A GENETIC EVALUATION PROGRAM FOR DAIRY SHEEP IN CANADA: PRELIMINARY RESULTS FROM A PROJECT IN QUEBEC

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Introduction

Recently, in Quebec, the dairy sheep industry has grown. Demand for fine cheeses has increased and consumers are requesting these new, local products. For producers, as for processors, production of large quantities of high quality milk has become a necessity. It is essential to identify animals with the potential for high milk production in order to achieve these objectives and to contribute to the profitability of dairy sheep farms. How is it possible to improve the milk production potential for sheep? In the past, the introduction of dairy breeds into the sheep population (mainly East Friesian) contributed to an improvement in the average milk production. Now, on many dairy farms, herds are mainly composed of dairy sheep purebred females (East Friesian, Lacaune, and a few British Milk sheep), hybrids of dairy breeds (crosses between two purebred sheep) and/or females with a high percentage of purebred dairy blood. In the absence of a specialized genetic evaluation program for dairy sheep, it was possible for producers to improve the milk production potential of their animals by selecting those that produced more milk. Milk production is a highly heritability trait, which means that the trait is more easily transmitted to the next generation when compared to other characteristics (such as prolificacy, for example). Selection based on the amount of milk produced by an animal can allow for overall improvement in this trait for the population. However, this type of selection has its limits, especially if we also wish to improve the milk quality (fat and protein level). Although quite heritable, selection on the amount of milk produced may be at the expense of milk composition. In fact, French studies show a negative genetic correlation between milk yield and protein level (-.047 ± 0.05), and between milk yield and fat content (-0.34 ± 0.07). These results indicate that selection based only on milk yield can be detrimental to the quality of the product. Since sheep milk is generally produced primarily for processing, maintaining its quality is essential (fat, protein, somatic cells). Given this situation, it seemed essential to develop a genetic program for dairy sheep within Quebec, and the entire country.

Summary of the project, goals and methodology

A project was developed in the fall of 2012 by the Quebec sheep industry (Federation of Producers of lambs and sheep of Quebec - FPAMQ) in collaboration with the Centre d'expertise en production ovine du Québec (CEPOQ – a center for research and development of the sheep industry), Valacta (a Center specialized in dairy cattle milk production) and the Center for Genetic Improvement of Livestock (CGIL) from the University of Guelph. The main objective of the project was to set up a Genetic evaluation program adapted for the dairy sheep industry through integration of precise measurements of milk sheep components. This project also included specific objectives:

- Develop a milk analysis system for precisely evaluating the components of sheep milk;
- Define the lactation curve of our local dairy sheep;
- Develop a North American Genetic Evaluation Program for Dairy sheep (online data base);
- Disseminate the genetic selection principles to sheep farmers in Quebec.

The project began during the spring of 2013 and data collection (for the purposes of the project) continued until fall of 2014. Although the project ended in December 2014, producers have continued to take production data on their flock. However, the results presented in this document only cover the period of 2013 and 2014. CEPOQ was responsible for project coordination and data collection, Valacta was responsible for milk samples and analyses and CGIL (Larry Schaeffer) was responsible for the development of the genetic evaluation program. CEPOQ also carried out statistical analysis using data included in the database.

To obtain the data necessary for the project, producers were to submit their flock inventory (complete permanent identification of each animal, date of birth, breed, and complete pedigree, if available) and lambing data to the genetic evaluation program, GenOvis. GenOvis is the Canadian genetic evaluation program available for meat sheep in Canada, which is managed by CEPOQ in Quebec. This program is also the result of a partnership between three organizations from the industry (CEPOQ, Ontario Sheep Marketing Agency, Canadian Sheep Breeders). The dairy sheep information was incorporated into GenOvis. In order to collect dairy data (milk yield, milk component), Valacta's staff was responsible for milk recording at the farm. Each month, a person from Valacta conducted test day records: the milk yield was recorded for PM and AM milking (or 24hs, in certain cases) and a milk sample was collected for each ewe. The milk samples were then sent to Valacta's laboratory (Sainte-Anne-de-Bellevue, Quebec, Canada). At the laboratory, the milk was tested for fat and protein content, somatic cell count, urea, lactose and beta-hydroxybutyrate (BHB).

In order to adapt the infrared analysis curves to sheep milk, Valacta validated calibration curves. It is important to mention that in the past, Valacta was using infrared analysis curves adapted for dairy cattle milk to estimate the milk component of other species (sheep, goat). This was probably not adequate since there are differences in the composition and structure of the main molecules of milk from one species to another and these differences can significantly influence the measurements. To this end, several series of milk samples were collected from the sheep milk producers to use as standards to calibrate the infrared analyzer. These analyses were designed to test the suitability of using standards prepared with sheep's milk instead of cows' milk. To develop the standards, tank samples were collected four times from each farm. The exact composition of these standards were determined by official chemical methods and compared with the values obtained by infrared analyzer.

