Calculation of a cow culling merit index including specific heterosis in a multibreed dairy population

NICOLÁS LÓPEZ-VILLALOBOS[1], MAURO PENASA[2], RICCARDO DAL ZOTTO[2], MARTINO CASSANDRO[2], WILFRIED BRADE[3,4], OTTMAR DISTL[3], ROSS EVANS[5] and ANDREW CROMIE[5]

[1]Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Palmerston North, New Zealand, [2]Department of Animal Science, University of Padova, Legnaro, Italy, [3]Institute for Animal Breeding and Genetics, University of Veterinary Medicine Hannover, Hannover, Germany, [4]Landwirtschaftskammer Niedersachsen, Fachbereich Versuchswesen Tier, Hannover, Germany, [5]Irish Cattle Breeding Federation, Highfield House, Newcestown Road, Bandon, Co. Cork, Ireland

Abstract

The objective of this study was to compare two models for the estimation of producing values (EPV) for lactation yields of milk, fat and protein, and calving interval (CI), which were combined in an index called the Cow Culling Merit Index (CMI), in Irish dairy cattle. Data comprised 188 927 records for production and 157 117 records for CI, collected on North American Holstein Friesian (HO), Friesian (FR), Jersey (JE), and Montbéliarde (MO) pure breeds, and some of their crosses. Cows calved from 2002 to 2006 and were from parities 1 to 5. Coefficients of specific heterosis for HO×FR, HO×JE, and HO×MO were calculated for each cow from parental breed information. The coefficient of general heterosis (GH) for each cow was obtained as the sum of the specific coefficients previously estimated. Model 1 included fixed effects of contemporary group, age at calving within parity, linear regression on gene proportions for FR, JE, and MO, and linear regression on the coefficient of expected GH. Additive genetic, permanent environmental, and error were random effects. Model 2 was based on Model 1 but GH was replaced by linear regressions on coefficients of expected specific heterosis for HO×FR, HO×JE, and HO×MO. Estimated producing values were calculated as the sum of estimated breeding value, permanent environmental and heterosis effects. The inclusion of coefficients of specific heterosis in the model did not produce re-ranking of animals but important differences in EPVs were observed in crossbred cows. These changes are important if EPVs are used to develop a culling merit index.

Keywords: crossbreeding, culling merit index, dairy cattle, genetic evaluation, heterosis

Zusammenfassung

Bildung eines Selektionsindexes für Milchkühe mit Einbeziehung der spezifischen Heterosis unter den Bedingungen des gleichzeitigen Vorhandenseins mehrerer Rassen

Das Ziel dieser Studie war ein Vergleich von zwei Modellen für die Schätzung des zu erwartenden Produktionswertes (EPV) für die Milch-, Fett- und Eiweißmenge sowie für das Kalbeintervall (CI) für Milchkühe, die anschließend zu einem Gesamtindex für Kühe (Cow Culling Merit Index, CMI) unter irischen Bedingungen weiter zusammengefasst wurden.

Die analysierten Daten umfassten 188 927 Datensätze für die Laktationsleistungen und 157 117 Datensätze für das Kalbeintervall (CI); basierend auf irischen Informationen von Kühen der Rassen nordamerikanische Holstein-Friesian (HO), Friesian (FR), Jersey (JE) und Montbéliarde (MO) sowie zugehörige Kreuzungen. Die Kühe kalbten von 2002 bis 2006 und hatten 1 bis 5 Trächtigkeiten. Die Koeffizienten für die spezifische Heterosis für HO×FR, HO×JE und HO×MO wurden für jede Kuh aus den elterlichen Rassen-informationen abgeleitet. Die Koeffizienten für die generelle Heterosis (GH) wurde für jede Kuh aus der Summe der zuvor geschätzten spezifischen Koeffizienten berechnet.

