

Genetic parameters for milk urea concentration and milk traits in New Zealand grazing dairy cattle

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Abstract

The aim of this study was to estimate genetic parameters for milk urea (MU), yields of milk (MY), fat (FY), crude protein (CPY) and lactose (LY), concentrations of fat (FP), crude protein (CPP) and lactose (LP) and efficiency of crude protein utilisation (ECPU) in grazing dairy cows. Data consisted of 1284 herd-test records of milk traits and MU from 468 mixed-breed cows in two herds. Univariate and bivariate repeatability animal models were used to estimate heritabilities (h^2) and genetic (r_G) and phenotypic (r_p) correlations among the traits. Estimates of h^2 for MU and ECPU were 0.24 and 0.11, whereas h^2 estimates for MY, FY, CPY and LY ranged from 0.10 to 0.20. Estimates of h^2 for FP, CPP and LP were 0.37, 0.59 and 0.19, respectively. The estimates of r_p for MU with other traits were near zero. The r_G of MU with MY (0.38), and of MU with LY (0.31) were positive and significant ($P < 0.01$) whereas the r_G of MU with FP (-0.80), CPP (-0.66) and LP (-0.76) were negative and significant ($P < 0.01$). The r_G between MU and ECPU was -0.09. These estimates of genetic parameters can be used to predict genetic responses to selection for reduction of MU.

Introduction

Milk production in New Zealand is based on cows grazing pastures that have a high protein content. Usually, from 5 to 35% of the nitrogen in pasture protein is converted into animal products (meat and milk protein) and the remaining nitrogen is excreted in faeces and urine (Saggar et al. 2005). This nitrogen excretion is of significant environmental concern (DairyNZ 2013) due to nitrate leaching contributing to aquatic eutrophication, as well as effects on air quality and greenhouse gas emissions through gaseous losses as ammonia and nitrous oxide. Thus, attention has focused on the relationship between nitrogen utilization in lactating cows and environmental pollution (Castillo et al. 2000).

In indoor milk production systems, there is an apparent relationship between concentration of urea nitrogen in milk and concentration of urea nitrogen in urine (Jonker et al. 1998; Kauffman & St-Pierre 2001; Spek et al. 2013). Milk urea nitrogen (MUN) has been proposed to be used as a selection tool, and therefore, an estimation of genetic parameters is needed. Estimates of heritabilities (h^2) for MUN range from 0.06 to 0.44 (Bastin et al. 2009; Hossein-Zadeh & Ardalan 2011; Miglior et al. 2007; Mitchell et al. 2005; Mucha & Strandberg, 2011; Stoop et al. 2007; Wood et al. 2003) with low phenotypic and genetic correlations with milk, fat and protein yields and the concentrations of fat and protein. The range of genetic parameter estimates is broad and may be due to the variation in the numbers of animals and the types of models used.

Different measures of protein efficiency in dairy cattle are found in the literature (Zamani et al. 2011): 1) Gross efficiency of crude protein calculated as crude protein in milk divided by crude protein intake; 2) Crude protein balance measured as the difference of crude protein intake and crude protein in milk; and 3) Residual crude

protein intake calculated as the difference between actual and predicted crude protein intakes. Other definitions include nitrogen-use efficiency calculated as nitrogen in milk divided by the total nitrogen intake (Castillo et al. 2000; Woodward et al. 2011) and metabolisable-protein efficiency calculated as protein in milk divided by intake of metabolisable protein (Wheaton et al. 2013).

In this paper, the selected measure of protein efficiency was defined as efficiency of crude protein utilisation (ECPU) calculated as the ratio of crude protein produced in milk to crude protein intake, expressed as a percentage. This measure is equivalent to the definition of gross efficiency of crude protein as defined by Zamani et al. (2011).

