Genetic correlations of milk fatty acid contents predicted from milk mid-infrared spectra in New Zealand dairy cattle

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ABSTRACT

The objective of this study was to estimate genetic correlations among milk fatty acid (FA) concentrations in New Zealand dairy cattle. Concentrations of each of the most common FA, expressed as a percentage of the total FA, were determined by gas chromatography on a specific cohort of animals. Using this data set, prediction equations were derived using mid-infrared (MIR) spectroscopy data collected from the same samples. These prediction equations were applied to a large data set of MIR measurements in 34,141 milk samples from 3,445 Holstein-Friesian, 2,935 Jersey, and 3,609 crossbred Holstein-Friesian × Jersey cows, sampled an average of 3.42 times during the 2007–2008 season. Data were analyzed using univariate and bivariate repeatability animal models. Heritability of predicted FA concentration in milk fat ranged from 0.21 to 0.42, indicating that genetic selection could be used to change the FA composition of milk. The *de novo* synthesized FA (C6:0, C8:0, C10:0, C12:0, and C14:0) showed strong positive genetic correlations with each other, ranging from 0.24 to 0.99. Saturated FA were negatively correlated with unsaturated (−0.93) and polyunsaturated (−0.84) FA. The saturated FA were positively correlated with milk fat yield and fat percentage, whereas the unsaturated FA were negatively associated with fat yield and fat percentage. Our results indicate that bovine milk FA composition can be changed through genetic selection using MIR as a phenotypic proxy.

Key words: genetic correlations, infrared spectrometry, crossbreeding

INTRODUCTION

The breeding goal for New Zealand dairy cattle has been to increase net farm income per unit of feed, with little focus given to improving the composition of milk proteins and fatty acids (FA). Cow milk fat typically contains 70% SFA, 25% MUFA, and 5% PUFA (Grummer, 1991). The FA composition of milk fat influences the technological properties of butter (MacGibbon and McLennan, 1987; MacGibbon and Taylor, 2006). Increasing the concentrations of C18:1 and C18:2 and reducing the concentrations of C8:0 to C14:0 FA improves the solid fat content at 10°C and, therefore, the spreadability of butter (MacGibbon and McLennan, 1987).

The concentration of FA in milk fat is affected by several factors (Hanuš et al., 2018), including diet (Palmquist et al., 1993; Dewhurst et al., 2006), stage of lactation and parity (Niero et al., 2016; Gottardo et al., 2017; Samková et al., 2018), and the natural genetic variation between cows (Soyeurt et al., 2006b; Stoop et al., 2008; Lehnert et al., 2015) and breeds (Auldist et al., 2004; Soyeurt et al., 2006b; Gottardo et al., 2017). Concentrations of individual FA are heritable (Arnould and Soyeurt, 2009; Krag et al., 2013; Bilal et al., 2014), indicating that there is sufficient genetic variation in FA content to implement a selection program to improve FA composition. However, the determination of individual concentrations of FA in individual cows through GC analyses is expensive and time consuming. Several studies (Soyeurt et al., 2006a; De Marchi et al., 2011; Lopez-Villalobos et al., 2014) have shown that it is possible to estimate FA concentrations by mid-infrared spectrometry. This technology is faster and cheaper than the reference chemical analysis. Using the predicted concentrations of individual FA by mid-infrared spectrometry, Soyeurt et al. (2006b, 2007) and Lopez-Villalobos et al. (2014) studied the genetic variation of FA and the differences across dairy breeds.

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Alteration of the fatty acid profile of cow milk can be desirable for 2 reasons (Hanuš et al., 2018): (1) from a human nutritional point of view, a lower proportion of SFA and a higher proportion of UFA, especially PUFA n-3, is desirable; and (2) from a processability point of view, higher proportions of UFA are preferred (i.e., easier spreadability of butter is desirable for consumers). The relationship between the amount of SFA in the diet for humans and the incidence of cardiovascular and coronary heart diseases has been widely investigated over several decades. However, recent reviews still do not reach consensus as to risks to the consumer from saturated fat intake (Lopez-Huertas, 2010; Hanuš et al., 2018; German et al., 2019). There are also problems associated with having high UFA content in milk fat, including its lower stability, increased oxidation, and possible sensory changes.

The desired FA profile of cow milk is still unknown and, therefore, a directional change in the fatty acid profile is difficult. Gibson (1991) and Majjala (2000) concluded that it was difficult to define the desired direction of change in milk fat composition before 2000. By 2009, Stoop (2009) reported that experts from the Netherlands suggested producing milk with lower fat percentage, lower proportions of C14:0 and C16:0, and higher proportions of UFA. At the present time (2020), the market for butter is forcing a reanalysis of these desired changes but based on updated knowledge on the effect of the FA profile on human health, milk fat processability into butter, cheese, and ice cream, shelf-life of dairy products, and flavors. If there were a market or processor drive for specific FA, this could be a method by which to alter the FA composition of milk and therefore the final product or product mix. Making desirable changes to the milk FA profile requires knowledge of the genetic and phenotypic correlations between FA to develop selection indices by which to select animals with the desired profile without affecting negatively production, reproduction, and survival traits. The objective of this study was to estimate genetic and phenotypic correlations for FA in pasture-fed New Zealand dairy cows.

MATERIALS AND METHODS

Calibration Equations

The method to develop the calibration equations to predict the most common FA was described by Lopez-Villalobos et al. (2014). A total of 848 milk samples were collected during the season 2003–2004 from 348 second-parity crossbred Holstein-Friesian × Jersey cows during peak, mid, and late lactation. These cows were part of a crossbreeding experiment designed to identify

QTL determining traits of economic importance in New Zealand dairy cattle (Spelman et al., 2001). Concentrations of FA in the 848 milk samples were determined by GC. The same milk samples were analyzed on a Foss MilkoScan FT6000 (Foss, Hillerød, Denmark) to provide the mid-infrared spectra. Wavenumbers related to water absorbance were removed from the spectra because these bands were found to have high noise levels (from 1,600 to 1,689 and from 3,048 to 3,666 cm^{-1}).

A principal component analysis using SAS software (version 9.1; SAS Institute Inc., Cary, NC) was undertaken across all FA and whole spectra to calculate the Mahalanobis distance for each sample. A sample was considered an outlier when the value of the FA or spectrum differed from the mean of the population by 3 or more times the Mahalanobis distance. Using this threshold, 12 of the 848 samples were considered outliers and discarded.

