

## New Zealand Society of Animal Production online archive

This paper is from the New Zealand Society for Animal Production online archive. NZSAP holds a regular annual conference in June or July each year for the presentation of technical and applied topics in animal production. NZSAP plays an important role as a forum fostering research in all areas of animal production including production systems, nutrition, meat science, animal welfare, wool science, animal breeding and genetics.

An invitation is extended to all those involved in the field of animal production to apply for membership of the New Zealand Society of Animal Production at our website [www.nzsap.org.nz](http://www.nzsap.org.nz)

[View All Proceedings](#)

[Next Conference](#)

[Join NZSAP](#)

The New Zealand Society of Animal Production in publishing the conference proceedings is engaged in disseminating information, not rendering professional advice or services. The views expressed herein do not necessarily represent the views of the New Zealand Society of Animal Production and the New Zealand Society of Animal Production expressly disclaims any form of liability with respect to anything done or omitted to be done in reliance upon the contents of these proceedings.

This work is licensed under a [Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License](http://creativecommons.org/licenses/by-nc-nd/4.0/).



You are free to:

**Share**— copy and redistribute the material in any medium or format

Under the following terms:

**Attribution** — You must give [appropriate credit](#), provide a link to the license, and [indicate if changes were made](#). You may do so in any reasonable manner, but not in any way that suggests the licensor endorses you or your use.

**NonCommercial** — You may not use the material for [commercial purposes](#).

**NoDerivatives** — If you [remix, transform, or build upon](#) the material, you may not distribute the modified material.

<http://creativecommons.org.nz/licences/licences-explained/>

## Estimation of lactation yield from repeated measures of test day yields

D.L. JOHNSON

Livestock Improvement Corporation, Private Bag 3016, Hamilton, New Zealand.

### ABSTRACT

Test day production records were combined into a measure of lactation yield for the purposes of genetic evaluation of lactation production in dairy cattle. The lactation yield estimation adjusts for test day environment, standardises lactation length, takes account of culling and weights test day records according to number of tests, stage of lactation at test and intervals between tests. Any combination of tests can be used allowing for inclusion of records in progress or incomplete lactation in genetic evaluation.

**Keywords:** animal model; dairy; lactation yield; genetic evaluation.

### INTRODUCTION

Genetic evaluation of dairy sires and cows for milk production traits is normally based on lactation yield (LY) which is estimated from test day (TD) records. Prediction of breeding values for lactation production traits is a two step procedure - from TD records to LY phenotype and then to breeding value for complete lactation. Current genetic evaluation for lactation production traits in New Zealand is carried out by separate processes for sire and cow evaluations. Within each of these processes separate methods have evolved for the calculation of LY from individual TD records.

In sire evaluation the area under the lactation curve is approximated by the sum of areas of rectangles. Each rectangle is based on a TD with height equal to that TD yield and width of base extending both sides of the test to the midpoints of the intervals between this test and adjacent tests (to a maximum of 60 days on either side). The number of days to the left of the first test is the interval between day 4 after calving and first test, and the interval to the right of the last test is assumed to be 15 days. We note some limitations of this method:

- Since the maximum width either side of a test is 60 days, if a missing or abnormal test causes valid tests to be separated by more than 120 days, the excess of days over 120 is ignored leading to “holes” in the LY calculation.
- The LY is not adjusted for lactation length. Actual lactation length is unknown since drying-off dates are generally not recorded - the assumed lactation length is calculated from calving to 15 days after the last herd test. However variation in calving date is normally accounted for by a month of calving effect in the genetic evaluation model.
- No account is taken of the number of tests contributing to the LY calculation.
- No account is taken of the environment affecting individual test days - it is assumed to “average out” over the lactation.

- Cows must be at least 100 days in milk for this calculation.

For cow evaluation, TD yields are adjusted to a fixed stage of lactation using standard lactation curves, the curves allowing for differences in shape due to breed, age and month of calving. The adjusted TD yields are expressed relative to a contemporary group average and used to update breeding and production indexes assuming a repeatability model within and across lactations. Although this method takes account of TD environment, number of tests and lactation length, we note:

- No allowance is made for variation between cows in the shape of the lactation curve.
- TD yields, within a lactation, are assumed to be equally correlated regardless of the intervals between tests.

Livestock Improvement Corporation has recently reviewed the procedures for genetic evaluation of dairy cattle in New Zealand. An across-breed genetic evaluation system, using an animal model, will be implemented in 1996 to replace the existing sire and cow evaluation systems (Harris *et al.*, 1996). One feature of the animal model is that both genders are processed together necessitating a review of the dual procedures, currently operating in the sire and cow systems, for calculation of LY from TD records. This paper outlines the method of calculation to be used with the implementation of the animal model genetic evaluation system.