Reports on the genetic variation for ECPU are scarce in the literature. Li et al. (1998) reported a h^2 of 0.13 ± 0.13 in Chinese Simmental cows, Hayes & Ageeb (2002) reported h^2 estimates of 0.10 ± 0.01 and 0.31 ± 0.03 at 90 and 305 days in milk in Canadian Holsteins, and Zamani et al. (2011) reported a value of 0.07 ± 0.05 in lactating Holstein cows in Iran. Few studies (Li et al. 1998; Zamani et al. 2011) have reported phenotypic and genetic correlations between ECPU and milk production and composition traits. The objective of this study was to estimate genetic parameters for milk urea (MU), milk production traits (yields of milk (MY), fat (FY), crude protein (CPY) and lactose (LY)), concentrations of fat (FP), crude protein (CPP) and lactose (LP) and ECPU in grazing dairy cows.

Material and methods

The present study was conducted at Massey University, Palmerston North, New Zealand, in two herds (Dairy 1 and Dairy 4). Dairy 1 contained 66 Holstein-Friesian (F), 55 Jersey (J) and 137 crossbred (F×J) cows milked once daily, and Dairy 4 contained 51 F, 3 J and 156 F×J cows milked

twice daily. Cows calved in spring 2016 and were milked until May 2017. There were 157 sires in their pedigrees and 41 sires had at least one progeny in both herds.

Details of the feeding system and management at each farm is provided by Correa-Luna et al. (2018). Each herd had access to fresh ryegrass (*Lolium perenne*)/white clover (*Trifolium repens*) pasture after milking. Dairy 1 cows were milked daily at 6.30 am throughout the season and received forage supplements at different times during the year including pasture silage, chicory (*Cichorium intybus*), red clover (*Trifolium pratense*), plantain (*Plantago lanceolata*), turnip (*Brassica campestris ssp. rapifera*) and lucerne (*Medicago sativa*).

Dairy 4 cows were milked daily at 5.30 am and 2.30 pm throughout the season. Maize silage was fed before the afternoon milking and concentrate pellets were fed twice daily during milking. In January and March, cows were fed other feed supplements, including dried distillers grains, pasture silage, and turnips.

For both herds, daily live weight (LW) measurements were generated using an automatic walk over scale in the exit race and body condition scores (BCS) measurements on a 10-point scale were assigned in synchrony with each herd-test by a single research technician. Yields of milk, FY, CPY and LY and somatic cell count (SCC) information were collected from five herd test records during the season. Somatic cell count score (SCS) was calculated as $SCS = \log_2(SCC)$.

Additionally, milk samples from each cow were taken at early-, mid- and late-lactation stages and analysed by MilkTestNZ (Hamilton, NZ) for the determination of MU (mg/dL) content and lactose percentage. Each MU record was converted into MU yield (MUY g cow/day) considering daily milk production.

Apparent dry matter intake (DMI = kg DM consumed/cow/day) was estimated based on total metabolisable energy (ME) requirements for maintenance, pregnancy, production and daily weight variation divided by ME content of any feed offered (Lopez-Villalobos et al. 2000). Content of crude protein from feed quality analyses were used to calculate crude protein intake (CPI). Daily ECPU was calculated as CPY divided by CPI and expressed as percentage. Milk urea yield was calculated as the multiplication of MU concentration by daily MY.

Single-trait animal models were used for estimation of h^2 , and bivariate animal models were used for estimation of genetic (r_G) and phenotypic (r_P) correlations. The mixed model included the fixed effects of herd test date, lactation number, stage of lactation, and covariables for deviation from mean calving date by herd, stage of lactation, the proportion of F and heterosis coefficients of $F \times J$; and the random effects of cow permanent environment, animal, and residual error. Estimates of (co)variance components were obtained using the restricted maximum likelihood procedure as implemented in the ASReml package (Gilmour et al. 2009) of VSN International Ltd.

Results

Descriptive statistics for the variables considered in this study are presented in Table 1. Milk yield, CPY, FY, LY and MUY showed coefficients of variation greater than 29%, whereas the concentrations of components showed smaller coefficients of variation; 18.6% for FP, 13.8% for CPP and 3.6% for LP. Concentration of MU showed a larger coefficient of variation (36.7%).

