Breeding values for dairy products from New Zealand heifers

N.W. Sneddon[1, 2], N. Lopez-Villalobos[1], R.E. Hickson[1], S.R. Davis[3] D.J. Garrick[1], L. Shalloo[4]

[1] Massey University, School of Agriculture, Palmerston North, New Zealand
Nick.Sneddon@fonterra.com (Corresponding Author)
[2] Fonterra, On-Farm Research and Development, Palmerston North, New Zealand
[3] Livestock Improvement Corporation, Hamilton, New Zealand
[4] Dairy Production Department, Teagasc Moorepark, Fermoy, Co. Cork, Ireland

Summary

Different milk products require milk of different composition for their optimal processing and production. Selection has been proposed as a method to alter the composition of milk to meet these optimal processing requirements through breeding. By applying a milk processing sector model to data on 5,797 mixed breed animals, estimated milk product yields for whole milk powder, skim milk powder, butter and cheese were produced. Estimated breeding values (EBVs) for these milk products can be used directly in index rankings, creating a greater flexibility in breeding programs than currently exists.

Keywords: milk products, breeding values, dairy, New Zealand

Introduction

Some milks are better suited for manufacture than others, requiring less standardisation before processing into different milk products. One measure of the suitability of milk to produce whole milk powder (WMP) is the ratio of protein to protein-plus-lactose, with a ratio of 0.38 being near optimal (Geary *et al.,* 2010; Sneddon *et al.,* 2014; Sneddon *et al.,* 2015; Sneddon *et al.,* 2016a). The milk produced by cows in New Zealand is typically deficient in lactose relative to the protein content of milk for WMP (Sneddon *et al.,* 2014). Previous research has highlighted the potential to estimate the yields of dairy products from either individual cows or entire dairy industries given herd test or similar data (Auldist *et al.,* 2004; Geary *et al.,* 2010; Capper & Cady, 2012; Bittante *et al.,* 2013; Bittante *et al.,* 2014; Sneddon *et al.,* 2015; Sneddon *et al.,* 2016a). These studies generate data which can be used to estimate the heritabilities for potential yields of different dairy products, including skim milk powder (SMP), WMP, cheese and butter (Sneddon *et al.,* 2016a).

The linear model software used to estimate the heritabilities of these different estimated product yields also produces estimated breeding values (EBVs) from the same analysis. If these product yield estimations are conducted on data held on animals within national databases it is possible that EBV for predicted product yields could be produced for all animals within a country. This study aimed to investigate whether EBVs for estimated milk product yields can be produced from a large dataset comprising animals with milk herd test records.

Material and methods

A milk-processing model developed at Massey University (Garrick & Lopez-Villalobos, 2000) which uses a mass-balance approach based on available fat, protein and lactose, was used to estimate yields of milk products for individual heifers at each herd test. Four scenarios were investigated representing different product portfolios; these were 100% of milk used for either WMP, SMP, cheese or butter. The model produced the maximal amount of the desired product given available components, with excess protein or fat being used to manufacture "by-products" which depending on the scenario were SMP (when producing butter), butter (when producing SMP), butter milk powder (BMP), casein or whey powder (WP).

Data

Herd-test records for milk, fat, protein and lactose (as monohydrate, back calculated to anhydrate (Sneddon *et al.,* 2015a) were available from 5,797 mixed-breed Livestock Improvement Corporation Sire Proving Scheme heifers from the 2010-2011 dairy season (Sneddon *et al.,* 2015a). The data comprised 1,056 Friesian (F), 774 Jersey (J) and 3,967 FxJ heifers. Total lactation yields of milk (TMY), fat (TFY), protein (TPY), lactose (TLY) and estimated yields of WMP, SMP, butter and cheese were calculated as the area under the curve from individual lactation curves modelled fitting a 5th order Legendre polynomial for milk, fat, protein, lactose, WMP, SMP, butter, cheese and somatic cell score (SCS; calculated as Log_2 (somatic cell count)) using ASReml (Gilmour *et al.,* 2009).

