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## Test-day model for national genetic evaluation of milk production traits

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### ABSTRACT

Genetic evaluation for milk, fat and protein yields, using 270-day lactation yields in an across-breed animal model (AM), has been performed in New Zealand since 1996. A new system has been developed to calculate breeding values from herd-test data. In the current AM, a 270-day lactation yield record is calculated based on 1 to 10 test-day records. The environmental effect of herd-test-day (HTD) is removed during the 270-day lactation yield calculation. However, this is done outside the AM, without reference to the genetic level of the HTD contemporary group. A test-day model (TDM) can simultaneously account for the fixed effects such as HTD contemporary groups, and the genetic, permanent environmental (PE) and temporary environmental random effects that affect the trait. By including the effect in the model, the TDM allows the environment specific to each test-day to be better taken into account, resulting in an improved accuracy of evaluation. A TDM can accommodate changes in the genetic and PE effects over time by fitting polynomials of time to these effects. A random regression (RR) TDM can accommodate changes in the genetic and PE effects over time by fitting Legendre polynomials of days in milk (DIM) to these random effects. The RR TDM allows each cow's lactation curve to have a different shape. TDM evaluations are more stable than evaluations obtained using 270-day lactations because they account for genetic differences in maturity rate and persistency of lactation. The sire breeding values (BVs) from the TDM were compared to those from the AM. For sires with more than 30 daughters, the correlations between the BVs from the two models were 0.990, 0.988 and 0.990 for milk, fat and protein yields, respectively. The TDM demonstrated improved stability for sires undergoing their widespread proof. There was less variation in the change in BVs for reproof sires from August through to October compared to the AM. The sires that show the greatest change during early reproof under the AM were sires that were outliers for their TDM persistency breeding values for their breed.

**Keywords:** milk production; genetic evaluation; test-day model; dairy cows.

### INTRODUCTION

The New Zealand (NZ) dairy industry is based on a pastoral system where the majority of cows calve in July and August so that peak milk production coincides with peak grass growth. Each "year", which starts in June and finishes in May, is referred to by the calendar year pertaining to the months June through December within the "year". However, year-round milk supply is accomplished by herds calving in the autumn, thus creating the spring and autumn calving seasons. In herds that calve in July and August, cows are generally dried off in April so that 270 days is considered to be the standard lactation length in NZ (Dairy Statistics, LIC 2006).

At Livestock Improvement, young sires are first proven based on the records of their two-year-old daughters in Sire Proving Scheme (SPS) herds. Estimation of genetic parameters is done using SPS herds because they are considered an unselected population. Herd testing for yield traits and somatic cell count (SCC) is generally done bimonthly in NZ herds so that most cows are tested between three to four times per lactation.

The current evaluation of milk, fat and protein yields involves combining herd test results to predict a 270-day yield deviation, corrected for test-day effects. These yield deviations are then used as the records for genetic evaluation. Currently, the system for genetic evaluation in NZ uses a single-trait repeatability animal model (AM), where production in different lactations is treated as repeated records of the same trait. This system was implemented in 1996 and is described by Harris *et al.*, (1996). The NZ dairy population contains primarily Friesian and Jersey cows, and unlike other countries, a substantial proportion of crosses between these breeds. To accommodate the crossbred cows and to allow across-breed comparisons, the animal model is a multiple-breed model where breed effects are modelled using genetic groups and the different breed heterozygosities are included as fixed covariates in the model. Genetic evaluations are run at three-weekly intervals.

Many countries have implemented, or are moving towards, test-day models (TDMs) for genetic evaluation of herd test data (de Roos *et al.*, 2003; Liu *et al.*, 2003; Schaeffer *et al.*, 2000). We