Im Modell 1 wurden die zugehörige Stallgefährtinnengruppe, das Kalbealter innerhalb der zugehörigen Trächtigkeitsnummer und die linearen Regressionskoeffizienten bezüglich der (theoretischen) Genanteile für FR, JE und MO einschließlich einem linearen Regressionskoeffizienten für die generelle Heterosis (GH) als fixe Effekte berücksichtigt. Der additiv-genetische Wert, der permanente Umweltfaktor sowie die zugehörige (restliche) Fehlerkomponente wurden als zufällige Effekte definiert. Das Modell 2 basierte auf Modell 1, aber die GH wurde jetzt durch einen linearen Regressionskoeffizienten für die spezifische Heterosis für HO×FR, HO×JE bzw. HO×MO ersetzt.

Die Produktionswerte wurden berechnet aus der Summe der geschätzten Zuchtwerte, den Effekten für die permannenten Umweltfaktoren und den Heterosiseffekten. Die Einbeziehung der Koeffizienten für die spezifische Heterosis in das Modell führte zwar nicht zu Rangfolgeveränderungen, aber deutlichen Differenzen in den EPVs; speziell bei den Kreuzungstieren. Diese Änderungen sind wichtig, wenn EPVs verwendet werden, um einen (Gesamt-) Produktionsindex für Kühe zu entwickeln.

Schlüsselwörter: Kreuzungszucht, Gesamtindex, Milchrinder, genetische Bewertung, Heterosis

Introduction

Commercial dairy cattle production in Ireland relies on several breeds, and the most important are North American Holstein Friesian (HO), Friesian (FR), Jersey (JE), and Montbéliarde (MO). Genetic evaluations across breeds are routinely computed by the Irish Cattle Breeding Federation (ICBF). The ICBF, in conjunction with Teagasc (the Irish farm research and advisory body), the Irish Department of Agriculture and other international collaborators, has developed a number of economic selection indexes suitable for Irish conditions and an overall index called the Economic Breeding Index (EBI). The aim of the EBI is to aid dairy farmers in identifying the most profitable bulls and cows for breeding dairy herd replacements. Milk production and fertility are the main contributors to farm profit and the economic weights in the selection index reflect their importance.

The across breed evaluation facilitates the comparison of estimated breeding values (EBV) on cows with differing breed contributions. Also, adjusting for heterosis allows more accurate selection of sires based on EBI through better estimation of the additive genetic effects. Farmers use the EBI to choose the best sires for the herd, to select cows to breed replacement heifers and as a tool for culling decisions. Estimated producing value (EPV) for traits of interest can be calculated for cows as the sum of their EBV plus

permanent environment and heterosis effects, and can be adopted to estimate the future performance of the animal in the same herd, which would be useful for the purpose of culling (HENDERSON 1975).

The current model of genetic evaluation adjusts for a coefficient of general heterosis, calculated for each animal on the basis of its total heterozygosity, without investigating the effect of specific breeds. This assumes that cows from different breed combinations (e.g. a first-generation HO×FR cow and a first-generation HO×JE cow) will express the same level of heterosis. Recently, PENASA *et al.* (2009) found that significantly different specific heterosis effects exist in the Irish dairy population.

The aim of this study was to investigate the effect of including coefficients of general and specific heterosis in the calculation of EPVs for lactation yields of milk, fat, and protein and calving interval (CI), which were then combined with economic values to calculate an index called the Cow Culling Merit Index (CMI).

Material and methods

Data

A total of 188 927 records of 305-d milk, fat, and protein yield, and 157 117 records of CI were used in the analysis. Production data were from 104 160 cows while CI information was available for 88 094 cows. Full details on datasets and breed structure of contemporary groups are reported in PENASA *et al.* (2009). Briefly, lactation yields adjusted to 305 days using the standard lactation curve method (OLORI and GALESLOOT 1999) were obtained from ICBF. Records on cows from parities 1 to 5 calving in the spring (January to June) from 2002 to 2006 were extracted. Four dairy breeds (HO, FR, JE, and MO) were identified as having enough records to estimate breed effects for the traits. The proportion of genes was calculated for each cow as:

$$\alpha_i^p = \frac{(\alpha_i^s + \alpha_i^d)}{2} \tag{1}$$

where α_i^p is the proportion of genes from breed *i* in the progeny, α_i^s is the proportion of breed *i* in the sire, and α_i^d is the proportion of breed *i* in the dam.

