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Genetic evaluation of multi-breed dairy sires in five environmental clusters within New Zealand

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Abstract

Many studies have shown dairy cattle sires (genotypes) and their daughters are sensitive to variation in feeding systems or thermal environment. The objectives of this study were 1) Quantify and cluster (CL) herd environment within New Zealand (NZ) based on milksolid (fat + protein; MS) yields per cow (a proxy for feeding system), a summer heat load index (HLI) and geographical location 2) Test for re-ranking of sires for yields of milk, fat or protein between the environmental clusters. Cluster averages ranged from 240 kg MS/cow, 67.9 HLI, and 37.1 ºS (CL1) to 343 kg MS/cow, 60.9 HLI and 45.4 ºS (CL5). A multi-breed repeatability sire model was used to estimate sire breeding values (EBV) in each of the five clusters. The genetic correlations between CL1 and CL5 ranged from 0.69 to 0.89, indicating significant re-ranking of sires between the clusters, which deviated significantly in environment. Large changes in sire EBV across clusters were observed for some sires (specialist genotypes), whereas, cluster environment had limited effects on the EBV of other sires (generalist genotypes). A breed x environment scaling effect was also observed where the difference in EBV's between Friesian and Jersey sires was greater in high yield-cool (eg. CL5) environments than in low yield-warm environments (eg. CL1). This information suggests it may be necessary to provide information to NZ farmers about the environmental sensitivity of individual sires and breeds.

Keywords: Environmental sensitivity, clustering, dairy cattle, New Zealand, multi-breed evaluation

Introduction

Numerous studies have reported the progeny of dairy sires vary in their ability to adapt to and achieve high performance levels in different nutritional and climatic environments; a type of genotype by environment interaction (Hayes *et al.*, 2003; Kolmodin *et al.*, 2002). Consequently, some farmers prefer to use sires that are proven in the system they have adopted and/or in the climate in which their herd is managed.

To test for re-ranking of genotypes amongst environments, herds which share similar climatic and production parameters can be clustered together (Zwald *et al.*, 2003). The genetic correlations or rank correlations between sire breeding values in each of these environmental clusters are then compared to determine if the genetic estimates obtained in one cluster are reliable for use in another environment or cluster. Classification of nutritional (or production) and climatic environment are generally based on herd-year-season (HYS) total, peak or standard deviations of herd milk, fat or protein yield (Calus and Veerkamp, 2003; Zwald *et al.*, 2003), regional measures of rainfall or temperature (Fikse *et al.*, 2003; Zwald *et al.*, 2003), or specific measures such as daily measures of temperature-humidity index from the nearest weather station (Hayes *et al.*, 2003; Ravagnolo and Misztal, 2000). Often, the greatest degree of sire re-ranking is observed using these environmental parameters.

By international standards, New Zealand (NZ) dairy herds achieve low yields per cow of 326 kg milksolids (MS; fat + protein). However, significant farm and regional differences exist in MS yields. For instance, Northland dairy herds (the far north of the North Island of NZ) achieve average MS yields of 244 kg compared to 355 kg for herds in the South Island of NZ (Anonymous, 2004). In addition, mean daily maximum air temperature for different dairy regions also varies by up to 5.0 ºC (NIWA, 2005).The genetic evaluation of NZ dairy cattle is undertaken using an animal model which analyses all breeds and breed crosses

simultaneously. Breeding value estimates of all animals are on the same scale allowing direct comparison of individual animals regardless of breed (Harris *et al.*, 1996).

The objectives of this study were to form environmental clusters of herds within NZ based on geographical location of the herd, adjusted herd mean MS yields per cow (a proxy for feeding level), and a summer heat load index (HLI) average using data from the meteorological station which was nearest to each herd. Performance in each environmental cluster would then be treated as a genetically distinct trait to determine if specific genotypes were better suited to one environment, and if re-ranking of sires occurred between environments.