have recently developed a system to calculate SCC breeding values (BVs) for the dairy industry using a random regression (RR) TDM. The next phase in the development of our genetic evaluation system is to use RR TDM for the genetic evaluation of milk, fat and protein yields. The RR TDMs that have been developed contain similar fixed effects, and use the same genetic grouping strategy, as are used currently for the repeatability models. However, the record for evaluation and the variance structures associated with the random effects are the key differences to the current system. In the current system, yield deviations from different lactations are treated as repeated records of the same trait. Hence, the same variance structure is imposed across all lactations. However, a cow's production is not likely to be the same trait genetically within or across lactation. Similarly, the environmental and non-additive genetic effects peculiar to each cow are likely to differ within and across the lactation. RR TD models, where Legendre polynomials (LP) of days in milk (DIM) are fitted to the animal and cow effects, can be used to model heterogeneity of variance of the genetic and permanent environmental (PE) effects. In a single-lactation RR model, a covariance matrix is fitted to each random effect. In multiple-lactation RR models, heterogeneity of variance of the random effect within and between lactations is accounted for by fitting the covariance matrix across the lactations.

The objectives of this study were to undertake the calculation of genetic parameters needed as inputs for the RR TDM, to develop computationally feasible strategies used to solve the resulting system of equations used for the national genetic evaluations, and to compare the results of the RR TDMs with those of the current genetic evaluation system.

## MATERIALS AND METHODS

### Genetic Parameter Estimation

Data for the analyses were obtained from cows that had their first lactation in Livestock Improvement's SPS herds in years 1995 to 2004. Where available, data from subsequent lactations of these cows, up to lactation six were included in the analyses. A total of 165,871 cows had first lactation records. These cows were the progeny of 2427 sires. The first-lactation cows had an average of 3.8 herd tests per cow. The breed composition of the first-lactation cows was 1% Ayrshires, 57% Holstein-Friesians, 22% Jerseys, and 20% crosses of these breeds. Two types of RR TDMs were examined to estimate covariance structures needed for the national evaluation. The first model was a

full RR model (RRF) where the covariance matrices for the sire and PE effects were fitted across all the lactations of interest, thus allowing complete generality of variance across the lactations. The second model was a RR correlation model (RRC) in which the same covariance structure was used across all lactations, but was modified by a factor to accommodate scale changes from one lactation to the next. This model assumed a constant correlation (genetic or PE) between lactations. A heterogeneous temporary environmental variance was fitted in both models by weighting each record according to the estimated error function obtained using the method of Kirkpatrick *et al.*, (1990). ASREML (Gilmour *et al.*, 2001) was used to estimate the covariance matrices for the two types of RR models.

### National Data

Individual herd test production records were extracted from the NZ national database. The extract was done in December 2006 and included all herd test milk records from 1987 onwards. The data included herd test date (HTD) and an indicator to identify herd test records from cows with induced lactations. Contemporary groups were defined on a test-day-parity-herd-season-year basis. Season was defined as spring or autumn calving. Pedigree, birth dates and breed data were extracted from the Animal Evaluation routine genetic evaluations for production. Ancestors were traced back to 1939. Animals born before 1960 were considered to be the base population. Birth date and herd test date data allowed the calculation of stage of lactation (DIM) for each herd test record. Breed and pedigree data allowed the calculation of average heterosis regression coefficients for each cow with production records for 4 different breed categories; Holstein-Friesian, Jersey, Ayrshire and other breeds, required for an across breed genetic evaluation.

### Statistical Model for National Genetic Evaluation

The model for the national genetic evaluation of milk, fat and protein yields was a multiple-lactation (ML) RR TDM where lactations 1, 2 and 3 are modelled as individual lactations and lactations 4, 5 and 6 together are modelled as one lactation under the same genetic control since the genetic correlations among these lactations were essentially one. Each lactation (1-6) is considered a different trait for modelling the permanent environmental effect.

A production TD yield measured on day of lactation,  $d$ , was modelled as:

$$y_{ijklmno} = htd_{ij} + age_{in} + ind_{im} + type_{il} + \sum_{s=1}^6 ht_{is} w_{ns}^h + \sum_{t=2}^5 \Phi_t(d) s_{it} + \sum_{t=1}^3 \Phi_t(d) a_{in} + \sum_{t=1}^3 \Phi_t(d) p_{i'n} + e_{ijklmno}$$

where:

- $y_{ijklmno}$  is the TD observation of milk volume, fat yield or protein yield,
- $i$  denotes lactation (1-4),
- $htd_{ij}$  is the  $j$ th herd-year-season-TD fixed effect for lactation  $i$ , with season referring to spring or autumn calving period,
- $age_{in}$  is the age at calving covariate, in days, for animal  $n$  nested within breed for lactation  $i$ ,
- $ind_{im}$  is the  $m$ th induced lactation fixed effect class for lactation  $i$  with induced classes representing induced or not induced lactation,
- $type_{il}$  is the  $l$ th record type fixed effect class for lactation  $i$  with type classes representing AM+PM, AM only, PM only or once-a-day milking TD record,,
- $ht_{is}$  is the linear regression coefficient for the  $s$ th heterosis effect for trait  $i$ ,
- $w_{ns}^h$  is the  $s$ th heterosis covariate for animal  $n$ ,
- $\Phi_t(d)$  is the standardised Legendre polynomial of order  $t$  calculated at days in milk  $d$ ,
- $s_{it}$  is the stage of lactation fixed effect for days in milk  $d$  of lactation  $i$  and order  $t$ ,
- $a_{in}$  is the random additive genetic effect of animal  $n$  for lactation  $i$ ,
- $p_{i'n}$  is the random non-additive genetic and permanent environment effect of animal  $n$  for lactation  $i'$  where  $i'$  denotes lactation number 1 to 6, and
- $e_{ijklmno}$  is the random residual associated with record  $y_{ijklmno}$

Heterosis factors were fitted to account for the effects of crossbreeding. Different factors were fitted by breed combination to account for different genetic distances among the major breeds. Genetic groups were assigned by breed, gender of missing parent, birth year and country of origin. Four breed classes were assigned genetic grouping, namely, Holstein-Friesian, Jersey, Ayrshire-Red, and other breeds. Genetic groups were assigned in 5-year intervals from 1960 to 1980 then yearly, with the first birth year group being prior to 1960. Country of origin was defined as NZ, North American and other. Gender of missing parent was defined as female or male. If a genetic group had less than 200 animals per group birth years were clustered. No clustering occurred across breed, origin or gender of parents genetic groups. The mixed model equations were solved using a preconditioned conjugate gradient solver (Stranden & Lidauer, 1999) and iteration on data with code reordering (Tsuruta *et al.*, 2001). For the national evaluation of the production traits, the convergence criteria for the model equations was  $<10^{-10}$ . The initial solution vector was populated with the solutions from previous runs to speed convergence.

## RESULTS AND DISCUSSION

A comparison of the results from RRF and RRC models was undertaken using the SPS data for lactations 1 to 3. An RRF analysis of lactations 1 to 6 was not computationally feasible. The results obtained by the RRF and RRC models were not identical. RRF model accommodates differences in the shape of the lactation curve from one lactation to another, whereas, the RRC model does not. However, the general shapes of the within-lactation curves from the models were similar and the differences between the estimated variances were small. As the number of traits, and hence number of parameters that need to be estimated increases, the problems in maximising the likelihood results in either poor or no estimates in the RRF model. The RRC model is a compromise but a practical one in which estimates can be obtained for greater than three lactations. For this reason, estimated (co)variance parameters from the RRC model were used for the national genetic evaluation. Table 1 provides the heritabilities and the genetic and phenotypic correlations between the four lactations for milk, fat and protein yields. The heritabilities are consistent with those reported by Harris *et al.*, (1996). The magnitudes of the heritabilities and genetic correlations are consistent with values reported in other countries (De Roos *et al.*, 2003; Lidauer *et al.*, 2003).

**Table 1:** Heritabilities (diagonal), genetic (below diagonal) and phenotypic (above diagonal) correlations lactations for milk volume, fat yield and protein yield calculated from the random regression correlation model.