Coefficients of specific heterosis were calculated between any pair of the four dairy breeds using the following identity (DICKERSON 1973):

$$\delta_{ij}^p = \alpha_i^s \alpha_j^d + \alpha_j^s \alpha_i^d \tag{2}$$

where δ_{ij}^p is the coefficient of expected heterosis between fractions of breeds *i* and *j* in the progeny, α_i^s and α_j^s are proportions of breeds *i* and *j* in the sire, and α_i^d and α_j^d are proportions of breed *i* and *j* in the dam. Three types of crosses (HO×FR, HO×JE, and HO×MO) were chosen to estimate specific heterosis effects because the distribution of cows across classes of coefficients of expected heterosis was suitable for this purpose (PENASA *et al.* 2009). The coefficient of general heterosis for each cow was obtained by summing coefficients of specific heterosis previously calculated.

Models

Tests for normality were used to assess the deviation of the data from the normal distribution. Because of the large number of records available, the deviation of all traits was statistically significant. Nevertheless, the values of skewness and kurtosis were relatively low, with the highest absolute values for CI (0.75 and 0.55, respectively), so that the application of linear models will be justified.

Breed and heterosis effects for lactation yields of milk, fat and protein, and CI were obtained in ASReml (GILMOUR *et al.* 2002) under the following univariate repeatability animal models:

Model 1: $\mathbf{y} = \mathbf{X_1 b_1} + \mathbf{X_2 b_2} + \mathbf{X_3 b_3} + \mathbf{Za} + \mathbf{Wc} + \mathbf{e}$ (3)

Model 2: $\mathbf{y} = \mathbf{X_1 b_1} + \mathbf{X_2 b_2} + \mathbf{X_4 b_4} + \mathbf{Za} + \mathbf{Wc} + \mathbf{e}$ (4)

where $\mathbf{y}$ is the vector of observations for lactation yields of milk, fat or protein, or CI, $\mathbf{b_1}$ is the vector of fixed effects of overall mean, contemporary group, and age at calving within parity, $\mathbf{b_2}$ is the vector of fixed regression coefficients of breed additive effects for FR, JE and MO (HO breed set to zero for comparison), $\mathbf{b_3}$ is a scalar of regression coefficient for GH, $\mathbf{b_4}$ is the vector of fixed regression coefficients for specific heterosis (HO×FR, HO×JE, and HO×MO), $\mathbf{a}$ is the vector of random additive genetic effects, $\mathbf{c}$ is the vector of random permanent environmental effects, $\mathbf{e}$ is the vector of residuals, and where $\mathbf{X_1}$, $\mathbf{X_2}$, $\mathbf{X_3}$, $\mathbf{X_4}$, $\mathbf{Z}$, and $\mathbf{W}$ are the incidence matrices relating fixed effects, fixed additive breed effects, fixed GH effects, fixed specific heterosis effects, random additive genetic effects, and random permanent environmental effects, respectively.

Variances of the random effects were considered as follows:

$$\mathrm{Var(a)} = \sigma_a^2 \mathbf{A}$$
$$\mathrm{Var(c)} = \sigma_c^2 \mathbf{I_c}$$ (5)
$$\mathrm{Var(e)} = \sigma_e^2 \mathbf{I_e}$$

where σ_a^2, σ_c^2, and σ_e^2 are the variances of animal, permanent environmental, and residuals effects, respectively, $\mathbf{A}$ is the numerator relationship matrix, $\mathbf{I_c}$ is an identity matrix of size c (the number of animals with records) and $\mathbf{I_e}$ is an identity matrix of size equal to the number of records for either production or CI traits. Heritabilities and repeatabilities for production were assumed in 0.35 and 0.55, respectively, which are those currently used for routine genetic evaluation of 305-d milk yield traits in Ireland (INTERBULL 2009). Heritability for CI was assumed in 0.04, again according to INTERBULL (2009), and repeatability in 0.08, according to the study of KEARNEY *et al.* (2004). Heritability for CI was comparable with estimates reported by DAL ZOTTO *et al.* (2007) in different environmental conditions.

