

Animal Model for New Zealand Dairy Cattle Evaluation

Bevin L. Harris

Research Scientist, Livestock Improvement, Private Bag 3016, Hamilton, New Zealand

July 1994

1 Introduction

This paper reports on the animal evaluation project which is responsible for developing an appropriate animal evaluation system for use in New Zealand. Since the introduction of the current sire evaluation system *over 20 years ago* there have been a number of developments which together justify a thorough review of the entire system used for providing genetic evaluations of dairy cattle in New Zealand. A detailed description of the current sire evaluation system used in New Zealand is given by Wickham & Stitchbury (1980).

2 Animal Models for Production and Liveweight

The animal model used for production is a repeated records, single trait, additive genetic effects and simple repeatability model (Henderson 1988). The statistical model for analysis of a cow with production yields is:

(1)

$$y_{ijklmno} = hsa_i + \sum_{r=1}^{c_h} w_r h_r + m_j + d_k + ab_{lm} + \sum_{r=1}^{c_g} q_r g_r + a_n + p_n + e_{ijklmo}$$

where:

$y_{ijklmno}$ is production yield o adjusted to a constant phenotypic standard deviation for animal n in herd-season-age contemporary group i , calving in calendar month j , in induced lactation class k , age-at-calving l , and of breed m ;

hsa_i is the fixed effect for herd-season-age contemporary group i ;
 m_j is the fixed effect for month of calving j ;
 d_k is the fixed effect for induced lactation nested within age k ;
 w_r is the contribution of heterosis class r to animal n ;
 h_r is the fixed effect for heterosis r with c_h classes;
 ab_{lm} is the fixed effect for age-at-calving class l nested within breed class m ;
 q_r is the contribution of genetic group r to the genetic merit of animal n ;
 g_r is the fixed effect for genetic group r with c_g classes;
 a_n is the random additive genetic effect for animal n ;
 p_n is the random non-additive genetic and permanent environment effect for animal n ; and

$e_{ijklmno}$ is the random residual.

The herd-season-age classes are assigned as a nested classification of herd, defined as a herd number at a map location; age defined in years: 2, 3, 4, 5 to 8 and greater than 8 years; and season defined as spring and autumn calving periods within each year. Month of calving is defined as a calendar month of calving: 1 to 12. Induced lactation is defined as induced or not induced nested within age. Age at calving is defined in months at parturition, with class 1 being less than 22 months, then proceeding in monthly divisions up to class 90 which is older than 109 months. The age at calving effect is nested within breed where breed has five classes: Holstein-Friesian, Jersey, Ayrshire, Jersey-Holstein-Friesian cross and other breeds. Animals with greater than $\frac{12}{16}$ of their genes originating from one breed were classified as that breed for nesting the age at calving effect within breed.

The animal model used for liveweight trait is similar to that for the production model. The statistical model for analysis of a cow with liveweight records is:

(2)

$$y_{ijklmno} = hsa_i + \sum_{r=1}^{c_h} w_r h_r + s_{jk} + ab_{km} + \sum_{r=1}^{c_g} q_r g_r + a_n + p_n + e_{ijklmno}$$

where:

$y_{ijklmno}$ is liveweight record o for animal n in herd-season-age contemporary group i at stage of lactation class j , of age class k , and in age-at-calving class l and of breed m ;

s_{jk} is the fixed effect for stage of lactation j when the cow was weighed nested with age class k ;

other effects defined as for Eqn[1].

The herd-season-age classes and age at calving are assigned as for the production animal model. Stage of lactation classes are defined in 10 day intervals from the date of calving to the date of weighing. Stage of lactation is nested within age to account for different growth curves for younger cows compared to mature cows.

