

USING A BIOLOGICAL MODEL OF LACTATION TO REASSESS DAIRY RECORDING AND GENETIC EVALUATION

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INTRODUCTION

Recent developments in the genetic evaluation of dairy animals have concentrated on using the desirable properties of the test-day model to genetically evaluate milk production (Ptak and Schaeffer, 1993). This methodology results in a single breeding value for each animal reflecting its level of daily milk production, adjusted for the many environmental influences and the shape of the lactation curve. Papers by Dijkstra *et al.* (1997) and Pollott (2000) have attempted to statistically model milk production throughout lactation in terms of the underlying biology, rather than by the more common empirical methods (see Masselin *et al.*, 1987 for a review). Daily milk yield throughout lactation can be thought of as the result of three processes; mammary cell differentiation in pregnancy and early lactation, cell death (apoptosis) throughout lactation and the secretion rate of differentiated mammary cells (Figure 1).

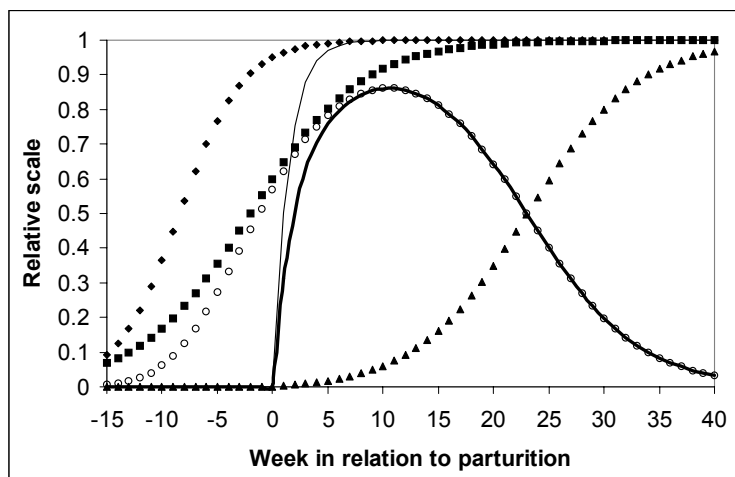


Figure 1. A schematic diagram of the biology of the mammary gland during pregnancy and a 40-week lactation, based on Knight and Wilde (1993), Wilde *et al.* (1997) and Knight *et al.* (1998) showing parenchyma cell production (◆), secretory cell differentiation (■), cells dying by apoptosis (▲), potentially active cells (○), secretion rate (–) and milk production (—) (Pollott, 2000)

This model has also been used to describe the production of milk components during lactation (Pollott, 2002). Analyses of dairy sheep data (Gootwine and Pollott, 2000 and 2002; Pollott and Gootwine, 2001) have shown that the parameters of the biological model are definable and repeatable characteristics of the animal and have some genetic basis. The objective of this paper is to explore the use of the biological model as the basis for improved genetic evaluations of dairy animals, and its implications for dairy recording.

MATERIALS AND METHODS

Milk production (M) on any given day (t) of lactation can be simply described as:

$$M_t = (\text{NDPC} - \text{NDCD}) S_{Mt} \quad [1] \text{ (Pollott, 2000)}$$

Where NDPC is the number of differentiated parenchyma cells produced to day t, NDCD is the number of differentiated parenchyma cells dying off to day t and S_{Mt} is the milk offtake rate per cell on day t (kg/cell/day; sometimes referred to as the secretion rate). Milk component production follows a similar pattern to milk yield throughout lactation. Model 1 has been shown to also describe the weight of any milk component such as fat (F), protein (Pr), lactose (L), water (W) or total solids (Tot; F + Pr + L) by substituting for M in Model 1 (Pollott, 2002). The only term to differ for the various components and milk yield is the offtake rate (S_{Ft} , S_{Prt} , S_{Lt} , S_{Wt} , S_{Tott}). Pollott (2002) has investigated the shape of the various offtake rate curves during lactation. Looked at in this way it is not surprising that there are high phenotypic and genetic correlations between the various milk and component weight traits since the number of active secretory cells is common to all of them.

The estimation of NDPC and NDCD from commonly-recorded farm data has been discussed by Pollott (2000) using two logistic curves with biologically meaningful parameters. These have been used to calculate a range of characteristics of the lactation curve such as total milk yield, peak yield, day of peak yield, rate of increase in milk production in early lactation and persistency.