A t-test was used to assess if effects for FR, JE, and MO were significantly different from HO as well as if heterosis effects were significantly different from zero.

Estimated breeding value (EBV) for animal k and for each trait was obtained as:

$$EBV_k = \alpha_{FR}\hat{g}_{FR} + \alpha_{JE}\hat{g}_{JE} + \alpha_{MO}\hat{g}_{MO} + \hat{a}_k$$ (6)

where α_{FR}, α_{JE}, and α_{MO} are proportions of FR, JE, and MO genes in animal *k*, respectively,

$\hat{g}_{FR}$, $\hat{g}_{JE}$, and $\hat{g}_{MO}$ are the estimated effects of FR, JE, and MO breeds, respectively, and $\hat{a}_k$ are the estimated random additive genetic effect for animal k.

Estimated producing value (EPV) of cow k with records was obtained according to the two models as:

Model 1: $EPV_k = EBV_k + \delta_{GH}\hat{h}_{GH} + \hat{c}_k$ (7)

Model 2: $EPV_k = EBV_k + \delta_{HO,FR}\hat{h}_{HO \times FR} + \delta_{HO,JE}\hat{h}_{HO \times JE} + \delta_{HO,MO}\hat{h}_{HO \times MO} + \hat{c}_k$ (8)

where δ_{GH} is the total heterozygosity of cow k, $\delta_{HO,FR}$, $\delta_{HO,JE}$, and $\delta_{HO,MO}$ are specific heterozygosities between HO×FR, HO×JE, and HO×MO of cow k, respectively, $\hat{h}_{GH}$ is the estimate of general heterosis effects, $\hat{h}_{HO \times FR}$, $\hat{h}_{HO \times JE}$, and $\hat{h}_{HO \times MO}$ are estimates of specific heterosis effects, and $\hat{c}_k$ is the solution for the permanent environmental effect of cow k.

Estimated producing values for lactation yields of milk, fat and protein, and CI were combined into an economic index useful for cow culling decisions. This index can be termed Cow Culling Merit Index (CMI) and was calculated for each cow as:

$CMI = (EPV_{milk} \cdot EV_{milk}) + (EPV_{fat} \cdot EV_{fat}) + (EPV_{protein} \cdot EV_{protein}) + (EPV_{CI} \cdot EV_{CI})$ (9)

Economic values (EV) may be estimated as suggested by PIETERS *et al.* (1997), and for the CMI were equal to −0.09 €/kg milk, 1.26 €/kg fat, 6.91 €/kg protein, and −11.97 €/day of CI (ICBF website, http://www.icbf.com) which are the current economic values included in the calculation of the EBI and used by farmers for the identification of the most profitable bulls and cows for breeding dairy herd replacements. The set of EVs used for the two indexes (CMI and EBI), should be different because the time horizon of each index is different. In particular, EVs for the CMI should aim to measure the future economic circumstances of the cow during her productive life while the EVs for the EBI should aim to measure the economic circumstances of the future progeny of the cow.

Results and discussion

Descriptive statistics for lactation yields and CI are shown in Table 1, along with estimates of crossbreeding effects obtained under the two models. Means and standard deviations were similar to those reported by EVANS *et al.* (2006) for commercial Holstein-Friesian cows.