The calibration equation for each FA was determined using partial least squares using SAS (version 9.1; SAS Institute Inc.). The optimum number of partial least squares (PLS) factors was determined by cross-validation from a maximum of 15 PLS factors allowed in the model. Fatty acid groups were defined by saturation (SFA and UFA) and by carbon chain length; short-chain (**SCFA**; 4 to 8 carbons), medium-chain (**MCFA**; 10 to 12 carbons), and long-chain (**LCFA**; 14 to 22 carbons). The coefficients of determination of cross-validation (R^2_{CV}) for the prediction equations were reported by Lopez-Villalobos et al. (2014). The R^2_{CV} to predict C8:0, C10:0, C12:0, C18:1 *cis*-9, and for groups of FA C18:1, MCFA, LCFA, SFA, and UFA were >0.8, and those for C4:0, C6:0, C14:0, C16:0, and PUFA were >0.70. The R^2_{CV} to predict n-3 and n-6 were lower (0.44 and 0.66, respectively).

Estimation of Breed Effects and Variance Components

The calibration equations were used to predict the concentration of each FA in milk fat in 34,141 milk samples from 3,445 Holstein-Friesian, 2,935 Jersey, and 3,609 crossbred Holstein-Friesian × Jersey cows sampled, on average, 3.42 times during the 2007–2008 season. These milk samples were part of the herd-testing program used to determine concentrations of fat, protein, lactose, and SCC in a Foss MilkoScan FT6000 instrument (Foss). For statistical analysis, SCC was analyzed as SCS, calculated as $\log_2(\text{SCC}/1,000)$. The Fourier-transform infrared spectrum for each milk sample was provided by Livestock Improvement Corp. (Hamilton, New Zealand). The same statistical procedure applied to the calibration data set was followed in this data set. Wavenumbers related to water

absorbance were removed and milk samples defined as outliers based on the Mahalanobis distance using principal components were discarded. No further edits were applied to the predicted values. The calibration data set (836 records) was merged with the prediction data set (34,141 records), and principal components analysis were performed on the spectra to evaluate variation in the spectra between the 2 data sets.

The cows were of different parities and distributed in 266 herds used for progeny testing of young bulls. The number of sires of the daughters providing records was 1,422. (Co)variance components to estimate heritability and repeatability for each predicted FA and genetic and phenotypic correlations among them were obtained using the statistical package ASReml version 3.0 (Gilmour et al., 2009) with univariate and bivariate repeatability animal models. In matrix notation, the bivariate model can be represented as follows:

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_2 \end{bmatrix} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{W}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{W}_2 \end{bmatrix} \begin{bmatrix} \mathbf{c}_1 \\ \mathbf{c}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix},$$

where $\mathbf{y}_1$ and $\mathbf{y}_2$ are the vectors of total lactation phenotypic measures for the 2 traits; $\mathbf{X}_1$, $\mathbf{X}_2$, $\mathbf{Z}_1$, $\mathbf{Z}_2$, $\mathbf{W}_1$, and $\mathbf{W}_2$ are design matrices relating the fixed, additive genetic, and cow permanent effects to the phenotypes, $\mathbf{b}_1$ and $\mathbf{b}_2$ are the vectors of fixed effects of parity number (1 to 10), herd-test-day, month of calving, the proportion of Jersey (proportion of Holstein-Friesian was not included in the model to avoid linear dependencies and was used as a base for comparison), heterosis Holstein-Friesian $\times$ Jersey for cows with records, $\mathbf{a}_1$ and $\mathbf{a}_2$ are the vectors of random effects of animal for each trait, $\mathbf{c}_1$ and $\mathbf{c}_2$ are the vectors of random effects of cow permanent environment for each trait, and $\mathbf{e}_1$ and $\mathbf{e}_2$ are vectors of residual errors. The distributional properties of the model with E and Var indicating the expectation and variance were as follows:

$$E \begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{bmatrix}$$

and

$$\text{Var} \begin{bmatrix} \mathbf{a}_1 \\ \mathbf{a}_2 \\ \mathbf{c}_1 \\ \mathbf{c}_2 \\ \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{A}\sigma_{a1}^2 & \mathbf{A}\sigma_{a1a2} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{A}\sigma_{a1a2} & \mathbf{A}\sigma_{a2}^2 & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{I}_1\sigma_{c1}^2 & \mathbf{I}_1\sigma_{c1c2} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{I}_1\sigma_{c1c2} & \mathbf{I}_1\sigma_{c2}^2 & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}_2\sigma_{e1}^2 & \mathbf{I}_2\sigma_{e1e2} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}_2\sigma_{e1e2} & \mathbf{I}_2\sigma_{e2}^2 \end{bmatrix},$$

where $\mathbf{A}$ is the numerator relationship matrix of order equal to the total number of animals in the pedigree file; σ_{a1}^2 , σ_{a2}^2 , and σ_{a1a2} are the animal (co)variance components for the 2 traits; $\mathbf{I}_1$ is an identity matrix of order equal to the number of animals with lactation records; σ_{c1}^2 , σ_{c2}^2 , and σ_{c1c2} are the cow permanent (co)variance components for the traits; $\mathbf{I}_2$ is an identity matrix of order equal to the number of records; and σ_{e1}^2 , σ_{e2}^2 , and σ_{e1e2} are the residual (co)variance components for the traits. Heritability (h^2) and repeatability (t) of a trait were calculated as

$$h^2 = \frac{\sigma_a^2}{\sigma_p^2} \text{ and}$$

$$t = \frac{\sigma_a^2 + \sigma_c^2}{\sigma_p^2},$$

and genetic (r_G) and phenotypic (r_P) correlations were calculated as

$$r_G = \frac{\sigma_{a1a2}}{\sigma_{a1} \times \sigma_{a2}} \text{ and}$$

$$r_P = \frac{\sigma_{p1p2}}{\sigma_{p1} \times \sigma_{p2}},$$

where σ_P^2 is the phenotypic variance for any trait calculated as $\sigma_P^2 = \sigma_a^2 + \sigma_c^2 + \sigma_e^2$.