The following data were considered in the genetic evaluation model for all evaluated animals:

- ATQ permanent identification for all animals (RFID tags) for GenOvis and Valacta database;
- Flock identification and province;
- Sheep breed or cross;
- Animal birth date;
- Age at first lambing, if available;
- Number of parities (first, second or later);
- Lambing data (lambing date, beginning of lactation);
- Number born (missing data for many ewes);
- Date of Test day record (for milk yield and milk quality);
- Number of days in milk on the test day record;
- Interval between start of PM test day record and start of AM test day record;
- Milk quality and quantity.

The main traits analyzed were AM milk yield, PM milk yield, 24h milk yield, fat and protein percentage (%), somatic cell count (SCC), urea (mg N/dl) and beta-hydroxybutyrate level (BHB, mmol/l). The lactation period considered for the genetic evaluation program covered the lactation period from days 5 to 220. Apart from this interval, this data was not considered in the lactation curve for the genetic evaluation. Note that a minimum of 4 complete test day records were needed to make an adequate lactation curve and perform genetic analysis on an animal (milk yield and/or milk component).

During 2013, 8 herds participated in the project and a ninth was added in 2014. On top of this data, it was possible to add all the production data already stored in Valacta's database, for a total of 2,878 sheep being sampled. There was a total of 3,023 animals with pedigree information included, of which 145 were rams and 1,277 were ewes.

During the project, many problems arose that impacted the analysis. In some cases, the permanent identification of the animal sampled was not complete (RFID tag - only 4, 5, 6 or 7 numbers were taken instead of 9), which created duplicates or unrecognized animals in the genetic evaluation database. In other cases, the lambing data was incomplete (lambing date or number of lambs born were missing). The sheep without lambing dates were rejected from analysis because it was impossible to trace the lactation curve. Clearly, this project has highlighted the importance good quality farm input data.

Genetic evaluation model. Model planned and current operational model.

When the project started, a genetic model was created and was planned for the Dairy sheep industry. The original model accounted for the following factors:

- Flock-year-season effects where years and seasons of lambing were separated for each flock. The seasons were going to be each month of lambing, but then this was reduced to two month seasons.
- Breed-Parity-Age-Season effects which assumed that there were different age groups within parities 1 and 2, and two-month seasons of lambing, and that these differed by breed definitions.
- Breed-Parity-Year-Season effects assumed year-season of lambing effects were different for each breed-parity group.
- Breed-Parity-Number Born effects assumed that the effect of number of lambs born differed for each breed-parity group.
- Breed-Parity-Milking Interval effects for AM and PM yield traits only were to account for the time elapsed between milkings, and that this effect was different for each breed-parity group.
- Animal Permanent Environmental effects, for each animal having test day records, and these would differ depending on parity.
- Animal Additive Genetic effects, for each animal in the pedigree.
- Residual effects, where the variance of residual effects could change during the lactation. Five intervals were created based on phenotypic standard deviations of test-day records of all traits. The intervals were:

  1) Days 5 to 48;
  2) Days 49 to 76;
  3) Days 77 to 111;
  4) Days 112 to 146;
  5) Days 147 to 220.

Unfortunately, some of the subclasses for the fixed factors had too few observations, and this caused problems with estimation. For example, because five regression coefficients needed to be estimated for each curve, that meant there should be a minimum of 6 observations per subclass for the fixed factors of the model. Many had less than 6 observations which led to estimation problems. Thus, the model was greatly simplified as follows:

- Breed-Parity-Age-Season effects were reduced to Breed effects;
- Breed-Parity-Year-Season effects were reduced to Year-Season effects. Thus, the same year-season effects were assumed to affect all breeds and parities similarly;
- Breed-Parity-Number born effects were reduced to Number Born effects;
- Breed-Parity-Milking Interval effects were reduced to Milking Interval effects, assumed the same for each breed and parity group. Milking interval effects applied only to AM or PM milk yield traits.

All other factors were the same as in the planned model.

As the amount of TD records gets larger over time, to where there are 20,000 or more records, then the model can be expanded back to the planned model for these fixed factors. However, the number of observations per level of each factor needs to be checked before expanding. Consequently, the operational model, now, is not the best model possible. The best model can not yet be applied given the amount of data available.