Breed effects obtained using the two models were similar. Estimates for milk and protein yield were always in favour of HO, the breed set as the reference in our study. Only fat production from Model 1 was significantly (*P*<0.05) higher for JE than HO cows, but the latter breed produced 1 680 kg more milk and 27.7 kg more protein than the former. These differences were larger compared to those reported by BUCKLEY *et al.* (2008) from an experimental trial comparing Holstein-Friesian, JE and their crosses under Irish grazing conditions. In that experiment, the JE produced 1 283 kg less milk and 19 kg less protein compared to Holstein-Friesian. However, fat yield from JE was 13.1 kg higher in BUCKLEY *et al.* (2008) than in our study. In New Zealand dairy cattle, the JE produced 904 kg less milk and 9.6 kg less fat compared to Holstein-Friesian cows (AHLBORN-BREIER and HOHENBOKEN 1991). In a study involving dairy herds in the United States, additive breed effects for JE were −2 962 kg for milk yield, −34 kg for fat yield and −47 kg for

protein yield compared to Holstein-Friesian (VANRADEN *et al.* 2007). Friesian and MO were similar for lactation yields (Table 1) and inferior than HO. Breed effects for MO cows agree with results reported by DILLON *et al.* (2003) in which the MO produced 875 kg less milk, 38 kg less fat, and 24 kg less protein than Holstein-Friesian cows. Breed effects for CI showed that FR and JE had significantly shorter CI compared to HO cows, regardless of the model used, while MO had shorter CI than HO only with Model 1.

General and specific heterosis effects for production traits were all positive and significantly different from zero ($P<0.001$). Heterosis effects for CI were negative but significantly different from zero only for HO×MO ($P<0.05$) indicating that HO×MO cows had shorter CI than the average of the parental purebreds. Heterosis estimates expressed as percentage of the overall mean were slightly lower than those reported in New Zealand (HARRIS 2005) and the United States (VANRADEN and SANDERS 2003) but similar to experimental results from BUCKLEY *et al.* (2008) and PENASA *et al.* (2007).

In general, crossbreeding effects from this study slightly differed from results reported by PENASA *et al.* (2009) using the same datasets. The differences are probably attributable to the shorter pedigree considered in our study (only cow, sire, dam and grandparents) and to the use of different softwares to obtain the estimates.

Table 1

Means, standard deviations, crossbreeding effects and standard errors (within brackets) for milk yield traits and calving interval obtained under two linear models

Mittelwerte, Standardabweichungen, Kreuzungseffekte und zugehörige mittlere Fehler (innerhalb der Klammern) für Milchleistungsmerkmale und das Kalbeintervall; basierend auf zwei linearen Modellen

	Milk, kg	Fat, kg	Protein, kg	Calving interval, d
Records, n	188 927	188 927	188 927	157 117
Mean	6 844	257	229	378
Standard deviation	1 471	56	47	38
Model 1				
Breed effects[1,2]				
FR	−778 (32)***	−25.1 (1.2)***	−20.1 (0.9)***	−10.9 (1.4)***
JE	−1 680 (72)***	5.3 (2.7)*	−27.7 (2.1)***	−10.5 (3.4)**
MO	−735 (53)***	−25.6 (2.0)***	−16.3 (1.5)***	−5.9 (2.4)*
General heterosis	277 (17)***	10.7 (0.6)***	8.8 (0.5)***	−1.5 (0.9)
Model 2				
Breed effects[1,2]				
FR	−751 (33)***	−23.9 (1.2)***	−19.2 (0.9)***	−11.4 (1.4)***
JE	−1 711 (75)***	2.5 (2.8)	−29.2 (2.2)***	−10.4 (3.6)**
MO	−748 (55)***	−26.1 (2.0)***	−16.6 (1.6)***	−4.6 (2.5)
Heterosis effects[3]				
HO×FR	256 (18)***	9.7 (0.7)***	8.0 (0.5)***	−1.1 (0.9)
HO×JE	496 (97)***	25.9 (3.6)***	21.4 (2.3)***	−2.1 (4.5)
HO×MO	460 (79)***	17.7 (3.0)***	11.5 (2.1)***	−10.2 (4.2)*

