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Prototype genetic evaluation in a New Zealand dairy sheep flock

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Abstract

Dairy sheep milking is an emerging industry in New Zealand, but at present there is no national breeding scheme. A prototype model for the genetic evaluation of dairy sheep was developed. Data were obtained from a flock of 123 crossbred ewes, over 479 monthly flock tests during the season 2015/16. Breeding values were estimated for lactation yields of milk, fat, protein and lactose, and for live weight, somatic cell score, first let-down time and yield, and number of lambs born, from a multiple-trait animal model. Heritabilities and phenotypic and genetic correlations required for the model were obtained from the literature, and phenotypic standard deviations were obtained from the data set. This prototype model to obtain estimated breeding values of animals in this flock can be extended to other dairy sheep farmers, to create selection schemes at industry level and start a systematic breeding program for the emerging New Zealand dairy sheep industry.

Keywords: dairy sheep; EBV; genetic evaluation; live weight

Introduction

Sheep dairy is an emerging industry in New Zealand, with the growth projected to reach two million sheep (Ardern et al. 2013) and the potential to be a billion dollar industry in 10 years' time (Griffiths 2015). The major factor currently limiting sheep dairy production in New Zealand is the extremely low number of sheep suitable for dairy production. The main suitable breed is the East Friesian, and within the breed no structured selection for milk production has taken place in New Zealand. There would be value in improving the genetic merit of dairy sheep in New Zealand, using quantitative genetic tools. Genetic evaluation is required to identify and select superior animals. Currently there is no national breeding scheme to ensure that genetic change will occur in a favourable direction, to produce milking ewes required for future production systems. Therefore, the objective of this paper was to develop a prototype system of genetic evaluation for dairy sheep in New Zealand.

Materials and methods

Data

The data set and pedigree information used in this study were for 123 crossbred ewes, each consisting of a mixture of East Friesian, Highlander, Polled-Dorset and Poltex breeds. The ewes were located on a commercial dairy sheep farm in Waiwhare, Hawkes Bay (-39.453684 latitude, 176.479725 longitude). Ewes were milked 2x daily, grazing lucerne and plantain/clover pastures. The farmers were interviewed to canvas their opinions on traits of importance for their farming business.

A total of 479 monthly flock milk tests (2-4 tests on each ewe), for milk volume and percentages of fat, protein and lactose and somatic cell count (SCC) were obtained over the 2015/16 milking season. Milk yields were recorded at the morning milking, while milk yields and samples for analysis were taken at the afternoon milking.

First let-down time (FLDT) and first let-down milk yield (FLDY) were measured during the test-day milkings. Waikato MKV milk meters (Waikato Milking Systems, New Zealand) were attached to each set of cups, and collected milk samples for each ewe during milking, while the time (s) was manually recorded as the time from when cups went on each ewe, to when they finished their first milk let down. First let down was considered to end once the milk flow slowed to a complete stop in the milk meters.

The live weight of each ewe was recorded 2-4 times throughout the season, enabling an average weight for each ewe during the lactation to be obtained.

The ewes were managed in two mobs (early and late lambing) of which the lambing date ranged from 6 July to 16 December 2015 with median lambing date of 31 July. In order to adjust for lambing date, a deviation of lambing date from the median lambing data of the flock was calculated for each ewe. Number of lambs born (NLB) was recorded for each ewe.

Statistical analysis and estimation of breeding values

Lactation curves for somatic cell score (SCS), daily yields of milk, fat, protein and lactose for each ewe were obtained using random regression models with the MIXED procedure of Statistical Analysis Software version 9.3 (SAS Institute Inc., Cary, NC, USA). An orthogonal polynomial of third order was chosen for fat and lactose daily yields, and an orthogonal polynomial of fourth order for milk and protein daily yields, selected based on the Akaike information criterion. SCS was calculated as Log_2(somatic cell count) at each flock test. Average somatic cell score (SCS) and lactation yields from day 1 to 150 of milk for each ewe were calculated from the predicted values of the individual lactation curves.

Breeding values for lactation yields of milk, fat, protein and lactose, and for live weight, somatic cell score, first let-down time and yield, and litter size at birth were estimated using the ASReml 3.0 software package (Gilmour

Table 1 Genetic parameters for traits[1] considered in the genetic evaluation of the Gunson's dairy sheep flock. Phenotypic (above diagonal) and genetic correlations (below diagonal).