Results and Discussion

Chemical analyses performed on sheep milk by Valacta's laboratory showed that the calibrations used for cow's milk (infrared analysis curve) were not suitable for sheep. Table 1 summarizes the impact of using cow's milk on the composition of the sheep milk samples. Very significant biases are noted for all components analyzed.

Table 1. Average differences between the reference methods and the infrared analyzer.

Average differences	Fat	Protein	Lactose
Before calibration adjustment (cow infrared)	-0.19	-0.17	0.13
After calibration adjustment (sheep infrared)	0.01	0.01	0.01

These results clearly illustrate the need to use sheep milk standards to generate calibration curves. After the infrared analyzer was calibrated with samples of sheep milk, the biases decreased considerably to acceptable levels, in absolute terms, and are now similar to the calibration process used for milk cows. In general, the mean differences for each component should be as close as possible to zero, which is equivalent to a very good correlation between the infrared analyzer and the chemical method.

Concerning the data used for the genetic evaluation program, a total of 19,302 test day records were extracted if ewes had a test day record with milk yield and/or components recorded (from any flock in the database). No limits were put on the actual yields, but this may be necessary in the future. Milk yields above 3 kg at one milking, for example were very rare. The earliest test day record was 1996/06/15 and the latest was 2014/11/06. After editing for days in milk between 5 and 220 days, there were 17,886 records. There were 6,427 records having only 1 test per day, 11,597 with AM and PM tests, and 37 with 24-hour milk yields only. There were three main dairy breeds represented in the data. These were East Friesian (EF), Lacaune (CU), and British Milk (BM). Ewes were assigned to one of ten breed groups as shown in the next table.

Table 2. Breed groups used in the genetic model and group composition records.

Group #	Breed composition	Records
1	75% EF or better (EF = East-Friesian)	10,669
2	75% CU or better (CU = Lacaune)	946
3	75% BM or better (BM = British Milk Sheep)	23
4	50% EF - 50% CU	681
5	50% EF - 50% BM	30
6	50% CU - 50% BM	0
7	50-74% EF	2286
8	50-74% CU	934
9	50-74% BM	71
10	All other	1221

Below are tables of raw means for the different breed groups. Tables 3 and 4 present the results for the main production traits evaluated during the study (milk yield, fat and protein content).

Table 3. Average milk production (kg/day) for each breed group.

Group #	Breed composition	AM milk	PM milk	24-h milk
1	75% EF or better	0.92	0.73	1.54
2	75% CU or better	1.10	0.66	1.20
3	75% BM or better	0.88	0.71	-
4	50% EF - 50% CU	0.97	0.71	0.85
5	50% EF - 50% BM	0.75	0.56	-
6	50% CU - 50% BM	-	-	-
7	50-74% EF	0.82	0.56	1.03
8	50-74% CU	0.96	0.62	1.07
9	50-74% BM	0.56	0.45	0.76
10	All other	0.81	0.55	0.66

While it is tempting to compare breeds to determine which are the most productive, the variable amount of data in the different purebreds or crossbreds proved to be a problem. In some cases, the amount of data came from only a few herds and in many cases, the performance could be explained by management decisions instead of the real potential of the breed. Statistical analyses were performed to determine the presence of significant effects (i.e. flock management) impacting the productivity of animals. However, to perform these analyses, breeds with small populations were removed from the analysis (BM and BM crosses). The following table shows the overall average productivity of sheep sampled and the significant effects observed. In this table, 76.9% of the data is represented by the East-Friesian and crosses.

Statistical analysis has shown that the parity (number of lambings, lactation number) had a significant effect on milk production and fat level. As we expected, ewes in their second lactation (and later), produced more milk, and also more fat, than ewes in their first lactation. However, statistical analyses did not demonstrate any effect of parity on milk protein content. Statistical analyses also showed a significant effect for a Breed*Flock interaction for all traits studied. In fact, in statistics, with an interaction between two variables (Breed*Flock), it is not possible to evaluate if the performance is the result of the breed alone, or the flock management alone. In

this case, this Breed*Flock interaction means that a breed may perform better than another, because of the flock management. This confirms that, with our current data, it is impossible to compare the breeds against each other. For lactose, the results showed similar levels between parities, flocks and breeds (no effect). As expected, lactose were also lower than observed for dairy cattle. Table 6 presents the results for somatic cell score (log of somatic cell count), urea and beta-hydroxybutyrate level.

Table 4. Fat, protein and lactose level (%) for each breed group.