Breed and heterosis effects

Least squares means for estimates of breed averages were obtained using a linear model in SAS version 9.4 (SAS Institute Inc., Cary NC, USA) with fixed effects of breed, month of calving and herd. Heterosis and breed effects were estimated using a linear model that included the fixed effects of month of calving and herd as class effects, and proportion of J, proportion of other breeds (including Ayrshire, Shorthorn, Brown Swiss) and heterosis between F and J, each fitted as covariates.

Genetic parameters

Single-trait animal models were used for estimation of heritabilities then bivariate animal models were used for estimation of genetic and phenotypic correlations. In matrix notation, the bivariate models can be represented as:

= (1)

where $\mathbf{y_1}$ and $\mathbf{y_2}$ are the vectors of total lactation phenotypic measures for the two traits, $\mathbf{X_1}$, $\mathbf{X_2}$, $\mathbf{Z_1}$ and $\mathbf{Z_2}$ are design matrices relating the fixed and additive genetic effects to the phenotypes, $\mathbf{b_1}$ and $\mathbf{b_2}$ are the vectors of fixed effects of herd, deviation from mean calving date (per herd), the proportion of J or other and pairwise heterosis coefficients of F×J, F×other and J×other, $\mathbf{u_1}$ and $\mathbf{u_2}$ are the vectors of random effects of animal for each trait, $\mathbf{e_1}$ and $\mathbf{e_2}$ are vectors of residual errors. The distributional properties were as follows:

E and Var = (2)

where **A** is the numerator relationship matrix of order 8,930, the total number of animals in the pedigree file; σ^2_{a1}, σ^2_{a2} and σ_{a12} are the animal (co)variance components for two traits; $\mathbf{I_1}$ is an identity matrix of order 5,797, the number of animals with lactation records; σ^2_{e1}, σ^2_{e2} and σ_{e12} are the residual (co)variance components for the traits. Estimates of (co)variance components were obtained using the Restricted Maximal Likelihood procedure in ASReml (Gilmour *et al.,* 2009). Heritability (h^2) was calculated as $h^2 =$ / ().

Estimated across-breed breeding values for TMY, TFY, TPY, TLY, fat percentage (FP), protein percentage (PP), lactose percentage (LP), protein-to-protein-plus-lactose ratio (P:PL), SCS, WMP, SMP, butter and cheese were calculated by adding the fixed effects estimates of the breed effects to the individual animal effects. Average breeding values for each breed were calculated for heifers, dams and sires. Liveweights for expressing product yields per kg or per ha were assumed to be 480, 440 and 400 kg for F, FxJ and J heifers respectively, based on published industry statistics (LIC & DairyNZ 2016). A stocking rate of 1,260kg liveweight/ha was chosen to express product yields per ha while representing the national average stocking rate of 2.86 for the FxJ breed group (LIC & DairyNZ 2016). Product yields per 1000 L of milk were calculated by dividing product yield by milk volume and multiplying by 1000.

Results

The total lactation yields, total lactation milk product potentials, heritabilities, heterosis and breed effect estimates are shown in Table 1. The J and FxJ heifers had greater estimated yields of butter than F heifers, while J heifers had the lowest estimated yields of WMP and SMP. Cheese yield was greatest from FxJ heifers, with no difference between J and F heifers. There was positive heterosis for butter and cheese yields, however, heterosis values for WMP and SMP were not significant.

The mean EBVs for milk yield and its components, as well as predicted milk product yields are shown in Table 2. All EBVs are relative to a base animal which produced 2,912 kg TMY, 123.4 kg TFY, 102.7 kg TPY and 149.8 kg TLY. Crossbred animals were the only animals with a consistent positive mean EBV for TMY, F had the lowest mean EBVs for TFY for sires, dams and heifers, while J animals had the lowest mean EBVs for TPY and TLY for sires, dams and heifers. For the concentration traits, J animals had the greatest mean EBVs for FP, PP, LP and P:PL F animals had the lowest mean EBVs for concentrations and FxJ EBVs between F and J animals. The J animals had the lowest mean EBVs for WMP, SMP and cheese yields, and had higher or similar EBVs for butter compared to FxJ animals for sires, dams and heifers.

