
THE PROCEEDINGS OF THE
NEW ZEALAND SOCIETY
OF
ANIMAL PRODUCTION
VOLUME 62 2002

Predicting cow production based on an estimate of animal genotype within a Whole Farm Model

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ABSTRACT

Modelling is being used to compare and contrast farm management strategies. A Whole Farm Model (WFM) has been developed that links models for cow metabolism ('Molly') and pasture growth driven by climate, with management policies. It has been evaluated against trial data and the challenge is to now use it for prediction. This requires that cows be initialized so that their production is determined by their environment and genotype. Livestock Improvement Corporation has developed a system of quantifying genotype through production values (or PV's). The aim of this study was to assess the ability of the WFM to predict Strain Trial cow production using PVmilk. The relationship between PVmilk and milk yield and composition was determined by allowing a parameter within 'Molly' to adjust so that predicted matched actual production for 3 Strain herds and one Jersey herd. WFM was then initialized using observed PVmilk to set genotype of each cow in 8 other Strain herds and farmlets were simulated for 2003/04 season. Predictions were considered useful if the prediction errors for milk yield and milksolids (629 L and 61 kg MS respectively) were lower than the observed standard deviations (825 L and 66 kg MS respectively) i.e. meaning model predictions of observed values were more accurate than simply using the mean as an estimate of observed values. The consistent under-prediction of milk yield and milksolids require further adjustments to the initialization of the model. PVmilk has the potential to set genotype in 'Molly', within the WFM.

Keywords: farm system; modelling; production value; genotype.

INTRODUCTION

Modelling is being used increasingly within farm systems research to compare and contrast management strategies. Once models have been shown to be robust and are able to accurately predict results they can be used to predict outcomes of different scenarios. In this way, models increase the return on research investment by extending the results of a particular trial.

We, and others have developed models to represent whole farm systems (Bright *et al.,* 2000; Cros *et al.,* 1999; Freer *et al.,* 1997; Marshall *et al.,* 1991; Rotz *et al.,* 1989a; Rotz *et al.,* 1989b). The models vary in their purpose and therefore in their application. Although the Whole Farm Model (WFM) was designed for research purposes, with the addition of economics it can be applied to actual farm systems (Neal *et al.*, 2005). It has been used to assess various farm systems (Beukes *et al.*, 2005a; Beukes *et al.*, 2005b) by setting cow genotype using observed production data. Here we test the ability to set the potential using some independently obtained estimate of a cow's genotype.

A cow's production is influenced by the quantity and quality of feed given to her and by her metabolic capacity to absorb, transport and convert nutrients into milk (Bargo *et al.,* 2003). The feed aspects are a component of her temporary environment, and the functional genes of an animal (genotype) control the metabolic processes that occur within the animal when a particular environment is imposed (Bryant *et al.,* 2005). In modelling a farm system it is important to try and model both aspects. The 'Molly' cow model (Baldwin, 1995) has equations representing the metabolic processes of digestion, absorption and conversion of nutrients into glucose, lipids and proteins, in the liver, muscle, adipose tissue, and into milk in the mammary gland. We have added energy losses for walking and growth of fetal tissues during pregnancy (Palliser *et al.,* 2001a; Palliser *et al.,* 2001b). 'Molly' therefore has the potential to predict milk yield (and composition) in cows given different feeds. The question is can she represent different genotypes? The aim of the study was to assess the ability of the WFM with 'Molly' to predict production of different farm systems with cows of differing genotype. We have used an approach to set a specific parameter in 'Molly' to represent her genotype, while the WFM, through climate-driven pasture growth and cow and pasture management policies, determined the temporary environment (Bright *et al.*, 2000; Wastney *et al.,* 2002).