2.1 Genetic Grouping

A grouping strategy developed by Robinson (1986), Westell (1984) and Westell, Quaas & VanVleck (1988) based on a proposal by Thompson (1979) in which a genetic group for each animal is derived from the genetic group effect of the animal's ancestors is used in the model. The mixed model equations are transformed with the QP transformation (Quaas & Pollack 1981) to solve for additive genetic merit directly. Procedures developed by Westell & VanVleck (1987) and Westell et al. (1988) enable the elements of numerator relationship matrix including genetic groups (D) to be computed directly using rules similar to those for computing the elements of the inverse of the numerator relationship matrix (Henderson 1975). In a multibreed animal model genetic groups are assigned by breed. In the case of an animal who is 3/4 breed A and 1/4 breed B with a known pure breed parent the phantom parent would be a 1/2A $\times$ 1/2B crossbred. Thus, the animal would be assigned to both the genetic groups for A and B with values of 1/2 for the unknown parent. The rules for forming D were modified for the multibreed situation. Genetic groups are assigned by the number of breeds present in the unknown parent, year of birth and country of origin.

2.2 Heterosis effects

Each animal can have up to four breed codes and the proportions of the genes from each of the four breeds are stored on database. Five breeds classes have been assigned to the New Zealand population:

1. Holstein Friesian
2. Jersey
3. Ayrshire
4. Non Ayrshire European Red breeds
5. Other breeds (beef breeds)

The coefficients for heterosis can be computed for specific crossbreeding designs (Dickerson 1973, Koch, Dickerson, Cundiff & Gregory 1985, Ahlborn-Brier & Hokenboken 1991, Panicke & Freyer 1992) or more generally for the heterosis coefficient for breed $i \times j$ as:

$$(3) \quad \text{het}_{i \times j} = [\mathbf{ps} \cdot \mathbf{pd}']_{ij} + [\mathbf{ps} \cdot \mathbf{pd}']_{ji}$$

where $\mathbf{ps}(\mathbf{pd})$ is the vector containing the percent of genes of each of the five breeds present in the sire (dam). The total heterozygosity for an individual is $(1 - \mathbf{ps}' \cdot \mathbf{pd})$ (VanRaden 1992). Assigning different heterosis coefficients for different breed combinations avoids the assumption that the genetic distances between breeds are the same.

2.3 Heterogeneous Variance Adjustment: Production Traits

The models for genetic evaluation (Eqn[1]) assume homogeneous variances across levels of fixed and random effects. However, there is substantial evidence for heterogeneity of variance across herds and herd-years (Hill, Edwards, Ahmed & Thompson 1983, Brotherstone & Hill 1986, Boldman & Freeman 1990). At present the production yields are standardised to a common phenotypic standard deviation across seasons by adjusting with a weighted combination of the herd-season-age phenotypic standard deviation and the population herd-season-age phenotypic standard deviation to avoid sampling error (Brotherstone & Hill 1986). The weighted combination standard deviation has weights directly proportional to the variances of herd-age-season standard deviation and population season-age standard deviation. Limits are imposed on the value of the weighted combination standard deviation using a 99% confidence range on the average herd-season-age phenotypic standard deviation.

Table 1: Data Description.

Trait	Mean (kg)	Number	SD
Milk Fat	154.2	10,993,084	30.4
Milk Volume	3265.9	10,993,084	674.9
Milk Protein	118.8	10,993,084	23.4
Liveweight	386.7	236,951	124.1

2.4 Computational Strategy

The mixed model equations are solved iteratively with the groups being solved as one block and each cow having the solutions for $\mathbf{a}$ and $\mathbf{p}$ solved simultaneously. Solutions were obtained by iterating on data (Schaeffer & Kennedy 1986, Misztal & Gianola 1988). Computing the initial fixed effect estimates and the diagonal elements of $\mathbf{MME}$ for parents and genetic groups requires reading the data file twice. The diagonal elements of $\mathbf{MME}$ for parents and genetic groups and the diagonal and right-hand-side elements for the fixed effects are stored in random access memory. After initial preparation the data file is read once for each iteration. The animal genetic merit and permanent environment are solved simultaneously. This method does not require prior estimates of the animal genetic merit solutions, thus animal genetic merit solutions for non-parents are not required to be stored in memory thereby reducing memory requirements.

3 Preliminary Results

The data for the animal models are described in Table 1. The yield data are from the years 1986 to 1994 and represent 5.9 million animals (including ancestors and young animals). The majority of cows calve in the months July to October to coincide with the onset of spring grass growth. A minority of the cows calve in March to May to supply the fluid milk industry. In New Zealand cows can have the lactation induced — that is the pregnancy is terminated up to 4 weeks before planned calving date. In the data 4.5% of the lactations were induced. Fifty-five percent of the lactations are from Holstein cows, 24% from Jersey cows, 18% from Holstein-Jersey crossbred cows and 2% from Ayrshire cows. There were 354,934 contemporary groups for the production traits with an average of 29.9 lactations

Table 2: Trait averages by breed (kg).

