)_i$ = milk yield on the i^{th} milking of the day

$(Fat)_i$ = fat yield on the i^{th} milking of the day

$(Protein)_i$ = protein yield on the i^{th} milking of the day

e_{ik} = random residual effect

An additional independent predictor variable, SCC on the i^{th} milking, was included in the prediction model for SCC only. Subclasses were defined as stage of lactation (seven classes) by parity (three classes). Hence, a total of 21 subclasses (i.e., $k = 21$) were defined. Preliminary analyses revealed heterogeneous means and variances for milk, fat and protein yield as well as SCC in different subclasses. Therefore, separate regression analyses were carried out within subclasses. The prediction equations were initially derived from 75% of the data randomly chosen, without replacement, from the entire data set using PROC SURVEYSELECT (SAS, 2004). The number of records per subclass varied from 18 to 411 in this data subset; the average number of records per subclass was 138.

Tests for comparing predicted yield with true yield

Prediction equations derived from 75% of the data were applied to the remaining 25% of the data. Predicted yields within subclasses were then combined into one dataset for statistical analysis. The comparison between predicted and true 24-h yield involved estimating the mean and variance of the bias. The average bias was computed as the mean of the difference

between true 24-h yield and predicted 24-h yield. The 25% and 75% quartiles of the bias were also estimated. Correlation analyses were performed using PROC CORR (SAS, 2004) between true and predicted yield as well as evaluating the independence of the residuals (i.e., difference between true and predicted yield).

The accuracy of predicting 24-h yield was investigated as:

$$\text{Accuracy} = (\sigma_{\text{true}}^2 / (\sigma_{\text{true}}^2 + \sigma_{\text{residual}}^2))$$

where:

σ_{true}^2 = variance of the true yield

$\sigma_{\text{residual}}^2$ = variance of the difference between the true yield and the predicted yield (i.e., variance of the residuals)

Prediction of true SCC *per se* may not be as important as identifying samples of high (e.g., $\geq 200,000$ cells/ml) somatic cell count. The figure 200,000 cells/ml was chosen to represent a milk sample exhibiting signs of infection (Dohoo and Leslie, 1991). Therefore, the sensitivity and specificity of predicted 24-h SCC at identifying samples with a true daily SCC $\geq 200,000$ cells/ml was investigated. Sensitivity was calculated as the proportion of true daily SCC $\geq 200,000$ cells/ml that had a predicted SCC $\geq 200,000$ cells/ml, and specificity was calculated as the proportion of true daily SCC $< 200,000$ cells/ml that had a predicted SCC of $< 200,000$ cells/ml. The standard error of sensitivity (Se) and specificity (Sp) was calculated as

$$\text{SE(Se)} = \sqrt{\frac{\text{Se} \cdot (1 - \text{Se})}{N_i}}$$

$$\text{SE(Sp)} = \sqrt{\frac{\text{Sp} \cdot (1 - \text{Sp})}{N_u}}$$

where N_i and N_u are the number of samples with a true daily SCC of $\geq 200,000$ cells/ml and the number of samples with a true daily SCC of $< 200,000$ cells/ml, respectively.

Results and Discussion

General performance

The mean and standard deviation of milk yield and composition are summarised in Table 1. Part-day milk yield varied from 0.8 kg to 46.7 kg. Part-day fat, protein and lactose percentages varied from 1.5% to 7.58%, 2.19% to 5.12%, and 3.31% to 5.44%, respectively. Part-day production and composition were similar to those reported previously across three Irish research herds (Berry *et al.*, unpublished). Daily composition was similar to average daily composition reported across all Irish milk recording herds in recent years (Irish Cattle Breeding Federation, 2004). However, the standard deviation of daily milk yield and composition are larger than reported by Berry *et al.* (2005) for research herds. Nevertheless, larger variation is expected in the current study given the larger expected diversity of genetic merit of animals and production systems across the 23 commercial herds included in the present study.

The ratio of AM milk yield to PM milk yield varied from 0.21 to 10.7; the average

Table 1. Mean and standard deviation (s.d.) for morning (AM), evening (PM) and daily milk production across all parities and stages of lactation

		Milk (kg)	Fat (%)	Protein (%)	SCC (000 cells/ml)
AM	Mean	15.5	3.25	3.32	258
	s.d.	4.97	0.65	0.31	
PM	Mean	11.5	4.05	3.37	354
	s.d.	4.13	0.75	0.32	
Daily	Mean	26.9	3.59	3.34	296
	s.d.	8.59	0.57	0.30	

was 1.4. The largest ratio (10.7) was an outlier representing one cow that produced 16 kg milk in the morning and 1.5 kg milk in the evening; this was despite the composition of the testday record being similar for the AM and PM samples. Following the removal of this outlier the ratios varied from 0.21 to 6.67. Correlations among AM yield, PM yield and true daily yield (results not shown) were similar to those previously reported by others (Berry *et al.*, 2005; Liu *et al.*, 2000).