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METHODS

1) Using an estimate of animal genotype to set Molly's potential milk yield

In 'Molly', potential yield is determined by setting a parameter for 'mature peak daily milk' (MPDM). Livestock Improvement Corporation (LIC) has developed a system of quantifying genetic potential for milk production of individual animals through a production value (PVmilk in litres (L)). The PVmilk is a measure of a cow's expected lifetime performance relative to a base of zero, an average 1985 born cow (Livestock Improvement Corporation, 1996). The relationship between PVmilk and the 'Molly' parameter, MPDM, was determined using observed data from a group of cows that were fully fed on pasture and with a wide range of PVmilk values. For this purpose observed data were used for seasonal milk production, seasonal milk composition and live weight from a Jersey herd (milked twice-a-day at Taranaki Research Station) and three herds (NZ-70 herd 2, NZ-90 herd 5, OS-90 herd 8) from the Dexcel HF Strain Trial (Macdonald *et al.,* 2005, Table 1) for the 2003/04 season. Cows in each of the four herds were grouped into three age groups, 2, 3 and 4+ years, and for every age group the average PVmilk was determined as well as average seasonal curves for milk, milk fat, milk protein and live weight. For each of the twelve 'average' cows the WFM's optimization procedure was used to optimize on the Molly parameter, MPDM, so that the differences between predicted and actual seasonal curves were minimized. The optimization procedure produced twelve 'optimum' parameter values for MPDM that were regressed against the twelve average values for PVmilk. The results showed a strong age effect on the relationship of PVmilk with MPDM. Three linear equations were subsequently developed, one for each age group:

2 yr: MPDM = 0.0068(PVmilk) + 19.305 ($R^2 = 0.74$)

3 yr: MPDM = 0.0046(PVmilk) + 23.766 ($R^2 = 0.77$)

4+ yr: MPDM = 0.006(PVmilk) + 25.444 ($R^2 = 0.68$)

2) Testing predicted and actual milk yields

The ability of 'Molly' to predict milk yield for cows with different genotype and under different temporary environments was tested using the Whole Farm Model (WFMv1.0.6.m) and cows in 8 herds (n=150 cows) from the Strain Trial (i.e., excluding herds 2, 5 and 8 used in the optimization process) (Table 1). Simulations for the 2003/04 year used daily climate data from NIWA Ruakura station, the McCall pasture model (McCall & Bishop-Hurley, 2003)(version 3.01), parameterized for the Waikato, and the 'Molly' cow model (version 4.16). The WFM (IBM VisualAge Smalltalk) is a framework that links published component models that are written in different languages (Sherlock & Bright, 1999; Sherlock *et al.*, 1997). At the start of the simulation (1 June 03) individual cow characteristics including live weight, BCS, date of last mating and next calving date, breed, age, and PVmilk were specified, together with size and pasture cover of the individual paddocks. Management policies were selected and defined based on those used in the trial. These policies included mating, drying-off, and feeding policies for cows and rotation lengths, minimum grazing residuals, conservation, and fertilizer application for pastures. The WFM stepped through the year, each day taking actions that mimicked those in the actual trial and calculated cow production, pasture growth, conservation and supplementary feeding.

Three strains of Holstein-Friesians were farmed in a range of feeding systems for 3 years. These included two high breeding worth ($BW) strains of either North American origin (OS-90) or NZ origin (NZ-90), and a low $BW strain of 1970 NZ Friesians (NZ-70). Systems were designed to

TABLE 1: Herd descriptions of the Dexcel HF Strain trial, involving 3 strains of Holstein Friesian [New Zealand cows of 1970's genetics (NZ-70); New Zealand cows of 1990's genetics (NZ-90); cows derived from Overseas 1990's genetics (OS-90)] at differing annual feed allowances (t DM/cow/year).

Herd	Strain	Annual feed allowance (t DM/c/y)	Pasture (t DM/c/y)	Supplement allowance (t DM/c/y)	Cows/ha
1	NZ-70	4.5	4.5	0	3.8
2	NZ-70	5.5	5.5	0	3.1
3	NZ-70	6.0	5.5	0.5	3.1
4	NZ-90	5.0	5.0	0	3.4
5	NZ-90	5.5	5.5	0	3.1
6	NZ-90	6.0	5.5	0.5	3.1
7	NZ-90	6.5	5.5	1.0	3.1
8	OS-90	5.5	5.5	0	3.1
9	OS-90	6.0	5.5	0.5	3.1
10	OS-90	6.5	5.5	1.0	3.1
11	OS-90	7	5.5	1.5	3.1

provide feed allowances of 4.5 to 7.0 t DM/cow/year, based on different stocking rates and supplement inputs (Table 1). When feed allowance was higher than 5.5 t DM/cow, additional feed was brought in above pasture grown.