Estimates of h^2 , repeatabilities, breed and heterosis effects are presented in Table 2. Live weight and CPP had the highest h^2 estimates (0.72 and 0.59, respectively).

Table 1 Means, standard deviations (SD), coefficients of variation (CV) and minimum (Min) and maximum (Max) values of milk quality and production, live weight, intakes and crude protein efficiency in grazing dairy cows from two herds in New Zealand.

Variable	N	Mean	SD	CV (%)	Min	Max
Yield, kg/day						
Milk	3,504	17.58	6.43	36.6	0.90	37.70
Fat	3,504	0.86	0.25	29.1	0.05	2.45
Crude protein	3,504	0.69	0.20	29.0	0.05	1.36
Lactose	1,286	0.95	0.33	34.7	0.15	1.93
Content, %						
Fat	3,504	5.10	0.95	18.6	1.77	8.86
Crude protein	3,504	4.07	0.56	13.8	2.75	6.51
Lactose	1,286	5.06	0.18	3.6	4.37	5.57
Somatic cell score ¹	3,496	5.54	1.57	28.3	0.00	12.43
Body condition score	3,504	4.44	0.38	8.6	3.28	5.62
Live weight, kg	3,504	491.1	65.0	13.2	333.9	684.0
Dry matter intake, kg/day	2,896	13.57	2.41	17.8	7.35	21.23
Crude protein intake, kg	2,896	2.48	0.47	19.0	1.18	4.53
ECPY ² , %	2,896	27.11	6.49	23.9	4.83	41.27
Milk urea, mg/dL	1,284	24.90	9.14	36.7	6.08	61.70
Milk urea yield, g/day	1,284	4.55	1.61	35.4	0.71	10.67

¹ Somatic cell score calculated as $SCS = \log_2(\text{somatic cell count})$.

² Efficiency of crude protein utilisation.

Table 2 Estimates of heritability (h^2), repeatability (t), variance components, heterosis and breed effects for milk traits, live weight, intakes and crude protein efficiency in grazing dairy cows from two herds in New Zealand.

Trait ¹	h^2	SE	t	SE	Variance components ²				Heterosis			Breed effect		
					σ_a^2	σ_c^2	σ_e^2	σ_{total}^2	F×J	SE	P	F-J	SE	
MY	0.20	0.08	0.50	0.02	2.1	3.2	5.3	10.6	0.78	0.37	0.0436	3.80	0.40	<.0001
FY	0.14	0.06	0.37	0.02	0.003	0.006	0.02	0.03	0.06	0.02	0.0006	0.01	0.02	0.3809
CPY	0.12	0.07	0.40	0.02	0.002	0.004	0.008	0.01	0.05	0.01	0.0001	0.08	0.01	<.0001
LY	0.20	0.09	0.46	0.03	0.005	0.007	0.01	0.03	0.05	0.02	0.0084	0.19	0.02	<.0001
FP	0.37	0.09	0.58	0.02	0.16	0.09	0.18	0.43	-0.04	0.08	0.5664	-1.12	0.08	<.0001
CPP	0.59	0.09	0.67	0.02	0.06	0.008	0.03	0.10	0.03	0.04	0.5274	-0.45	0.04	<.0001
LP	0.19	0.11	0.59	0.03	0.004	0.008	0.008	0.02	0.04	0.02	0.0144	-0.08	0.02	<.0001
SCS	0.10	0.08	0.55	0.02	0.20	0.87	0.86	1.9	0.05	0.16	0.7767	0.35	0.17	0.0475
BCS	0.35	0.12	0.88	0.008	0.03	0.04	0.009	0.08	0.01	0.04	0.8162	-0.06	0.04	0.1317
LW	0.72	0.12	0.95	0.003	1249	410	78	1737	12.0	5.87	0.0418	105	6.04	<.0001
DMI	0.29	0.11	0.69	0.02	0.42	0.57	0.44	1.4	0.60	0.15	<.0001	1.69	0.15	<.0001
CPI	0.26	0.10	0.65	0.02	0.01	0.02	0.02	0.05	0.13	0.03	<.0001	0.30	0.03	<.0001
ECPU	0.11	0.08	0.50	0.02	0.04	1.5	1.9	3.5	0.56	0.23	0.0157	-0.05	0.24	0.9262
MU	0.24	0.09	0.42	0.03	6.3	5.0	15.4	26.8	0.10	0.60	0.8764	2.73	0.62	<.0001
MUY	0.19	0.09	0.54	0.03	0.36	0.61	0.83	1.80	0.23	0.16	0.1628	1.46	0.17	<.0001

