

ESTIMATING BREEDING VALUES FOR SHEEP: ESTIMATES OF GENETIC PARAMETERS AND TRENDS IN A CROSSBRED POPULATION OF DAIRY SHEEP

Thomas W. Murphy¹ and David L. Thomas²

¹Montana State University, Bozeman, Montana, USA

²University of Wisconsin-Madison, Madison, Wisconsin, USA

Background

The overall goal of most North American dairy sheep producers is to decrease operational costs while increasing enterprise returns, thereby maximizing profitability. From a management standpoint, it may be fairly straightforward to identify areas where you can decrease costs and increase returns. You can invest in new feeders that limit the amount of hay wastage, you can plant varieties of grasses and legumes that will extend the grazing season, and you can find alternative markets for your lamb, milk, and cheese, to name a few. However, from a breeding and selection standpoint, identifying individual animals that will provide your operation with more saleable product in the future is not so clear-cut. The following sections will identify important concepts in genetic evaluation, some results from the Spooner Agricultural Research Station's (ARS) historic data base, and practices that are necessary in order to implement a successful genetic improvement program.

Important Concepts in a Genetic Evaluation Program

There is no question that an across-flock genetic evaluation program for North American dairy sheep would be desirable. It would enable producers to more accurately identify genetically superior rams and ewes. Because of environmental influences, the performance of an individual for a trait (e.g., milk yield, fat content, litter size) is not necessarily an accurate indicator of its true genetic merit for that trait. Therefore, accurately identifying and correcting for environmental effects (i.e., non-genetic effects) is key to an effective genetic improvement program.

The Basic Genetic Model

The phenotype of an animal, or its performance for a trait that can be seen or measured, has several components that can be formulized mathematically as:

$$PP = \mu + BBBB + GGGGBB + EE \text{ (Bourdon, 2000).}$$

An animal's phenotype or performance (P) is the summation of the population mean performance (μ) and the animal's breeding value (BV), gene combination value (GCV), and environmental (E) deviations. The true breeding value of an individual is the sum of the independent effects of all its genes that affect a quantitative trait. The gene combination value of an individual represents favorable and unfavorable interactions within and between genes, and is dependent upon the entire genotype of the animal. The environmental effect of an individual represents all of the non-genetic effects which influence its performance. Breeding values, gene combination values, and environmental effects can be positive or negative and are centered around zero. Therefore, individuals can have similar phenotypes but very different breeding values, gene combination values, and environmental effects.

Environmental effects such as nutrition and management are not inherited in future generations. Furthermore, parents pass a random sample of half of their genes, and not their genotypes, to their progeny, so the gene combination value of an individual is not inherited in a predictable manner from his/her parents. However, since a parent transmits half of his/her genes to each

progeny, the expectation is that half of each parent's breeding value is transmitted to each offspring. Consequently, breeding value is of major importance to animal breeders. Since the number of genes and their independent effects on performance traits are not known, the true breeding values of animals are not known. Lucky for us, breeding values can be estimated from the similarities among related animals for phenotypic performance. However, in order to accurately estimate breeding values, we must first identify the non-genetic effects which can influence the phenotype of dairy sheep and adjust the phenotype for these effects in some manner.

Many research projects have been conducted at the University of Wisconsin-Madison's Spooner ARS to determine the effects of various nutritional, management, health, and animal factors (e.g., lamb sex, lamb type of birth, ewe age) on the performance of dairy sheep. While many of these non-genetic effects are very important for determining the level of performance and profitability, they can mask breeding value differences among animals if they are applied differentially to sheep in the flock. As many of these non-genetic factors as possible need to be accounted for in order to accurately estimate breeding values of dairy sheep. The following subsections will discuss the important non-genetic effects that influence dairy ewe performance.

Non-genetic effects on dairy ewe performance – lamb rearing systems

Early research at the Spooner ARS focused on the effects of different lamb rearing systems on lamb and ewe performance (McKusick et al., 2001). Ewes in the first weaning system (DY1) stopped nursing their lambs 24-36 h postpartum, and the ewes were then machine milked twice per d for the remainder of their lactation. Ewes in the second weaning system (DY30) nursed their lambs for 30 d postpartum during which time they were not milked. After weaning of their lambs at approximately 30 d of age, the ewes were milked twice per d for the remainder of their lactation. Ewes in the final weaning system (MIX) were separated from their lambs each night and milked once per d in the morning. After milking, the ewes rejoined their lambs where they stayed for the remainder of the day until evening when they were again separated from their lambs overnight. This process continued until their lambs were weaned at 30 d of age, at which time the ewes were milked twice per d for the remainder of their lactation.

Table 1. Ewe and lamb performance in the three weaning systems from McKusick et al. (2001).

Trait	Weaning System		
	DY1	DY30	MIX
<i>Ewe traits, n</i>	31	33	35
Lactation length, d	183.4 ± 5.4 ^a	182.9 ± 5.5 ^a	179.2 ± 5.1 ^a
Machine milking, d	182.4 ± 5.4 ^a	152.3 ± 5.5 ^b	178.2 ± 5.1 ^a
Milk yield, kg	260.1 ± 9.7 ^a	171.7 ± 9.9 ^b	235.8 ± 9.1 ^c
Fat, %	5.1 ± 0.1 ^a	4.8 ± 0.1 ^{a,b}	4.5 ± 0.1 ^b
Protein, %	5.3 ± 0.1 ^a	5.2 ± 0.1 ^a	5.1 ± 0.1 ^a

^{a,b,c}Means within a row without a common superscript are different ($P < 0.05$).