RESULTS

Mean and Coefficient of Variation

Descriptive statistics of daily milk production levels and concentrations of the main FA are presented in Table 1. Mean daily milk yield was 17.07 L/d and contents of fat, protein and lactose were 4.93, 3.79, and 4.87%, respectively. Milk yield traits had higher coefficients of variation (**CV**) than contents of milk components and FA. A low CV (4%) was found for SCFA (C4:0 to C8:0) and higher CV (13%) was found for MCFA. The highest CV were found for n-6 (23%), C18:2 *cis*-9,*trans*-11 (26%), and C20:0 (33%). The CV for the entire SFA and UFA were low, 4 and 9%, respectively, and PUFA had a higher CV (11%).

Saturated FA averaged 71.09%, UFA averaged 28.95%, and PUFA averaged 4.10% of the total FA.

The most abundant SFA were C14:0, C16:0, and C18:0, averaging 10.53, 23.92, and 12.20% of the total FA, respectively. The FA C18:1 *cis*-9, the most prominent among the UFA, averaged 16.95% of the total FA. The mean of LCFA was 78.75%, with a large range from 66.93 to 100.29%. Supplemental Figure S1 (<https://doi.org/10.3168/jds.2019-17971>) shows the distribution of milk samples from the 2 data sets (calibration and prediction) along the 2 principal components. It can be observed that the calibration data set is fully represented in the prediction data set.

Heritabilities and Repeatabilities

Estimates of variance components, heritabilities, and repeatabilities of daily milk yields and concentration of the main FA are presented in Table 2. These estimates were obtained using the univariate repeatability animal model. Estimates of heritability and repeatability for percentages of fat, protein, and lactose were higher than the respective estimates for yields of fat, protein, and lactose. Estimates of h^2 for SFA were higher than estimates of h^2 for UFA and PUFA. The standard errors of

Table 1. Descriptive statistics of daily yields of milk, fat, protein and lactose, and concentrations of fat, protein, lactose, and fatty acids (FA) in New Zealand cows sampled in 2007 (n = 34,140)

Trait	Mean	SD	CV	Minimum	Maximum
Milk yield, kg/d	17.07	6.45	38	0.60	50.20
Fat yield, kg/d	0.81	0.27	33	0.02	2.34
Protein yield, kg/d	0.63	0.22	35	0.02	1.97
Lactose yield, kg/d	0.83	0.32	39	0.03	2.51
Fat, %	4.93	0.92	19	2.22	8.11
Protein, %	3.79	0.42	11	2.55	5.73
Lactose, %	4.87	0.19	4	4.23	5.40
SCS ¹	6.33	1.65	26	2.32	14.27
Fatty acid, % of total FA					
C4:0	4.14	0.23	6	2.95	4.89
C6:0	2.62	0.12	5	2.10	3.24
C8:0	1.64	0.11	7	1.14	2.19
C10:0	3.63	0.40	11	1.91	5.49
C10:1	0.26	0.04	15	0.14	0.44
C12:0	3.79	0.54	14	1.81	6.19
C12:1	0.13	0.02	15	0.08	0.21
C14:0	10.53	1.03	10	7.15	14.98
C16:0	23.92	2.39	10	16.71	32.97
C18:0	12.20	2.77	23	1.44	25.45
C18:1 <i>cis</i> -9	16.95	2.37	14	8.39	24.76
C18:1 <i>cis</i> -7	4.64	0.96	21	1.44	8.04
C18:2 <i>cis</i> -9, <i>cis</i> -12	1.21	0.21	17	0.52	2.13
C18:2 <i>cis</i> -9, <i>trans</i> -11	0.84	0.22	26	0.01	1.77
C20:0	0.12	0.04	33	0.01	0.22
n-3 ²	1.12	0.18	16	0.50	1.84
n-6 ³	1.28	0.29	23	0.23	2.36
SCFA ⁴	8.40	0.37	4	6.45	10.13
MCFA ⁵	7.81	0.97	13	4.06	12.17
LCFA ⁶	78.75	4.51	6	66.93	100.29
SFA ⁷	71.09	3.01	4	59.73	81.97
UFA ⁸	28.95	2.75	9	18.44	37.81
PUFA ⁹	4.10	0.47	11	2.42	5.86

¹Calculated as $\log_2$ (SCC/1,000).

²n-3 = sum of all n-3 fatty acids.

³n-6 = sum of all n-6 fatty acids.

⁴SCFA = short-chain fatty acids; sum of C4:0, C6:0, and C8:0.

⁵MCFA = medium-chain fatty acids; sum of C10:0, C10:1, C12:0, and C12:1.

⁶LCFA = long-chain fatty acids; sum from C14:0 to C22:0.

⁷SFA = sum of C4:0, C6:0, C8:0, C10:0, C12:0, C13:0, C14:0, C15:0, C16:0, C17:0, C18:0, C20:0, and C22:0.

⁸UFA = sum of PUFA and C10:1, C12:1, C14:1, C16:1, C17:1, C18:1 *cis*-9, C18:1 *trans*-11, C20:1 *cis*-11, and C24:1.

⁹PUFA = sum of C18:2 *cis*-9,*trans*-11, C18:3n-3 *cis*-9,*cis*-12,*cis*-15, C20:2n-6 *cis*-11,*cis*-14, C20:3n-6 *cis*-8,*cis*-11,*cis*-14, C20:4n-6 *cis*-5,*cis*-8,*cis*-11,*cis*-14, C20:3n-3 *cis*-11,*cis*-14,*cis*-17, C20:4n-3 *cis*-8,*cis*-11,*cis*-14,*cis*-17, C20:5n-3 *cis*-5,*cis*-8,*cis*-11,*cis*-14,*cis*-17, C22:4n-6 *cis*-7,*cis*-10,*cis*-13,*cis*-16, C22:5n-6 *cis*-4,*cis*-7,*cis*-10,*cis*-13,*cis*-16, C22:5n-3 *cis*-7,*cis*-10,*cis*-13,*cis*-16,*cis*-19, and C22:6n-3 *cis*-4,*cis*-7,*cis*-10,*cis*-13,*cis*-16,*cis*-19.

h^2 estimates were ≤ 0.03 . The highest h^2 estimates were for C16:0 and C20:0 (0.42), and the lowest h^2 estimates were for C18:1 *cis*-7 (0.21) and C18:2 *cis*-9,*trans*-11 (0.21).