Breed	Fat	Protein	Volume	Liveweight
Holstein	156.8	123.0	3547.6	429.0
Jersey	152.4	110.7	2672.8	326.6
Ayrshire	147.8	122.2	3394.2	363.2
Holstein-Jersey Crosses	159.1	120.5	3244.0	387.0

per contemporary group. There were 8,198 contemporary groups for the liveweight with an average of 28.8 weights per contemporary group. The trait averages by breed are given in Table 2.

The heterosis estimates for the four traits from the animal model are given in Table 3. The estimates of heterosis in the production traits for Holstein-Jersey crosses are in agreement with prior estimates reported by Ahlborn-Brier & Hokenboken (1991). The breeding values for all traits were adjusted to a genetic base (mean breeding value of zero) consisting of cows born in 1985 with all traits measured. The means, ranges and standard deviations of the breeding values for sires born in 1988 and 1989 with at least 20 daughters for the four traits are given Table 4. The breeding values from the animal model give an estimate of the genetic distances between the breeds. The genetic distances between the different breeds are consistent with the average production averages in Table 2. The separation of the breeds is clearly seen in Figures 1 and 2 which show the distributions of the sire breeding values for 3 major breeds for protein yield and liveweight respectively. The distributions of the protein breeding values for Holstien and Jersey breeds and the Holstein-Jersey crossbred cows are shown in Figure 3 for 150 randomly selected herds which are milk recording in 1993/94. The mean breeding value of the Holstein-Jersey crossbred cows is 7.0 (kg) which is close the mid-point between the Holstein and Jersey means, 15.1 (kg) and -1.9 (kg) respectively.

Estimates of genetic trend were calculated from the average breeding values of sires with at least 20 daughters born from 1984 to 1989 by breed. Using sires born from 1984 to 1989 ensures that they have daughters with first lactation data in the animal model analysis. The estimates of genetic trend are given in Table 5 and the average breeding values for Jersey sires by birth year is illustrated in Figure 4 for protein yield.

The Jerseys appear inferior to Holsteins in terms of per cow milk pro-

Table 3: Heterosis estimates (kg).

Breed	H×J	H×A	A×J
Fat	8.2	3.4	10.9
Protein	6.4	3.3	8.3
Volume	137.8	90.2	201.3
Liveweight	0.8	0.0	1.5

duction. However, because of the pasture based farm systems in New Zealand where net farm income is related to production per hectare of land, the Jersey and Holstein herds are comparable on a net income basis since the Jersey herds have higher stocking rates (cows per hectare). The *genetic worth* index accounts for the effects of liveweight as well as milk production on net farm income to rank animals economically across breeds. Figure 5 illustrates the range in genetic worth values for sires with at least 20 daughters born in 1988/89 by breed. The average genetic worth of the sires likely to have widespread usage in the population of the Holstein and Jersey breeds are very close.

Table 4: Summary statistics for breeding values of sires born in 1988-89 with at least 20 daughters (kg).

		Fat			
Breed	N	Mean	SD	Max	Min
All Breeds	498	11.4	12.1	47.8	-34.0
Holstein	295	16.9	10.2	47.8	-18.6
Jersey	171	2.5	9.4	24.6	-34.0
Ayrshire	29	9.6	11.8	36.8	-13.0
		Protein			
Breed	N	Mean	SD	Max	Min
All Breeds	498	7.3	12.5	44.7	-30.4
Holstein	295	14.5	8.8	44.7	-20.5
Jersey	171	-5.3	7.7	17.5	-30.4
Ayrshire	29	8.2	8.4	29.0	-7.2
		Volume			
Breed	N	Mean	SD	Max	Min
All Breeds	498	219.1	512.9	1421.1	-1119.8
Holstein	295	553.8	282.3	1421.1	-300.8
Jersey	171	-371.4	263.3	446.3	-1119.8
Ayrshire	29	309.8	281.1	997.0	-326.4
		Liveweight			
Breed	N	Mean	SD	Max	Min
All Breeds	498	6.4	42.3	108.2	-74.6
Holstein	295	37.1	20.3	108.2	-19.5
Jersey	171	-44.9	12.4	-9.29	-74.6
Ayrshire	29	-2.3	19.6	31.4	-50.8

Table 5: Genetic trend estimates from sires born in 1984-89 with at least 20 daughters.