Model 1   repeatability animal model with coefficient of general heterosis,   Model 2   repeatability animal model with coefficients of specific heterosis,   [1]Breed effects of North American Holstein Friesian were set to zero for comparison,   [2]FR Friesian, JE Jersey, MO Montbéliarde,   [3]HO×FR North American Holstein Friesian × Friesian, HO×JE North American Holstein Friesian × Jersey, HO×MO North American Holstein Friesian × Montbéliarde, breed effects significantly different from HO (the reference breed) at *$P<0.05$, **$P<0.01$, ***$P<0.001$, heterosis effects significantly different from zero at *$P<0.05$, **$P<0.01$, ***$P<0.001$

The purpose of this study was to compare the effect of including a coefficient of general heterosis (Model 1) and coefficients of specific heterosis (Model 2) on the calculation of EPVs for milk, fat, and protein yield, and CI. Correlation coefficients between EPVs estimated by the models were higher than 0.95, indicating little re-ranking of animals for each of the traits.

Table 2 shows means and standard deviations of EPVs for the different traits and for different breed groups. Average EPVs from the models were similar across breed groups with only few exceptions. Compared to Model 1, Model 2 produced significantly ($P<0.05$) lower average EPVs for CI in FR cows, significantly ($P<0.05$) lower average EPVs for fat yield in JE cows, significantly ($P<0.05$) higher average EPVs for CI in MO cows, significantly ($P<0.05$) higher average EPVs for fat and protein yield in HO×JE cows, and significantly ($P<0.05$) lower EPVs for CI in HO×MO cows.

Means and standard deviations of CMI across breed groups are in Table 2. The CMI is a measure of the farm profitability under Irish grazing conditions. Based on estimates from Model 2, the values show that among the straightbred groups, the JE had higher farm profitability than HO, FR, and MO cows. These results agree with findings of LÓPEZ-VILLALOBOS *et al.* (2000) showing that under New Zealand conditions JE had higher farm profitability than Holstein-Friesian and Ayrshire breeds.

The CMI captures permanent environmental and heterosis effects which are expressed by the cow during its productive life. North American Holstein Friesian×JE had the highest average CMI, followed by HO×MO and HO×FR cows. Very similar results were reported by LÓPEZ-VILLALOBOS *et al.* (2000) in New Zealand and BUCKLEY *et al.* (2008) in Ireland showing that aggregate effects of Holstein-Friesian × JE heterosis for individual traits result in a significant economic heterosis.

Using the estimates of general heterosis obtained under Model 1 and considering milk, fat, protein, and CI, the economic aggregate heterosis was 68 €. The corresponding economic aggregates for specific heterosis under Model 2 were 59 € for HO×FR, 139 € for HO×JE, and 200 € for HO×MO. The economic heterosis reported in the United States cows ranged from $ 163 to $ 197 depending on the economic values of the merit indexes (VANRADEN and SANDERS 2003).

The effect of including specific heterosis compared to only including general heterosis in the estimation of CMI is shown in Table 2. Model 2 increased significantly ($P<0.05$) the average value of CMI for FR, HO×JE, and HO×MO but decreased significantly ($P<0.05$) the average value of CMI for JE and MO cows. However, correlation coefficients between CMI estimated from the two models were higher than 0.96 for each of the breed groups suggesting little re-raking of cows based on CMI.

The inclusion of specific heterosis effects did not produce any major re-ranking of cows but important differences in EPVs can be observed, especially in HO×JE and HO×MO cows. These changes are important if EPVs are used to develop a culling merit index.