Correlations Among Production Traits

The genetic and phenotypic correlations among all traits considered in this study are presented in Table 3. The standard errors of these estimates were ≤ 0.06 . The correlations between yields traits were high and

positive. The genetic correlations of milk yield with fat percentage and protein percentage were moderate and negative (-0.52 and -0.53 , respectively) and the corresponding phenotypic correlations were also negative but weaker (-0.26 and -0.36).

Milk and protein yields had positive genetic correlations with SCFA and negative correlations with MCFA and LCFA. Milk and protein yields had a negative genetic correlation with SFA and positive correlations with UFA and PUFA. Fat yield had the opposite trend, being negatively correlated with SCFA, UFA, and

Table 2. Estimates of variances, heritability, and repeatability for production traits and concentrations of fatty acids (FA) in New Zealand dairy cattle

Item	Residual	Genetic	Cow	Total	Heritability		Repeatability	
					Estimate	SE	Estimate	SE
Milk yield, kg/d	5.19	2.82	2.33	10.32	0.27	0.02	0.50	0.01
Fat yield, kg/d	0.015	0.004	0.006	0.025	0.16	0.02	0.39	0.01
Protein yield, kg/d	0.007	0.002	0.003	0.012	0.20	0.02	0.42	0.01
Lactose yield, kg/da	0.013	0.007	0.005	0.025	0.27	0.02	0.49	0.01
Fat, %	0.184	0.175	0.043	0.402	0.44	0.03	0.54	0.01
Protein, %	0.034	0.031	0.018	0.083	0.37	0.03	0.59	0.01
Lactose, %	0.006	0.004	0.001	0.011	0.35	0.03	0.46	0.01
SCS ¹	0.954	0.177	0.908	2.040	0.09	0.02	0.53	0.01
Fatty acid, % of total FA								
C4:0	0.013	0.008	0.003	0.024	0.33	0.02	0.45	0.01
C6:0	0.004	0.002	0.001	0.006	0.28	0.02	0.40	0.01
C8:0	0.003	0.002	0.001	0.006	0.31	0.02	0.42	0.01
C10:0	0.042	0.026	0.008	0.076	0.33	0.02	0.45	0.01
C10:1	<0.001	<0.001	<0.001	0.001	0.38	0.03	0.51	0.01
C12:0	0.072	0.045	0.015	0.132	0.34	0.02	0.45	0.01
C12:1	<0.000	<0.000	<0.000	<0.000	0.39	0.03	0.51	0.01
C14:0	0.228	0.161	0.051	0.440	0.36	0.03	0.48	0.01
C16:0	0.979	0.905	0.251	2.135	0.42	0.03	0.54	0.01
C18:0	1.581	0.530	0.096	2.207	0.24	0.02	0.28	0.01
C18:1 <i>cis</i> -9	1.015	0.642	0.231	1.888	0.34	0.03	0.46	0.01
C18:1 <i>cis</i> -7	0.107	0.035	0.028	0.170	0.21	0.02	0.37	0.01
C18:2 <i>cis</i> -9, <i>cis</i> -12	0.008	0.004	0.001	0.013	0.32	0.02	0.41	0.01
C18:2 <i>cis</i> -9, <i>trans</i> -11	0.015	0.005	0.003	0.024	0.21	0.02	0.36	0.01
C20:0	<0.000	<0.000	<0.000	0.001	0.42	0.03	0.52	0.01
C22:0	0.006	0.004	0.001	0.010	0.36	0.02	0.45	0.01
n-3 ²	0.014	0.010	0.003	0.027	0.38	0.03	0.48	0.01
n-6 ³	0.063	0.050	0.015	0.128	0.39	0.03	0.51	0.01
SCFA ⁴	0.345	0.137	0.030	0.513	0.27	0.02	0.33	0.01
MCFA ⁵	0.834	0.625	0.277	1.736	0.36	0.03	0.52	0.01
LCFA ⁶	1.787	0.983	0.424	3.194	0.31	0.02	0.44	0.01
SFA ⁷	1.706	1.314	0.462	3.482	0.38	0.03	0.51	0.01
UFA ⁸	0.034	0.016	0.011	0.061	0.26	0.02	0.44	0.01
PUFA ⁹	5.189	2.805	2.327	10.320	0.27	0.02	0.50	0.01

¹Calculated as $\log_2$ (SCC/1,000).

²n-3 = sum of all n-3 fatty acids.

³n-6 = sum of all n-6 fatty acids.

⁴SCFA = short-chain fatty acids; sum of C4:0, C6:0, and C8:0.

⁵MCFA = medium-chain fatty acids; sum of C10:0, C10:1, C12:0, and C12:1.

⁶LCFA = long-chain fatty acids; sum from C14:0 to C22:0.

⁷SFA = sum of C4:0, C6:0, C8:0, C10:0, C12:0, C13:0, C14:0, C15:0, C16:0, C17:0, C18:0, C20:0, and C22:0.

⁸UFA = sum of PUFA and C10:1, C12:1, C14:1, C16:1, C17:1, C18:1 *cis*-9, C18:1 *trans*-11, C20:1 *cis*-11, and C24:1.

⁹PUFA = sum of C18:2 *cis*-9,*trans*-11, C18:3n-3 *cis*-9,*cis*-12,*cis*-15, C20:2n-6 *cis*-11,*cis*-14, C20:3n-6 *cis*-8,*cis*-11,*cis*-14, C20:4n-6 *cis*-5,*cis*-8,*cis*-11,*cis*-14, C20:3n-3 *cis*-11,*cis*-14,*cis*-17, C20:4n-3 *cis*-8,*cis*-11,*cis*-14,*cis*-17, C20:5n-3 *cis*-5,*cis*-8,*cis*-11,*cis*-14,*cis*-17, C22:4n-6 *cis*-7,*cis*-10,*cis*-13,*cis*-16, C22:5n-6 *cis*-4,*cis*-7,*cis*-10,*cis*-13,*cis*-16, C22:5n-3 *cis*-7,*cis*-10,*cis*-13,*cis*-16,*cis*-19, and C22:6n-3 *cis*-4,*cis*-7,*cis*-10,*cis*-13,*cis*-16,*cis*-19.