Trait	h^2	σ_p	LL	MY	FY	PY	LY	LW	SCS	FLDT	FLDY	NLB
LL	0.13	1845		0.61	0.84	0.88	0.61	0.00	0.00	0.00	0.00	0.00
MY	0.27	2197	0.61		0.89	0.97	0.89	0.12	-0.25	0.08	0.25	0.11
FY	0.21	11.07	0.84	0.88		0.86	0.80	0.12	0.06	0.06	0.20	-0.03
PY	0.24	7.53	0.88	0.94	0.92		0.18	0.11	0.02	0.06	0.20	0.00
LY	0.27	7.11	0.61	0.70	0.60	0.60		0.12	-0.22	0.06	0.20	0.11
LW	0.65	51.87	0.00	0.47	0.66	0.65	0.47		0.00	0.00	0.00	0.01
SCS	0.09	2.89	0.00	-0.13	0.31	0.19	-0.49	0.00		0.44	0.51	0.00
FLDT	0.42	419.97	0.00	0.10	0.03	0.01	0.10	0.00	0.44		-0.52	0.00
FLDY	0.38	0.02	0.00	0.06	-0.01	0.07	0.06	0.00	0.51	-0.52		0.00
NLB	0.11	0.42	0.00	0.21	-0.14	-0.03	0.07	-0.01	0.00	0.00	0.00	

[1]h^2 = heritability, σ_p = phenotypic standard deviation, LL = lactation length, MY = milk yield, FY = fat yield, PY = protein yield, LY = lactose yield, LW = live weight, SCS = somatic cell score calculated as Log2(somatic cell count), FLDT = first let-down time, FLDY = first let-down yield, NLB = number of lambs born

et al. 2009) with multiple-trait animal model. The model included the fixed effects of lactation number and deviation from median lambing date and the random effect of animal. The pedigree file was compiled of information for two generations, including 11 known sires and 189 dams.

Genetic and residual variances and covariances derived from genetic parameters are presented in Table 1. Heritability and genetic correlations are averages of values published in the literature. Phenotypic standard deviations were obtained from the data set using the linear model that included the fixed effect of lactation number and the deviation from the median lambing date of the flock. When published estimates of genotypic and phenotypic correlations were not found, genetic correlations were assumed to be equal to phenotypic correlations obtained from the data set. Due to observations being few in number, breed and heterosis effects were not included.

Results

Descriptive statistics for the animal traits considered in this study are presented in Table 2. The coefficients of variation were 38% for lactation length and between 42 and 47% for yields.

The least squares means of each trait for different lactation numbers are shown in Table 3. Means for lactation length, FLDT, FLDY and live weight in first lactation ewes were significantly ($P<0.05$) lower than those in older ewes. Lactation yields for fat, protein, and lactose all increased with increasing lactation number ($P<0.05$) up to the fourth lactation and then declined in fifth-lactation animals.

Distributions of estimated breeding values (EBVs) for some of the traits considered in the genetic evaluation are presented in Figure 1. All EBVs follow a normal distribution. The range of milk yield EBVs was 70 kg (-35 to +35 kg per lactation), and fat yield was 4 kg (-1.5 to +2.5 kg). Distribution for live weight EBVs showed some skew above zero. Somatic cell score EBVs were normally distributed with one outlier with a desirable negative breeding value of -1.25. Milk flow EBVs ranged from -16 to +20 seconds for first let-down time and -0.125 to +0.1 kg for first let-down yields. Estimated breeding values for lactation length ranged from -25 to +30 days while NLB EBVs were between -0.15 and +0.30 lambs.

Table 2 Descriptive statistics of variables considered in the genetic evaluation of the Gunson's dairy sheep flock for the 2015/16 season.

Trait	n	Mean	SD	Min	Max	CV
LL (days)	122	126.0	48.0	44.0	208.0	38
Lactation yield (kg)						
Milk	122	234.0	101.0	47.5	526.0	43
Fat	122	16.5	7.2	2.7	38.7	43
Protein	122	13.0	6.1	2.8	28.9	47
Lactose	122	12.6	5.3	2.5	27.1	42
LW (kg)	92	75.9	8.4	52.0	99.3	11
SCS	121	17.5	1.7	15.1	22.4	10
FLDT (s)	121	78.8	22.2	45.0	157.6	28
FLDY (L)	121	0.5	0.2	0.2	0.9	33
NLB	115	2.0	0.7	1.0	5.0	34

Where, LL = lactation length, LW = live weight, SCS = somatic cell score calculated as Log2(somatic cell count), FLDT = first let-down time, FLDY = first let-down yield, NLB = number of lambs born.
SD = standard deviation and CV = coefficient of variation.

