Genetic parameter estimates for post-weaning growth, ultrasound, and carcass traits in Canadian heavy lambs

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Summary

Carcass traits have a major influence on the profitability of meat lamb production, but lack of genetic parameters for these traits in local breeds and production systems has limited their genetic improvement in Canada. This research presents the first genetic parameter estimates for carcass traits and their correlations to other economically important post-weaning growth and ultrasound traits for Canadian heavy lambs. Carcass traits were found to be moderately heritable, with heritability estimates ranging from 0.17 ± 0.02 for hot carcass weight to 0.32 ± 0.02 for carcass conformation score. Estimated genetic correlations between carcass and post-weaning growth and ultrasound traits were generally favourable, but unfavourable correlations among carcass traits emphasize the need for index selection. The results of this research provide the parameter estimates necessary for future inclusion of carcass traits into the Canadian national sheep genetic evaluation system.

Keywords: genetic parameters, sheep, carcass, growth, ultrasound

Introduction

The Canadian sheep industry, with a national inventory of approximately 816,000 animals (Statistics Canada, 2017), is small in comparison to other major Canadian livestock industries. Nevertheless, a growing demand for lamb meat has led to greater interest in production efficiency and the quality of marketed product. The Canadian national sheep genetic evaluation system (GenOvis, www.genovis.ca) provides weekly genetic evaluations for growth, ultrasound, and reproductive traits. However, the lack of genetic evaluations for carcass traits and scarcity of ultrasound measurements have limited genetic improvement of traits measured post-weaning. In the province of Quebec, heavy lambs (lambs under 365 days of age with a carcass weight greater than 16.4 kg) are marketed through the Heavy Lamb Sales Agency (HLSA). Producer payment through the HLSA utilizes a price grid classification system, thus rewarding producers that are able to meet target carcass weight (20.0 to 24.0 kg), muscularity (scores of 5), and fatness levels (7 to 12 mm). This system is generating carcass records in a quantity that would allow for genetic evaluation of these traits (Les Éleveurs d'ovins du Québec, 2017).

Genetic selection provides a cumulative and permanent way to improve traits relative to a given breeding objective. International genetic parameter estimates (e.g., Brito et al., 2017) suggest that carcass yield and quality traits are moderately heritable, therefore, it is likely that improvement to carcass yield and quality would be attainable through genetic selection. Production systems and breeds used in Canada, such as the Canadian and Rideau Arcott, differ considerably from major sheep producing regions, thus population-specific genetic parameter estimates for these traits are needed. The objectives of this research were to estimate heritabilities for carcass traits and to estimate their genetic correlations to currently evaluated post-weaning growth and ultrasound traits.
for a Canadian heavy lamb population.

**Material and methods**

**Data**

Data used in this research was obtained from commercial producers and processors, thus, animal utilization approval was not required. Carcass yield and quality data was collected on over 80,000 commercial lambs marketed through the HLSA between January 2011 and August 2013. Lambs were slaughtered at an average slaughter age (SAGE) of 172 days. Carcass data included hot carcass weight (HCWT), carcass fat depth at the GR site, measured 110 millimetres from the midline on the 12th rib (FATGR), and average carcass conformation score (CONF), calculated as the average of shoulder, loin and leg primal cut conformation scores. Primal cut conformation scores are subjective measurements of muscularity, and scores range from a minimum of 1 to a maximum of 5 (Government of Canada, 1992). Tattoo numbers were used to match 16,565 carcass records to lambs with GenOvis management, pedigree, and growth and ultrasound trait records. Growth and ultrasound trait records for all ancestors of animals with carcass records were also extracted and included post-weaning weight (PWWT), ultrasound eye muscle depth (EMDUS) and average ultrasound fat depth (FATUS). Lambs were weaned at an average of 55 days and live traits were recorded at an average of 98 days.

Records with missing management or pedigree information were removed from the data set. Only carcass records that met the criteria of being a heavy lamb (HCWT ≥ 16.4 kg and SAGE ≤ 365 d) and growth trait records that were within the biologically plausible ranges given by Schaeffer and Szkotnicki (2015), were retained for analysis. To remove suspected outliers, phenotypes were adjusted for sex, birth and rearing type, dam age, breed composition and age at measurement, and records were removed if the residual value of the phenotype was greater than three standard deviations from the mean. Lastly, records from contemporary groups, defined as management group within year within producer, with fewer than three animals were removed. The final dataset contained a total of 29,923 animals, of which 14,441 animals had carcass records. Descriptive statistics for the traits are presented in Table 1. Representative of the Canadian commercial sheep population, only 29.0% of animals with carcass records were purebred.

Pedigree information was extracted from GenOvis and trimmed using the pedigree package (Coster, 2013) in R software version 3.4.0 (R Core Team, 2015) to remove branches without records. The final pedigree included 37,885 animals over 21 generations. Animals with records were the progeny of 2,760 sires and 17,451 dams, and had an average pedigree depth of 10.4 generations. Consistent with group mating practices, all animals with records had dam pedigree information, however 5,633 animals with records had unknown sires.