Table 3. Phenotypic (above the diagonal) and genetic (below the diagonal) correlations between fatty acids (FA) in New Zealand dairy cattle

Trait ¹	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1. MY		0.73	0.90	0.99	-0.26	-0.36	0.01	-0.12	0.34	0.15	0.04	-0.08	-0.22	-0.14	-0.25	-0.22
2. FY	0.53		0.79	0.72	0.40	-0.01	0.02	-0.08	-0.02	0.21	0.28	0.28	0.25	0.26	0.20	0.22
3. PY	0.86	0.69		0.89	-0.07	0.03	-0.01	-0.09	0.13	0.16	0.11	0.05	0.02	0.02	-0.02	-0.01
4. LY	0.99	0.53	0.86		-0.26	-0.36	0.12	-0.15	0.36	0.14	0.01	-0.12	-0.24	-0.18	-0.28	-0.27
5. F%	-0.52	0.44	-0.23	-0.51		0.53	-0.01	-0.06	-0.49	0.14	0.42	0.56	0.73	0.61	0.69	0.65
6. P%	-0.53	0.14	-0.06	-0.53	0.73		-0.08	0.11	-0.55	0.03	0.19	0.34	0.62	0.41	0.61	0.54
7. L%	-0.07	0.05	-0.08	0.07	0.11	-0.01		-0.22	0.25	-0.07	-0.27	-0.35	-0.16	-0.40	-0.31	-0.46
8. SCS	0.01	0.05	0.10	-0.02	0.04	0.10	-0.21		-0.24	-0.16	-0.05	0.05	-0.01	0.10	0.10	0.14
9. C4:0	0.48	-0.24	0.15	0.50	-0.73	-0.71	0.13	-0.25		0.58	0.14	-0.20	-0.37	-0.37	-0.62	-0.52
10. C6:0	0.03	0.06	0.02	0.01	0.04	0.01	-0.15	-0.21	0.48		0.86	0.64	0.40	0.50	0.20	0.35
11. C8:0	-0.18	0.21	-0.07	-0.21	0.41	0.28	-0.30	-0.12	0.01	0.86		0.93	0.66	0.85	0.60	0.72
12. C10:0	-0.31	0.26	-0.13	-0.36	0.61	0.46	-0.35	-0.02	-0.33	0.64	0.94		0.75	0.98	0.80	0.89
13. C10:1	-0.43	0.30	-0.11	-0.45	0.79	0.73	-0.13	-0.06	-0.51	0.41	0.70	0.80		0.83	0.91	0.81
14. C12:0	-0.37	0.27	-0.15	-0.43	0.70	0.55	-0.37	0.02	-0.47	0.52	0.87	0.99	0.84		0.88	0.95
15. C12:1	-0.44	0.31	-0.12	-0.48	0.80	0.72	-0.25	0.04	-0.69	0.24	0.65	0.83	0.94	0.90		0.91
16. C14:0	-0.44	0.28	-0.15	-0.50	0.76	0.67	-0.38	0.05	-0.60	0.38	0.75	0.91	0.88	0.96	0.94	
17. C16:0	-0.50	0.39	-0.13	-0.50	0.93	0.82	0.02	-0.04	-0.74	0.07	0.42	0.62	0.87	0.72	0.86	0.84
18. C18:0	0.21	-0.34	-0.02	0.21	-0.57	-0.49	-0.04	0.01	0.39	-0.25	-0.48	-0.57	-0.81	-0.60	-0.76	-0.60
19. C18:1 <i>cis</i> -9	0.49	-0.25	0.14	0.49	-0.80	-0.81	-0.01	-0.10	0.62	-0.29	-0.63	-0.79	-0.83	-0.84	-0.86	-0.85
20. C18:1 <i>cis</i> -7	0.36	-0.08	0.25	0.33	-0.48	-0.37	0.56	-0.15	0.40	-0.09	-0.29	-0.42	-0.32	-0.48	-0.38	-0.58
21. C18:2 <i>cis</i> -9, <i>cis</i> -12	0.50	-0.35	0.14	0.48	-0.89	-0.82	-0.14	-0.03	0.65	-0.10	-0.39	-0.57	-0.84	-0.65	-0.78	-0.73
22. C18:2 <i>cis</i> -9, <i>trans</i> -11	0.16	-0.19	0.26	-0.09	-0.38	0.04	0.19	0.09	0.06	-0.17	-0.24	-0.25	-0.03	-0.24	-0.04	-0.24
23. 20:0	0.48	-0.43	0.15	0.47	-0.95	-0.77	-0.04	-0.01	0.71	-0.16	-0.54	-0.73	-0.89	-0.80	-0.90	-0.84
24. n-3 FA	0.49	-0.36	0.14	0.45	-0.88	-0.78	-0.31	-0.03	0.68	0.03	-0.25	-0.44	-0.73	-0.52	0.37	-0.59
25. n-6 FA	0.48	-0.42	0.14	0.20	-0.93	-0.78	-0.21	0.04	0.66	-0.13	-0.45	-0.62	-0.87	-0.69	0.63	-0.76
26. SCFA	0.26	-0.07	0.08	0.26	-0.34	-0.37	-0.06	-0.26	0.81	0.90	0.59	0.28	0.01	0.13	-0.17	-0.03
27. MCFA	-0.36	0.27	-0.14	-0.41	0.68	0.53	-0.36	0.00	-0.42	0.56	0.90	0.99	0.84	1.00	0.89	0.94
28. LCFA	-0.22	0.16	-0.20	-0.23	0.38	0.14	-0.05	-0.02	-0.45	-0.47	-0.29	-0.14	-0.06	-0.06	0.05	0.07
29. SFA	-0.50	0.31	-0.22	-0.54	0.86	0.69	-0.23	0.00	-0.67	0.23	0.61	0.79	0.75	0.85	0.82	0.91
30. UFA	0.52	-0.29	0.18	0.53	-0.85	-0.80	0.06	-0.09	0.65	-0.26	-0.62	-0.80	-0.83	-0.86	-0.86	-0.90
