Genetic parameters for lactose and its relationship with concentrations and ratios of other milk components

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Abstract

The objective of this study was to estimate genetic parameters for milk yields, milk concentrations and ratios of milk components. Herd-test records from 268 Jersey cows from a Waikato dairy farm were obtained along with pedigree information. Genetic and phenotypic (co)variances for daily yields of milk (MY), fat (FY), protein (PY), milksolids (MSY; FY + PY) and lactose (LY), percentages of fat, protein, and lactose, and ratios of protein to fat (P:F) and protein to protein plus lactose (P:PL), and somatic cell score, were obtained with single trait and bivariate animal models using a restricted maximum likelihood methodology. The models included the fixed effects of month of calving and days in milk, modelled using an exponential curve, lactation number and the random effects of animal and cow permanent environment effects were also included in the model. Heritability estimates were 0.50 ± 0.12 (standard error) for MY, 0.25 ± 0.10 for FY, 0.30 ± 0.12 for PY, 0.27 ± 0.11 for MSY, 0.50 ± 0.12 for LY, 0.24 ± 0.04 for P:F ratio and 0.53 ± 0.04 for P:PL ratio. The genetic correlations for daily yields were high and positive. The genetic correlation between MSY and P:F ratio was -0.35 indicating that increases in MSY under the current breeding objective will decrease the P:F ratio, thus departing from an optimal ratio for whole milk powder processing.

Keywords: genetic parameters; lactose; ratios

Introduction

Estimations of genetic parameters for daily yields of milk (MY), fat (FY), protein (PY), milksolids (MSY) (FY + PY) and lactose (LY), percentages of fat (FP), protein (PP), and lactose (LP), and ratios of protein to fat (P:F) and protein to protein plus lactose (P:PL) and somatic cell score (SCS) in the same study are scarce in the literature. Most papers publish only a subset of these traits or an incomplete list of correlations (Roman et al. 1999; Johnson et al. 2000; Roman et al. 2000; Pryce & Harris 2006; Miglior et al. 2007). Roman & Wilcox (2000) obtained estimates of genetic parameters for 18 milk production traits using a bivariate animal model with 374 first lactation records collected between 1969 and 1987. In the present paper we have attempted to estimate the genetic parameters of 11 milk production traits in a single herd of 268 Jersey cows.

Determination of the heritable factors in milk production is an integral part of animal breeding, and genetic correlations are required to determine the response to selection on breeding objectives. The P:PL ratio is important for optimal processing of milk for whole milk powder. A P:PL ratio of approximately 0.39 (Geary et al. 2010) in milk is required to produce whole milk powder without having a requirement for standardisation. A ratio below 0.39 will require the addition of protein or the removal of lactose using ultra filtration. On the contrary, a ratio above 0.39 requires either the removal of protein using ultra filtration or the addition of lactose.

This paper reports the results of a pilot study conducted to develop a prototype model for the estimation of genetic parameters for production traits including lactose, which could be replicated using a larger data set representative of New Zealand dairy cattle.

Materials and methods

Data

The records used in this study were from a commercial dairy farm in the Waikato region of New Zealand (coordinates 38.17296 S, 175.828757 E) which included ancestry information for 268 Jersey cows sired by 58 Jersey bulls. The bulls are of both New Zealand and Danish bloodlines, with 16 of the bulls being bred from within the herd. The remainder of the bulls are of Livestock Improvement Corporation, CRV Ambreed, and Viking Genetics breeding.

Individual animal records for milk production from herd tests were collected during the 2011/12 production season. At the time of analysis, three herd tests were available for this study. The herd test data provided daily MY, FP, PP, LP, and somatic cell count (SCC). Fat percentage, PP and LP were determined by an infrared milk analyser (Foss MilkoScan FT120, Foss Electric, Hillerød, Denmark) to provide Fourier transform infrared spectral data where the lactose content is estimated as lactose monohydrate. From the herd test data FY, PY, LY, MSY, SCS, P:F ratio and P:PL ratio were calculated and subsequently used in the analysis. SCS was calculated as $\text{Log}_2(\text{SCC})$. Each herd-test became a repeated observation of the same cow in the same lactation.

Table 1 Mean, standard deviation, minimum and maximum values for the measured milk traits in a Jersey herd.