There were differences in ewe performance between the weaning systems (Table 1). Most notably, ewes in the DY1 group produced 10% and 51% more volume of milk than MIX and DY30 ewes, respectively. Fat content was similar between DY1 and DY30 ewes, but DY1 ewes had a higher fat content in their milk than MIX ewes. Many different weaning systems are practiced in North American dairy sheep operations, and this is an important environmental effect

that will need to be accounted for to be able to accurately estimate breeding values for lactation traits.

Non-genetic effects on dairy ewe performance – nutritional, biological, and systematic effects

Several studies at the Spooner ARS have evaluated the effect of various ewe nutritional treatments on lactation performance. One early project was conducted in 1998 and utilized 97 East Friesian-cross ewes that had been fed in drylot until mid-lactation. For the remainder of lactation, 48 ewes stayed in drylot while 49 grazed orchard grass-kura clover pasture (unpublished data; Thomas et al., 2014). The ewes that had access to pasture produced, on average, 10.5% more milk throughout lactation than the drylot ewes.

Most dairy sheep operations in North America rely heavily on pasture, but additional supplementation with various concentrate feeds is common. In a 2006 research trial, 96 East Friesian and Lacaune crossbred, mature ewes in mid-lactation were assigned to one of four treatments that supplemented whole shelled corn at a level of 0.00, 0.41, 0.82, or 1.24 kg of dry matter per ewe per day (Mikolayunas et al., 2008). Treatment means of ewe performance for several traits are shown in Table 2. Ewes that were supplemented with 0.82 or 1.24 kg of whole shelled corn had higher daily milk yields than ewes supplemented with no or 0.41 kg of corn. Ewes supplemented with 1.24 kg of corn had a lower milk fat percentage than the other groups. Protein percentage in milk was not different among the treatment groups (Mikolayunas et al., 2008). Because of these increases in performance from supplementation, lactating ewes at the Spooner ARS have been supplemented with approximately one pound of whole shelled corn at each milking since 2007.

Table 2. Performance of mid-lactation, pastured ewes supplemented whole shelled corn at varying levels from Mikolayunas et al. (2008).

Trait	Whole shelled corn supplementation (kg dry matter/ewe/day)			
	0.00	0.41	0.82	1.24
<i>Ewe traits, n</i>	24	24	24	24
Test day milk yield, kg	1.30 ± 0.03 ^a	1.32 ± 0.03 ^a	1.41 ± 0.03 ^b	1.44 ± 0.03 ^b
Fat, %	6.26 ± 0.11 ^b	6.40 ± 0.11 ^b	6.09 ± 0.11 ^b	5.89 ± 0.11 ^a
Protein, %	5.29 ± 0.04	5.41 ± 0.04	5.37 ± 0.04	5.39 ± 0.04

^{a,b}Means within a row without a common superscript are different ($P < 0.05$).

Ewe nutrition programs are likely very different from farm to farm. Along the same lines, climatic conditions are variable from year to year. Finally, performance differences obviously exist between ewes of different ages. However, the effects of farm, year, and ewe age, among others, are non-genetic, environmental effects that can be accounted for in an across-flock genetic evaluation program.

Genetic effects on dairy ewe performance – breed differences and heterosis

The East Friesian and Lacaune breeds originated in Germany and France, respectively, under different climatic and management environments. It is therefore likely that these breeds differ in performance for one or more traits. Haenlein (2007) reported breed averages for dairy sheep breeds commonly milked in Europe and Asia, and some of the findings are presented in Table 3. German East Friesian had 135 d longer lactations and produced 362 kg more milk and 21 kg more fat in a lactation than French Lacaune, but French Lacaune had 0.92% higher fat content in their milk than the German East Friesian. However, dairy sheep producers in these two countries

likely have different husbandry and nutrition programs, and these environmental effects cannot be accounted for in this report.

Table 3. Average performance for European dairy sheep breeds in their home country from Haenlein (2007).

Country	Breed	Trait ^a		
		LL (d)	MY (kg)	FY (kg)
France	Corsica	170	108	9
	Lacaune	165	270	20
Germany	East Friesian	300	632	41
Italy	Sarda	200	158	11
	Churra	150	150	11
Spain	Latxa	180	210	16
	Manchega	210	300	28

^aLL = lactation length, MY = total lactation milk yield, FY = total lactation fat yield.

In addition to differences that may exist among breeds, crossbred animals often perform better than the average of purebreds that make up the cross because of heterosis or hybrid vigor. In crossbred populations like the flock at the Spooner ARS, individuals may vary in their amount of retained heterosis, which may result in differences in performance. Gootwine and Goot (1996) estimated the effect of heterosis on performance in Awassi and EF ewes. They found positive effects of individual heterosis for prolificacy, milk yield, and lactation length as F₁ ewes were estimated to gestate 0.10 more lambs, yield 47 kg more milk, and milk 9 d longer than the average of purebred EF and Awassi ewes.

