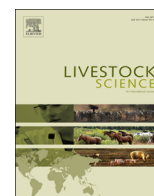




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Estimation of genetic parameters for milk traits in cows milked once- or twice-daily in New Zealand



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ABSTRACT

The objective of the present study was to estimate genetic parameters for milk yields, average somatic cell score (SCS) and milk composition traits in dairy cows milked either once a day (OAD) or twice a day (TAD) in New Zealand. The data set comprised 124,620 and 194,631 lactation records from OAD and TAD populations, respectively, during the period 2008–2012. Overall, estimates of parameters were similar between milking frequencies (MF), although heritabilities of production traits tended to be greater in the TAD cows. Estimates of heritability in OAD and TAD were: 0.33 and 0.36 for milk yield; 0.21 and 0.26 for fat yield; 0.22 and 0.25 for protein yield; and 0.12 and 0.12 for SCS, respectively. Estimates of correlations were similar across MF, in particular the genetic correlation between milk yield and protein yield (0.84 for TAD and 0.85 for OAD). Estimates of genetic correlations between SCS and other traits tended to be close to zero in both populations. The results indicate that genetic progress can be lower in the OAD population due to lower phenotypic and genetic variances compared to the TAD population. However, a potential disadvantage is that evaluating both dairy populations together could lead to systematic inaccuracies and biases in the estimation of breeding values for the population milked OAD as future dams.

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1. Introduction

The estimation of genetic parameters for milk yield and milk composition traits has been well documented in New Zealand (Ahlborn and Dempfle, 1992; Johnson et al., 2000; Pryce and Harris, 2006; Sneddon et al., 2015) and overseas (Berry et al., 2003; Rupp and Boichard, 1999). In those studies, the genetic parameters were estimated with records from cows milked twice-a-day (TAD), which is the standard milking frequency (MF) for dairy cattle in New Zealand. However, since the late 1990s, milking once-a-day (OAD) has been adopted by some farmers for herd management and lifestyle benefits (Clark et al., 2006; Davis et al., 1999).

In New Zealand, the prevalent breeds used in the dairy industry are Holstein–Friesian (F), Jersey (J) and their crosses (F × J), which represent 37.0%, 11.7% and 42.6% of the national herd, respectively (LIC and Dairy NZ, 2014). In an experimental study, Clark et al. (2006) reported a significant MF by breed interaction for the milk production traits. This interaction corresponds to a scaling effect, in which the breed groups perform differently with differing MF but without changing the ranking among them (Hammami et al.,

2009). However, from the study of Clark et al. (2006), a large variability in production has been observed in cows milked OAD compared to TAD, in particular in F cows, where some OAD F cows yielded as much as the highest F milked TAD (Hickson et al., 2006). This large variability might suggest that the apparent genetic merit of cows for production can change depending upon the MF environment.

In the New Zealand dairy industry, the genetic merit of an animal is evaluated according to the breeding worth index (BW) (Lopez-Villalobos and Garrick, 2005). The BW index is calculated as weighting the estimated breeding values (EBVs) for lactation yields of milk (MY), fat (FY) and protein (PY), somatic cell score (SCS), live weight, fertility and residual survival, with their respective economic values. In this index, bulls and cows are ranked according to their expected ability to produce more profitable replacements, which represents the genetic superiority or inferiority of an animal to convert 5 t of dry matter into farm profit. Given the MF by breed interaction reported by Clark et al. (2006), OAD farmers might be concerned if genetic evaluation is affected by this interaction since phenotypic and genetic parameters are population and environment specific, and may have different magnitudes. The response to selection of a particular trait is affected by genetic correlations and phenotypic variance and in particular heritability (Lopez-Villalobos, 2012). Therefore, accurate estimates of genetic parameters are required to develop an

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effective and comprehensive breeding programme for the OAD population.

The aim of this study was to estimate genetic parameters for milk yields, average SCS and milk composition traits in dairy populations milked either OAD or TAD in New Zealand.

2. Materials and methods

2.1. Data

Lactation records of MY, FY and PY recorded from 2008 to 2012, and pedigree information were provided by Livestock Improvement Corporation (LIC, Hamilton, New Zealand). Fat percentage (FP) and protein percentage (PP) were calculated as the ratio between FY or PY and MY. Protein to fat ratio (P:F) was calculated from these estimates. Another data set provided by LIC containing herd-test records of somatic cell count (SCC) was used to calculate average somatic cell score (SCS) during the same period. Somatic cell score was calculated as $SCS = \log_2(SCC)$ (Harris and Winkelman, 2004).

Total lactation records were sorted based on a code to determine if the cow was milked OAD or TAD. Once-a-day herds were identified as those where 100% of the cows were milked OAD all season. Using the GPS Visualizer (Schneider, 2012), TAD herds were selected within a radius of 20 km of the OAD herds. In some cases, in a given single map co-ordinate a OAD herd was surrounded by several TAD herds; in such cases, all TAD herds were selected. Any herds with less than 50 cows were removed from the dataset. Only records from spring calving cows in their first five lactations with lactation lengths comprised between 150 and 305 days were considered. Lastly, only records from F, J and their crosses were considered, discarding data from animals without information on breed composition.

The breed composition for each cow was determined with the following equation:

$\alpha_i^p = \frac{(\alpha_i^s + \alpha_i^d)}{2}$, where α_i^p is the proportions of genes from breed *i* in the cow, α_i^s and α_i^d are proportion of breed *i* in the sire and dam, respectively, and *i* is breed F or J. Pure breed cows were defined as having a breed composition of $\geq 93.75\%$ from a single breed.