Materials and Methods

Initial data consisted of milk, fat and protein total yield deviation (Johnson, 1996) records from animals which were in Livestock Improvement's Sire Proving Scheme herds (e.g. only those herds that participated in progeny testing of young sires) from 1989 to 2003. A pedigree file with ancestors, traced back to the 1940's in many instances, was used to construct a sire-maternal grand-sire pedigree. For each animal in the dataset, the breed proportions of overseas Holstein Friesian (HF), New Zealand Friesian (NZF), Jersey (J) and other (O) which included Ayrshire, Guernsey, Milking Shorthorn were calculated. Individual animal heterosis and recombination coefficients were calculated for each of the major breed crosses using the method outlined by VanRaden and Sanders (2003).

Meteorological data was obtained for 65 stations throughout NZ from the National Institute of Water and Atmospheric Research (NIWA) from 1989 to 2002. Daily meteorological data for humidity, temperature, wind speed and solar radiation was then used to calculate summer heat load indices (HLI; Casteneda *et al.,* 2004). Herds and meteorological stations were then spatially located on a map using ArcView GIS version 3.2 (ESRI, 1999). The nearest meteorological station with complete climate data (within a 50 km radius) to each herd-year-season (HYS) was then used as the measure of summer HLI for that particular HYS. Adjusted MS yield for each HYS was obtained using the GLM procedure of SAS (SAS, 1999) by fitting a model which included the effects of HYS, age, breed and days in milk. HYS groups were subsequently clustered based on adjusted MS yield per cow, summer HLI, and latitude using the FASTCLUS procedure of SAS (SAS, 1999), which uses the k-means algorithm. The choice of the number of clusters was based on the occurrence of peaks in the cubic clustering criterion or F-statistic.

The statistical model applied to each cluster was a univariate multi-breed repeatability sire-maternal grand-sire model. In matrix notation, the full model was as follows:

$$\mathbf{y = Xb + ZQg + Zs + Wp + Hh + e}$$

where

y	is the vector of records for milk, fat or protein total yield deviation
b	is the vector of the fixed effect of HYS, covariate effects of age at parturition date (in months, fitted as a linear and quadratic effect) and parturition date deviation from the mean HYS parturition date
g	is the vector of genetic group effects
s	is the vector of random additive genetic effects of sire
p	is the vector of permanent environment effects of cow
h	is the vector of covariate effects of breed, heterosis and recombination
X, Z, Q, W and H	are incidence matrices associating records with the elements of **b**, **g**, **s**, **p** and **h**, respectively
e	is the vector of random residuals

The breed effects considered were for HF, J, and Other, effectively setting the breed solution for NZF to zero. The heterosis and recombination effects considered were for HF x J, HF x NZF, J x NZF, and the major breeds of HF, NZF and J combined x Other. Variance components, and solutions for random and fixed effects were calculated in each cluster using the AIREML program of Johnson and Thompson (1995). Random sire solutions (**s**) were subsequently transformed to (**u**) or estimated breeding values (EBV) using: **u = Qa + 2s,**

where **Q** is a matrix relating fractions of breed group effects to the sire, with these fractional compositional effects proportional to the breed composition of the sire, **a** is a vector of fixed additive breed group effects or breed group means, and **s** is a vector of random additive genetic effects for sire (Arnold *et al.*, 1992). The reliability of each sire in each cluster was calculated using the information source method of Harris and Johnson (1998) and these values were then applied to calculate the genetic correlation between EBV in different clusters using the method proposed by Calus *et al.* (2002).

Results and Discussion

The total analysed data set included 443,879 records and 10,464 HYS after all data edits were applied. Approximately 30 % of available data was lost due to farms not having HLI data from a meteorological station within the defined 50 km radius. A total of 1,973 sires had a daughter represented in each cluster, and 54 sires had at least 20 daughters in each cluster. Five clusters were formed, CL1 and CL2 consisted of low and medium MS yield herds respectively in warm regions of the North Island (Table 1). CL3 was comprised of medium to low MS yield herds from Auckland (North Island) to the base of the South Island with a mild climate. CL4 herds had high MS yields and were located throughout NZ in mild climates. CL5 herds had the highest mean MS yield, and were primarily from the south of the South Island in a cool climate.