The correlations between traits are in Table 3. There was no significant phenotypic correlation between TFY and P:PL, or genetic correlation between FP and LP. There were positive genetic and phenotypic correlations between total yield traits and milk product yields. Protein percentage had a negative genetic correlation with all product traits except for cheese which was not significant, LP had a genetic and phenotypic correlations with both WMP and SMP, and a negative genetic correlations with butter.

Table 4 presents the estimated product yields per kg of liveweight, per ha and per 1000 L of milk. The J heifers were estimated to produce greater yields of butter and cheese per kg of liveweight, per ha, and per 1000 L of milk. The F heifers were estimated to produce greater yields of WMP and SMP per 1000L of milk, there were no differences in WMP or SMP yields per kg and per ha between F or J heifers.

Table 1. Means and standard errors of lactation yields, breed effects, heterosis, and heritabilities of milk and milk product potentials from Holstein-Friesian (F), Jersey (J) and crossbred (FxJ) first lactation heifers.

	F		FxJ		J		Breed effect			Heterosis			h^2
	Mean	SE	Mean	SE	Mean	SE	F-J	SE	P-value	FxJ	SE	P-value	
Days in Milk	212[b]	1.81	214[a]	1.71	213[ab]	1.94	-1.78	1.58	0.264	1.97	1.30	0.130	
Milk yield (kg)	3121.8[a]	48.3	2947.0[b]	45.7	2751.6[c]	51.7	633.3	41.5	<.001	93.6	34.2	0.006	0.23 ± 0.04
Fat yield (kg)	142.9[c]	2.25	149.9[a]	2.13	147.0[b]	2.41	-1.00	1.96	0.610	11.8	1.62	<.001	0.15 ± 0.04
Protein yield (kg)	113.6[a]	1.69	112.3[a]	1.59	107.7[b]	1.80	12.5	1.46	<.001	5.86	1.20	<.001	0.14 ± 0.03
Lactose yield (kg)	160.0[a]	2.47	151.6[b]	2.34	142.0[c]	2.64	30.9	2.12	<.001	5.06	1.75	0.004	0.22 ± 0.04
Fat percentage	4.63[c]	0.05	5.11[b]	0.05	5.38[a]	0.06	-1.09	0.04	<.001	0.16	0.04	<.001	0.45 ± 0.06
Protein percentage	3.70[c]	0.02	3.86[b]	0.02	3.97[a]	0.02	-0.39	0.02	<.001	0.05	0.02	0.002	0.40 ± 0.05
Lactose percentage	4.86[c]	0.01	4.88[b]	0.01	4.89[a]	0.01	-0.05	0.01	<.001	0.01	0.01	0.942	0.35 ± 0.05
Protein-to-protein-plus-lactose ratio	0.42[a]	0.002	0.43[b]	0.002	0.44[c]	0.002	-0.02	0.001	<.001	0.003	0.001	0.002	0.42 ± 0.06
Somatic cell score	5.89	0.09	5.92	0.09	5.87	0.11	0.01	0.08	0.936	0.07	0.07	0.325	0.11 ± 0.03
Whole milk powder (kg)	347.6[a]	6.08	316.6[b]	5.75	290.2[c]	6.51	92.6	5.20	<.001	4.74	4.29	0.26	0.31 ± 0.05
Skim milk powder (kg)	232.0[a]	4.09	210.9[b]	3.87	193.1[c]	4.38	62.7	3.49	<.001	2.94	2.88	0.308	0.31 ± 0.04
Butter (kg)	168.8[b]	2.84	179.1[a]	2.68	176.3[a]	3.04	26.1	4.86	<.001	25.4	4.01	<.001	0.16 ± 0.04
Cheese (kg)	358.9[b]	5.60	364.9[a]	5.30	351.6[b]	5.99	-4.86	2.47	0.049	15.3	2.04	<.001	0.13 ± 0.03

Values with different letters denote significant differences P<0.05.

Table 2. Mean estimated breeding values for milk yield, components and estimated milk products from Holstein-Friesian (F), Jersey (J) and crossbred (FxJ) first lactation heifers, dams and sires.