Group #	Breed composition	Fat %	Protein %	Lactose %
1	75% EF or better	5.70	4.86	4.74
2	75% CU or better	5.51	5.04	4.73
3	75% BM or better	5.95	5.27	4.69
4	50% EF - 50% CU	5.88	5.20	4.68
5	50% EF - 50% BM	5.81	5.43	4.75
6	50% CU - 50% BM	-	-	-
7	50-74% EF	5.74	4.97	4.71
8	50-74% CU	5.58	5.01	4.73
9	50-74% BM	4.76	4.89	4.62
10	All other	5.80	4.90	4.71

Table 5. Average milk yield, fat and protein content for all breeds (except BM) and effects of breeds, parity and flock.

Item	Average	Min-Max	Effects
Milk (kg/day)	1.39 ± 0.79	0.10 to 5.80	P B*F
Fat (%)	5.72 ± 1.31	1.63 to 13.33	P B*F
Protein (%)	4.92 ± 0.71	1.65 to 12.41	B*F

* Significant effects ($p < 0.05$) B = Breed P = Parity F = Flock.

According to Somatic cell count (SCC) and Somatic cell score (SCS), the data presented in table 6 is the result of a logarithmic adjustment that allows analysis through the genetic evaluation program. The results (from lab analysis) show that somatic cell count (SCC) averaged 736,000 for all breeds evaluated during the study (results from 1000 to 9 999 000 SSC). This result is too high and needs to be reduced. Our statistical analysis shows a significant breed*flock interaction. Some flocks had high levels of SCC (over 1 000 000), which probably affected the data.

For urea, our statistical analysis showed a significant effect of parity on the level of milk urea. Second, and subsequent, parity ewes showed higher levels of urea than first parity ewes. We also observed a significant flock effect for this element with some flocks showing higher levels of urea (39.9 mg N/dl). Again, our analysis showed a significant effect for breed*flock interaction. Three flocks showed high levels of urea, which is probably a reflection of feed management.

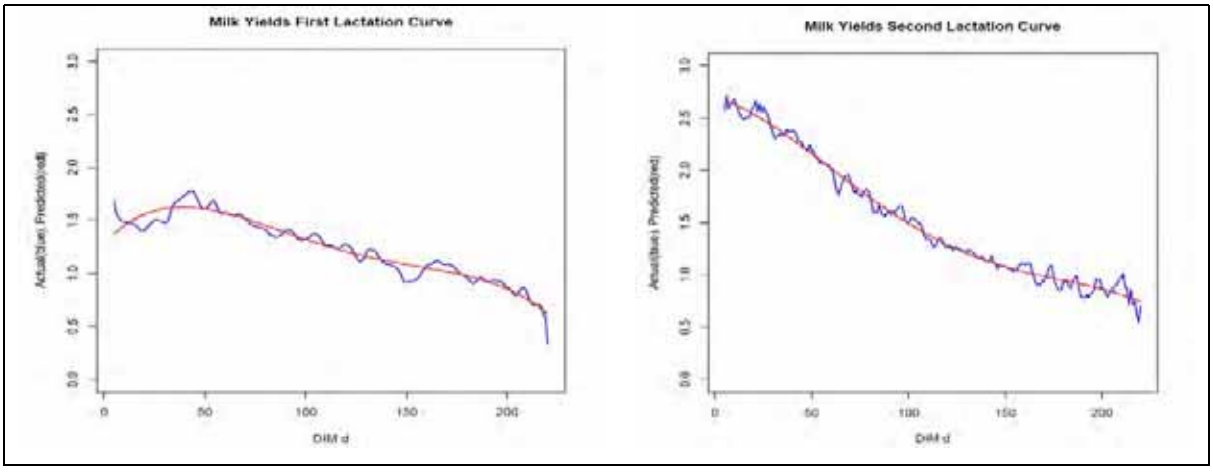
For BHB, analyses were done using the “Cetolab” analysis from Valacta. Cetolab was developed for dairy cattle and many samples where needed to adjust the analyses to correctly determine BHB level for this species. For dairy cattle, Cetolab is useful to identify cattle affected by ketosis. With this analysis, we know that cattle showing BHB levels over 0.20 mmol/l are af-