Somatic cell count varied from 7,000 to 9,928,000 cells/ml; SCC of nine records was 9,999,000 cells/ml which is the maximum count recordable in the national database. In total, 1,031 records (27% of the data set) had a daily SCC $\geq 200,000$ cells/ml. The ratio of AM SCC to PM SCC varied from 0.012 to 181.25 thereby indicating considerable diurnal variation.

Correlations between AM SCC, PM SCC and true daily SCC are summarised in Table 2. The correlations in Table 2 indicate that both AM SCC or PM SCC closely resembled daily SCC. The Spearman correlations reflect the strength of the linear relationship in cow ranking for SCC based on either AM, PM or daily SCC (i.e., weighted sum of AM and PM SCC); this criterion will be most influential in culling decisions rather than SCC level *per se*. Furthermore, the results demonstrate that even without the implementation of prediction equations the ranking of cows on either AM or PM SCC is similar to ranking on daily SCC; this was despite considerable diurnal variation being observed for SCC.

The sensitivity and specificity of the AM sample as an indicator of daily SCC $\geq 200,000$ was 82% (s.e. = 1.2%) and 99% (s.e. = 0.2%), respectively; the corresponding results for the PM sample were 95% (s.e. = 0.7%) and 93% (s.e. = 0.5%), respectively. The accuracy of predicting

Table 2. Pearson (above diagonal) and Spearman (below diagonal) correlations between morning (AM), evening (PM) and true daily (DAY) somatic cell count

Sample	Sample		
	AM	PM	DAY
AM		0.80	0.96
PM	0.86		0.94
DAY	0.96	0.95	

daily SCC from only using AM SCC or PM SCC was 0.92 and 0.85, respectively.

Prediction using information on either an AM or PM sample

The ability of the prediction equations to estimate daily milk, fat, and protein yields from either AM or PM samples is summarised in Table 3. There was a tendency for daily yield predicted from the AM sample to, on average, underestimate true daily yield; the opposite was true for daily yield predicted from PM samples. In contrast to Berry *et al.* (2005), mean bias was not zero. This is because in the present study, unlike that of Berry *et al.* (2005), the prediction equations were applied to an independent dataset. The systematic underestimation and overestimation of true yield by AM and PM samples, respectively suggest that a milk recording scheme alternating between AM and PM samples would be superior when predicting lactation yield; this agrees with previous studies (Berry *et al.*, 2005; Dickenson and McDaniel, 1970; Schaeffer and Rennie, 1976).

The mean square error across traits was higher than those reported by Berry *et al.* (2005) but was similar to those reported by Schaeffer *et al.* (2000). The lower mean square error reported by Berry *et al.* (2005) is expected since Berry *et al.* (2005) applied their prediction equations to the same data as was used to derive the equations while Schaeffer *et al.* (2000) applied their prediction equations to an

Table 3. Accuracy, correlation between predicted daily yield and true daily yield, mean square error (MSE), mean, 25% percentile (Q1) and 75% percentile (Q3) of the residuals from predicting 24-h milk yield, fat yield, protein yield or somatic cell count (SCC) from either a morning (AM) or evening (PM) sample in an independent data set

Sample		Accuracy	Correlation	MSE	Mean	Q1	Q3
AM	Milk	0.93	0.96	5.88	-0.16	1.20	-1.48
	Fat	0.84	0.90	0.018	-0.010	0.069	-0.077
	Protein	0.92	0.95	0.006	-0.005	0.038	-0.047
	SCC	0.91	0.95	84747	-5.2	46.5	-19.2
PM	Milk	0.88	0.93	9.98	0.06	1.69	-1.52
	Fat	0.83	0.87	0.019	0.005	0.085	-0.071
	Protein	0.87	0.92	0.011	0.002	0.055	-0.050
	SCC	0.88	0.93	115257	-3.1	41.3	-22.1

independent data set. The mean square error is a good indicator of the fit of the model and reflects both the bias and the variance of the bias. The lower mean square error and higher accuracy of prediction from AM records included in the prediction equation agree with previous studies (Berry *et al.*, 2005; Liu *et al.*, 2000) suggesting the superiority of AM records at predicting 24-h yield compared to PM records. The accuracy of prediction was similar to that reported by Berry *et al.* (2005) but lower than that reported by Schaeffer *et al.* (2000). Examination of the quartiles reveals that 50% of the predicted milk yields were within ± 1.7 kg of the true milk yield; this represents an error of 6% of the mean.