Discussion

The breeding objective of a genetic improvement program requires the identification of the most important traits that will affect overall farm profit (Harris et al. 1984). Traits chosen to be included in the selection criteria were: total yields of milk, fat and protein, first let-down time and yield, live weight, somatic cell score, and number of lambs born. This study provides estimates of breeding values for these economically importance traits.

Average milk production was 234 kg from an average of 126 days in milk. Although milk production was greater than that reported in other flocks (116 kg over 147 days) before the introduction of East Friesian ewes to New Zealand (Gosling et al. 1997), more recent production records of a selection of high-performing East Friesian cross ewes in

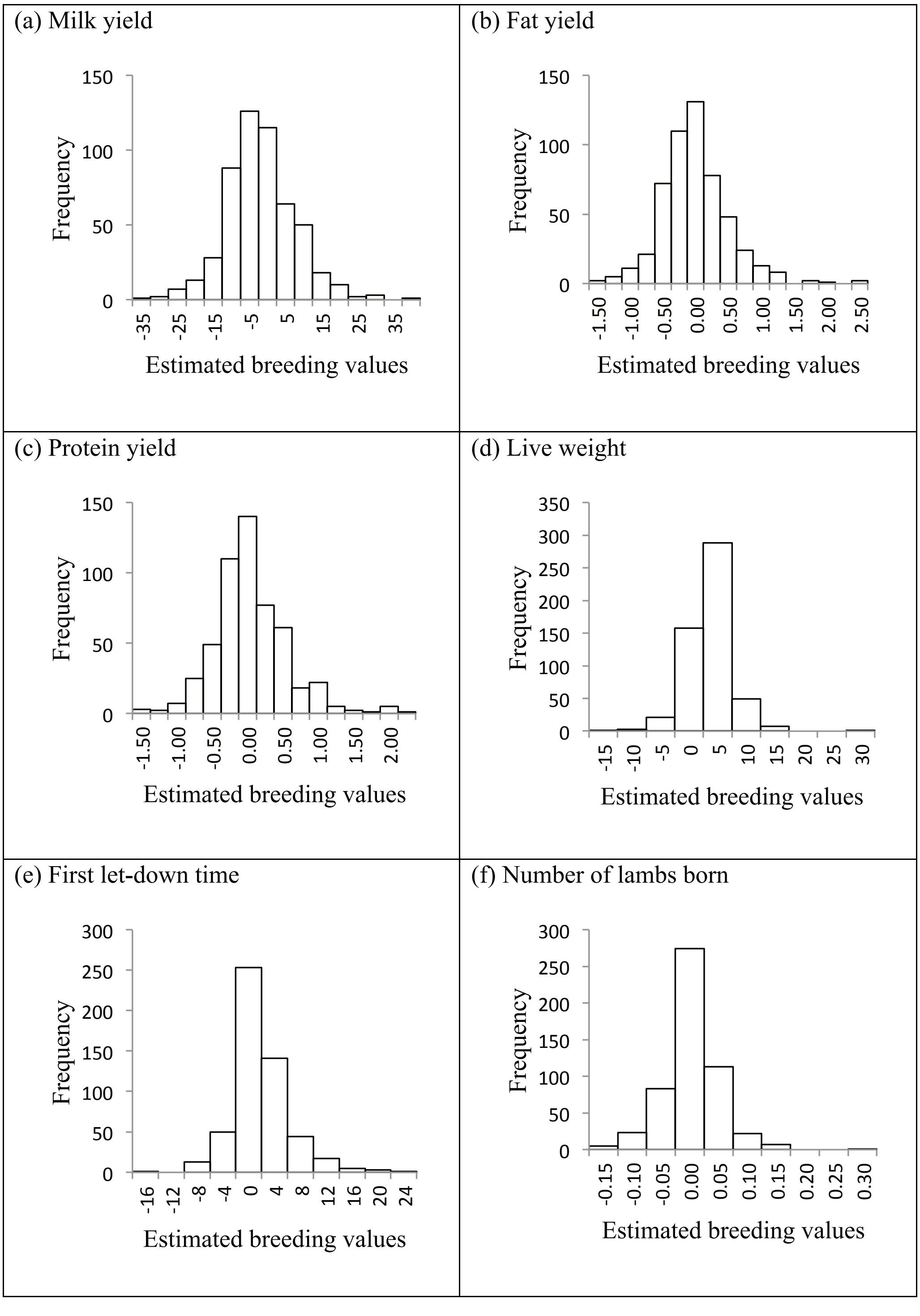
Table 3 Lactation length, predicted yields at 150 days in milk, milking characteristics, live weight and litter size of the Gunson's dairy ewes of different lactation number. Data are means and standard errors (SE).