Total milk yield has been shown to be closely related to a single yield measure in lactation (Persaud and Simm, 1991) or, using the curves described above, to two measures of lactation (Maximum secretion potential and persistency; $r = 0.98$; Pollott, 2002). Also there is a close correlation between lactose and water secretion rate, and hence total milk secretion (due to the large proportion of TMY comprising water; 88% approx). Milk yield is commonly thought of as a single entity and the production of its components as separate selection criteria. However, looked at with the biological model described above, daily milk yield is the product of the number of active parenchyma cells and the secretion rates of the four major constituents outlined above (Model 2).

$$M_t = (\text{NDPC} - \text{NDCD}) \times (S_{Ft} + S_{Prt} + S_{Lt} + S_{Wt}) \quad [2] \text{ (Pollott, 2002)}$$

Water dominates the other three and is highly correlated with lactose production. Fat and protein secretion appear to be largely unrelated but fat and water secretion are highly negatively related (Pollott, 2002).

RESULTS AND DISCUSSION

How could this fresh look at milk production affect the way the production of milk and its components are considered? Traditional selection for milk yield alone may increase the number of cells, secretion rate of components, particularly water (the dilution effect of selecting for milk yield) or increase persistency (or a combination of these). It may be desirable to control this process more precisely. For example, in the case of very high yielding cows, increased persistency may be a more welfare-friendly way of increasing total milk yield than increasing cell numbers. Breeding for increased persistency may also relieve managers from the constant pressure to achieve 365-day calving intervals by having extended lactations. This approach may also have a beneficial effect on fertility since infertility problems are often linked to the very high daily yields in early lactation. A lower-flatter curve at the same total milk yield may be more desirable.

Where volume of output *per se* is important it may be economically more efficient to select for increased cell numbers and water content but limit fat and protein production. In situations where consumer demand is for high protein/low fat milk then selection objectives will look to increase protein secretion rates, limit fat secretion rate increases and maybe increase cell numbers. If payment is on protein percent then limiting water output may also be a target.

These ideas raise a number of important questions about measuring, recording and selecting for milk yield and its components. As Pollott (2000) points out, the separation of the number of active parenchyma cells from the secretion rate of individual cells is not possible under current milk recording regimes. This would require a means to estimate either the number of active parenchyma cells in a mammary gland or the secretion rate of the average active cell, or preferably both. This would be a key breakthrough that would allow a more precise method of selection in dairy breeding programmes. Developments in scanning technology could allow the operator to 'see' into the mammary gland and pick out active cells, the level of apoptosis or some other key indicator of mammary activity. Alternatively a humane and commercially applicable way of taking an udder biopsy in order to assess the level of secretory activity of cells in the udder would be useful. Either, or both these approaches could provide the necessary information to enable more precise selection schemes to be devised. An estimate of the number of active parenchyma cells would immediately allow Models 1 and 2 to be used, with commonly recorded information, to estimate more precise measures of what is happening during lactation to cell number and secretion rates.

Secondly is the monthly test-day record an absolute necessity? Certainly by measuring all lactating cows every month a good estimate of transitory environmental effects with which to adjust the data is obtained. There is additional spin-off in terms of management information available to the herd owner. However, much of the post-peak recording is not adding new information to selection decisions, over and above the 2 or 3 records needed to estimate persistency. It could be argued that current recording methods poorly estimate pre-peak characteristics of lactation and that there is more to be gained from a better knowledge of how a cow reaches peak yield, and the factors which affect it. In this case weekly records from parturition to peak may be more useful.

Thirdly, test-day methods are somewhat cumbersome for the amount of information that they produce. Using biologically-based lactation curves and the resulting characteristics of the lactation curve (Pollott, 2000) may simplify genetic evaluation procedures, provide more informative statistics about the lactations of the animals and allow the analysis of simple traits and their relationships. In addition, these new lactation curves could provide the herd manager with a range of other useful management information about the cow.

CONCLUSION

Biologically-based models of lactation have been used to assess the possibilities for improving milk recording and the genetic evaluation of dairy animals. New models provide a greater insight into what is happening to the dairy animal during lactation. They may also provide a more precise way of selecting for the varying selection objectives of different dairy industries. The development of new technology to estimate active secretory cell number, apoptosis or cell secretion rate will make these new methods even more precise and valuable as an aid to selection.

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