31. PUFA	0.50	-0.43	0.21	0.48	-0.95	-0.71	0.00	0.03	0.64	-0.12	-0.45	-0.63	-0.81	-0.70	-0.78	-0.76
Trait	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	
1. MY	-0.31	0.09	0.25	0.10	0.22	-0.02	0.23	0.23	0.23	0.27	-0.12	-0.06	-0.20	0.25	0.21	
2. FY	0.27	-0.18	-0.12	-0.15	-0.26	-0.26	-0.37	-0.24	-0.31	0.14	0.27	0.05	0.22	-0.20	-0.36	
3. PY	-0.05	-0.03	-0.02	0.04	0.00	0.06	0.01	-0.02	0.01	0.16	0.04	-0.06	-0.03	0.00	0.04	
4. LY	-0.32	0.08	0.24	0.13	0.19	-0.08	0.24	0.19	0.45	0.27	-0.16	-0.09	-0.24	0.26	0.19	
5. F%	0.86	-0.41	-0.55	-0.39	-0.70	-0.37	-0.91	-0.69	-0.81	-0.13	0.61	0.15	0.63	-0.69	-0.85	
6. P%	0.68	-0.30	-0.70	-0.20	-0.55	0.18	-0.58	-0.62	-0.56	-0.27	0.40	0.00	0.44	-0.66	-0.45	
7. L%	-0.12	-0.19	-0.08	0.55	-0.20	0.27	0.02	-0.34	-0.22	0.05	-0.37	-0.30	-0.39	0.03	-0.17	
8. SCS	0.08	0.07	-0.05	-0.10	0.06	0.01	-0.03	0.03	0.04	-0.21	0.07	0.12	0.14	-0.06	0.05	
9. C4:0	-0.64	0.04	0.31	0.30	0.19	0.02	0.45	0.38	0.27	0.83	-0.31	-0.48	-0.59	0.33	0.24	
10. C6:0	0.06	-0.25	-0.34	-0.12	-0.23	-0.20	-0.22	-0.06	-0.24	0.93	0.56	-0.35	0.13	-0.37	-0.28	
11. C8:0	0.37	-0.29	-0.51	-0.31	-0.28	-0.31	-0.49	-0.20	-0.38	0.66	0.89	-0.10	0.51	-0.56	-0.42	
12. C10:0	0.57	-0.33	-0.63	-0.41	-0.35	-0.30	-0.64	-0.33	-0.47	0.36	0.99	0.03	0.69	-0.69	-0.50	
13. C10:1	0.85	-0.56	-0.69	-0.27	-0.61	-0.08	-0.82	-0.65	-0.73	0.10	0.81	0.06	0.64	-0.71	-0.66	
14. C12:0	0.68	-0.33	-0.65	-0.46	-0.36	-0.30	-0.69	-0.39	-0.49	0.19	1.00	0.13	0.77	-0.71	-0.52	
15. C12:1	0.84	-0.46	-0.70	-0.34	-0.49	-0.08	-0.78	-0.13	0.15	-0.13	0.86	0.16	0.74	-0.73	-0.58	
16. C14:0	0.79	-0.29	-0.65	-0.55	-0.40	-0.29	-0.70	-0.43	-0.52	0.01	0.93	0.21	0.83	-0.74	-0.55	
17. C16:0		-0.39	-0.64	-0.43	-0.62	-0.26	-0.86	-0.70	-0.74	-0.26	0.66	0.27	0.76	-0.73	-0.74	
18. C18:0	-0.64		0.68	-0.33	0.81	-0.49	0.65	0.74	0.80	-0.14	-0.35	0.66	0.17	0.61	0.66	
19. C18:1 <i>cis</i> -9	-0.85	0.69		0.07	0.76	-0.18	0.74	0.79	0.80	-0.07	-0.66	0.42	-0.32	0.94	0.71	
20. C18:1 <i>cis</i> -7	-0.51	-0.17	0.31		0.04	0.80	0.28	-0.03	0.07	-0.05	-0.41	-0.22	-0.53	0.38	0.34	
21. C18:2 <i>cis</i> -9, <i>cis</i> -12	-0.92	0.77	0.85	0.30		-0.14	0.79	0.88	0.96	-0.04	-0.38	0.50	-0.08	0.80	0.91	
22. C18:2 <i>cis</i> -9, <i>trans</i> -11	-0.26	-0.38	0.07	0.73	0.05		0.14	-0.19	-0.05	-0.22	-0.12		-0.32	-0.14	-0.01	
23. 20:0	-0.94	0.74	0.91	0.36	0.92	0.19		0.78	0.89	0.06	-0.69	0.08	-0.53	0.82	0.87	
24. n-3	-0.84	0.71	0.81	0.20	0.96	0.03	0.88		0.91	0.15	-0.39	0.30	-0.21	0.76	0.83	
25. n-6	-0.95	0.78	0.88	0.26	0.97	0.11	0.97	0.95		-0.02	-0.50	0.37	-0.24	0.84	0.95	
26. SCFA	-0.34	0.02	0.12	0.07	0.28	-0.24	0.25	0.37	0.26		0.26	-0.43	-0.16	-0.08	-0.07	
27. MCFA	0.70	-0.61	-0.83	-0.49	-0.64	0.00	-0.79	-0.51	-0.68	0.18		0.08	0.74	-0.71	-0.53	
28. LCFA	0.26	0.40	0.09	-0.43	-0.10		-0.14	-0.08	-0.12	-0.55	-0.09		0.67	0.33	0.28	
29. SFA	0.86	-0.36	-0.84	-0.69	-0.73	-0.17	-0.86	-0.62	-0.77	-0.17	0.83	0.37		-0.44	-0.33	
30. UFA	-0.91	0.62	0.97	0.49	0.87	-0.16	0.92	0.80	0.89	0.16	-0.84	-0.09	-0.93		0.84	
31. PUFA	-0.94	0.66	0.84	0.36	0.94	-0.14	0.94	0.91	0.97	0.25	-0.69	-0.25	-0.84	0.90		