The sensitivity and specificity of identifying a daily SCC $\geq 200,000$ using the prediction equations was 96% (s.e. = 0.6%) and 92% (s.e. = 0.5%), respectively for the AM sample; the corresponding values for the PM sample were 93% (s.e. = 0.8%) and 92% (s.e. = 0.5%), respectively. The high mean square error associated with SCC was attributable mainly to a few large individual SCC values. When AM SCC was restricted to be less than 10,000,000 cells/ml the mean square error

was reduced by 10,000; the mean square error halved when AM SCC $> 5,000,000$ were removed from the analysis.

Accuracy of predicting 24-h SCC from AM samples was reduced through the use of the prediction equations compared to using the AM sample itself; however, the sensitivity was increased through the use of the prediction equations. Accuracy of predicting 24-h SCC was increased through the use of the prediction equations including PM SCC compared to using the PM sample alone; however, the sensitivity and specificity were reduced through the use of the prediction equations. Similarly, the correlations between predicted daily SCC and true daily SCC were lower than correlations between AM or PM SCC and daily SCC. The authors are unaware of any previous study that investigated the efficacy of predicting 24-h SCC (or the existence of subclinical mastitis indicated as a binary variable) from part-day SCC samples. Nevertheless, the results suggest little or no benefit of using prediction equations to estimate 24-h SCC, or to identify samples exhibiting subclinical mastitis (i.e., $\geq 200,000$ somatic cells/ml).

Graphical examination of the residuals against predicted yield revealed no obvi-

ous trend. Absolute correlations between residuals and predicted yields were less than 0.10 for milk, fat and protein yields; the majority were not significantly different from zero. This suggests randomness of the error. Correlations between residual and predicted SCC varied from 0.10 to 0.14 and were significantly different from zero. This suggests a systematic bias towards the underestimation of relatively high SCC and the overestimation of relatively low SCC. Nevertheless, such correlations were strongly influenced by testday records with exceptionally high SCC. Graphical examination of the relationship between the residuals and month of calving revealed no trend. Correlations between the residuals and month of calving were generally not significantly different from zero indicating no systematic linear bias across months of calving.

Estimation of daily yield using two consecutive milk weights and only one composition in a prediction equation

A supplementary scenario was investigated whereby two milk weights (both AM and PM) were available with either an AM or PM milk composition. The accuracy of prediction of daily fat and protein yield from two consecutive milk weights and

either an AM or PM composition is summarised in Table 4.

In agreement with Schaeffer *et al.* (2000) the accuracy of predicting 24-h fat and protein yields increased when both milk weights were available for inclusion in the prediction equation; the mean square error of the variance also decreased across both studies. The accuracy of predicting 24-h protein yield was 1.00 and 0.99 from AM or PM samples, respectively; Schaeffer *et al.* (2000) also reported accuracies of 0.995 and 0.99, respectively. The accuracy of predicting 24-h fat yield from AM (0.93) or PM (0.90) samples was in agreement with Schaeffer *et al.* (2000) who reported accuracies of 0.93 and 0.92, respectively.

From derived daily fat and protein yield, fat and protein percentage were calculated and compared to true daily fat and protein percentage. For daily fat percentage, 50% of the predicted records were within $\pm 0.2\%$ of the true value; the corresponding figure was $\pm 0.04\%$ for protein percentage.