Genetic and non-genetic parameters

From the basic genetic model presented earlier, it is evident that phenotypic differences among animals can occur because of differences in breeding value, gene combination value, and/or environmental effects. The magnitude of population differences in phenotype, breeding value, gene combination value, and environment is quantified through their respective variances. The heritability of a trait is calculated as the ratio of breeding value variance to phenotypic variance and ranges from 0 to 1. Heritability is an important concept for many reasons, one of which is that it tells us how accurately an animal's own phenotypic performance serves as a predictor of its true breeding value. When a trait has a high heritability (> 0.60), an animal's performance is a pretty good indicator of their genetic merit and the opposite is true for traits with low heritability (< 0.20).

We are usually interested in genetically improving more than one trait at a time. For example, we might want to increase milk and the component yields, percent fat and protein, and lactation length. Meanwhile we might want to decrease somatic cell count and mature body size. Many genes can have an effect on more than one trait. Because of this, when we genetically improve one trait we may intentionally or unintentionally change other traits. This genetic relationship between traits is called a genetic correlation, and its value ranges from -1 to +1. A strong positive genetic correlation (> +0.80) between two traits indicates a large number of the same genes affect both traits in the same direction, i.e., an animal with a high breeding value for trait 1 will tend to have a high breeding value for trait 2. On the other hand, two traits with a strong negative genetic correlation (< -0.80) indicates a large number of the same genes affect both traits, but in different directions, i.e., an animal with a high breeding value for trait 1 will tend to

have a low breeding value for trait 2.. However, a positive genetic correlation is not necessarily good and a negative genetic correlation is not necessarily bad. For example, if milk yield and somatic cell count have a positive genetic correlation in a population, genetic improvement in milk yield would potentially come with increased somatic cell count.

Genetic evaluation of Spooner ARS dairy sheep

Data description

The lambing season at the Spooner ARS generally began in late January and lasted until late March. Following weaning of their lambs, ewes began 2x per d milking until late lactation (mid-August) when the whole flock was switched to 1x milking. Milk recording took place, on average, every 4 weeks throughout lactation. A ewe's p.m. and a.m. records were summed for an estimated daily yield, and samples were taken from each ewe's a.m. test day milk and sent to an independent lab to estimate fat and protein content and somatic cell count (SCC).

Individual test day records were combined to estimate 180 day adjusted milk (180d MY), fat (180d FY), and protein (180d PY) yields as well as average percent fat (%F) and protein (%P) through 180 days. For ewes that reared their own lambs for any time period (MIX or DY30), test day records prior to 30 days in lactation were not included in 180 day lactation records. The MIX and DY30 rearing systems were considered together (DY+), and distinguished from DY1 ewes whose 180 d performance was estimated from the first day of milking.

Individual SCC records were transformed to somatic cell score (SCS) with the following equation (Ali and Shook, 1980; Shook, 1993):

$$SCS_t = \frac{SCC_t}{100} + 3$$

where SCS_t is the calculated SCS on test day t and SCC_t is the SCC (thousands of cells per mL of milk) on test day t . The arithmetic mean of individual test day SCS records throughout lactation (LSCS) was then calculated for each ewe.

Breed composition and retained heterosis

In this analysis, non-dairy breed composition was considered as one breed group in addition to the percentage of East Friesian (EF) and Lacaune (LA) breeding of each animal. The breed composition of each individual was calculated as:

$$b_{ii}^{jj} = \frac{1}{2} b_{SS_{ii}}^{jj} + b_{DD_{ii}}^{jj}$$

where b_{ii}^{jj} is the calculated percent of the j^{th} breed (EF, LA, non-dairy) of individual i and $b_{SS_{ii}}^{jj}$ ($b_{DD_{ii}}^{jj}$)

is the percent of the j^{th} breed of the sire(dam) of i . Then, proportion retained heterosis (H) could be calculated for each individual as:

$$HH_{ii} = 1 - \sum_{jj=1}^3 b_{SS_{ii}}^{jj} b_{DD_{ii}}^{jj}$$

Statistical models

The ewe traits of interest were number of lambs born (NLB), LSCS, 180d MY, 180d FY, 180d PY, %F, and %P. Ewes were removed from the analyses if they were less than 12.5% dairy breeding (EF + LA), had a machine milking length less than 70 d, were culled or died mid-lactation, or were treated for mastitis or other illness at any point during lactation. Additionally, a LSCS record needed to be the average of at least 3 individual test dates to be included in the analysis. After editing the dataset, there were 5,438 NLB records from 1,969 individual ewes and 4,696 LSCS and , 4,763 180d MY, 180d FY, 180d PY, %F, and %P records from 1,688 individual ewes.

To estimate the non-additive genetic effects on ewe performance, univariate linear mixed models included the fixed effects of year of lambing (1995 – 2015), weaning system (included for lactation traits only; DY1 or DY+), age of ewe (1 – 6 years), and the random effect of ewe. Additionally, ewe's EF and LA breed composition and individual retained heterosis were fit as linear covariates. All ewe traits were analyzed using the MIXED procedure of SAS (Version 9.3).

After the significant non-additive genetic effects for each trait were determined, two multiple-trait repeatability models were employed in ASReml (Version 4) from which genetic parameters of and among traits were estimated and breeding values were predicted. The first model jointly analyzed NLB, 180d MY, 180d FY, 180d PY, and LSCS while the second model analyzed NLB, 180dMY, %F, %P, and LSCS. Estimated breeding values of ewes with records were then regressed onto their year of birth to determine the genetic trend in traits over the years.