¹ MY = milk yield, FY = fat yield, CPY = crude protein yield, LY = lactose yield, FP = fat percentage, CPP = crude protein percentage, LP = lactose percentage, SCS = somatic cell score calculated as $SCS = \log_2(\text{somatic cell count})$, BCS = body condition score, LW = liveweight, DMI = dry matter intake, CPI = crude protein intake, ECPU = efficiency of crude protein utilisation, MU = milk urea concentration, MUY = milk urea yield.

² σ_a^2 = genetic variance, σ_c^2 = permanent environmental variance, σ_e^2 = residual error variance, σ_{total}^2 = sum of all variances, F×J = heterosis effect of Holstein-Friesian Jersey crossbred, F-J = breed effect expressed as the difference between Holstein-Friesian and Jersey.

Somatic cell count and ECPU had the lowest h^2 estimates (0.10 and 0.11, respectively). Estimates of h^2 for production traits (MY, FY, CPY and LY) varied between 0.10 and 0.20, and estimates of h^2 for concentration traits were generally higher with estimates for FP and CPP being 0.37 and 0.59 respectively, however, the h^2 for LP was lower (0.19). The estimate of h^2 was low for ECPU (0.10), and moderate for MU (0.24) and MUY (0.19). Body condition score and LW had the greatest repeatabilities of all the traits (0.88 and 0.95 respectively), while the milk-production traits had moderately high repeatabilities. Milk urea, MUY and ECPU had moderate repeatabilities, which were similar to those of the milk production traits.

Breed effects (F-J) were significant for almost all traits, except for FY, BCS and ECPU. The breed effect of F cows was 105 kg LW, 3.80 kg MY, -1.12% FP, -0.45% CPP, 2.73 mg/dL MU and 1.46 g/day MUY, compared to purebred J cows. First cross F×J heterosis effects were significant for MY, FY, CPY and LY but not significant for milk composition traits, including SCS and MU.

Genetic and phenotypic correlations among traits are presented in Table 3. The r_G and r_p among MY, FY, CPY and LY were high; the r_G and r_p between MY and LY were close to 1. Milk yield and MU showed a moderate positive r_G (0.38) with a lower r_p (0.19). The r_G between ECPU and MU was not significantly different from zero (-0.09), whereas there was a low r_p (0.12).

The r_p among MUY, yields and intake traits were high (>0.48). The r_p between MUY and ECPU was moderate (0.35), and between MUY and MU was high (0.80), whereas

the r_p of MUY with FP and CPP were moderate and negative. The r_G between MUY and the other traits followed the same trend as the corresponding r_p , but became more negative with FP, CPP, LP and SCS. Moderately high and positive r_G were obtained between MUY and LW (0.65), MUY and DMI (0.51), and MUY and CPI (0.49). In the opposite direction, moderately high and negative r_G were obtained between MUY and BCS (-0.81), and MUY and ECPU (-0.34).

Discussion

The large overall coefficient of variation for the traits analysed in this study can be explained by differences in milking frequency and feed levels used in the farms, and also by the breed differences. Dairy 1 cows were milked once a day and had a more balanced number of cows from the three breed groups, whereas Dairy 4 cows were milked twice a day and had few J cows.

Breed and heterosis for production and milk composition-traits estimated in the present study are similar to previous research in commercial herds (Lopez-Villalobos et al. 2014). The breed effect (F-J) for MU concentrations and MUY in this study were significant, indicating that a purebred F cow had in average 2.73 mg/dL higher concentration of MU and produced 1.46 g of MU more than a purebred J cow. This result does not agree with the result reported by Kauffman and St-Pierre (2001), who reported no significant difference between Holstein and Jersey cows for MUN concentration, but this could reflect the differences between MU and MUN.