Milk Yield				
Lactation	1	2	3	4
1	0.361	0.758	0.721	0.678
2	0.917	0.358	0.815	0.771
3	0.905	0.983	0.361	0.836
4	0.864	0.959	0.984	0.353
Fat Yield				
Lactation	1	2	3	4
1	0.336	0.756	0.700	0.656
2	0.921	0.327	0.801	0.751
3	0.900	0.983	0.325	0.820
4	0.859	0.956	0.984	0.317
Protein Yield				
Lactation	1	2	3	4
1	0.308	0.747	0.689	0.639
2	0.904	0.306	0.803	0.747
3	0.893	0.976	0.306	0.827
4	0.846	0.945	0.982	0.304

**Table 2:** Summary statistics for the national herd test data by lactation and breed of cow.

<b>Lactation 1</b>						
<b>Breed</b>	<b>Cows(n)</b>	<b>Herd tests</b>	<b>Herd tests/cow</b>	<b>Milk Volume (L/day)</b>	<b>Fat Yield (kg/day)</b>	<b>Protein Yield (kg/day)</b>
Holstein Friesian	4,467,083	15,323,898	3.43	13.81	0.60	0.48
Jersey	1,462,301	5,244,125	3.59	10.14	0.58	0.41
Ayrshire	117,961	474,634	4.02	12.25	0.54	0.44
HFxJ Cross	2,757,140	9,034,632	3.28	12.83	0.63	0.47
Other	386,239	1,285,559	3.33	12.50	0.59	0.46
<b>Lactation 2</b>						
<b>Breed</b>	<b>Cows(n)</b>	<b>Herd tests</b>	<b>Herd tests/cow</b>	<b>Milk Volume (L/day)</b>	<b>Fat Yield (kg/day)</b>	<b>Protein Yield (kg/day)</b>
Holstein Friesian	3,704,550	12,923,039	3.49	16.12	0.71	0.56
Jersey	1,264,199	4,559,076	3.61	11.58	0.67	0.48
Ayrshire	99,502	401,944	4.04	14.19	0.62	0.51
HFxJ Cross	2,226,128	7,390,238	3.32	14.94	0.74	0.56
Other	305,697	1,026,459	3.36	14.55	0.69	0.54
<b>Lactation 3</b>						
<b>Breed</b>	<b>Cows(n)</b>	<b>Herd tests</b>	<b>Herd tests/cow</b>	<b>Milk Volume (L/day)</b>	<b>Fat Yield (kg/day)</b>	<b>Protein Yield (kg/day)</b>
Holstein Friesian	3,227,586	11,247,396	3.48	17.69	0.78	0.62
Jersey	1,120,629	4,029,004	3.60	12.54	0.73	0.52
Ayrshire	85,988	345,908	4.02	15.63	0.69	0.56
HFxJ Cross	1,858,796	6,165,826	3.32	16.31	0.81	0.61
Other	250,329	839,663	3.35	15.98	0.76	0.59
<b>Lactations 4-6</b>						
<b>Breed</b>	<b>Cows(n)</b>	<b>Herd tests</b>	<b>Herd tests/cow</b>	<b>Milk Volume (L/day)</b>	<b>Fat Yield (kg/day)</b>	<b>Protein Yield (kg/day)</b>
Holstein Friesian	3,503,337	24,488,123	6.99	18.44	0.81	0.64
Jersey	1,227,221	8,861,750	7.22	12.98	0.75	0.54
Ayrshire	94,511	752,609	7.96	16.50	0.72	0.60
HFxJ Cross	1,809,006	12,392,623	6.85	16.96	0.83	0.64
Other	240,660	1,635,553	6.80	16.73	0.79	0.62

**Table 3:** Summary statistics for milk volume, fat yield and protein yield sire breeding values for sires with at least 30 herd tested daughters.