The rank correlation within testday (with a minimum of 20 cows per testday) between fat yield estimated using prediction equations incorporating either AM or PM samples and true fat yield varied from 0.83 to 0.97 and from 0.83 to 0.96, respec-

Table 4. Accuracy, correlation between predicted yield and true yield, mean square error (MSE), mean, 25% percentile (Q1) and 75% percentile (Q3) of the residuals from predicting 24-h milk yield, fat yield, protein yield or somatic cell count (SCC) from both morning (AM) and evening (PM) milk weights simultaneous with either an AM or PM composition sample

Sample		Accuracy	Correlation	MSE	Mean	Q1	Q3
AM	Fat	0.93	0.96	0.007	-0.004	0.044	-0.046
	Protein	1.00	1.00	0.000	0.001	0.010	-0.009
	SCC	0.91	0.95	83181	-5.7	48.2	-19.1
PM	Fat	0.90	0.95	0.010	0.003	0.058	-0.054
	Protein	0.99	1.00	0.001	0.001	0.013	-0.012
	SCC	0.88	0.93	115180	-2.9	46.0	-26.3

tively. The rank correlation within testday (with a minimum of 20 cows per testday) between daily protein yield predicted from AM or PM samples and true protein yield varied from 0.98 to 1.00 and from 0.97 to 0.99, respectively. Therefore, the ranking of cows for predicted daily fat or protein yield on any given testday was very similar to cow ranking based on true 24-h fat or protein yields.

The sensitivity and specificity of identifying daily SCC $\geq 200,000$ using an AM sample incorporated within a prediction equation including two milk weights were 95% (s.e. = 0.7%) and 91% (s.e. = 0.5%), respectively; the corresponding values for the PM sample were 94% (s.e. = 0.7%) and 92% (s.e. = 0.5%), respectively. These are very similar to previous results where only one milk weight was included in the prediction equation thereby suggesting no additional advantage of the availability of a second milk weight.

However, farmers may only be interested in identifying the cows with the highest SCC. The rank correlation within herd-testday between predicted 24-h SCC from AM samples and true 24-h SCC varied from 0.83 to 0.97. The rank correlation within herd-testday between predicted 24-h SCC from PM samples and true 24-h SCC varied from 0.76 to 0.97.

No obvious graphical trend was observed between the residuals and predicted yields. Absolute correlations between residuals and predicted fat and protein yield were not significantly different from zero indicating total randomness of the error. Correlations between residuals and predicted SCC were 0.10 and 0.14 but were strongly influenced by testday records with exceptionally high SCC.

Graphical examination of the relationship between the residuals and month of calving revealed no trend. Correlations between the residuals and month of calv-

ing were generally not significantly different from zero indicating no systematic linear bias across months of calving.

Definition of milking interval

Four alternative definitions of milking interval were created: cow-testday milking interval in minutes; cow-testday milking interval rounded to the nearest half hour; average herd-testday milking interval, and average herd milking interval across the study period. The effect of the definition of milking interval on the mean square error of prediction for daily yield using either an AM or PM sample incorporated into a prediction equation, with one milk weight is illustrated in Figure 1.

Indications are that milking interval defined as individual cow-testday interval measured in minutes was most accurate (i.e., yields the lowest mean square error). The mean square error generally increased when cow-testday interval was rounded to the nearest half-hour, and was further increased when milking interval was defined as average herd-testday and herd average milking interval. The authors are unaware of any other study that has evaluated the effect of milking interval definition on the prediction of 24-h yield from part-day samples. Both Berry *et al.* (2005) and Schaeffer *et al.* (2000) used herd milking interval rounded to the nearest half hour.

The effect of alternative milking interval definitions diminishes when two milk weights are included in the prediction model; this is partly attributable to the reduced importance of milking interval when two milk weights are included in the model. This therefore suggests that in the absence of a device to record cow test-day milking interval average herd/testday milking interval could be supplied by the farmer. The average herd milking interval implemented on the testday of milk recording would be superior.

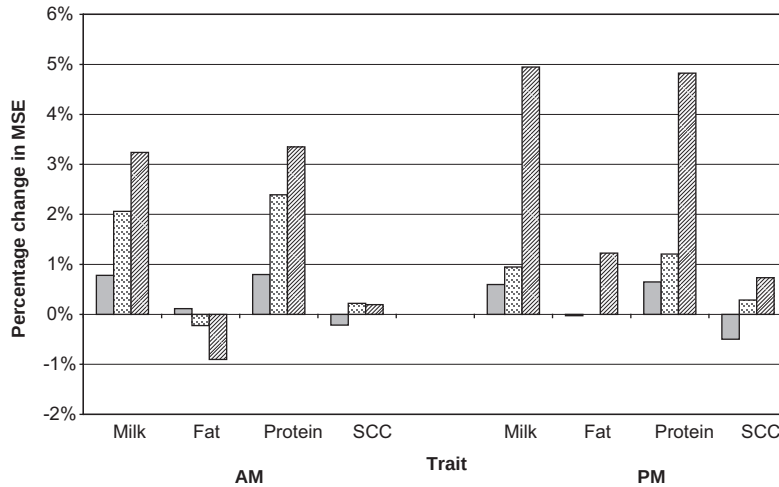


Figure 1: Percentage change in mean square error (MSE) when milking interval is defined as cow-testday interval rounded to the nearest half hour (full bars); average herd-testday (spotted bars), or average herd (striped bars) compared to cow-testday interval measured in minutes using either a morning (AM) or evening (PM) sample.