¹MY = milk yield, FY = fat yield, PY = protein yield, LY = lactose yield, F% = fat percentage, P% = protein percentage, L% = lactose percentage; SCFA = short-chain fatty acids; MCFA = medium-chain fatty acids; LCFA = long-chain fatty acids. All groups are as defined in Table 1.

PUFA and positively correlated with SFA. The phenotypic and genetic correlations of SCS with the different FA were low, except for a moderate negative correlation with C4:0 and C6:0. The genetic and phenotypic correlations of milk yield with n-3 and n-6 FA were moderately positive.

Fat and protein percentage had positive genetic correlations with SFA and negative correlations with UFA and PUFA. Among individual FA, fat percentage had a strong positive (0.93) genetic correlation with C16:0 and a strong negative (−0.80) correlation with C18:1 *cis*-9. The genetic correlation between C18:0 and fat percentage was moderately negative (−0.57) and that between C12:0 and fat percentage was positive (0.70).

Genetic Correlations Among De Novo Fatty Acids

Strong positive genetic and phenotypic correlations among C6:0 to C16:0 were found in this study (Table 3). However, the correlations of C4:0 with other FA did not follow the same trend. The C4:0 had a moderate positive genetic correlation with C6:0, zero with C8:0, negative with C10:0, C10:1, C12:0, C14:0 and C16:0, and positive with FA C18:0 or greater.

The genetic correlations of C16:0 with C4:0, C18:0, and C20:0 and all of the FA of the C18:1 and C18:2 groups were moderately to strongly negative, but genetic correlations of C16:0 with C8:0, C10:0, C10:1, C12:0, C12:1, and C14:0 were strongly positive (from 0.42 to 0.87). The phenotypic correlations of C18:0 and C18:1 *cis*-9 with saturated short to medium-chain FA (C6:0, C8:0, C10:0, C12:0, C14:0, and C16:0) were negative. The SFA had negative correlations with UFA (−0.93) and PUFA (−0.84) and the genetic correlation between UFA and PUFA was strong and positive (0.90).

The genetic and phenotypic correlations between n-3 and n-6 were strong and positive. The phenotypic and genetic correlations of n-3 and n-6 with C4:0, C18:0, and C18:1 *cis*-9 were strongly positive, whereas correlations with C10:0, C01:1, C12:0, C14:0, and C16:0 were strong and negative.

DISCUSSION

Mean and Coefficient of Variation

The levels of milk production found in this study were similar to other values reported in New Zealand (Auldist et al., 2004) in cows under grazing conditions. However, the cows in this study produced less milk with higher concentrations of fat and protein compared with Canadian Holstein cows fed TMR (Fleming et al., 2018) or Italian Brown Swiss, Holstein-Friesian, Jersey,

Simmental, and Alpine Grey cows fed forage or hay and concentrate (Manuelian et al., 2019). The mean values of the FA found in this study were typical of New Zealand dairy cattle (MacGibbon, 1996; Auldist et al., 2004). Of the total FA, 71.09% were SFA and 28.95% were UFA, which were similar to other reported populations (Grummer, 1991). The concentration of PUFA was 4.10%, which agrees well with the value reported by Grummer (1991). MacGibbon and Taylor (2006) reported C16 and C18:1 as the major FA in milk in New Zealand. The mean reported values were 27.9 and 17.2%, respectively, with ranges of 23.6 to 31.4% and 14.9 to 22% respectively. These values agree with the values estimated in this study. The ratio of n-6 to n-3 estimated in this study was 1.14, which is similar to that for US organic milk and desirable for human health (Benbrook et al., 2013). The optimal ratio of n-6 to n-3 FA is estimated to be close to 2.0. An excess of n-6 FA can interfere with the utilization of n-3 FA and thereby limit their numerous health benefits, such as reducing the risk of cardiovascular disease, diabetes, and obesity (Benbrook et al., 2013). Some predicted values of LCFA were 100%, which indicates some level of overprediction by the calibration equation using mid-infrared spectra.

Heritabilities and Repeatabilities

Heritabilities and repeatabilities for yields of milk, fat, and protein and for concentrations of fat, protein, and lactose found in this study agree well with other estimates in New Zealand dairy cattle (Sneddon et al., 2015). The estimates of heritabilities for FA in this study were generally higher than those reported by Bobe et al. (2008) in American Holstein cows, by Mele et al. (2009) in Italian Holstein cows, by Soyeurt et al. (2007) in mixed-breed population of the Walloon region of Belgium, and by Krag et al. (2013) in Danish Holstein cows, but agree well with the estimates reported by Stoop (2009) in Dutch Holstein cows. The estimates of heritabilities for FA reported by Pegolo et al. (2016) in Italian Brown Swiss cows were obtained from a well-designed experiment and FA were determined using GC, with variance components estimated using Bayesian animal models. Their estimates were, in general, lower than ours, and those authors argued that comparisons of heritability estimates among the various studies are difficult because of differences in the analytical methods (GC or spectroscopy), the method of expressing FA contents (g/100 g of milk, g of FA/100 g of fat, or g of FA/100 g of total FA), sample size, breed, parity number, stage of lactation, and the statistical methods (e.g., sire, animal model and random

regression). However, the heritability estimates for FA indicate that differential selection could be used to change the FA composition of milk through genetics.

The estimates of repeatabilities for FA found in this study were, in general, higher than those reported by Bobe et al. (2008) in American Holstein cows and by Soyeurt et al. (2007) in dairy cattle from different breeds in the Walloon region of Belgium. Our estimates of repeatabilities for FA indicate that cows with a high proportion of a particular FA maintained that consistently high level throughout the lactation.

Correlations Among Production Traits

The estimates of phenotypic and genetic correlations between yield traits were similar to the values reported in other studies, including lactose (Sneddon et al., 2015; Costa et al., 2019).

Somatic cell score and lactation yields of milk, fat, and protein are traits included in the breeding objective of New Zealand dairy cattle. The economic values of these traits used in the genetic evaluation of February 2019 were $-\$37.3/\text{unit}$ of SCS, $-\$0.092/\text{L}$ of milk, $\$3.49/\text{kg}$ of fat, and $\$4.38/\text{kg}$ of protein.

The current study estimated phenotypic and genetic correlations of milk production traits and SCS with FA to be used for later studies and predicted correlated responses under different selection scenarios to modify the fatty acid profile of the New Zealand milk. In the Netherlands, Stoop (2009) used selection index theory to illustrate that selection for protein yield could produce positive correlated responses in the proportions of C14:0 and UFA and negative correlated responses in the proportions of C16:0 in milk fat of Dutch Holstein cattle.