Trait	Mean	Standard deviation	Minimum	Maximum
Milk yield (kg/day)	16.2	3.7	6.7	29.1
Fat yield (kg/d)	0.83	0.19	0.22	1.65
Protein yield (kg/d)	0.64	0.14	0.29	1.05
Lactose yield (kg/d)	0.82	0.19	0.32	1.46
Milksolid yield (kg/d)	1.47	0.32	0.53	2.61
Fat content (%)	5.17	0.67	3.03	7.44
Protein content (%)	3.98	0.29	2.76	4.83
Lactose content (%)	5.09	0.15	4.61	5.58
Protein : Fat ratio	0.78	0.10	0.53	1.41
Protein : Protein + lactose ratio	0.44	0.02	0.35	0.51
Somatic cell count (cells/mL) (SCC)	121.0	244.4	10	3267
Somatic cell score ($\log_2$(SCC))	6.13	1.27	3.32	11.6

Data analysis

The data for lactation number had to be modified due to the sample size. This created four lactation groups, first lactation, second lactation, third lactation, and fourth and above lactations. The same characterisation was completed for calving month where three months of calving were condensed into two, July and August. Few cows calved outside of these two months.

Components of (co)variances to estimate heritability, repeatability and genetic correlations for the different traits were obtained using the statistical package ASREML (Gilmore et al. 2009) with a mixed linear model that included the fixed effects of lactation number, month of calving and days in milk modelled using an exponential curve (Wilmink 1987) and the random effects of cow, to account for repeated samples in the same cow, and an additive genetic animal effect. The pedigree file included 268 cows, 58 sires and 225 dams. The average number of daughters per sire was 4.6.

Heritability was calculated as $[\sigma^2_a/(\sigma^2_a + \sigma^2_c + \sigma^2_e)]$ and repeatability was calculated as $[(\sigma^2_a + \sigma^2_c)/(\sigma^2_a + \sigma^2_c + \sigma^2_e)]$ where σ^2_a, σ^2_c, and σ^2_e are the additive genetic, cow and residual variances, respectively.

Genetic correlations (r_g) were estimated as:

$$r_g = \frac{\sigma_{g12}}{\sigma_{g1} \times \sigma_{g2}}$$

where σ_{g12} is the genetic covariance between Trait 1 and Trait 2, equivalent to σ_{a12}; σ_{g1} is the genetic additive standard deviation for Trait 1, equivalent to $\sqrt{\sigma^2_{a1}}$; and σ_{g2} is the genetic additive standard deviation for Trait 2, equivalent to $\sqrt{\sigma^2_{a2}}$.

Phenotypic correlations (r_t) were estimated as:

$$r_t = \frac{\sigma_{t12}}{\sigma_{t1} \times \sigma_{t2}}$$

where σ_{t12} is the phenotypic covariance between Trait 1 and Trait 2, equivalent to $\sigma_{a12} + \sigma_{p12} + \sigma_{e12}$; σ_{t1} is the phenotypic standard deviation for Trait 1, equivalent to $\sqrt{\sigma^2_{a1} + \sigma^2_{p1} + \sigma^2_{e1}}$; and σ_{t2} is the phenotypic standard deviation for Trait 2, equivalent to $\sqrt{\sigma^2_{a2} + \sigma^2_{p2} + \sigma^2_{e2}}$.

Results

The average daily yields for the milk traits are shown in Table 1 along with their associated standard deviations and range values. This herd of cows is currently achieving above national average milk production, with higher daily milk, fat and protein yields. The national averages for Jersey cows are 13.7 kg milk, 0.78 kg fat and 0.57 kg protein per day (Livestock Improvement Corporation 2012).
Estimates of heritability and repeatability of the 11 traits are presented in Table 2 and genetic and phenotypic correlations are presented in Table 3.

Discussion

The estimated heritability for MY of 0.50 is higher than the 0.36 reported by Pryce & Harris (2006). These authors used a much larger data set containing 169,661 animals from the sire proving scheme and with a national breed representation. The standard errors of the estimates of heritability in this study were much larger than the standard errors reported by Pryce and Harris (2006). Most likely due to the small data set used in this study, as well as the single herd environment which reduces the levels of environmental effects which can be identified and accounted for. This is also evident when compared with the average h^2 results published in Johnson et al. (2000) of 0.27, 0.26, 0.20, and 0.26 for MY, FY, PY, and LY respectively. Overall, the heritability estimates are similar to published figures for small datasets of Jersey cattle (Roman et al. 2000).

The genetic correlations estimated in this study are comparable with both internationally (Maijala & Hanna 1976; Wilcox 1978; Welper & Freeman 1992; Roman & Wilcox 2000; Miglior et al. 2007) and nationally (Johnson et al. 2000, Pryce & Harris 2006) published figures. These estimates can be used to predict the responses to selection from different breeding objectives and selection indices. Selection on MSY may result in increases in MY, FY, PY and LY. However, the correlations between MY and the concentration and ratio traits were negative.

Table 2 Estimates of variance components, heritability and repeatability with their associated standard errors for milk production traits in a Jersey herd. Somatic cell score = $\log_2$ (Somatic cell count (cells/mL)).