	Base cow	Sires			Dams			Heifers		
		F	FxJ	J	F	J	FxJ	F	J	FxJ
N		99	74	107	632	401	1820	1056	774	3967
Milk yield (kg)	2912	-3.75	5.58	-27.15	-2.41	-2.59	1.20	2.15	0.31	6.02
Fat yield (kg)	123.4	-0.42	2.62	1.91	0.01	1.93	2.11	0.16	2.01	1.75
Protein yield (kg)	102.7	-0.18	-4.68	-10.89	-0.13	-10.82	-4.37	-0.06	-10.78	-4.65
Lactose yield (kg)	149.8	-0.33	-12.07	-28.02	-0.28	-27.71	-11.27	-0.16	-27.60	-11.99
Fat percentage	4.31	-0.02	0.50	1.00	0.01	0.99	0.44	0.01	1.00	0.46
Protein percentage	3.49	-0.004	0.15	0.36	0.002	0.35	0.14	0.002	0.35	0.15
Lactose percentage	4.79	-0.003	0.02	0.05	0.0004	0.05	0.01	0.002	0.05	0.02
Protein-to-protein-plus-lactose ratio	40.1	-0.01	0.87	1.98	0.01	1.94	0.79	0.01	1.96	0.85
Somatic cell score	5.41	0.003	-0.05	0.05	0.00	0.04	-0.05	0.002	0.05	-0.02
Whole milk powder (kg)	338	-0.77	-36.45	-84.19	-0.79	-82.98	-34.16	-0.51	-82.85	-36.18
Skim milk powder (kg)	226	-0.50	-24.74	-57.08	-0.54	-56.25	-23.19	-0.34	-56.16	-24.54
Butter (kg)	335	-0.25	4.03	4.00	0.06	3.97	3.74	0.38	4.07	3.08
Cheese (kg)	318	-0.52	-8.03	-23.38	-0.27	-23.03	-7.66	0.08	-22.97	-8.90

Table 3. Estimated genetic and phenotypic correlations for milk yield, components and estimated product yields.

	TMY	TFY	TPY	TLY	FP	PP	LP	P:PL	SCS	WMP	SMP	Butter	Cheese
TMY		0.75	0.93	0.99	-0.35	-0.31	-0.06ns	-0.24	-0.07	0.95	0.95	0.73	0.88
TFY	0.43		0.84	0.74	0.31	0.10	-0.07	0.14	-0.03ns	0.60	0.59	0.94	0.91
TPY	0.87	0.54		0.91	-0.14	0.05ns	-0.06ns	0.09	-0.05ns	0.80	0.79	0.82	0.96
TLY	0.98	0.40	0.82		-0.36	-0.31	0.09	-0.30	-0.09	0.97	0.97	0.72	0.87
FP	-0.68	0.37	-0.46	-0.70		0.67	-0.04ns	0.60	0.07	-0.50	-0.50	0.27	0.01ns
PP	-0.70	-0.11	-0.26	-0.74	0.83		-0.01ns	0.93	0.08	-0.50	-0.50	0.13	0.07
LP	-0.17	-0.21	-0.30	0.02ns	-0.04ns	-0.11		-0.37	-0.15	0.15	0.15	-0.05ns	-0.04ns
P:PL	-0.58	-0.04ns	-0.14	-0.68	0.60	0.94	-0.44		0.13	-0.49	-0.50	0.18	0.11
SCS	-0.19	0.07	-0.17	-0.21	0.24	0.14	-0.12	0.16		-0.11	-0.11	-0.01ns	-0.04ns
WMP	0.94	0.26	0.68	0.98	-0.76	-0.84	0.12	-0.81	-0.21		0.99	0.58	0.74
SMP	0.93	0.26	0.67	0.97	-0.76	-0.84	0.13	-0.82	-0.21	0.99		0.58	0.74
Butter	0.45	0.99	0.54	0.40	0.35	-0.14	-0.26	-0.05ns	0.03ns	0.27	0.26		0.88
Cheese	0.76	0.79	0.92	0.72	-0.18	-0.03ns	-0.02ns	-0.08	-0.10	0.57	0.56	0.81	

TMY: Total Milk Yield, TFY: Total Fat Yield, TPY: Total Protein Yield, FP: Fat Percentage, PP: Protein Percentage, LP: Lactose Percentage, P:PL: Protein-to-Protein-plus-Lactose Ratio, SCS: Somatic Cell Score, WMP: Whole Milk Powder, SMP: Skim Milk Powder.
Genetic correlations shown below the diagonal and phenotypic above.
NS = Correlation not significantly different from zero P>0.05.