The phenotypic and genetic correlations of SCS with the different FA were generally low, except for a moderate negative correlation with C4:0 and C6:0. Soyeurt et al. (2007) and Bilal et al. (2014) reported that SFA (C12:0, C14:0, C16:0, and C18:0) tended to be negatively correlated with milk yield, but UFA (C18:1 and C18:2) had weak positive correlations with milk yield. The results from this study confirm the strong negative association of milk yield with C12:0 and C14:0, but the genetic correlations of milk yield with unsaturated C18:1 and C18:2 were moderately positive in the present study. Interestingly, the genetic and phenotypic correlations of milk yield with n-3 and n-6 FA were moderately positive. These correlation estimates suggest that positive correlated responses would be expected when milk yield is increased. However, in the construction of selection indices to modify the concentrations of n-3

and n-6 in milk fat, the strong and negative correlations (from -0.78 to -0.93) of these FA with fat and protein percentages need to be considered (Table 3).

Several studies (Soyeurt et al., 2007; Stoop et al., 2008; Bilal et al., 2014) have reported that fat and protein percentages have positive genetic correlations with SFA and negative correlations with UFA and PUFA, indicating that genetic gains in the concentrations of fat and protein in milk may result in fat with higher content of SFA but lower contents of UFA and PUFA.

The strong positive genetic correlation between fat percentage and C16:0 and the strong negative genetic correlation between fat percentage and C18:1 *cis*-9 found in this study were also reported by Schennink et al. (2007) and Stoop et al. (2008) in Dutch Holsteins and by Bilal et al. (2014) in Canadian Holsteins. This suggests that selection against high palmitic acid (C16:0) concentration in milk fat will lead to low milk fat percentage, which might be undesirable for the dairy industry from an economic perspective (Nafikov et al., 2015). However, Soyeurt et al. (2007), in a study with multiple breeds, noted that not all SFA were negatively correlated with fat percentage. They reported that the genetic correlation between C18:0 and fat percentage was high (0.84). Bilal et al. (2014) reported in Canadian Holsteins a negative correlation (-0.10). In our study, the corresponding genetic correlation was moderate and negative (-0.57). This apparent contradiction may be due to the underlying genetics of the crossbred cows used in our study.

In agreement with other studies (Soyeurt et al., 2007; Bilal et al., 2014), the genetic correlation between C18:1 and fat percentage was strong and negative (-0.80). MacGibbon (1996) illustrated that concentration of C18:1 was negatively correlated with the hardness of the milk fat.

Genetic Correlations Among De Novo Synthesized Fatty Acids

Even-chain saturated C6:0–C14:0 and a fraction of C16:0 are synthesized de novo in the mammary gland from SCFA formed by microbial digestion of carbohydrates in the rumen (Palmquist et al., 1993); therefore, strong positive genetic and phenotypic correlations among these FA were estimated in this study. Similar results were reported by Karijord et al. (1982) in Norway, Krag et al. (2013) and Buitenhuis et al. (2014) in Denmark, Bilal et al. (2014) in Canada, and Pegolo et al. (2016) in Italy. The phenotypic and genetic correlations of C4:0 with other de novo synthesized FA in the mammary gland were zero or negative. This

trend was similar to the trend reported by Stoop et al. (2008) in Dutch Holstein cows and by Bilal et al. (2014) in Canadian Holstein cows. The genetic correlations of C16:0 with C8:0, C10:0, C10:1, C12:0, C12:1, and C14:0 were strong and positive (from 0.42 to 0.87); C18:0 showed the opposite correlations to C16:0. This difference for C18:0 is likely because C18:0 is part of a group of FA absorbed from blood, whereas a fraction of the C16:0 is synthesized *de novo* in the mammary gland. The C18:0 in the blood is a consequence of the extent of biohydrogenation in the rumen of C18 UFA from the feed. Thus, the concentrations of C16:0 and C18:0 in milk fat are influenced by different factors (Palmquist et al., 1993). Oleic acid (C18:1 *cis*-9) can be produced from stearic acid (C18:0) under the action of Δ^9 -desaturase enzyme activity. The genetic and phenotypic correlations between C18:0 and C18:1 *cis*-9 were strong and positive (0.69 and 0.68). Pegolo et al. (2016) also reported a positive genetic correlation (0.60) between these 2 FA. The negative genetic correlations of C18:1 with saturated short- to medium-chain FA (C6:0, C8:0, C10:0, C12:0, C14:0, and C16:0) could be due to the known effect of C18:1 as the main compensation for changes in SCFA (Palmquist et al., 1993). The mid to strong (negative) phenotypic correlations of C18:0 and C18:1 *cis*-9 with saturated short- to medium-chain FA (C6:0, C8:0, C10:0, C12:0, C14:0, and C16:0) may be also explained because these cows were grazing pasture with high amounts of C18:0 and C18:1 decreasing the *de novo* fat synthesis of saturated short- to medium-chain FA (C6:0, C8:0, C10:0, C12:0, C14:0; Grummer, 1991; Hurtaud et al., 2010). The genetic correlation between SCFA and LCFA in our study was -0.55 , which is opposite to the reported value of 0.70 reported by Narayana et al. (2017). This apparent contradiction may be explained by the differences in the definitions of the length of the carbon chain, and the expression of concentration of FA; in our study, FA were expressed as grams per 100 g of total FA, whereas the Narayana et al. (2017) expressed concentration as grams per 100 g of milk.

The strong negative genetic correlation between SFA and UFA found in this study has also been reported in most studies (Krag et al., 2013; Buitenhuis et al., 2014; Pegolo et al., 2016; Hein et al., 2018), although other studies (Soyeurt et al., 2007; Narayana et al., 2017) have reported strong (>0.6) positive genetic correlations over the lactation. This apparent contradiction is due to the expression of concentration of FA; Soyeurt et al. (2007) and Narayana et al. (2017) expressed concentration as grams per 100 g of milk, whereas the other studies expressed concentration as grams per 100 g of total FA.

CONCLUSIONS

The current study provided estimates of genetic and phenotypic correlations between milk production traits and content of FA in New Zealand dairy cattle. These estimates suggest that the FA profile must have been changed as a result of current selection indices and breeding objectives of the dairy industry. The estimates of genetic parameters reported in this study are useful data for the definition of feeding or breeding strategies aimed at improving milk with better characteristics for human health and improved processing ability of high-fat dairy products.

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