Table 3 Estimates of genetic (below diagonal) and phenotypic (above diagonal) correlations among milk urea and constituents in grazing dairy cows from two herds in New Zealand.

MY	FY	CPY	LY	FP	CPP	LP	SCS	BCS	LW	DMI	CPI	ECPU	MU	MUY
SE	0.70	0.01	0.97	-0.32	0.03	0.00	0.03	-0.27	0.20	0.04	0.77	0.01	0.19	0.03
MY	0.52	0.21	0.67	0.02	-0.08	0.03	0.03	-0.19	0.09	0.03	0.71	0.01	0.12	0.03
FY	0.68	0.15	0.85	0.01	-0.13	0.03	0.03	-0.22	0.16	0.03	0.75	0.01	0.18	0.03
CPY	0.99	0.01	0.51	0.25	-0.35	0.03	0.03	-0.24	0.22	0.04	0.71	0.02	0.17	0.03
LY	-0.67	0.16	0.20	0.24	-0.10	0.28	-0.63	0.10	-0.14	0.04	-0.07	0.03	-0.19	0.03
FP	-0.75	0.12	-0.02	0.22	-0.09	0.24	-0.74	0.16	-0.09	0.04	-0.17	0.03	-0.16	0.03
CPP	-0.30	0.32	0.28	0.35	-0.26	0.37	-0.20	0.37	0.51	0.26	0.08	0.23	-0.08	0.04
LP	0.03	0.40	0.47	0.48	0.21	0.48	-0.27	0.44	0.30	0.39	0.19	0.30	-0.12	0.03
SCS	-0.44	0.25	-0.03	0.30	-0.36	0.30	0.27	0.28	0.56	0.25	0.33	0.20	-0.12	0.03
BCS	0.64	0.15	0.48	0.19	0.58	0.18	0.75	0.15	-0.31	0.16	-0.32	0.13	-0.17	0.04
LW	0.86	0.07	0.83	0.09	0.93	0.06	0.87	0.09	-0.28	0.22	-0.39	0.18	0.02	0.04
DMI	0.80	0.10	0.82	0.10	0.91	0.07	0.69	0.16	-0.29	0.23	-0.37	0.19	0.16	0.03
CPI	0.01	0.37	0.63	0.41	0.59	0.27	-0.19	0.44	0.23	0.36	0.55	0.26	0.12	0.03
ECPU	0.38	0.26	-0.21	0.33	0.01	0.34	0.31	0.28	-0.80	0.20	-0.66	0.20	-0.09	0.40
MU	0.62	0.18	0.04	0.36	0.23	0.33	0.56	0.20	-0.82	0.18	-0.81	0.17	0.96	0.07
MUY														

¹ MY = Milk yield, FY = Fat yield, CPY = Crude protein yield, LY = Lactose yield, FP = Fat percentage, CPP = Crude protein percentage, LP = Lactose percentage, SCS = Somatic cell score calculated as $SCS = \log_2(\text{somatic cell count})$, BCS = Body condition score, LW = Liveweight, DMI = Dry matter intake, CPI = Crude protein intake, ECPU = Efficiency of crude protein utilisation, MU = Milk urea concentration, MUY = Milk urea yield.

The genetic parameters for production traits in the present study are similar to those previously reported, both for New Zealand dairy heifers (Sneddon et al. 2015) and cows milked once a day at Dairy 1 (Lembey et al. 2016). The estimate of h^2 for MU found in the current research is higher than the estimates reported by Stoop et al. (2007) (0.14), Bastin et al. (2009) (0.13) and Mucha and Strandberg (2011) (0.16) and similar to the estimates reported by Mitchell et al. (2005) (0.22) and Hossein-Zadeh and Ardalan (2011) (0.10 to 0.33); but lower than the estimates of Miglior et al. (2007) (0.38) and Wood et al. (2003) (0.59). Yield of MU as calculated in this study had a h^2 estimate of 0.19, however, no other estimates for MUY were found in the literature.