	Fat	Protein	Volume	Lwt
Breed	kg/yr	kg/yr	l/yr	kg/yr
Holstein	1.70	1.07	32.0	1.49
Jersey	3.15	1.70	36.3	0.23
Ayrshire	2.56	0.81	30.1	0.08

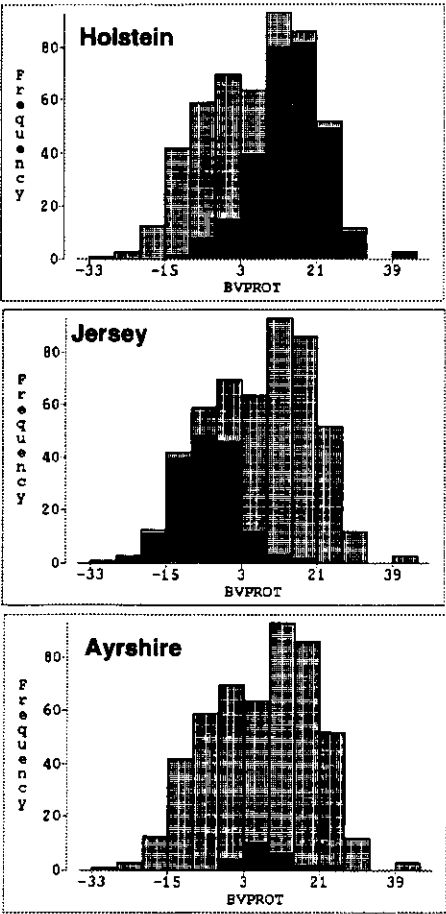


Figure 1: Distribution of protein breeding values from sires born in 1988/89 with at least 20 daughters. Dark area is distribution for that breed.

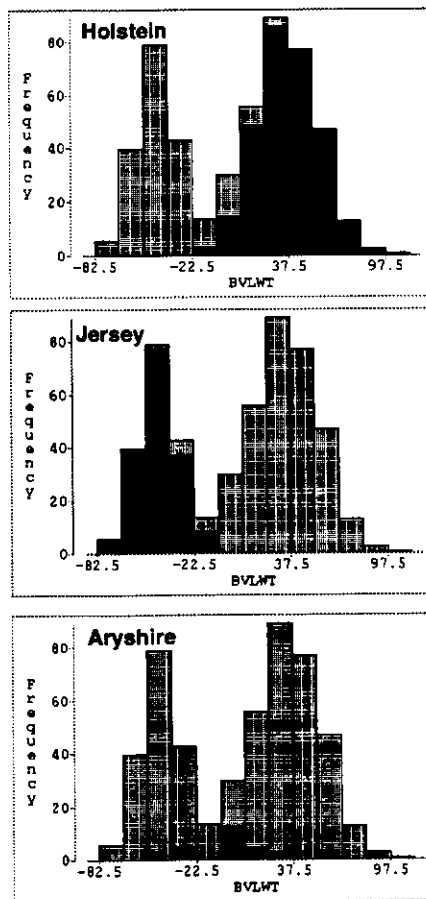


Figure 2: Distribution of liveweight breeding values from sires born in 1988/89 with at least 20 daughters. Dark area is distribution for that breed.