Table 4. Milk product yields per kg of liveweight, per ha, and per 1000 L of milk for Holstein-Friesian (F), Jersey (J) and FxJ crossbred heifers

	Per kg of liveweight			Per hectare (ha)			Per 1000 litres of milk		
Product	F	FxJ	J	F	FxJ	J	F	FxJ	J
Measure	480 kg	440 kg	400 kg	1,260 kg/ha (2.63 cows/ha)	1,260 kg/ha (2.86 cows/ha)	1,260 kg/ha (3.15 cows/ha)			
WMP	0.724	0.720	0.726	912.5	906.6	914.1	111	107	105
SMP	0.483	0.479	0.483	609.0	603.9	608.3	74	72	70
Butter	0.352	0.407	0.441	443.1	512.9	555.3	54	61	64
Cheese	0.748	0.829	0.879	942.1	1044.9	1107.5	115	124	128

WMP: Whole Milk Powder, SMP: Skim Milk Powder.

Discussion and Conclusion

The use of BLUP procedures in conjunction with milk processing modelling and estimation of product yields could allow for the production of EBVs for dairy product yields at the same time as generating EBVs for milk and milk components as part of a standard national breeding program. Previous studies have found that selection on P:PL as a predictor of WMP production would have a negative impact on the suitability of milk for WMP (Sneddon *et al.,* 2016b), as this was due to the imbalance in the heritabilities of the numerator and denominator in this ratio, (0.29 for protein percentage and 0.50 for lactose percentage, Gunsett, 1984). Accordingly, considerable emphasis would be required to make a small change in genetic gain for this aggregate trait. It has been proposed that selection on milk product estimates themselves could be conducted, however, before this can be investigated their heritabilities had to be calculated (Bittante *et al.,* 2013, Bittante *et al.,* 2014, Sneddon *et al.,* 2016a) and it had to be determined if EBVs for milk product yields could be calculated using processing modelling with nationally recorded data.

The correlations between milk products and total milk yields were positive, with TLY and WMP being highly correlated. The negative correlation between P:PL and WMP and SMP is expected as the current P:PL is above optimal for WMP production (Sneddon *et al.,* 2014). As expected an increase in total yields of milk components increases the total product yield possible from that milk. More concentrated milks are better suited to the production of cheese and butter (Auldist *et al.,* 1996; Sneddon *et al.,* 2016c) and therefore require a different product portfolio in order to optimise the outputs of products from the milk. In the study of Sneddon *et al.* (2016c) the yields of WMP and SMP per 1000 L were greater from F and FxJ animals, with a lower P:PL in milk from F and FxJ animals overcoming the more concentrated milk of the J animals. Increasing the concentration of milk components may not necessarily increase the total yields of milk products where there is an optimal ratio of milk components, such as WMP or SMP. For example, J heifers have a greater PP in their milk, however, the increase in LP is not of the same order which decreases their WMP potential relative to F heifers (Sneddon *et al.,* 2016c). In the study of Sneddon *et al.* (2016b) differential selection upon MY and LY allowed selection index theory to move the population average towards the optimal milk composition faster than a very high relative weighting on a ratio trait, with little impact on the other traits of interest. However, there is a risk that if the product portfolio changes due to volatile changes in demand the milk will no longer be optimal for the new product mix.

This study has shown that it may be possible to run milk processing models on milk test records held in national databases to produce genetic parameters, heterosis values and EBVs for milk products when conducting routine animal evaluations. There may be a requirement to run the milk processing models separate from the national animal evaluations, where the outputs of milk processing models are then attributed to the animals which had these yields estimated. The production of milk product genetic parameters and breeding values may allow for greater flexibility to be built into dairy industries over time. As product mixes change to meet export market requirements the product EBVs within the national breeding objective could be altered to move the national herd towards this future goal. Future research should evaluate the potential for including these product traits into selection indices to determine the impact of selection on a trait for a milk product yield.

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