The mean value of ECPU was 27.1% (SD=6.49) which is the same value reported for Iranian indoor dairy cows (Zamani et al. 2011). Comparison with other studies is difficult because of the differences in the definitions of protein efficiency. Wheadon et al. (2013) reported estimates of metabolisable protein efficiency of 0.283 and 0.302 for low- and high-Breeding Worth cows, respectively. Castillo et al. (2000) reported values of 17% and 28% for nitrogen use efficiency in high- and low-nitrogen fertilizer use in dairy systems, respectively, and Woodward et al. (2013) reported values of 18% and 22% of nitrogen-use efficiency in low- and high-Breeding Worth cows, respectively. The h^2 estimate for ECPU in this study was 0.11, which is similar to the values reported by Zamani et al. (2011) in Iranian indoor cows fed total mixed rations, Li et al. (1998) in Chinese Simmental cows, and Hayes & Ageeb (2002) in Canadian Holstein cows in early lactation.

The weak r_p between MU and milk traits, while having strong negative r_G with milk composition, could be explained by the variability in the crude protein of the diet of cows under New Zealand grazing conditions. The crude protein content of the diet varies more than the production level it would support, meaning that the r_p are weaker due to the greater variance of one trait while the r_G are unaffected by this phenotypic variation of the diet. This is most evident in the r_G of MU with FP, CPP, and LP. The r_G of MU with FP, CPP, LP and LW also seem to follow a biological drive: as FP, CPP and LP increase MU decreases and as LW increases so does MU. The negative r_G between MU and CPP in this study agrees with the negative values (-0.11 to -0.24) reported by Rzewuska and Strabel (2013) in Polish commercial herds, but contradicts the positive value of 0.27 reported by Stoop et al. (2007) in Dutch cattle. This strong negative r_G between MU and CPP found in this study suggests that cows producing milk with low MU concentration may partition nitrogen away from MU and towards other nitrogen pathways such as milk protein, which was reflected in the positive r_G estimates of ECPU with CPP (0.55) and CPY (0.59).

Previous research has shown MUN to be a reliable predictor of urinary nitrogen excretion by dairy cows (Jonker et al. 1998; Kauffman & St-Pierre 2001) and MUN has been suggested as a non-invasive tool to select cows for low urinary N excretion and higher nitrogen-use efficiency. However, more genetic studies are required because the r_p are affected by several environmental factors. For example, Woodward et al. (2013) found no significant relationship between MUN and nitrogen-use efficiency, indicating that MUN is not a good indicator of nitrogen-use efficiency. In the current study the r_p between MU and ECPU was significant but low (0.12, SE=0.03) and the r_G was not significantly different from zero, confirming that MU will not be a good genetic tool to improve genetic merit for ECPU. Furthermore, the estimate of the r_p between MUY with ECPU was moderately positive ($P < 0.001$) suggesting that cows with high MUY are also phenotypically of high ECPU, but the r_G was not significant, indicating that selection for high MUY will not produce genetic correlated responses on ECPU.

Both gaseous nitrogen emissions and nitrate leaching from dairy farms are of high concern to the New Zealand dairy industry. Various approaches have been attempted to mitigate the economic and environmental impacts of nitrogen losses (Saggar et al. 2005). One approach is to reduce the amount of urinary nitrogen excreted by the cows, but this variable is difficult to measure. Prediction equations have been developed to estimate urinary nitrogen based on MUN output in milk and crude protein content of the diet in indoor systems, by controlling the amount of crude protein in the diet (Jonker et al. 1998; Kauffman & St-Pierre 2001; Spek et al. 2013). Further research is required to validate these equations in grazing systems and to estimate the r_G of total urinary nitrogen excretion with production and protein-efficiency traits to develop optimal selection indexes that maximise farm profit, minimise nitrogen emissions and improve ECPU.

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