Trait	Variance				Heritability	Repeatability
	Additive genetic	Permanent environment	Residual error	Total		
Milk yield (kg/day)	3.73	1.22	5.53	7.48	0.50 ± 0.12	0.67 ± 0.03
Fat yield (kg/d)	0.006	0.005	0.014	0.025	0.25 ± 0.10	0.45 ± 0.04
Protein yield (kg/d)	0.0033	0.0027	0.0047	0.01	0.30 ± 0.12	0.56 ± 0.04
Lactose yield (kg/d)	0.0095	0.0032	0.0064	0.019	0.50 ± 0.12	0.67 ± 0.03
Milksolid yield (kg/d)	0.017	0.015	0.030	0.062	0.27 ± 0.11	0.52 ± 0.04
Fat content (%)	0.12	0	0.24	0.36	0.33 ± 0.05	0.34 ± 0.05
Protein content (%)	0.039	0.002	0.025	0.066	0.58 ± 0.11	0.61 ± 0.04
Lactose content (%)	0.012	0	0.007	0.019	0.64 ± 0.03	0.64 ± 0.03
Protein : Fat ratio	0.002	0	0.007	0.010	0.24 ± 0.04	0.24 ± 0.04
Protein : Protein + lactose ratio	0.0017	0	0.0016	0.0033	0.53 ± 0.04	0.53 ± 0.04
Somatic cell score	0.48	0.34	0.69	1.52	0.33 ± 0.11	0.54 ± 0.04

Selection for increased yields may decrease SCS as the estimated genetic correlation between yields and SCS are negative. However, selection for increased concentration of milk components may increase the SCS in cows because the estimated genetic correlations between concentrations and SCS are positive.

The highest positive genetic correlation is that of MY and LY (0.99 ± 0.01). These two traits also have the highest phenotypic correlation (0.99 ± 0.01), which indicates that an increase in MY will be accompanied with an increase in LY. This, however, has a negative effect on LP as the genetic and phenotypic correlations between MY and LP are nil to negative. While this relationship between lactose and milk yield is well known, the authors wished to determine if the concentration of lactose could be altered through selection. For whole milk powder production it would be a positive step to be able to produce milk with a lower ratio between protein and solids not fat. In this study the herd-test data did not contain a measure of mineral content so P:PL ratio was calculated instead. The negative genetic correlation (-0.76 ± 0.15) between MY and P:PL ratio shows that an increase in MY could decrease the P:PL ratio and move populations under selection towards animals which produce a milk more suited to whole milk powder production. It is difficult to determine the validity of the genetic and phenotypic correlations for the P:PL ratio as few estimates for this parameter have been published. Instead parameters related to a fat to solids not fat ratio are published.

It can be seen in Table 3 that increases in total MSY have the potential effect of decreasing the P:F ratio over time with selection. This is most likely because increases in FY are greater than PY due to the larger genetic and phenotypic variation in FY. This herd does, however, appear to produce milk with a higher P:F ratio of 0.78 than the national average for Jersey cattle of 0.72 (Livestock Improvement Corporation 2012).

There is variation in both the LY and LP within the studied herd. It may therefore be inferred that this variation could be even larger across a larger genetic and environmental sample. The variation for LY could be as wide as 0.32 to 1.46 kg/day and the variation for LP as wide as 4.61 to 5.51%. While this variation is small, it is present and allows the possibility to selectively breed cows to increase the proportion of lactose in the milk. Larger variation in lactose content is seen in other studies (Johnson et al. 2007) where it is postulated that it is possible to split herds on their lactose percentage. This could decrease the P:PL ratio closer to levels required for efficient whole milk powder production, a ratio which is estimated to be 0.39 (Geary et al. 2010). In the studied herd this would require the P:PL ratio to be reduced from 0.44 to 0.39. This could be achieved by increasing the LY, as well as the LP of the milk. A change of the magnitude required would be difficult to achieve given the smaller genetic variation in this trait and the negative correlations with other production traits.

However, differences in P:PL ratios between farms are difficult to determine at the processing stage, because milk collection tankers contain milk from several farms with a range of P:PL ratios. As lactose is not a component of the current payment system, customisation of milk collection to avoid the mixing of milk from herds with varying P:PL ratios is impractical. As the values reported in this paper are only from one farm, wider industry data would be required to substantiate this hypothesis.

Conclusion

Estimates of h^2, repeatability, genetic and phenotypic (co)variances for the milk components and ratios in this pilot study were obtained using a small number of animals in a single Jersey herd. Despite the small size of the herd the derived genetic parameters

Table 3 Estimates of genetic correlations ± standard error below the diagonal, and phenotypic correlations ± standard error above the diagonal, for milk production traits in a Jersey herd. Somatic cell score calculated as $\log_2$ of the somatic cell count.