Coefficients of expected heterosis for individual cows ($h_{F \times J}$) was calculated using the following equation (Dickerson, 1973):

$h_{F \times J} = \alpha_F^s \alpha_J^d + \alpha_J^s \alpha_F^d$, where α_F^s and α_J^s are proportion of breeds F and J in the sire, and α_J^d and α_F^d are proportion of breeds J and F in the dam, respectively.

The final dataset used for statistical analysis contained 124,620 lactations from 298 OAD herds and 194,631 lactations from 350 TAD herds. The population included 9,122 and 26,239 purebred F cows in OAD and TAD herds, respectively. The purebred J cows were 18,417 and 13,129 in OAD and TAD herds, respectively. Finally, crossbred F × J cows were 38,180 and 50,956 in OAD and TAD herds, respectively. The breed proportions were: 13.9% and 29.1% F cows, 28.0% and 14.5% J cows, and 58.1% and 56.4% F × J cows in

OAD and TAD herds, respectively. Jersey cows were more represented in the OAD population compared to F and F × J cows likely because farmers choose Jersey cows when they change to OAD milking. Experimental results show that reduction in milk production per cow and per hectare caused by OAD in Jersey cows is less than the reduction in F and F × J cows (Cooper, 2000; Clark et al., 2006). Number of lactation records, yield averages and coefficients of variation for each trait considered in the analysis are presented by breed group and MF in Table 1.

2.2. Estimation of variance and covariance components

Heritability, repeatability, correlations and their standard errors were calculated with restricted maximum likelihood (REML) procedures using the ASReml 3.0 software package (Gilmour et al., 2009). Estimates of variance components required for the calculation of heritabilities and repeatabilities for each trait were assessed using a single-trait repeatability animal model. A bivariate repeatability animal model was used to assess the estimates of covariance components required for the calculation of phenotypic and genetic correlations.

2.2.1. Single-trait animal model

A single-trait repeatability animal model was represented as follows (Mrode, 2014):

$$y = Xb + Za + Wp + e,$$

where **y** is the vector of observations for each of the traits MY, FY, PY, SCS, FP, PP and P:F; **b** is the vector of fixed effects, **a** is the vector additive genetic effects; **p** is the vector of random permanent environmental effects; and **e** is the vector of random residual effects. **X**, **Z** and **W** are incidence matrices relating records to fixed animal, additive genetic and permanent environmental effects, respectively.

The effects included in **b** were contemporary group (CG) defined as the combination of herd-season-lactation number; the regression coefficient associated with the linear effect of proportion of F; the regression coefficient associated with the linear effect of coefficient of heterosis; and the regression coefficient associated with linear effect of deviation days from median calving date of the herd in a given season.

The following expectation (*E*) of the variables was assumed: $E(y) = Xb$; $E(a) = 0$; $E(p) = 0$ and $E(e) = 0$. It was also assumed that the residual and permanent environmental effects were independently distributed, therefore $\text{var}(a) = A\sigma_a^2$; $\text{var}(p) = I\sigma_p^2$; $\text{var}(e) = I\sigma_e^2 = R$ and $\text{var}(y) = ZAZ'A\sigma_a^2 + WIW'R + R$,

where σ_a^2 is the animal variance, σ_p^2 is the permanent environmental variance, σ_e^2 is the random residual variance, and **A** is the numerator relationship matrix between all cows considered in the data set. The size of the matrix **A** was 110,671 animals in the OAD population and 149,593 animals in the TAD population. Identity matrix (**I**) corresponds to the number of cows with

Table 1
Mean (coefficient of variation, %) for milk production traits by breed group and milking frequency.

| Breed | MF ^a | N | MY (kg) | FY (kg) | PY (kg) | SCS | FP (%) | PP (%) | P:F (%) |
|-------------------|-----------------|---------|--------------|--------------|--------------|-------------|-------------|------------|-------------|
| Holstein–Friesian | 1 | 16,936 | 3,275 (33.3) | 149.2 (32.4) | 122.2 (32.6) | 6.56 (21.4) | 4.61 (14.3) | 3.75 (7.4) | 0.82 (12.4) |
| | 2 | 57,018 | 4,503 (27.8) | 195.9 (27.6) | 162.1 (27.6) | 6.12 (21.0) | 4.39 (14.0) | 3.61 (7.2) | 0.83 (12.4) |
| Crossbred F × J | 1 | 71,066 | 3,009 (31.2) | 156.9 (30.3) | 121.8 (30.5) | 6.37 (20.7) | 5.28 (13.7) | 4.07 (7.7) | 0.78 (12.1) |
| | 2 | 109,339 | 3,973 (29.2) | 194.6 (28.0) | 152.1 (28.4) | 6.06 (20.7) | 4.96 (14.3) | 3.85 (7.7) | 0.79 (12.4) |
| Jersey | 1 | 36,618 | 2,575 (27.6) | 151.5 (28.1) | 110.6 (27.7) | 6.27 (20.0) | 5.91 (11.0) | 4.30 (6.6) | 0.73 (9.9) |
| | 2 | 28,274 | 3,234 (26.0) | 186.0 (26.6) | 133.7 (26.0) | 6.09 (20.0) | 5.77 (11.4) | 4.14 (7.1) | 0.72 (10.3) |

N=Number of observations; MY=milk yield; FY=fat yield; PY=protein yield; SCS=somatic cell score; FP=fat percentage; PP=protein percentage; P:F=protein to fat ratio.

^a MF=milking frequency, 1=milking once-daily and 2=milking twice-daily.

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