Age, weaning system, breed, and heterosis effects on ewe performance

Least squares means for main fixed effects and solutions for breed composition and retained individual heterosis obtained from the univariate models for ewe traits are shown in Tables 4a and 4b. Large ($P < 0.01$) differences existed among ewe ages for yields of milk, fat, and protein adjusted to 180 days (Table 4a). Yields were lowest in first parity ewes, peaked in the third or fourth parity, then decreased until 6 years of age. Not surprisingly, the type of weaning system impacted ($P < 0.01$) yield traits as well. Ewes that had their lambs weaned shortly after birth (DY1) produced 57.3 kg more milk, 3.6 kg more fat, and 2.9 kg more protein in 180 days than ewes that reared their lambs for approximately 30 d (DY+).

Ewe EF and LA breed composition affected ($P < 0.001$) all 180 day adjusted yield traits (Table 4a). A 100% EF ewe is expected to produce 149 kg (14.9 kg x 10) more milk, 6.5 kg more fat, and 5.9 kg more protein in 180 days than a 100% non-dairy ewe. Similarly, a 100% LA ewe is expected to produce 120 kg more milk, 7.2 kg more fat, and 5.7 kg more protein in 180 days than a 100% non-dairy ewe. A 100% EF ewe is expected to produce 28.2 kg more milk in 180 days ($P < 0.001$) than a 100% LA ewe, but performances between the two dairy breeds were similar for 180 d FY ($P > 0.08$) and 180 d PY ($P > 0.57$).

Age affected ($P < 0.05$) percentage of milk component traits (%F and %P), lactation average somatic cell score, and prolificacy in ewes (Table 4b). Percentage fat and protein in milk generally increased with ewe age, peaking in the fourth and later parities, and similar trends were found for LSCS and NLB. Weaning system also impacted ($P < 0.05$) %F, %P, and LSCS, as ewes that reared their lambs for some time (DY+) had 0.15% lower fat content, 0.04% lower protein content, and a 0.24 higher average LSCS than ewes that did not rear their lambs (DY1).

Table 4a. Least-squares means (\pm standard errors) for the main effects of ewe age (Age) and weaning system (Wean) and solutions for ewe breed and heterosis effects for 180 d adjusted milk (180d MY), fat (180d FY), and protein yield (180d PY).

Effect	Level	Trait		
		180d MY (kg)	180d FY (kg)	180d PY (kg)
Age	1	180.9 \pm 1.84 ^d	10.3 \pm 0.11 ^d	8.63 \pm 0.09 ^d
	2	262.9 \pm 2.11 ^b	15.3 \pm 0.13 ^c	12.9 \pm 0.10 ^b
	3	286.9 \pm 2.43 ^a	17.2 \pm 0.15 ^a	14.4 \pm 0.12 ^a
	4	281.7 \pm 2.92 ^a	17.5 \pm 0.18 ^a	14.2 \pm 0.14 ^a
	5	256.6 \pm 3.53 ^b	16.1 \pm 0.22 ^b	13.0 \pm 0.17 ^b
	6	233.8 \pm 4.67 ^c	14.7 \pm 0.29 ^c	11.9 \pm 0.23 ^c
Wean	DY1	279.1 \pm 1.92 ^a	17.0 \pm 0.12 ^a	14.0 \pm 0.09 ^a
	DY+	221.8 \pm 2.84 ^b	13.4 \pm 0.18 ^b	11.1 \pm 0.14 ^b
	EF	14.9 \pm 1.13 [*]	0.652 \pm 0.068 [*]	0.587 \pm 0.053 [*]
Breeding [‡]	LA	12.0 \pm 1.21 [*]	0.720 \pm 0.074 [*]	0.570 \pm 0.058 [*]
	H _I	3.25 \pm 0.62 [*]	0.221 \pm 0.037 [*]	0.166 \pm 0.029 [*]

^{a,b,c,d}Means within a trait and effect are different ($P < 0.05$).

^{*}Coefficient is different from zero ($P < 0.001$).

[‡]EF = ewe percentage East Friesian breed composition; LA = ewe percentage Lacaune breed composition; H_I = percentage retained individual heterosis. EF, LA, and H_I solutions are expressed per 10% increase.

Table 4b. Least-squares means (\pm standard errors) for the main effects of ewe age (Age) and weaning system (Wean) and solutions for ewe breed and heterosis effects for percentage milk fat (%F) and protein (%P), number of lambs born (NLB), and somatic cell score (LSCS).

Effect	Level	Trait			
		%F	%P	LSCS	NLB (n)
Age	1	5.68 \pm 0.02 ^e	4.80 \pm 0.01 ^d	2.85 \pm 0.04 ^c	1.63 \pm 0.01 ^d
	2	5.76 \pm 0.02 ^d	4.95 \pm 0.01 ^c	2.73 \pm 0.04 ^d	1.88 \pm 0.02 ^c
	3	5.92 \pm 0.02 ^c	5.01 \pm 0.01 ^b	2.81 \pm 0.05 ^{c,d}	2.12 \pm 0.02 ^b
	4	6.09 \pm 0.02 ^b	5.05 \pm 0.01 ^a	2.88 \pm 0.06 ^{b,c}	2.20 \pm 0.03 ^a
	5	6.15 \pm 0.03 ^a	5.06 \pm 0.01 ^a	3.04 \pm 0.08 ^{a,b}	2.10 \pm 0.03 ^b
	6	6.13 \pm 0.04 ^{a,b}	5.07 \pm 0.02 ^a	3.12 \pm 0.10 ^a	2.24 \pm 0.05 ^a
Wean	DY1	6.03 \pm 0.02 ^a	5.01 \pm 0.01 ^a	2.78 \pm 0.04 ^b	-
	DY+	5.88 \pm 0.02 ^b	4.97 \pm 0.01 ^b	3.02 \pm 0.06 ^a	-
	EF	-0.110 \pm 0.005 [*]	-0.075 \pm 0.005 [*]	ns	ns
Breeding [‡]	LA	ns	-0.025 \pm 0.005 [*]	0.087 \pm 0.012 [*]	-0.026 \pm 0.004 [*]
	H _I	ns	ns	ns	0.014 \pm 0.004 [*]

^{a,b,c,d,e}Means within a trait and effect are different ($P < 0.05$).