Latitude (linear) and summer HLI (linear and quadratic) both had significant effects ($P<0.001$) on HYS MS yields when fitting a GLM in SAS (SAS, 1999). HYS MS yields increased with more southern latitudes and declined with increases in summer HLI with a greater reduction in HYS MS yield occurring as summer HLI exceeded 70. The effect of heat stress on MS yield is similar to the findings of Hayes *et al.* (2003) in relation to temperature humidity index.

Table 1: Means of descriptive Herd-Year group variables for each cluster

	CL1	CL2	CL3	CL4	CL5	ALL
Number of records	89,061	132,166	107,192	85,394	30,066	443,879
Number of HYS	2,542	3,010	2,420	1,798	694	10,464
Environmental parameters: Mean (std. Dev)						
MS yield (kg/cow)	240 (41.6)	293 (52.5)	269 (41.4)	337 (56.2)	343 (62.9)	283 (74.2)
Summer HLI	67.9* (1.7)	67.9 (1.4)	64.1 (1.5)	65.2 (1.6)	60.9 (1.8)	66.0 (2.6)
Latitude (ºS)	37.1 (1.1)	37.4 (1.0)	39.8 (1.0)	40.1 (1.5)	45.4 (1.3)	39.0 (2.4)

*equivalent to a maximum temperature of 24 °C and 90 % humidity

Heritability was highest for milk yield (0.25 to 0.33), followed by protein (0.20 to 0.24) and fat (0.16 to 0.21) yields (Table 2). The values are similar to those estimated in NZ by Ahlborn and Dempfle (1992) and for the predominantly-NZ cluster in a study of Zwald *et al.* (2003). Heritability and heterogeneity of variance components (data not shown) for milk, fat and protein yields increased at increasing levels of production, which is consistent with other studies (Hayes *et al.*, 2003; Hill *et al.*, 1983). Fat yield was influenced most strongly by environment, as was reported by Weigel et al. (1999) for pasture-fed dairy cattle in the United States. They postulated this was due to large variations in pasture quality in the warmer summer months which affects fat percentage. A study by Litherland *et al.* (2002) also found considerable seasonal and regional variations in pasture quality in NZ, with the lower values in the warmer regions expected to reduce daily intake of metabolisable energy.

The genetic correlations for estimated breeding values for the most reliably proven Friesian and J sires (minimum of 20 daughters in each cluster) between clusters generally declined with increasing deviation in environment between clusters (Table 2). EBV estimated across ALL environments was generally reliable for use in different clusters, but was least reliable for use in extreme environments such as CL5 and CL1. Very low genetic (0.69 to 0.89) correlations were observed between clusters 1 and 5 where the difference in MS yield, HLI and latitude was 103 kg MS/cow, 7.0 units and 8.3 ºS, respectively. A similar low genetic correlation estimate of 0.75 for milk yield was observed in an international study by Zwald et al. (2003) when comparing a predominantly North Island of NZ cluster (daily peak milk yield per cow of 17.3 kg) with another cluster which consisted of herds from the South Island of NZ and northern Europe (23.7 kg milk). The results of the current study, and that of Zwald et al.

(2003) indicate re-ranking of genotypes can occur between widely different environments within New Zealand.

Table 2: Heritability[1] and genetic[2] correlations between clusters for total lactation yield deviations of milk, fat and protein

	CL1	CL2	CL3	CL4	CL5	ALL
Milk						
CL1	0.25 (0.014)	1.00	0.97	0.90	0.89	1.00
CL2	1.00	0.31 (0.014)	0.85	0.90	1.00	1.00
CL3	0.97	0.88	0.32 (0.016)	1.00	0.73	0.97
CL4	0.98	0.96	1.00	0.33 (0.017)	0.75	0.99
CL5	0.85	0.72	1.00	1.00	0.30 (0.029)	0.95
All	1.00	0.97	1.00	1.00	0.99	0.30 (0.010)
Fat						
CL1	0.16 (0.011)	1.00	1.00	0.88	0.69	1.00
CL2	0.93	0.21 (0.011)	1.00	0.89	0.86	1.00
CL3	0.74	0.64	0.20 (0.012)	0.84	0.73	1.00
CL4	0.73	0.78	0.92	0.21 (0.013)	0.72	0.96
CL5	0.70	0.79	0.86	1.00	0.20 (0.024)	0.91
All	0.90	0.91	0.93	1.00	1.00	0.20 (0.008)
Protein						
CL1	0.20 (0.013)	1.00	1.00	1.00	0.73	1.00
CL2	0.94	0.24 (0.012)	0.95	0.96	0.81	1.00
CL3	0.95	0.76	0.24 (0.014)	1.00	0.63	1.00
CL4	0.94	0.92	1.00	0.24 (0.015)	0.74	1.00
CL5	0.80	0.71	1.00	1.00	0.23 (0.026)	0.87
All	0.99	0.96	0.98	1.00	1.00	0.23 (0.008)