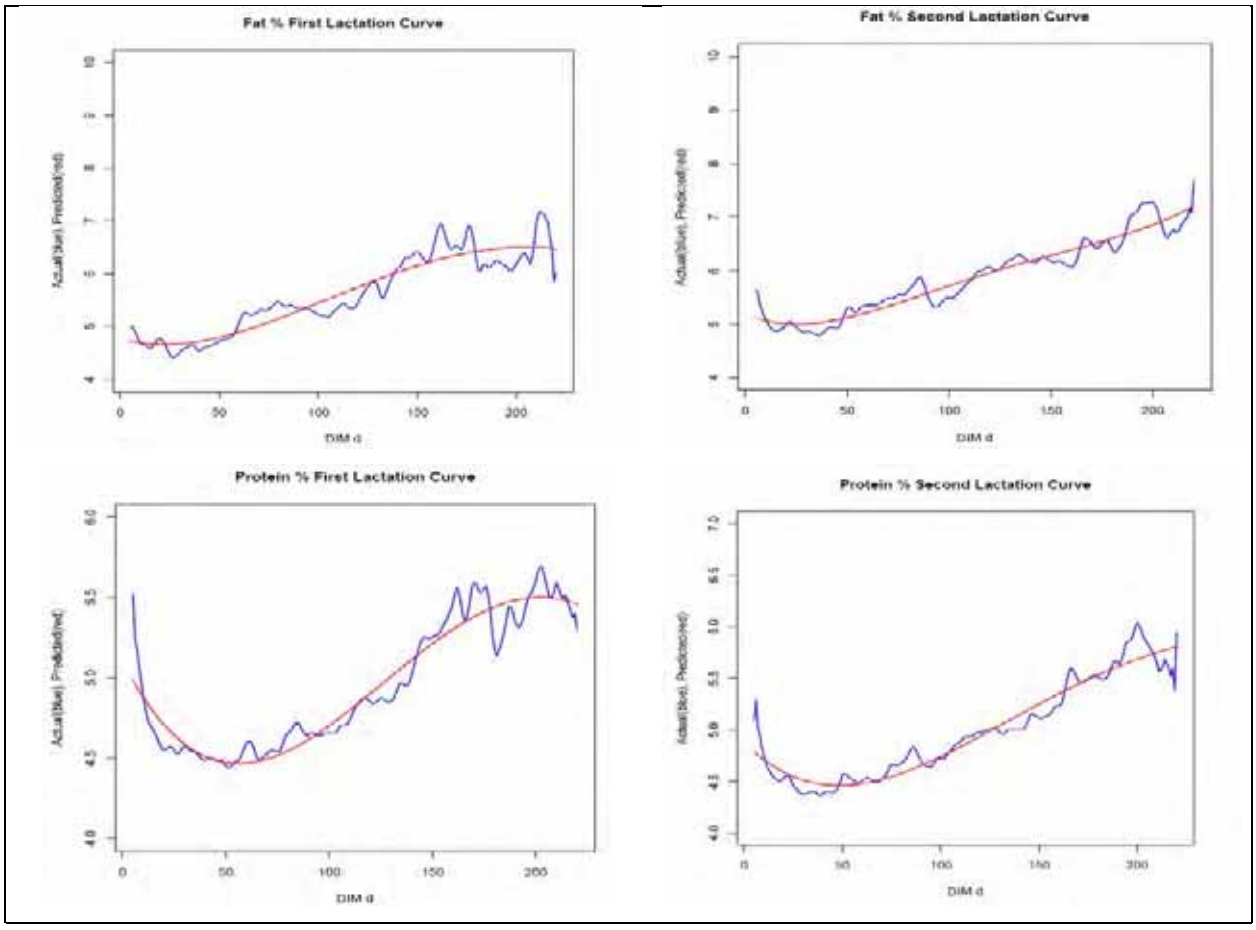
fected by ketosis and cattle showing levels between 0.15-0.20 mmol/l are suspected to have ketosis. In dairy cattle, BHB can be used as a quantitative result to positively diagnose ketosis. For sheep, the results are not as clear because Cetolab has not been calibrated and tested for them. For sheep, BHB levels should only be compared between animals within a flock or between different flocks. It is possible to determine that one animal has a higher BHB level than another, but it is not possible to diagnose ketosis. The statistical analysis showed that the ewe's parity had a significant effect on BHB. First parity ewes showed higher levels of BHB than multiparous females. First parity ewes also had high BHB levels in the first weeks of gestation and some cases remained high. A significant flock effect was also observed for BHB, with two flocks showing almost twice the average farm level of BHB (>0.30 mmol/l). Considering that BHB is a reflection of energy metabolism, producers with ewes showing sudden rises in, or sustained elevation of, BHB levels should question their feeding program in preparation for lambing. Should the energy level of the feeding program be adjusted? Is the body condition score appropriate? Is the voluntary feed intake adequate? These are all questions that need to be addressed in order to ensure the females are properly prepared for a good, persistent lactation.

Table 6. Somatic cell score (SCS), urea and beta-hydroxybutyrate (BHB) level for each breed group.