Acknowledgements

Table 2

Means and standard deviations (within brackets) of estimated producing values for milk yield traits and calving interval obtained under two linear models for different breed groups

Mittelwerte und Standardabweichungen (innerhalb der Klammern) für geschätzte Produktionswerte für Milchleistungsmerkmale und das Kalbeintervall für verschiedene Rassengruppen bei Anwendung von zwei verschiedenen Modellen

| | Breed group[1] | | | | | | |
	HO	FR	JE	MO	HO×FR	HO×JE	HO×MO
Milk, kg							
Model 1	133 (533)	−603 (460)	−1676 (413)	−681 (453)	−38 (525)	−360 (437)	−79 (429)
Model 2	132 (533)	−581 (460)	−1705 (413)	−694 (453)	−40 (524)	−281 (444)	−32 (446)
Model 1 - Model 2	0.9 (0.8)	−21.7 (3.0)	29.5 (3.2)	12.9 (1.7)	1.9 (3.4)	−78.7 (65.1)	−46.7 (60.3)
Fat, kg							
Model 1	4.2 (20.7)	−17.0 (18.6)	6.9 (18.6)	−24.1 (18.2)	2.2 (20.7)	22.3 (16.6)	0.9 (15.6)
Model 2	4.2 (20.7)	−16.0 (18.6)	4.3 (18.6)	−24.6 (18.2)	2.1 (20.7)	29.0 (17.5)	2.7 (16.2)
Model 1 - Model 2	0.0 (0.0)	−1.0 (0.1)	2.6 (0.3)*	0.5 (0.1)	0.1 (0.2)	−6.7 (3.5)*	−1.8 (2.3)
Protein, kg							
Model 1	6.2 (16.3)	−13.1 (15.0)	−27.4 (13.0)	−14.8 (15.0)	3.2 (16.6)	6.3 (13.5)	3.4 (13.8)
Model 2	6.1 (16.3)	−12.4 (15.0)	−28.9 (13.0)	−15.1 (15.0)	3.1 (16.5)	10.2 (13.5)	4.5 (13.8)
Model 1 - Model 2	0.0 (0.0)	−0.7 (0.1)	1.5 (0.2)	0.3 (0.0)	0.1 (0.1)	−3.9 (2.4)*	−1.1 (1.8)
Calving interval, d							
Model 1	0.4 (4.1)	−9.1 (2.9)	−10.4 (3.3)	−5.7 (3.3)	−3.2 (4.1)	−6.2 (3.2)	−6.5 (3.2)
Model 2	0.4 (4.1)	−9.5 (2.9)	−10.3 (3.3)	−4.3 (3.3)	−3.2 (4.1)	−6.3 (3.2)	−11.4 (3.2)
Model 1 - Model 2	0.0 (0.0)	0.4 (0.0)*	−0.1 (0.0)	−1.3 (0.0)*	−0.1 (0.1)	0.1 (0.3)	4.9 (1.8)*
CMI, €							
Model 1	31.0 (102.8)	51.5 (90.1)	94.1 (85.9)	−3.8 (91.4)	66.9 (100.8)	178.6 (77.2)	108.9 (84.4)
Model 2	30.6 (102.8)	60.4 (90.1)	82.4 (86.0)	−21.5 (91.4)	65.8 (100.8)	207.8 (79.8)	173.7 (90.4)
Model 1 - Model 2	0.4 (0.3)	−8.9 (1.1)*	11.7 (1.2)*	17.7 (0.5)*	1.1 (1.4)	−29.2 (19.0)*	−64.8 (31.7)*

Model 1 repeatability animal model with coefficient of general heterosis,   Model 2 repeatability animal model with coefficients of specific heterosis,   [1]HO North American Holstein Friesian, FR Friesian, JE Jersey, MO Montbéliarde, HO×FR North American Holstein Friesian × Friesian, HO×JE North American Holstein Friesian × Jersey, HO×MO North American Holstein Friesian × Montbéliarde,   *means significantly different from zero at $P<0.05$

References

Ahlborn-Breier G, Hohenboken WD (1991) Additive and nonadditive genetic effects on milk production in dairy cattle: evidence for major individual heterosis. J Dairy Sci 74, 592-602