3) Statistics

Results of predicted versus observed values for milk yield and milksolids were visually compared for individual cows. Statistical analysis was only performed on herd level results, as individual animals may under- or over-achieve their potential milk yield due to environmental conditions beyond the scope of the model e.g. health reasons. On a herd level this effect will be minimized. The root mean square of prediction error (RMSPE), defined as the square root of the sum of the predicted-minus-observed values squared divided by the number of observations was calculated (Tedeschi, 2005). Predictions were considered useful if the RMSPE was lower than the observed standard deviation (SD) i.e. meaning model predictions of observed values were more accurate than simply using the mean as an estimate of observed values. Residual error was calculated

$$\text{Residual error} = \sqrt{[(\text{RMSPE})^2 - (1/n\sum(\text{predicted-observed}))^2]}$$

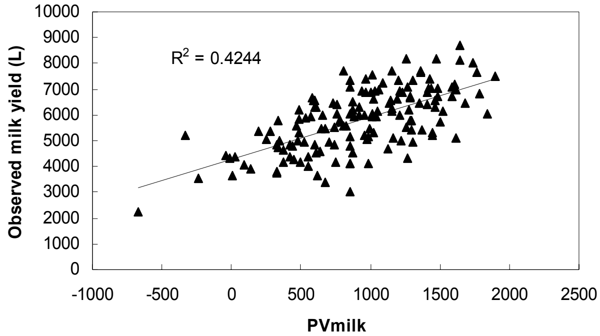
and expressed as a percentage of RMSPE. Residual error is regarded as of greater concern in model evaluation because it indicates some conceptual flaw or systematic error in the model. Mean bias is a measure indicating consistent error in the model.

$$\text{Mean bias \%} = 100 - \text{Residual error \%}$$

RESULTS AND DISCUSSION

In addition to milk yield, several farm variables predicted by the WFM were compared to observed values to ensure the modelled cows were being fed in the same way as in the trial. Specifically, pasture growth rate (kg DM/ha/d), pasture cover (kg DM/ha), live weight (kg/cow), BCS, pasture and supplement intakes (kg DM/cow/d) were compared to observed values on a monthly basis (data not shown). Observed milk yields are shown against PVmilk for all eight herds in Figure 1. Milk yield ranges from 2000 to 9000 L/cow and PVmilk ranged from -600 to +1800 (Figure 1). Some variability in yield at each PVmilk is due in part to the different feeding levels for each herd (Table 1).

FIGURE 1: Observed milk yield (L) vs PVmilk for all cows (n = 150) in the eight herds. A trend line with R^2 value is also given.



For eight herds, with average PVmilk ranging from 346 to 1301L, RMSPE for milk yield and milksolids were lower than the SD of the observed values (629 vs 825 L and 61 vs 66 kg MS/cow respectively) (Table 2), meaning model predictions of observed values were more accurate than simply using the mean as an estimate of observed values. The RMSPE as % of the mean (= Mean Prediction Error, MPE) was 10.9% for milk and 13.3% for milksolids (Table 2). Model predictions are considered to be satisfactory, adequate, or

TABLE 2: Herd results for eight herds of the Dexcel HF Strain trial. See Table 1 for herd descriptions.

	PVmilk (L/cow)		Milk yield-observed (L/cow)		Milk yield-predicted (L/cow)		Milk yield ratio	Milksolids - observed (kg/cow)		Milksolids-predicted (kg/cow)		Milksolids ratio
Herd	Mean	SD	Mean	SD	Mean	SD	(P/O)[1]	Mean	SD	Mean	SD	(P/O)
1	346	440	4358	1013	3976	753	0.91	349	78	305	67	0.88
3	385	291	5310	765	4668	841	0.88	426	53	369	74	0.87
4	885	317	5249	993	4819	929	0.92	426	78	381	84	0.89
6	974	399	5812	1078	5189	1243	0.89	501	85	410	112	0.82
7	839	339	6251	973	5509	883	0.88	536	89	437	76	0.81
9	1195	392	5468	1063	5573	912	1.02	414	66	446	84	1.08
10	1153	383	6671	1000	5796	761	0.87	507	76	464	69	0.91
11	1301	335	6843	827	6002	666	0.88	523	77	482	60	0.92
Mean	885		5745		5192			460		412		
SD	357		825		672			66		58		
RMSPE					629					61		
MPE %					10.9					13.3		
Residual error as % of RMSPE					22.5					36.7		
Mean bias as % of RMSPE					77.5					63.3		