^{*}Coefficient is different from zero ($P < 0.001$).

^{ns}Coefficient is not different from zero ($P > 0.15$).

[‡]EF = ewe percentage East Friesian breed composition; LA = ewe percentage Lacaune breed composition; H_I = percentage retained individual heterosis. EF, LA, and H_I solutions are expressed per 10% increase.

Relative to non-dairy breeding, EF and LA breeding had a negative effect on %P but only EF breeding had a negative effect on %F (Table 4b). A 100% EF ewe is expected to have 1.1% less ($P < 0.001$) fat content and 0.75% less ($P < 0.001$) protein content than a 100% non-dairy ewe. A 100% LA ewe is expected to have 0.25% less ($P < 0.001$) protein content but similar ($P > 0.16$) fat content than a 100% non-dairy ewe. A 100% LA ewe is expected to have 0.5% more ($P < 0.001$) protein content than a 100% EF ewe. A 100% EF ewe is expected to have a similar ($P > 0.92$) performance for NLB and LSCS than a non-dairy ewe. However, LA breed composition adversely ($P < 0.01$) affected LSCS and NLB, as a 100% LA ewe is expected to have a 0.87 higher average LSCS and gestate 0.26 fewer lambs than a 100% EF or non-dairy ewe (Table 4b).

Estimates of genetic parameters

Genetic and non-genetic parameter estimates across traits are displayed in Tables 5a and 5b. Prolificacy and LSCS were estimated to be lowly heritable in both models (0.07 to 0.08 and 0.13, respectively). This indicates that, although genetic progress can certainly be made in NLB and LSCS, an individual's phenotype for these traits is a poor predictor of their true genetic merit. Milk, fat, and protein yields adjusted to 180 days were all moderately heritable (0.26 to 0.32). Percentage fat and protein in milk were both highly heritable (0.53 and 0.61, respectively). These heritability estimates for lactation performance traits are within the range that has been reported in dairy cattle and goats, as well as European dairy sheep populations.

Prolificacy (NLB) was estimated to have low genetic correlations with the 180 d adjusted yield traits (-0.06 to 0.05) and LSCS (0.07 ± 0.18). The yield traits were all highly positively genetically correlated with one another (0.91 to 0.96), indicating that genetic improvement in 180d MY will result in genetic improvement in 180d FY and 180d PY as well. Milk, fat, and protein yields adjusted to 180 days were all moderately positively, and unfavorably, genetically correlated with LSCS (0.29 ± 0.13 , 0.40 ± 0.13 , and 0.29 ± 0.13 , respectively). Therefore, one downfall of focusing solely on genetic improvement of milk yield is that increased susceptibility to mastitis will likely follow.

Table 5a. Estimates of heritability on the diagonal and genetic correlations (above diagonal) of and among number of lambs born per ewe lambing, 180 d adjusted milk yield, 180 d adjusted fat yield, 180 d adjusted protein yield, and lactation average somatic cell score.

Traits ^a	NLB	180d MY	180d FY	180d PY	LSCS
NLB	0.07 ± 0.02	0.05 ± 0.14	-0.06 ± 0.15	0.02 ± 0.14	0.07 ± 0.18
180d MY	-	0.32 ± 0.04	0.91 ± 0.02	0.96 ± 0.01	0.29 ± 0.13
180d FY	-	-	0.26 ± 0.04	0.94 ± 0.01	0.40 ± 0.13
180d PY	-	-	-	0.30 ± 0.04	0.29 ± 0.13
LSCS	-	-	-	-	0.13 ± 0.03

^aNLB = number of lambs born per ewe lambing; 180d MY = 180 d adjusted milk yield; 180d FY = 180 d adjusted fat yield; 180d PY = 180 d adjusted protein yield; LSCS = lactation average test-day somatic cell score.

Percentage fat and protein in milk were positively genetically correlated with each other (0.60 ± 0.05), but both were negatively genetically correlated with 180d MY (-0.31 ± 0.08 and -0.34 ± 0.08 , respectively) (Table 5b). Again, if milk yield is the only selection criteria for North American dairy sheep, future generations will experience decreases in component content which could have negative consequences for cheese makers. The estimated genetic correlation between

LSCS and %P was low (0.03 ± 0.11), however, LSCS and %F were moderately positively genetically correlated (0.21 ± 0.11). Interestingly, NLB and %P were not genetically correlated (-0.01 ± 0.12), but the estimated genetic correlation between NLB and %F was moderately negative (-0.26 ± 0.12).

Table 5b. Estimates of heritability on the diagonal and genetic correlations (above diagonal) of and among number of lambs born per ewe lambing, 180 d adjusted milk yield, percentage fat in milk, percentage protein in milk, and lactation average somatic cell score.