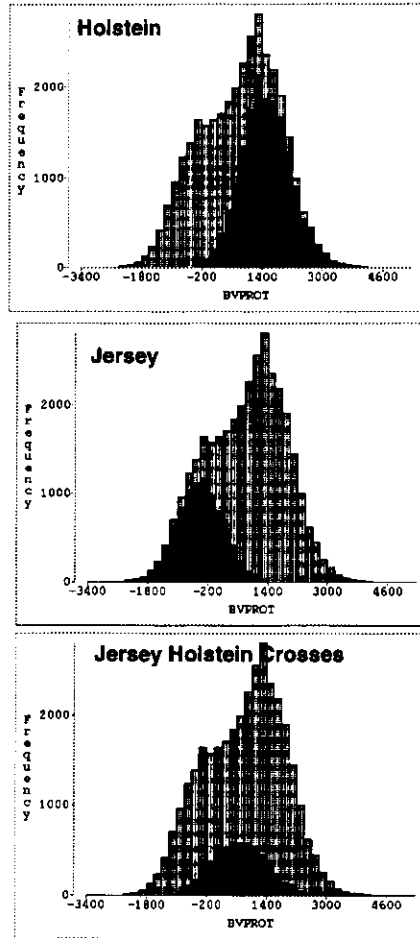


Figure 3: Distribution of protein breeding values for cows from 150 randomly chosen herds. Dark area is distribution for that breed (scale is $BV \times 100$ (kg)).

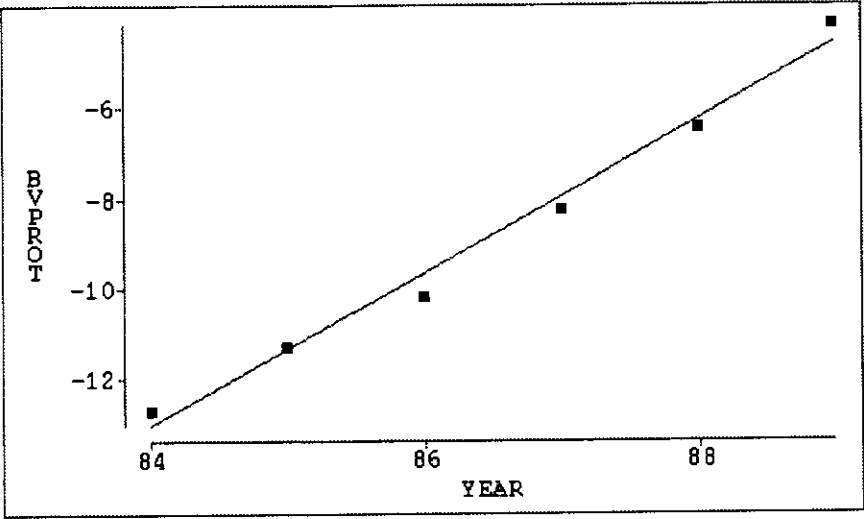


Figure 4: The average breeding values of jersey sires with at least 20 daughters born from 1984 to 1989 (kg).

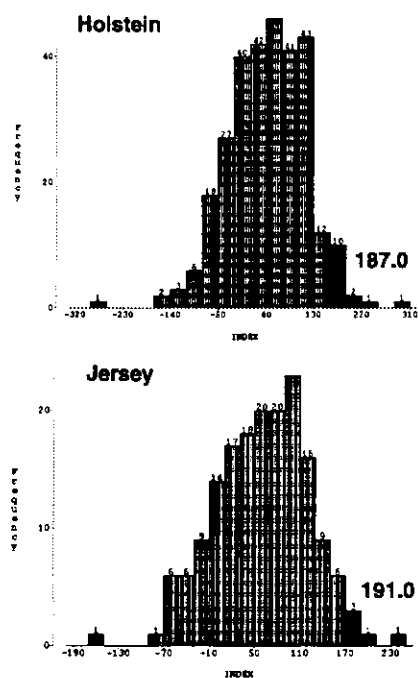


Figure 5: Distribution of genetic worth economic index for sires with at least 20 daughters born in 1988/89 (kg). Dark area indicates the sires likely to be used heavily with the mean of the group above.