National use of predicted yield

Given the favourable results reported herein, prediction equations were re-derived using the full data set. Correlations between previously derived solutions (75% of the data) and solutions from the whole data set were all greater than 0.98 for fat and protein yield when two milk weights were included in the prediction equation. The correlation between previous solutions and new solutions for AM SCC was 0.62; the corresponding correlation for PM SCC was 0.49. This suggests that the prediction equations for SCC are not robust and question their usefulness in predicting daily SCC since AM/PM SCC records alone are a good indicator of daily SCC. Nevertheless, the reduced accuracy of predicting SCC is not surprising given the considerable variation in SCC between two consecutive records.

The use of prediction equations for fat and protein yield is relatively simple and can easily be incorporated within the national database. The procedures

utilised to estimate daily yield from part-day samples using prediction equations is summarised in Appendix 1.

As national genetic evaluations of milk production progress towards testday models that utilise all individual testday records in the genetic evaluation model, cognisance may have to be taken of whether the testday yield is a true or predicted yield. Computational demands will possibly restrict the feasibility of treating the two types of testday yields as separate traits in a multi-trait testday model evaluation. Thus, to treat predicted and true daily yield as the same trait the genetic correlation between traits should be unity and the (co)variance structure among testdays should be similar across the two yield types. Data limitations in the present study did not allow estimation of genetic correlations between true and predicted testday yields or the estimation of auto-correlations among different lactation stages. Liu *et al.* (2000) reported a trend

in autocorrelations among lactation stages that was similar for both true and predicted yield; the autocorrelations were slightly lower in absolute terms for predicted yield and decreased as the distance between stages increased (Liu *et al.*, 2000).

Figure 2 illustrates the ratio of the variance of predicted daily fat yield to true daily fat yield across the different stages of lactation defined herein. The ratio of predicted daily protein yield to true protein yield across lactation is shown in Figure 3. The variance of either predicted

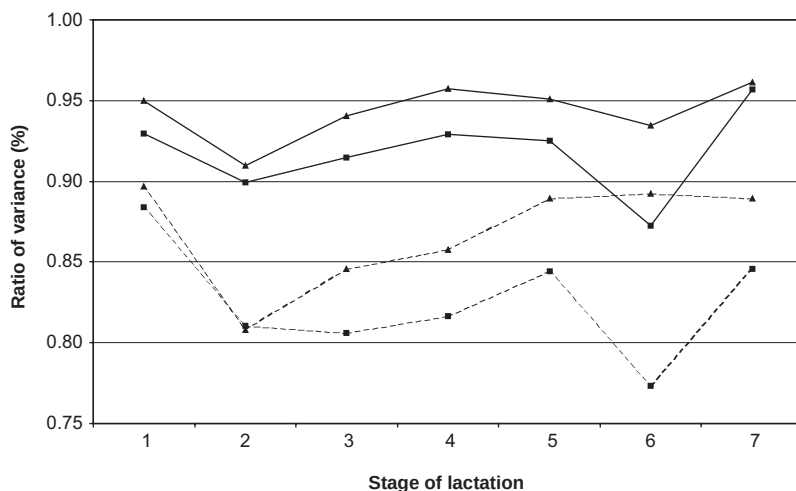


Figure 2: Ratio of the phenotypic variance of AM-predicted daily fat yield (▲) and PM-predicted daily fat yield (■) to true daily fat yield. Ratios are presented for prediction equations incorporating one (----) or two (—) milk weights.