Traits ^a	NLB	180d MY	%F	%P	LSCS
NLB	0.08 ± 0.02	0.06 ± 0.17	-0.26 ± 0.12	-0.01 ± 0.12	0.06 ± 0.17
180d MY	-	0.31 ± 0.04	-0.31 ± 0.08	-0.34 ± 0.08	0.30 ± 0.13
%F	-	-	0.53 ± 0.04	0.60 ± 0.05	0.21 ± 0.11
%P	-	-	-	0.61 ± 0.04	0.03 ± 0.11
LSCS	-	-	-	-	0.13 ± 0.03

^aNLB = number of lambs born per ewe lambing; 180d MY = 180 d adjusted milk yield; %F = percentage fat in milk; %P = percentage protein in milk; LSCS = lactation average test-day somatic cell score.

Genetic trend in the Spooner ARS Flock

The predicted breeding values for 180d MY (180d MY EBV) for ewes with records are plotted against their year of birth in Figure 1. The dashed and solid black lines pass through the mean 180d MY EBV with and without the addition of breed effects, respectively, for each birth year. From 1994 to 2014, there has been an increase of 2.20 ± 0.11 kg per year in 180d MY EBV. However, most of this genetic gain can be attributed to the more recent time period of 2002 to 2014 (3.08 ± 0.21 kg per year), as there was actually a genetic decrease (-1.55 ± 0.37 kg per year) from 1994 to 2002. The reason for this is likely because in the early years, the Spooner ARS flock was managed with the goal of increasing the proportion of dairy breeding in the flock as fast as possible rather than selecting animals for their additive genetic merit for lactation performance. The upward trend in response since 2002 was due to simple phenotypic selection on dam's milk yield because the calculation of EBVs and their use in selection for this flock only started very recently.

The increase in milk yield of 2.20 kg per year from 1994 to 2014 (or 3.08 kg per year from 2002 to 2014) in the Spooner ARS flock is generally similar, and sometimes greater, than the gains seen in national genetic improvement programs in Europe. In Spain, genetic evaluation programs are in place for the Churra, Black-Faced Latxa, Blond-Faced Latxa, and Manchega breeds. These programs report genetic gains in milk yield of 2.97, 2.95, and 0.82 liters per year in Black-Faced, Blond-Faced, and Manchega sheep, respectively (Legarra et al., 2003; Jurado et al., 2006). (Note: 1 liter of sheep milk = 1.036 kg = 2.279 lb.). The Sarda breed in Italy also has a genetic improvement program and has reported a genetic gain of 2.0 liters per year in past years (Carta et al., 2009).

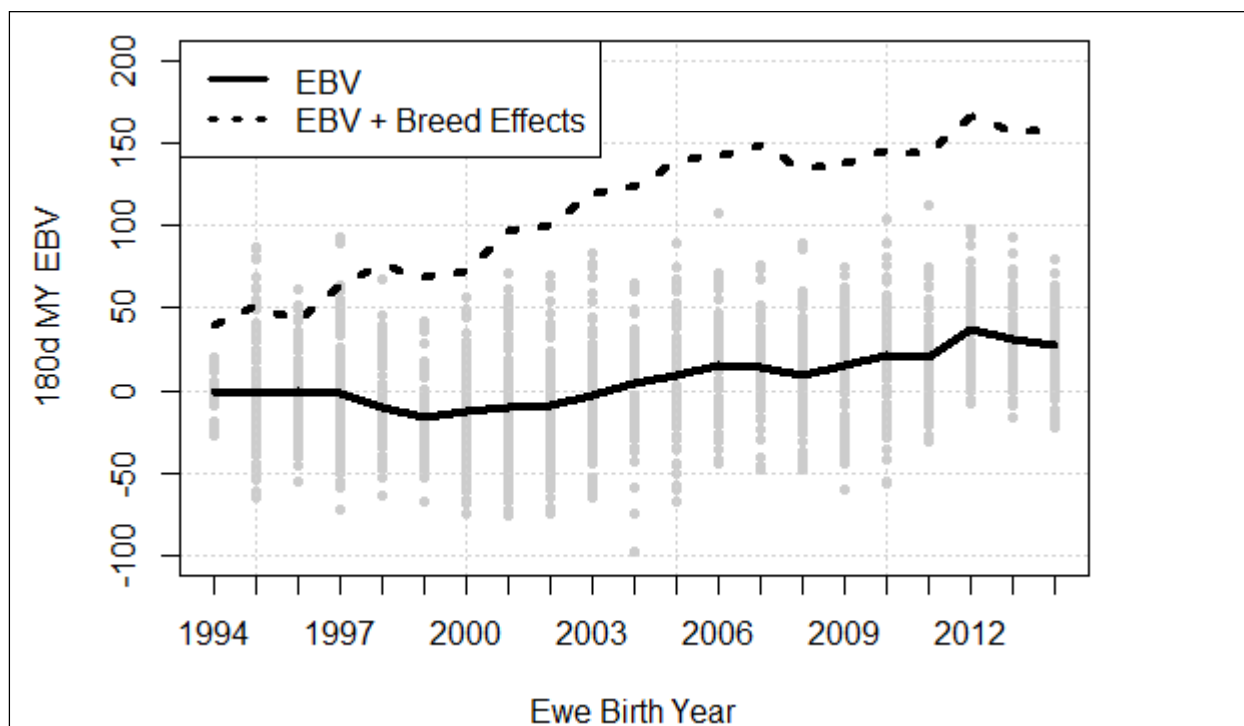


Figure 1. Ewe predicted breeding values (gray closed circles) for 180 d adjusted milk yield (180d MY EBV), adjusted for breed effects, and plotted against their year of birth. The solid black trend line passes through the mean 180d MY EBV for each year. The dashed black line passes through the mean 180d MY EBV with the addition of breed effects for each year.