References

- Ahlborn-Brier, G. & Hokenboken, W. D. (1991), 'Additive and non-additive genetic effects on milk production in dairy cattle: Evidence for major heterosis', *J. Dairy Sci.* **74**, 592–602.
- Boldman, K. G. & Freeman, A. E. (1990), 'Adjustment for heterogeneity of variances by herd production level in dairy cow and sire evaluation', *J. Dairy Sci.* **73**, 503–512.
- Brotherstone, S. & Hill, W. G. (1986), 'Heterogeneity of variances amongst herds for milk production', *Anim. Prod.* **42**, 297–303.
- Dickerson, G. E. (1973), Inbreeding and heterosis in animals, in 'Animal breeding and genetics symposium in honor of Dr. J. L. Lush', American Society of Animal Science, Champaign, Illinois, USA, pp. 54–77.
- Henderson, C. R. (1973), Sire evaluation and genetic trends, in 'Animal breeding and genetics symposium in honor of Dr. J. L. Lush', American Society of Animal Science, Champaign, Illinois, pp. 10–41.
- Henderson, C. R. (1975), 'Best linear unbiased estimation and prediction under a selection model', *Biometrics* **31**, 423–447.
- Henderson, C. R. (1988), 'Theoretical basis and computational methods for a number of different animal models', *J. Dairy Sci.* **71** (Supplement 2), 1–17.
- Hill, W. G., Edwards, M. R., Ahmed, M. K. & Thompson, R. (1983), 'Heritability of milk yield and composition at different production levels and variability of production', *Anim. Prod.* **36**, 59–68.
- Jones, L. P. & Goddard, M. E. (1990), Five years experience with the animal model for dairy cattle evaluations in Australia, in 'Fourth World Congress on Genetics Applied to Livestock Production Volume XIII', Edinburgh, U.K., pp. 382–385.
- Koch, R. M., Dickerson, G. E., Cundiff, L. V. & Gregory, K. E. (1985), 'Heterosis retained in advance generations of crosses among Angus and Hereford', *J. Anim. Sci.* **60**, 1117–1132.
- Misztal, I. & Gianola, D. (1988), Indirect solutions of mixed model equations, in G. H. Schmidt, ed., 'The animal model workshop', American Dairy Science Association, Champaign, Illinois, pp. 99–106.

- Panicke, L. & Freyer, G. (1992), 'Heterosis estimation for production traits in dairy cattle', *Arch. Tierz.* **35**, 537–549.
- Quaas, R. L. & Pollack, E. J. (1981), 'Modified equations for the sire model with groups', *J. Dairy Sci.* **64**, 1503–1509.
- Robinson, G. K. (1986), 'Group effects and the computing strategies for models for estimating breeding values', *J. Dairy Sci.* **69**, 3106–3112.
- Schaeffer, L. R. & Kennedy, B. W. (1986), 'Computing strategies for solving mixed model equations', *J. Dairy Sci.* **71**, 338–342.
- Thompson, R. (1979), 'Sire evaluation', *Biometrics* **35**, 339–345.
- VanRaden, P. M. (1992), 'Accounting for inbreeding and crossbreeding in genetic evaluations of large populations', *J. Dairy Sci.* **75**, 3136–3144.
- Visscher, P. M. & Hill, W. G. (1992), 'Heterogeneity of variance and dairy cattle breeding', *Anim. Prod.* **55**, 321–329.
- Weigel, K. A. & Gianola, D. (1993), 'Computationally simple Bayesian method for estimation of heterogeneous within-herd phenotypic variances', *J. Dairy Sci.* **76**, 1455–1465.
- Westell, R. A. (1984), Simultaneous evaluation of sires and cows for a large population of dairy cattle, PhD thesis, Cornell University, Ithaca, New York, USA.
- Westell, R. A., Quaas, R. L. & VanVleck, L. D. (1988), 'Genetic groups in an animal model', *J. Dairy Sci.* **71**, 1310–1318.
- Westell, R. A. & VanVleck, L. D. (1987), 'Simultaneous evaluation of sires and cows for a large population of dairy cattle', *J. Dairy Sci.* **70**, 1006–1012.
- Wickham, B. W. & Stitchbury, J. W. (1980), Cow and sire evaluation in New Zealand, Technical report, Farm Production Division, New Zealand Dairy Board, Private Bag 3016, Hamilton, New Zealand.
- Wiggans, G. R., Misztal, I. & VanVleck, L. D. (1988), 'Implementation of animal model for genetic evaluations of dairy cattle in United States', *J. Dairy Sci.* **71**, 54–69.
- Wiggans, G. R. & VanRaden, P. M. (1992), 'Method and effect of adjustment for heterogeneous variance', *J. Dairy Sci.* **75**, 54–69.