Buckley F, Begley N, Prendiville R (2008) Crossbreeding the dairy herd – a real alternative. Irish Grassland Assoc J 42, 5-17

Dal Zotto R, De Marchi M, Dalvit C, Cassandro M, Gallo L, Carnier P, Bittante G (2007) Heritabilities and genetic correlations of body condition score and calving interval with yield, somatic cell score, and linear type traits in Brown Swiss cattle. J Dairy Sci 90, 5737-43

Dickerson GE (1973) Inbreeding and heterosis in animals. Proc of the Animal Breeding and Genetics Symposium in honor of Dr. JL Lush. Am Soc Anim Sci and Am Dairy Sci Assoc, Champaign, IL, 54-77

Dillon P, Buckley F, O'Connor PO, Hegarty D, Rath M (2003) A comparison of different dairy cow breeds on a seasonal grass-based system of milk production 1. Milk production, live weight, body condition score and DM intake. Livest Prod Sci 83, 21-33

Evans RD, Wallace M, Shalloo L, Garrick DJ, Dillon P (2006) Financial implications of recent declines in reproduction and survival of Holstein-Friesian cows in spring-calving Irish dairy herds. Agric Syst 89, 165-83

Gilmour AR, Gogel BJ, Cullis BR, Wellham SJ, Thompson R (2002) ASReml User Guide. Release 1.1. VSN International Ltd., Hemel Hempstead, Hertfordshire, UK

Harris BL (2005) Breeding dairy cows for the future in New Zealand. N Z Vet J 53, 384-9

Henderson CR (1975) Use of all relatives in intraherd prediction of breeding value and producing abilities. J Dairy Sci 58, 1910-16

Interbull (2009) Description of National Genetic Evaluation Systems for dairy cattle traits as applied in different Interbull member countries. http://www-interbull.slu.se/national_ges_info2/framesida-ges.htm. [last access 02.08.2009]

Kearney JF, Schutz MM, Boettcher PJ, Weigel KA (2004) Genotype by environment interaction for grazing versus confinement. II. Health and reproductive traits. J Dairy Sci 87, 510-6

López-Villalobos N, Garrick DJ, Holmes CW, Blair HT, Spelman RJ (2000) Profitabilities of some mating systems for dairy herds in New Zealand. J Dairy Sci 83, 144-53

Olori VE, Galesloot PJB (1999) Projection of partial lactation records and calculation of 305-day yields in the Republic of Ireland. Proc of the 1999 Interbull Meeting, Zurich, Switzerland, 26-27 August, Bulletin 22, 149-54

Penasa M, Dal Zotto R, Cecchinato A, de Jong G, Cassandro M (2007) Effect of crossbreeding on milk yield traits and somatic cell score in dairy cattle. Ital J Anim Sci 6 (Suppl 1), 186-8

Penasa M, López-Villalobos N, Evans RD, Cromie AR, Dal Zotto R, Cassandro M (2009) Crossbreeding effects on milk yield traits and calving interval in spring-calving dairy cows. Accepted for publication in J Anim Breed Genet

Pieters T, Canavesi F, Cassandro M, Dadati E, van Arendonk JAM (1997) Consequences of differences in pricing systems between regions on economic values and revenues of a national dairy cattle breeding scheme in Italy. Livest Prod Sci 49, 23-32

VanRaden PM, Sanders AH (2003) Economic merit of crossbred and purebred US dairy cattle. J Dairy Sci 86, 1036-44

VanRaden PM, Tooker ME, Cole JB, Wiggans GR, Megonigal JH Jr (2007) Genetic evaluations for mixed-breed populations. J Dairy Sci 90, 2434-41

Corresponding author:

NICOLÁS LÓPEZ-VILLALOBOS
email: n.lopez-villalobos@massey.ac.nz

Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Private Bag 11-222, Palmerston North, New Zealand