However the French Lacaune genetic evaluation program has reported greater genetic gains than other programs in Europe and is an indication of the high rates of genetic gain that are possible. Between 1980 and 1994, a genetic gain of 6 liters per year was reported for the nucleus flocks of the French Lacaune (Barillet et al., 2001) when the main selection criterion was on milk yield. Since then, despite incorporating component traits into the selection criteria, the French Lacaune program still reports a genetic gain of 5 liters per year (Carta et al., 2009). France also has genetic evaluation programs for the Corsican, Red-Faced Manech, Black-Faced Manech, and Basco-Béarnaise breeds, which report milk yield genetic gains of 0.81, 4.33, 3.19, and 3.53 liters per year, respectively (Astruc et al., 2002).

Selection for multiple traits

The main goal of most dairy sheep farms is to make a profit, which is dependent upon the efficient production of quality lamb and milk. Many traits contribute to profitability including number of lambs born, lamb survival, lamb growth rate, ewe milk yield, milk composition, and ewe health. The most efficient way to select for net merit or net profit is to select on an index that includes all traits of economic value and weights the traits by coefficients that take into account trait heritabilities, correlations with other traits, and net economic values.

However, developing a good selection index is no easy task. The most difficult task is to obtain good estimates of the net economic value of a unit change in each trait. For example, what is the net economic value of increasing lactation milk yield by 1.0 kg? The increased income from

the extra 1.0 kg of milk is easy to calculate, but the cost of producing the extra 1.0 kg of milk is not so easy to determine. How much more feed does it take to produce the extra milk, how much longer does it take to milk a ewe with more milk production, what is the effect of the extra milk on the incidence of mastitis, etc., etc. etc.? While determining the net economic value of a kg of milk may not be easy, determining the net economic value of some other traits, such as milk protein percentage, may be even more difficult.

Regardless of the challenges, a publicly available software package, ECOWEIGHT (Wolf et al., 2011a, b), was used to develop net profit selection indexes for dairy sheep using genetic parameters estimated from the Spooner ARS flock records and costs of inputs and prices for products from the Spooner ARS operation or estimated from national or regional sources. The traits included were NLB, lamb birth weight (BW), lamb 30 day weight (WW), 180d MY, 180d FY, 180 d PY, %F, and %P.

Indexes were calculated for two general production scenarios: 1) MILK - all milk sold to a processor on a weight basis with no premiums/discounts for percentage of fat and protein and 2) CHEESE - all milk processed into cheese on the farm. In both scenarios, the combined effects of changes in the non-lactation traits of NLB, BW, and WW only accounted for 5% to 14% of the changes in profitability. Under the MILK scenario, a change in 180 d MY accounted for over 80% of the change in profitability, and in the CHEESE scenario, a change in fat and protein (either % or yield) accounted for 73% to 84% of the change in profitability. Since it is important for cheese processing to maintain a high content of fat and protein in sheep milk, the recommended index, including only lactation traits, was:

$$\text{Net Profit Index} = (1.2 \times \text{EBV}_{180\text{dMY}}) + (280 \times \text{EBV}_{\%F}) + (268 \times \text{EBV}_{\%P})$$

Does selection on EBVs work?

Of course, the answer to the above question is “yes.” An EBV is an estimate of genetic value of an animal, and selection on an estimate of genetic value, assuming that it is a good estimate calculated in a proper manner, is a better selection criterion than selecting on the raw phenotypic record. While we know this is true, it is always good to have some data that demonstrates this truism for non-believers.

A small retrospective study was conducted using the 2014 first lactation 180 d MY records of 76 ewe lamb replacements born in 2013 at the Spooner ARS (Murphy, 2015). Three possible selection criterion were considered for the ewe lambs: 1) their dam’s actual 180 d MY in 2013, 2) their dam’s 180 d MY adjusted for age of dam and number of lambs born to the dam in 2013, and 3) their dam’s EBV for 180 d MY considering all lactation records of the dam and her relatives collected through 2013.

Presented in Table 6 is the average 180 d MY in 2014 of the “best” 38 ewe lambs compared with the average 180 d MY of the “worst” 38 ewe lambs based on the three selection criterion. When ewe lambs were ranked by their dam’s actual (raw) 180d MY, the top ½ produced, on average, 5.7 kg (12.5 lbs.) more than the bottom ½, but this difference was not statistically significant ($P > 0.60$). Next, when the 2013-born ewe lambs were ranked by their dam’s adjusted 180d MY, the top ½ produced 12.1 kg (26.6 lbs.) more than the bottom ½ in 2014, but this difference also was not statistically significant ($P > 0.25$). Finally, when the ewe lambs were ranked by their dam’s EBV for 180d MY, the top ½ tended to produce more ($P < 0.07$), 20.2 kg (44.4 lbs.) on average, than the bottom ½ in their first lactation.