[1]heritability (standard errors) on diagonal
[2]HF genetic correlations above diagonal, and J below diagonal

The difference in average EBV between J and Friesian sires increased as production environment (MS yield) improved, a type of breed x environment scaling effect. For example, the difference between the average EBV of Friesian and J sires for milk, fat and protein was the least (-618, +0.2, and –9.4 kg, respectively) in a poor environment (CL1), and greatest (-1011, -1.6 and –17.5 kg, respectively) in a good environment (CL5). The breed x environment scaling effect is also illustrated in Figure 1, which compares the EBV's of two Friesian sires and two J sires, as a function of cluster MS yield. Similarly, Oldenbroek (1988) also observed that the difference in milk, fat and protein yield and feed intake between J and Friesian cattle was greater on a concentrate diet than on a roughage diet.

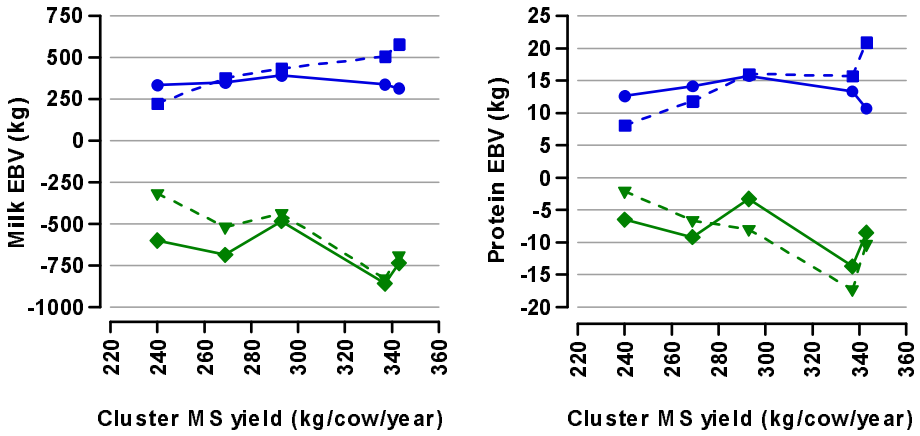

Figure 1: Estimated breeding values for milk and protein for two Friesian (■ and ●) and two Jersey (▼ and ◆) sires, illustrated as a function of cluster MS yield.

The information presented in Figure 1, illustrates sire re-ranking across the environmental gradient and also illustrates differences in environmental sensitivity of certain sires. For example, the milk and protein EBV of the Friesian sire represented by "●" is only slightly affected by production environment, this could be referred to as a generalist genotype.

Whereas, the milk and protein EBV of two other sires represented by the "■" and "▼" are influenced by production environment (specialist genotypes). The Friesian sire represented by a "■" ranks highly when its daughters are managed in a superior environment, whereas the Jersey sire represented by a "▼" improves its ranking when daughters are managed in challenging environments where animals are likely to be underfed at certain stages throughout the year.

Conclusions

The results illustrated there was significant re-ranking of sires and a scaling effect for breeds between very different environments. This suggests it may be necessary to provide information to farmers about the environmental sensitivity of sires and breeds under the range of New Zealand environments. Further studies are needed to determine if other environmental parameters such as herd size, rainfall and altitude influence EBV for sires and breed groups.

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