### METHODS

#### Model

The estimation of LY is carried out within herd x year x season x age contemporary groups, the same groups defined in the animal model (Harris *et al.*, 1996). Let  $y_{ik}$  denote the performance of cow  $k$  at test  $i$  for any of the three traits milk volume, fat and protein yields. Then  $y_{ik}$  has expectation  $\mu_{ik}$  which is assumed to be represented by a linear model on the log scale

$$\ln \mu_{ik} = m_i + a t_{ik} + b \ln t_{ik} \quad [1]$$

where  $m_i$  is a parameter reflecting the environment of test

$i, t_{ik}$  is the number of days in milk for cow  $k$  at test  $i$  and  $a$  and  $b$  are shape parameters. The functional form of equation [1] is essentially that of Wood (1967) with a different intercept corresponding to each test. The regression terms in  $t_{ik}$  take account of the variation in days in milk so that cows can be compared as if they were at the same stage of lactation.

**Variance Structure**

A cow’s production phenotype changes with stage of lactation and therefore can be represented as a function of time. The traditional way of analysing the quantitative genetics of such traits involves focusing on phenotypes (TD yields) at a small number of stages of lactation, essentially making discrete what is intrinsically a continuous process. A covariance matrix based on discrete traits can then be used to determine a covariance function which gives the covariance between any two stages of lactation.

Covariance matrices were derived from a study of data of 1000 randomly selected herds, from the New Zealand database, for each of 3 seasons 1990-1992 (Johnson, 1994, unpublished). Briefly, stage of lactation was divided into nine 30-day intervals with each stage treated as a different trait. Genetic and phenotypic parameters were estimated from the sire component of covariances using REML in a multi-trait model. A correlation function for which the phenotypic correlation depends only on the number of days between stages of lactation was an adequate fit to the covariance data. Thus the phenotypic correlation between TD yields at days  $t_1$  and  $t_2$  is assumed to be

$$r_p(t_1, t_2) = \tau (1 - \rho |t_1 - t_2|) \quad [2]$$

where  $\tau < 1$  and  $\rho > 0$  are constants depending on the trait.

We model the variance of TD records by assuming a constant coefficient of variation, independent of stage of lactation, and the function [2] to take account of repeated measures on the same cow. Generalised least squares (GLS) is used to estimate the parameters of model [1].

**Lactation Yield Estimation**

The objective is to find a function of TD records that has maximum correlation with LY and Best Linear Prediction (BLP; also known as selection index) is used for this purpose. The estimation of LY is then a linear combination of test day residuals, deviations of observed test day yields from their fitted values estimated using model [1], the index weighting factors being derived from the covariance structure of TD yields. LY is expressed as a deviation from the contemporary group average - it is unnecessary to add a constant to the prediction which would ultimately have no influence on genetic evaluations.

**Lactation Expansion Factors**

The predicted LY will have less genetic variance than a true LY, based on the accumulation of daily yields, because the predictions include a regression factor to allow for reduced accuracy. The variance of the prediction will depend on the number of tests available and stage of lactation at each test. In order to equate the genetic vari-

ance of predicted and true records, and make assumptions of the animal model and data agree, one can either expand the predicted record (VanRaden *et al.*, 1991) or modify the mixed model equations (Weller, 1988).

If  $Y$  denotes the true yield and  $P$  its prediction based on TD records then we consider a scalar  $x$  such that

$$E(x.P | Y) = Y$$

i.e. the true yield  $Y$  is the best predictor of the expanded record  $x.P$ . It follows that the theoretical expansion factor  $x$  is given by

$$x = \text{var } Y / \text{var } P = 1 / [\text{corr}(P, Y)]^2$$

which is the inverse squared correlation between predicted and true value.

It is assumed by using the expansion factor that both genetic and permanent environmental variance is stabilised. To compensate for this expansion, the temporary environmental variance is higher and so expanded records will receive less weight in the animal model. If  $r$  is the between lactation repeatability then the variance of  $Y$  can be decomposed as

$$\text{var } Y = r. \text{var } Y + (1-r). \text{var } Y$$

where the latter term represents temporary environmental variance. We also have

$$\text{var}(x.P) = x^2. \text{var } P = x. \text{var } Y = r. \text{var } Y + (x-r). \text{var } Y$$

so that the ratio of temporary environmental variance of true record to expanded record is the lactation weight

$$w = (1-r)/(x-r)$$

a number between 0 and 1, which is applied to each record in the animal model along with modification of design matrices to take account of the expansion (Harris, 1995).

Estimates of genetic variance used in the animal model will need to reflect that of the true yield  $Y$  and will therefore be higher than previous estimates based on the average of say ten TD records. The lactation weight will compensate for the higher heritability. Table 1 illustrates the (expanded) index weights to predict 270-day LY for milk volume using up to 4 tests as the season progresses. The last TD record receives the largest weight for part records. After 9 monthly tests all the index weights will be close to 30 with a lactation weight of about 0.86.