These results suggest that selection on the basis of any objective record is better than random selection without objective information, but selection on the best estimate of genetic value (the dam's EBV in this case) is the most effective.

Table 6. Least square means \pm standard errors for 180d MY of ewe lambs whose dam was in the top or bottom half among all dams for 3 selection criteria.

Dam Group	Selection Criterion		
	Raw 180d MY, kg	Adjusted 180d MY, kg	EBV 180d MY, kg
Top ½	212.7 \pm 7.8	215.8 \pm 7.6	219.8 \pm 7.5
Bottom ½	207.0 \pm 7.7	203.7 \pm 7.7	199.6 \pm 7.6
Top - Bottom	5.7	12.1	20.2*

* $P < 0.07$.

Conclusions

There are several practices that are necessary to adopt before a genetic improvement program can be implemented for North American dairy sheep flocks. First and foremost, routine milk recording (i.e., every 4 weeks) needs to be implemented by participating flocks. Additionally, accurate pedigrees of all animals need to be maintained and genetic relatedness among animals within and between flocks has to be determined. This requires single-sire matings and a single national animal identification system that is capable of tracking animals that move from flock to flock and sires that are used in multiple flocks. Finally, genetic improvement only comes with a great deal of record-keeping and a lot of patience.

Buzzwords like “genomics” often conjure up images of being able to extract DNA from an animal at birth and immediately determining their genetic potential. Indeed, other livestock industries are able to implement such technologies. However, the only reason they can do so is because their genomic breeding values are backed by many, many years of parentage identification, performance recording, and pedigree-based estimated breeding values. The American sheep industry needs to start at the basics before such state-of-the-art technologies are feasible.

Traditionally, the North American dairy sheep industry has relied on importing European germplasm as its main source of genetic improvement. To a lesser extent, replacement animals have been selected on their performance or the performance of their close female relatives. Though these methods can yield appreciable genetic gains, importing foreign genetics may continue to be heavily regulated and expensive, and phenotypic selection is inaccurate for lowly or moderately heritable traits. A genetic evaluation program would be an invaluable development for North American dairy sheep, but it comes with a cost, and key practices must first be implemented.

References

- Ali, A. K. A. and G. E. Shook. 1980. An optimum transformation for somatic cell concentration in milk. *J. Dairy Sci.* 63:487-490.
- Astruc, J. M., F. Barillet, A. Barbat, V. Clément, and D. Boichard. 2002. Genetic evaluation of dairy sheep in France. 7th World Congr. Genet. Appl. Livest. Prod., Montpellier, France. 01:45.
- Barillet, F., C. Marie, M. Jacquin, G. Lagriffoul, and J. M. Astruc. 2001. The French Lacaune dairy sheep breed: use in France and abroad in the last 40 years. *Liv. Prod. Sci.* 71:17-29.

- Bourdon, R. M. 2000. Understanding animal breeding. 2nd Ed. Prentice-Hall, Inc., Upper Saddle River, NJ.
- Carta, A., S. Casu, and S. Salaris. 2009. Invited review: Current state of genetic improvement in dairy sheep. *J. Dairy Sci.* 92:5814-5833.
- Gootwine, E. and H. Goot. 1996. Lamb and milk production of Awassi and East-Friesian sheep and their crosses under Mediterranean environment. *Small Rum. Res.* 20:255-260.
- Haenlein, G. F. W. 2007. About the evolution of goat and sheep milk production. *Small Rum. Res.* 68:3-6.
- Jurado, J. J., M. Serrano, and M. D. Pérez-Guzmán. 2006. Análisis del progreso genético obtenido en el esquema de selección de la raza ovina Manchega. *ITEA J.* 102:41-54.
- Legarra, A., E. Ugarte, and F. Arrese. 2003. Analysis of the genetic progress in the Latxa breed breeding program. *Informacio Tecnico-Economica Agraria* 99A:192-202.
- McKusick, B. C., D. L. Thomas and Y. M. Berger. 2001. Effects of weaning systems on commercial milk production and lamb growth of East Friesian dairy sheep. *J. Dairy Sci.* 84:1660- 1668.
- Mikolayunas, C. M., D. L. Thomas, K. A. Albrecht, D. K. Combs, Y. M. Berger, and S. R. Eckerman. 2008. Effects of supplementation and stage of lactation on performance of grazing dairy ewes. *J. Dairy Sci.* 91:1477-1485.
- Murphy, T. W. 2015. Estimated breeding values do predict future performance. Proc. 63rd Annual Spooner Sheep Day, Dept. Anim. Sci., Univ. Wisconsin-Madison. pp. 3-8.
- Shook, G. E. 1993. Genetic improvement of mastitis through selection on somatic cell count. *Veterinary Clinics of North America – Food Animal Practice.* 9:563-581.
- Thomas, D. L., Y. M. Berger, B. C. McKusick and C. M. Mikolayunas. 2014. Dairy sheep production research at the University of Wisconsin-Madison, USA – a review. *J. Anim. Sci. and Biotech.* 5:22.
- Wolf, J., M. Wolfová, Z. Krupová, and E. Krupa. 2011. User's manual for the program package ECOWEIGHT, Version 5.1.1. Part 3A: program EWSH2 for sheep, Version 1.0.2.
- Wolf, J. and M. Wolfová. 2011. User's manual for the program package ECOWEIGHT, Version 5.1.1. Part 3B: program GFSH for gene flow in sheep, Version 1.0.3.