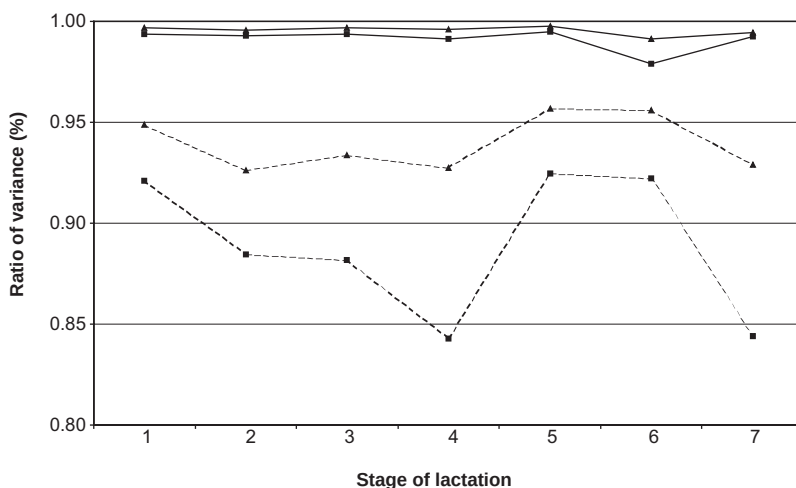


Figure 3: Ratio of the phenotypic variance of AM-predicted daily protein yield (▲) and PM-predicted daily protein yield (■) to true daily protein yield. Ratios are presented for prediction equations incorporating one (----) or two (—) milk weights.

fat or protein yield was consistently less than the true variance, and the variance of predicted yield from the AM part-day sample were consistently higher than the variance of predicted yield from the PM sample, corroborating previous studies (Liu *et al.*, 2000). A lower variance of predicted yield is expected since:

$$\text{Var}[\text{Yield}_{\text{TRUE}}] = \text{Var}[\text{Yield}_{\text{PREDICTED}}] + \text{Var}[\text{Yield}_{\text{TRUE}} - \text{Yield}_{\text{PREDICTED}}]$$

Thus, unless the predicted yield is a perfect estimate of true yield, $\text{Var}[\text{Yield}_{\text{TRUE}} - \text{Yield}_{\text{PREDICTED}}]$ (i.e., the variance of the residual) will be greater than zero. Nevertheless, the variance of predicted yield resembled the true yield variation more closely when two milk weights were included in the prediction equation.

VanRaden, Wiggans and Ernst (1991) suggested expanding predicted yields by dividing by the accuracy of the respective prediction equation. Such expansions result in identical genetic and permanent environmental variance in predicted and true testday yields, but the error variance of the predicted yields is larger, thereby reducing the heritability of testday yield (VanRaden *et al.*, 1991). The reduction in heritability of the test-day records manifests as an animal's own phenotypic record(s) receiving less weight in the breeding value estimation procedures. This is expected to be more of an issue in cow rather than sire breeding value estimation, since a sire generally has more daughter records across a range of milk recording systems (Liu *et al.*, 2000).

Conclusions

The results clearly show that daily yield can be accurately predicted from either an AM or PM sample. However, the

accuracy of predicting daily yield can be increased by the inclusion of two milk weights in the prediction model. Therefore, do-it-yourself milk recording provides an accurate alternative to current supervised milk recording schemes available in Ireland.

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Appendix 1.

Prediction equations were derived for each subclass of parity (1, 2, ≥ 3) and days in milk (0–49, 50–99, 100–149, 150–199, 200–249, 259–299, ≥ 300). For example, the prediction equation of a first lactation cow with a milk testday at 83 days in milk is:

$$\begin{aligned} \text{FAT}_{\text{DAY}} &= 0.226686148 + (-0.019860586 \times \text{INT}_{\text{PM-AM}}) \\ &+ (-0.02133069 \times \text{MILK}_{\text{AM}}) + (0.037295198 \times \\ &\text{MILK}_{\text{PM}}) + (1.199585129 \times \text{FAT}_{\text{AM}}) + (0.40690312 \\ &\times \text{PROTEIN}_{\text{AM}}) \\ \text{FAT}_{\text{DAY}} &= -0.085085796 + (0.013486432 \times \text{INT}_{\text{PM-AM}}) \\ &+ (0.0294658 \times \text{MILK}_{\text{AM}}) + (-0.014821905 \times \\ &\text{MILK}_{\text{PM}}) + (1.324716931 \times \text{FAT}_{\text{PM}}) + (0.035625646 \\ &\times \text{PROTEIN}_{\text{PM}}) \end{aligned}$$

A cow was present on a farm with a milking interval of 8.28 hours between AM and PM milking. The cow had an AM milk yield, fat percent and protein percent of 8.7 kg, 3.13% fat, 3.23% protein, respectively, and a PM milk yield, fat percent and protein percent of 4.4 kg, 4.44% and 3.12%, respectively. Therefore, this cow produced a fat yield of 0.468 kg. Predicted fat yield from the AM sample and PM sample were 0.482 kg and 0.481 kg, respectively.