Trait	Milk yield (kg/d)	Fat yield (kg/d)	Protein yield (kg/d)	Lactose yield (kg/d)	Milksolids yield (kg/d)	Fat content (%)	Protein content (%)	Lactose content (%)	Protein to fat ratio	Protein to protein plus lactose ratio	Somatic cell score
Milk yield (kg/d)		0.79 ± 0.02	0.92 ± 0.01	0.99 ± 0.01	0.89 ± 0.01	-0.14 ± 0.04	-0.32 ± 0.05	-0.06 ± 0.06	-0.08 ± 0.05	-0.26 ± 0.05	-0.18 ± 0.05
Fat yield (kg/d)	0.83 ± 0.09		0.80 ± 0.02	0.77 ± 0.02	0.97 ± 0.01	0.46 ± 0.04	-0.11 ± 0.05	-0.15 ± 0.05	-0.54 ± 0.03	-0.03 ± 0.05	-0.13 ± 0.05
Protein yield (kg/d)	0.97 ± 0.09	0.81 ± 0.10		0.90 ± 0.01	0.92 ± 0.01	-0.05 ± 0.05	0.05 ± 0.05	-0.09 ± 0.05	0.03 ± 0.04	0.09 ± 0.05	-0.16 ± 0.05
Lactose yield (kg/d)	0.99 ± 0.01	0.81 ± 0.10	0.97 ± 0.05		0.86 ± 0.01	-0.17 ± 0.05	-0.34 ± 0.05	0.09 ± 0.06	-0.06 ± 0.05	-0.32 ± 0.05	-0.19 ± 0.05
Milksolids yield (kg/d)	0.91 ± 0.06	0.97 ± 0.02	0.95 ± 0.03	0.90 ± 0.06		0.28 ± 0.04	-0.05 ± 0.05	-0.14 ± 0.05	-0.34 ± 0.05	0.01 ± 0.05	-0.15 ± 0.05
Fat content (%)	-0.19 ± 0.19	-0.26 ± 0.33	-0.55 ± 0.28	-0.65 ± 0.19	-0.27 ± 0.32		0.28 ± 0.04	-0.19 ± 0.05	-0.82 ± 0.02	0.32 ± 0.04	0.06 ± 0.05
Protein content (%)	-0.84 ± 0.13	-0.87 ± 0.25	-0.83 ± 0.30	-0.87 ± 0.13	-0.95 ± 0.28	0.41 ± 0.17		-0.12 ± 0.06	0.28 ± 0.04	0.92 ± 0.01	0.09 ± 0.05
Lactose content (%)	-0.12 ± 0.18	-0.31 ± 0.23	-0.09 ± 0.22	0.02 ± 0.18	-0.28 ± 0.21	-0.17 ± 0.20	0.02 ± 0.17		0.14 ± 0.04	-0.46 ± 0.04	-0.07 ± 0.05
Protein to fat ratio	-0.07 ± 0.25	-0.53 ± 0.23	0.09 ± 0.30	0.01 ± 0.25	-0.35 ± 0.28	-0.61 ± 0.11	0.21 ± 0.22	0.47 ± 0.20		0.19 ± 0.04	0.03 ± 0.04
Protein to protein plus lactose ratio	-0.76 ± 0.15	-0.56 ± 0.25	-0.50 ± 0.26	-0.81 ± 0.14	-0.57 ± 0.24	0.54 ± 0.16	0.90 ± 0.02	-0.36 ± 0.13	0.01 ± 021		0.11 ± 0.05
Somatic cell score	-0.39 ± 0.23	-0.42 ± 0.28	-0.47 ± 0.28	-0.36 ± 0.23	-0.49 ± 0.29	0.19 ± 0.27	0.16 ± 0.22	0.16 ± 0.21	0.05 ± 0.29	0.07 ± 0.22	

compare well with published estimates. The farm used, while above the national breed average daily production for MY, PY, and FY, was also found to have a P:PL ratio that is above the optimal ratio (0.44 vs. 0.39) considered most suited for whole milk powder production. The derived estimates thus suggest that through selection on LY and LP it may be possible to develop animals which produce milk better suited to the production of whole milk powder. However blending of milk, as occurs with the standard collection procedures removes any potential differences between herds by blending milk from the high and low ratio herds. While benefiting whole milk powder production, selection on lactose concentration may have a negative effect of reducing the total yields of milk components; consequently reducing the total yield of milk products. Under the current milk pricing procedures this would result in a reduced net return per cow milked.

Acknowledgements

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