Lactation no.	n	LL	SE	MY	SE	FY	SE	PY	SE	LY	SE	SCS	SE	FLDT	SE	FLDY	SE	LW	SE	NLB	SE
1	22	92.2^{b}	9.7	208^{c}	10	12.9^{d}	0.7	10.9^{c}	0.62	10.7^{c}	0.58	16.7^{c}	0.36	63.1^{b}	4.4	0.36^{b}	0.03	63.0^{c}	3.0	1.5^{b}	0.16
2	48	125.9^{a}	6.5	266^{b}	7	18.8^{c}	0.49	14.9^{b}	0.42	14.2^{b}	0.39	17.4^{bc}	0.24	78.3^{a}	3.0	0.48^{a}	0.02	73.8^{b}	1.2	2.0^{a}	0.09
3	24	138.5^{a}	9.2	265^{b}	10	18.9^{bc}	0.69	15.6^{ab}	0.59	14.6^{b}	0.55	18.0^{ab}	0.36	78.7^{a}	4.3	0.48^{a}	0.03	81.4^{a}	1.6	2.0^{a}	0.13
4	6	140.8^{a}	18.5	324^{a}	20	22.2^{a}	1.38	18.0^{a}	1.19	17.4^{a}	1.10	17.7^{abc}	0.69	93.0^{a}	8.4	0.59^{a}	0.06	75.0^{ab}	3.2	2.3^{a}	0.26
5	22	142.8^{a}	9.7	288^{ab}	10	20.6^{ab}	0.72	16.0^{ab}	0.62	15.2^{ab}	0.58	18.2^{a}	0.36	91.9^{a}	4.4	0.54^{a}	0.03	78.2^{a}	1.6	2.1^{a}	0.14

LL = lactation length, MY = milk yield, FY = fat yield, PY = protein yield, LY = lactose yield, SCS = somatic cell score = Log2(somatic cell count), FLDT = first let-down time, FLDY = first let-down yield, LW = live weight, NLB = number of lambs born.

^{a,b,c,d} Means with different superscripts are significantly different ($P<0.05$).

Figure 1 Distribution of estimated breeding values for 150-day yields for milk (a), fat (b) and protein (c), live weight (d), first let-down time (e) and number of lambs born (f) of the Gunson's dairy sheep flock.



New Zealand (McMillan et al. 2014) were 120 kg greater than the average of the flock in this study. The sheep from this commercial flock achieved similar production levels to a study of East Friesian ewes in the United States (260 kg; McKusick et al. 2001), but higher production levels than the East Friesian ewes in the Australian study (107 kg; Morgan et al. 2006).

Milk production changes with age in Awassi (Gootwine & Pollott 2000) and Latxa sheep (Gabina et al. 1993). The study on Latxa ewes showed milk yield, by age of ewes followed a quadratic trend, with one-year-old ewes producing the lowest milk yields and maximum yields occurring between four and seven years of age. A similar effect was observed in this study, with age having a significant effect on yields of milk, fat and protein, and ewe live weight.

This genetic evaluation showed large ranges of estimated breeding values for the different traits that may be the result of the diverse breed composition of the flock. This creates an opportunity to identify superior animals to be parents for the following generation and to achieve genetic gain. It is recommended that the farmers use a selection index to rank ewes and rams and produce genetic gain for each of the traits in the right direction and right proportion toward improvement of the breeding objective, still to be defined by the industry. This prototype model can be extended to other dairy sheep farmers and propose selection schemes to produce genetic gain at the industry level.

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