[1] Predicted/Observed

unsatisfactory, when MPE is <10%, between 10 and 20%, or >20% (Fuentes-Pila *et al*., 1996). Ratios of Predicted to Observed (P/O) for milk yield and milksolids showed that predictions were generally within 15% of herd means. However, there was a consistent under-prediction by the model, which is confirmed by the trend lines in Figures 2 and 3 being above the 1:1 lines. This consistent error was also confirmed by the relatively large proportion of total error comprised of mean bias. Residual error contributed a relatively smaller proportion to the total error (Table 2). Predicted and observed milk yields for the 2003/04 season are shown for a representative herd (Figure 4). Both observed and predicted yields fluctuated across PVmilk as cows differed by age (and therefore potential yield), but predicted yields were consistently below the observed for this herd.

The encouraging aspect of this exercise was that model predictions followed the observed trends determined by cow age and genotype. The model still requires some adjustment to resolve the consistent error resulting in under-prediction. However, we conclude that under predominantly grazing systems PVmilk has the potential to set an initialization parameter in 'Molly' cow model to predict milk yield, when quantity and quality of feed varies as simulated by WFM.

FIGURE 2: Observed vs predicted milk yield (L). A 1:1 line and trend line with R^2 value is also given.

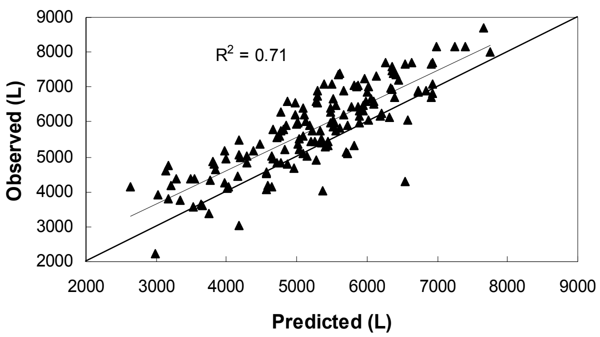


FIGURE 3: Observed vs Predicted milksolids (MS). A 1:1 line and trend line with R^2 value is also given.

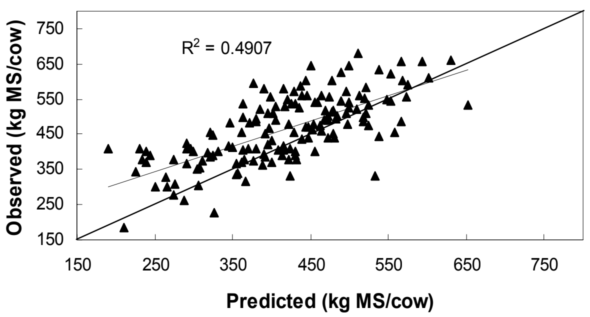
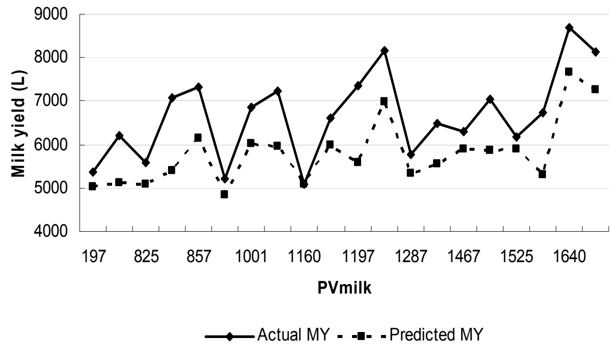


FIGURE 4: Observed and predicted milk yield for the 2003/04 season vs PVmilk for herd 10 of the Strain trial.



ACKNOWLEDGEMENTS

We acknowledge the funding of Dairy InSight (project 10079).

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