	<b>Milk Volume (L)</b>				
	<b>Number</b>	<b>Mean</b>	<b>Standard Deviation</b>	<b>Minimum</b>	<b>Maximum</b>
All Breeds	9582	508	698	-1409	2152
Holstein-Friesian	5419	999	379	-371	2152
Jersey	765	-327	348	-1409	707
Ayrshire	765	390	311	-532	1227
Other Breeds	234	5	328	-238	261
	<b>Fat Yield (kg)</b>				
	<b>Number</b>	<b>Mean</b>	<b>Standard Deviation</b>	<b>Minimum</b>	<b>Maximum</b>
All Breeds	9582	15.3	17.9	-65.9	67.9
Holstein-Friesian	5419	22.4	14.0	-26.8	68.0
Jersey	7484	6.8	17.5	-50.2	57.0
Ayrshire	765	1.3	14.1	-34.3	44.1
Other Breeds	234	-12.0	16.0	-65.9	29.0
	<b>Protein Yield (kg)</b>				
	<b>Number</b>	<b>Mean</b>	<b>Standard Deviation</b>	<b>Minimum</b>	<b>Maximum</b>
All Breeds	9582	16.8	17.3	-40.0	67.2
Holstein-Friesian	5419	27.1	12.5	-16.2	67.2
Jersey	7484	-0.1	11.7	-40.0	37.2
Ayrshire	765	11.0	9.9	38.6	-15.9
Other Breeds	234	1.5	10.0	-23.8	26.1

The average milk, fat and protein TD yields across parities 1 to 6 based on 128,422,059 herd test records from 9,190,724 cows were 14.6(l), 0.70(kg) and 0.54(kg) respectively. The summary statistics for the national data by lactation number and breed of cow are given in Table 2.

The BV from the TDM is calculated as the simple average of the four 270-day lactation (from 3 to 270 DIM) BVs. Table 3 provides within and across breed summary statistics for sires. The sire BVs from the RR TDM were compared with those from the national repeatability AM run done on the 20th December 2006. A comparison among sires that have at least 30 herd test daughters was undertaken. The correlations between the national RR TDM and national AM BVs were 0.990, 0.988 and 0.990 for milk, fat and protein, respectively. The regression coefficients for the regression of the BVs from the RR TDM on the national repeatability AM BVs were 1.07, 1.05 and 0.984 for milk, fat and protein, respectively. The within-breed correlations between the sire BVs from the RR TDM and repeatability AM were all above 0.97. Schaeffer *et al.*, (2000) compared the BVs from a 305-day lactation model to those obtained from a RR TD model. The correlations between the BVs were 0.97, or higher, for Holstein sires and greater than 0.98 for Jersey bulls. Lidauer *et al.*, (2003) found correlations of 0.975, or higher, between Ayrshire sires evaluated using the two models. The results of this study are in line with other published work.

The stability of the RR TDM BVs as the season progressed was compared to those from the current system. There were 28 reproof sires in 2007 season which had initial protein BVs in June 2006 based on an average of 236 daughters and subsequent BVs in December 2006 based on an average of 6441 daughters. The standard deviation of the difference in breeding values from June to December was calculated for the 28 sires. The RR TDM showed smaller changes due to reproof with a standard deviation of 1.22 kg compared to the current system which had a standard deviation of 3.99 kg. The sires that show the greatest reproof changes in the current system also have the more extreme lactation persistency BVs. The correlation between reproof change and persistency BV was -0.12 (not significantly different from 0) and 0.60 for RR TDM and current system, respectively.

## CONCLUSION

The study shows that estimation of genetic and PE parameters for large scale RR TDMs is computationally feasible provided that the covariance structure among lactations is simplified.

The simplification to the covariance structure in this application had little effect on estimated variances and thus only very small impacts on the RR TDM BVs. A national RR TDM genetic evaluation including lactations 1 through 6 is computationally feasible provided prior solutions are used as starting values. A routine evaluation RR TDM run currently takes under 24 hours per trait to complete, which is within time required for a national evaluation to be feasible.

Comparisons of the RR TDM with the current AM BVs are consistent with the results reported by previous studies. The re-ranking of sires and cows is considerably smaller than was reported with the change from the Breeding Index system to the current AM system (Harris *et al.*, 1996). The RR TDM is better statistically equipped to cope with differences among cows in terms of maturity and persistency. Maturity differences are taken into account by modelling each lactation separately so that individual animals can show differing rates of maturity rather than assuming that all lactations are repeated records of each other. Also, the RR TDM fits a curve to each individual for each lactation allowing individuals to have differing shapes of lactation and consequently differing levels of lactation persistency. Initial evidence from the 2007 season suggests that the RR TDM gives better stability of BVs than the current system. The RR TDM should provide improved accuracy of the estimated breeding values and should improve the response to selection for production under BW.

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