**TABLE 1:** Index weighting factors, and lactation weight, for estimation of 270-day milk volume based on 1 through 4 herd tests at 60 day intervals starting at day 20.

test	stage of lactation				lactation weight
	20	80	140	200	
1	224				.30
2	87	139			.49
3	55	75	107		.66
4	48	59	69	82	.75

**DISCUSSION**

We list the main features of the LY calculations.

- TD yields are adjusted for stage of lactation using data from the contemporary group itself. However for small contemporary groups, estimation of the shape parameters  $a$  and  $b$  will be less reliable and standard

shape parameters have been included as prior information by modifying the diagonal and right-hand side of the GLS estimating equations for model [1]. As contemporary group size increases, the influence of standard shape parameters decreases. By expressing TD yields as deviations from the contemporary group curve we are implicitly defining a lactation curve specific to each cow.

- We eliminate environmental effects that influence the production of all cows on a particular TD. This is important when combining TD yields for cows with different combinations of valid tests.
- Since any number of tests can be used to calculate LY, cows which for any reason have not completed their lactation will not be disadvantaged. This will eliminate need for the minimum 100 day rule in the current sire evaluation system.
- For the same reason as above, genetic evaluations can be carried out at any stage of the season.
- LY is based on a fixed length of lactation (270 days) which reduces variation due to calving date and drying-off date. Thus the decision of individual farmers to dry-off or milk-on does not influence genetic evaluations.
- The number of tests and intervals between tests influences the reliabilities of the genetic evaluations.
- Culling poor producing cows during the season has the effect of increasing the average production at subsequent tests which will in turn introduce a downward bias to contemporary group comparisons at these tests for cows remaining in the herd relative to tests prior to culling. The GLS estimation takes account of culling when estimating the parameters of the model [1].

One can also use actual expansion factors based on the ratio of genetic variances of actual and predicted records. The actual and theoretical expansion factors were mostly similar for this data set as was the case in the study of Pander and Hill (1993). Actual expansion factors have not been considered further at this stage - the theoretical expansion factors are readily available from the LY calculation and are intuitively appealing in their simplicity.

Further research should consider the variance structure of TD records. The assumption of constant coefficient of variation and the form of [2] may be better specified

using the smoothing technique of Kirkpatrick *et al.* (1994). A limitation of combining TD records into one measure of LY is that it does not allow for selection of specific characteristics of the lactation curve, such as persistency, or allow for a price premium for shoulder milk. Genetic correlations between different stages of lactation are less than unity and in fact decrease with increasing days between tests similar to phenotypic correlations. However about 90% of the genetic variation in lactation production is associated with simultaneous increases or decreases in production at all stages of lactation and so there are not strong trade-offs between early and late lactation (Kirkpatrick *et al.*, 1994). Modeling TD records, rather than LY, using random regressions to fit a separate lactation curve for each cow (Schaeffer and Dekkers, 1994) or a multivariate TD model using reduced rank genetic covariance matrices (Wiggans and Goddard, 1996) are areas of research requiring further investigation which may lead to future development of the New Zealand genetic evaluation system for dairy cattle.

## REFERENCES

- Harris, B.L.; Clark, J.M.; Jackson, R.G. 1996. Across breed evaluation of dairy cattle. *Proceedings of the New Zealand Society of Animal Production* **56**: 12-15.
- Harris, B.L. 1995. Animal evaluation methods for New Zealand dairy cattle. Livestock Improvement Corporation technical report.
- Kirkpatrick, M.; Hill, W.G.; Thompson, R. 1994. Estimating the covariance structure of traits during growth and ageing, illustrated with lactation in dairy cattle. *Genetical Research Cambridge* **64**: 57-69.
- Pander, B.L.; Hill, W.G. 1993. Genetic evaluation of lactation yield from test day records on incomplete lactation. *Livestock Production Science* **37**: 23-36.
- Schaeffer, L.R.; Dekkers, J.C.M. 1994. Random regressions in animal models for test-day production in dairy cattle. *Proceedings of the 5th World Congress on Genetics Applied to Livestock Production* **18**:443-446.
- Weller, J.I. 1988. Inclusion of partial lactations in the genetic analysis of yield traits by differential weighting of records. *Journal of Dairy Science* **71**: 1873-1879.
- VanRaden, P.M.; Wiggans, G.R.; Ernst, C.A. 1991. Expansion to projected lactation yield to stabilize genetic variance. *Journal of Dairy Science* **74**: 4344-4349.
- Wiggans, G.R.; Goddard, M.E. 1996. A computationally feasible test day model with separate first and later lactation genetic effects. *Proceedings of the New Zealand Society of Animal Production* **56**: 19-21.
- Wood, P.D.P. 1967. Algebraic model of the lactation curve in cattle. *Nature* **216**: 164-165.