Group #	Breed composition	SCC	Urea mg N/dL	BHB mmol/L
1	75% EF or better	12.07	22.37	0.14
2	75% CU or better	11.47	21.30	0.16
3	75% BM or better	11.74	19.03	0.21
4	50% EF - 50% CU	11.59	20.81	0.14
5	50% EF - 50% BM	12.72	20.39	0.14
6	50% CU - 50% BM	-	-	-
7	50-74% EF	11.45	21.75	0.12
8	50-74% CU	11.17	22.06	0.16
9	50-74% BM	9.87	22.55	0.08
10	All other	11.35	21.64	0.13

The figures below show the lactation curves for the main trait evaluated in the study for first parity and second parity and following (milk yield, fat and protein content).





Effect of number born. The number of lambs born to start a lactation has an influence on the amount of milk produced by the ewe. Up to 7 lambs were recorded in the dairy data. However, there were less than 10 such lambing amongst later parity ewes. For first parity, dairy ewes, the upper limit was 4 and there were very few of those. The prolificacy was affected by breeds and number of parity. However, with the small population of this study, but mostly, because of the large amount of variation, it is hard to evaluate the effect of each trait. Table 7 present the number of record for single, twin, triplet or quad for all ewe in the database.

Table 7. Number of records for number born.

Number born	Number of records	% of record
Single	5170	28.6
Twin	9873	54.7
Triplet	2676	14.8
Quad +	342	1.9

The average number of lambs born (for all breeds) was 1.90 lambs born/lambing. The result of the effect of the number born on the milk production at first parity, second parity and later, are presented in tables 8 and 9.

Table 8. First Parity - effect of number of lambs born.

Trait	(2)-(1)	(3)-(1)	4)-(1)
AM milk (220d)	2.92	3.01	-
PM milk (220d)	1.14	1.95	-
24h milk (220d)	-0.03	1.16	-
Fat (%)	0.00	0.10	-
Protein (%)	0.10	0.20	-
SCS	0.06	0.11	-

Table 9. Second Parity and later - effect of number of lambs born.

Trait	(2)-(1)	(3)-(1)	4)-(1)
AM milk (220d)	3.87	3.92	-
PM milk (220d)	1.55	3.98	-
24h milk (220d)	6.27	7.82	-
Fat (%)	-0.03	-0.04	-
Protein (%)	0.10	0.20	-
SCS	0.06	0.11	-

There seems to be more milk produced by ewes with two lambs over ewes with one lamb, and a slight increase of ewes with three lambs over ewes with two. There were not enough observations to know if this trend continued with 4 lambs born. In any case, these are small increases.

Accuracies and Percentiles of EBVs. The most important part of this project was the development of the Dairy Sheep Genetic Evaluation Program to obtain EBVs for the traits analyzed in the population. Accuracies and percentile rankings were calculated for each trait using the same selection index approximation as used in the evaluations for growth and reproduction (for meat sheep). So the factors included into the accuracies are:

- The number of test day records for an animal;
- The number of female progenies that also have test day records.
- The sire and his number of daughters;
- The dam and her number of test day records;
- The dam and her number of daughters.

Genetic correlations between traits are not taken into account in the accuracy calculations. Thus the accuracies are conservative estimates, and deliberately kept lower than they might be.

As said previously, there were a total of 3,023 animals in the pedigree information, of which 145 were rams and 1277 were dams of ewes. Only 12 animals were inbred. Tables 10 and 11 present the range of the EBVs calculated on the population. The EBVs are expressed in the unit of each trait for complete 220 days lactation. In these Tables, the EBVs are presented for the whole population, so they are not described for each breed. Milk, fat, protein, and lactose yields are yields over the entire lactation from day 5 to 220 days. The percentages are the average daily percentage, as for SCS, urea, and BHB.

Table 10. EBVs Range for the traits measured on the population for ewe in first parity – results for the genetic evaluation run done in April 2015.

Trait	Minimum	Maximum	Average EBV	SD
Milk yield, kg	-171	213	-10.8	46.0
Fat yield, kg	- 9.8	13.5	- 0.7	2.7
Protein yield, kg	- 8.4	11.2	- 0.4	2.3
Lactose yield, kg	- 7.9	10.3	- 0.6	2.2
Fat %	- 0.85	1.14	- 0.01	0.29
Protein %	- 0.64	1.04	0.06	0.21
Lactose %	- 0.73	0.41	- 0.03	0.12
SCS	- 1.91	2.64	- 0.01	0.46
Urea	- 4.65	7.20	- 0.20	1.28
BHB	- 0.09	0.11	0.00	0.02

Table 11. EBV range for the traits measured on the population for ewe in second parity and later – results for the genetic evaluation run done in April 2015.

Trait	Minimum	Maximum	Average EBV	SD
Milk yield, kg	-267	333	-17.9	64.4
Fat yield, kg	-15.8	17.3	-1.3	3.9
Protein yield, kg	-13.2	15.0	-0.8	3.2
Lactose yield, kg	-12.4	15.8	-0.9	3.0
Fat %	-1.13	1.41	-0.02	0.36
Protein %	-0.75	1.28	0.08	0.24
Lactose %	-0.68	0.32	-0.02	0.10
SCS	-2.05	2.90	-0.03	0.66
Urea	-6.34	9.97	-0.24	1.49
BHB	-0.08	0.12	-0.01	0.02

As an example in interpreting these previous data, the best ewe (first parity) from the dairy sheep population could produce, on average, 213 kg more milk than the average first parity ewe of the same breed. In order to help producers, percentiles are available and allow to identify quickly the best animals in the population for each trait.

Estimates of Variances. Tables 12 and 13 present the proportions of total variation that can be explained by genetics (heritability), permanent environment of the animal (flock, management, etc.), the rest being explained by the flock-year season effect (as explained in the genetic model below).

In the tables, the estimates of the proportion of genetic variances (heritability) out of the total variance remain high for the dairy traits. In the literature, Barillet (1994) studied 130,409 ewes from 2,670 rams, and reported heritabilities of 0.30, 0.28, and 0.29 for milk, fat and protein yields for the Lacaune breed of France. In a paper published in 2007, Barillet et al., report moderate heritability for milk, fat and protein yield (~0.30) and higher heritabilities for fat and protein contents (~0.50–0.60). Oravcova (2007) gave values of 0.15, 0.10, and 0.25 for milk, fat, and protein for 2,196 test day records (much less data than our population) of Lacaune ewes from Slovakia. Bauer et al. (2012) studied Lacaune and East Friesian ewes in the Czech Republic with a data set of similar size to the Quebec population. They found a heritability for milk yield

of 0.28. The work of Banos et al. (2005) with Chios sheep of Greece was more similar to the current analyses (in terms of models and methods), based on 42,675 test day records from 75 flocks. They used records from day 40 to 240 of lactation. For our study, the estimates of the Genetic evaluation run done in April 2015 where lower than the previous reports, which was expected. In fact, the estimates are expected to decrease to their true level as the number of test day records and flocks increase (more data in the genetic database). More data means that there are more animals of various genetic backgrounds, so there is a better picture of the entire genetic pool for dairy production. At the moment, only 145 different rams are represented and 1277 dams of ewes, and a good number of these are related to ancestors from one flock in Ontario. This may explain why the heritabilities are still high in the calculation, since this is a small population and many animals are linked in their pedigree.

Table 12. Proportions of Total Variation for each trait for Parity 1 ewes.

Trait	Genetic	Perm. Env.	Flock-YS
AM milk yield, kg	0.597	0.207	0.195
PM milk yield, kg	0.594	0.206	0.199
24-h milk yield, kg	0.510	0.228	0.261
Fat %	0.378	0.153	0.466
Protein %	0.587	0.155	0.257
Lactose %	0.699	0.155	0.145
SCS	0.703	0.113	0.177
Urea	0.425	0.130	0.443
BHB	0.577	0.217	0.205

Table 13. Proportions of Total Variation for each trait for Parity 2 and later ewes.

Trait	Genetic	Perm. Env.	Flock-YS
AM milk yield, kg	0.678	0.160	0.161
PM milk yield, kg	0.681	0.157	0.162
24-h milk yield, kg	0.608	0.173	0.218
Fat %	0.430	0.151	0.416
Protein %	0.541	0.141	0.317
Lactose %	0.696	0.147	0.155
SCS	0.759	0.062	0.174
Urea	0.487	0.093	0.417
BHB	0.575	0.206	0.219

Given the high heritabilities (as mentioned earlier) the accuracies for EBVs can be good for ewes. With the number of data available for this first genetic evaluation run, ewes having several daughters and 5 or more test day records can have accuracies around 60%. Rams with more than 20 daughters can reach accuracies close to 80%.

The following tables present the genetic correlation of traits between parities. In summary, the genetic correlations show a moderate link between parities for milk production (AM, PM and 24h milk), but high correlations for the other traits.

Table 14. Genetic correlation of traits between parities.

Trait	Genetic correlation
AM Milk	0.53
PM Milk	0.58
24h Milk	0.56
Fat %	0.90
Protein %	0.88
Lactose %	0.87
SCS	0.90
Urea	0.79
BHB	0.76

The following table present the genetic correlation among traits within parities (for Parity 1 and Parity 2 and later). In the table, the genetic correlations for parity 1 are presented above the diagonal (dark cells) and the genetic correlations for parity 2 are below the diagonal.

Table 15. Genetic correlations among traits within parities. Parity 1 above the diagonal (dark cells) and parity 2 below the diagonal.

Trait	Milk	Fat %	Protein %	Lactose %	SCS	Urea	BHB
Milk	-	-0.12	-0.21	0.23	-0.13	0.26	-0.19
Fat %	-0.28	-	0.59	0.04	0.05	-0.19	-0.14
Protein %	-0.30	0.64	-	-0.11	-0.02	-0.25	-0.17
Lactose %	0.09	-0.04	-0.07	-	-0.04	0.14	-0.35
SCS	-0.25	-0.01	0.06	-0.08	-	-0.23	0.19
Urea	0.16	-0.17	-0.27	0.04	-0.53	-	-0.20
BHB	-0.22	0.06	-0.04	-0.28	0.34	-0.35	--

Genetic correlations among traits for parity 1 and parity 2 and later are quite similar to the ones reported in the literature, but lower in many cases. In fact, in a publication from Barillet et al, 2007, the authors report that milk yield is negatively related to contents and generally more strongly to protein content (∼−0.40) than to fat content (∼−0.30). In our study, genetic correlations were of -0.28 and -0.30, respectively for fat content and protein content at parity 1, and of -0.12 and -0.21 for parity 2 and later for the same traits. It is difficult to explain why the correlation between milk and protein is low at parity 2 and later (-0.12) compared to that in the literature. As written in Barillet et al, 2007, negative correlation between milk and content is a well-established dairy trait in ruminants, but exceptions to this general pattern can happen for different breeds in varying environmental conditions. In our study, this may be explained by a lack of data in the genetic evaluation database. Our results also show a high positive correlation between fat and protein contents for both parity 1 (+0.59) and parity 2 and later (+0.64). This is high compare to what is reported by Barillet (2007), with positive moderate correlations of + 0.20 -0.30. In summary, in our study, even if the negative correlations are a little lower between milk yield and fat-protein contents, our results suggest that a selection only based on milk production may be detrimental to milk content. In the future, as more data will be captured in the Dairy Sheep Genetic Evaluation Program, index must be developed to find a compromise between milk yield

and milk content. This genetic selection index will need to be implemented in order to improve simultaneously milk yield and content with the ultimate objective to increase cheese yield and cheese output.

Conclusions

This project demonstrated the need for on farm data capture quality. Permanent identification of animals, pedigree depth, complete and well detailed lambing data are essentials. Producers in- terested in genetic evaluation should therefore be prepared to note these items to obtain complete and reliable genetic results. For producers, it is possible to send only milk production data to the genetic evaluation program (AM, PM, 24-h milk). However, this method does not allow generat- ing EBVs for selecting on milk composition (protein, fat contents). Our results show that selec- tion based solely on dairy production could be to the detriment of dairy components. Milk ana- lyzes represent a cost to producers. Henceforth, adjustment of the calibration curves better justi- fies this investment, since the analyzed data are now representative of the real composition of sheep milk. Although these analyzes have a cost, they are essentials to an effective selection for milk quantity and quality. A minimum of 4 test day records allows for a more accurate lactation curve and a more reliable genetic evaluation. These test day do not need to be done 30 days apart, some producers doing the test day record every 40-60 days to reduce the cost.

To date, the Canadian dairy sheep genetic evaluation program has been completed. As soon as more than 20,000 to 25,000 reliable and complete data are available in the genetic database, it will be possible to use the preliminary genetic model that was developed by the geneticist Larry Schaeffer. For now, the genetic program uses a simplified model. Producers are currently send- ing their data to the Center of Expertise in Quebec Sheep Production to be captured in the ge- netic program by the staff. Animal identification issues still exists and several producers fail to provide lambing data, which cause trouble to the genetic evaluation program. This makes it im- possible to trace the lactation curve. Thus a change in the lambing period routines is essential for obtaining genetic data on dairy performance (need to have complete and accurate lambing data).

In the coming months, geneticists are preparing dairy export data files (EBVs, reports) and will test import files containing on farm data (milk yield, milk content). The section for lambing data capture is reliable and complete in the genetic evaluation system GenOvis. There is still work to be done, but Canada will soon be able to offer a genetic evaluation program for North American dairy sheep.

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