**Statistical analyses**

ASReml statistical software (Gilmour et al., 2015) was used for genetic parameter estimation. The model for each trait included fixed effects of sex, birth and rearing type, dam age, and age at measurement as a covariate. The carcass trait models also included a fixed effect of year-month of slaughter to account for seasonal and market differences that might influence when an animal was slaughtered. To account for the large number of crosses in the data, breed effects were modelled by including breed composition fractions for the seven most common breeds as covariates. The seven most common breeds included maternal (Rideau Arcott, Romanov, Polypay), dual-purpose (Polled Dorset) and terminal (Suffolk, Canadian Arcott and Hampshire) breeds. Random effects in the models included the animal additive genetic effect and contemporary group. Although there is evidence of maternal effects on some post-weaning growth and carcass traits (Ingham et al., 2007; Mortimer et al., 2010), maternal effects were not estimated due to inadequate data structure. Variance component estimates from univariate and bivariate animal models were used to estimate
heritabilities and correlations, respectively.

Table 1. Trait descriptions and summary statistics

<table>
<thead>
<tr>
<th>Trait</th>
<th>N</th>
<th>Range</th>
<th>Mean ± SD</th>
<th>CV%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hot carcass weight, HCWT (kg)</td>
<td>14,441</td>
<td>16.4 - 31.7</td>
<td>23.2 ± 2.3</td>
<td>9.9</td>
</tr>
<tr>
<td>Carcass fat depth at the GR site, FATGR (mm)</td>
<td>14,441</td>
<td>1.0 - 19.0</td>
<td>11.0 ± 3.3</td>
<td>30.0</td>
</tr>
<tr>
<td>Carcass conformation score, CONF</td>
<td>14,441</td>
<td>2.0 - 4.0</td>
<td>3.1 ± 0.6</td>
<td>17.8</td>
</tr>
<tr>
<td>Post-weaning weight, PWWT (kg)</td>
<td>26,763</td>
<td>8.0 - 65.0</td>
<td>33.0 ± 8.1</td>
<td>24.5</td>
</tr>
<tr>
<td>Ultrasound eye muscle depth, EMDUS (mm)</td>
<td>1,299</td>
<td>10.6 - 36.6</td>
<td>26.8 ± 3.8</td>
<td>14.2</td>
</tr>
<tr>
<td>Ultrasound fat depth, FATUS (mm)</td>
<td>1,299</td>
<td>0.9 - 10.8</td>
<td>3.8 ± 1.4</td>
<td>36.9</td>
</tr>
</tbody>
</table>

1N: number of records; SD: standard deviation; CV%: coefficient of variation; : phenotypic variance.

Results and discussion

Genetic parameter estimates for post-weaning growth and carcass traits are presented in Table 2. Heritability estimates were generally moderate and ranged from 0.16 ± 0.06 for EMDUS to 0.32 ± 0.02 for CONF, which suggests that there is potential to improve carcass and post-weaning growth traits in the Canadian heavy lamb population through selection. Hot carcass weight was found to have a heritability of 0.17 ± 0.02, which is similar to the heritability estimate of 0.19 reported by Brito et al. (2017), but on the low end of literature estimates (0.19 to 0.37) (Greeff et al., 2008). In agreement with literature estimates, FATGR (0.30 ± 0.02), CONF (0.32 ± 0.02) and PWWT (0.25 ± 0.01) were all moderately heritable (Mortimer et al., 2010; Einarsson et al., 2015). Ultrasound fat depth (FATUS), with a heritability of 0.22 ± 0.05, was within the range of estimates found in the literature (0.15 to 0.42) (Mortimer et al., 2010; Einarsson et al., 2015), but EMDUS had a relatively low heritability (0.16 ± 0.06) compared to literature estimates (0.22 to 0.41) (Greeff et al., 2008; Karamichou et al., 2007).

Table 2. Genetic parameter estimates for carcass and growth traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>HCWT</th>
<th>FATGR</th>
<th>CONF</th>
<th>PWWT</th>
<th>EMDUS</th>
<th>FATUS</th>
</tr>
</thead>
<tbody>
<tr>
<td>HCWT</td>
<td>0.17 ± 0.02</td>
<td>0.35 ± 0.01</td>
<td>0.22 ± 0.01</td>
<td>0.29 ± 0.02</td>
<td>0.25 ± 0.05</td>
<td>0.21 ± 0.07</td>
</tr>
<tr>
<td>FATGR</td>
<td>0.15 ± 0.07</td>
<td>0.30 ± 0.02</td>
<td>0.35 ± 0.01</td>
<td>0.35 ± 0.01</td>
<td>0.30 ± 0.02</td>
<td>0.29 ± 0.04</td>
</tr>
<tr>
<td>CONF</td>
<td>0.04 ± 0.07</td>
<td>0.48 ± 0.05</td>
<td>0.32 ± 0.02</td>
<td>0.00 ± 0.01</td>
<td>0.02 ± 0.00</td>
<td>0.01 ± 0.01</td>
</tr>
<tr>
<td>PWWT</td>
<td>0.38 ± 0.05</td>
<td>-0.11 ± 0.05</td>
<td>-0.22 ± 0.05</td>
<td>0.25 ± 0.01</td>
<td>0.64 ± 0.02</td>
<td>0.52 ± 0.03</td>
</tr>
<tr>
<td>EMDUS</td>
<td>0.71 ± 0.19</td>
<td>0.25 ± 0.19</td>
<td>0.19 ± 0.18</td>
<td>0.54 ± 0.08</td>
<td>0.16 ± 0.06</td>
<td>0.41 ± 0.03</td>
</tr>
<tr>
<td>FATUS</td>
<td>0.24 ± 0.17</td>
<td>0.49 ± 0.14</td>
<td>0.31 ± 0.14</td>
<td>0.63 ± 0.08</td>
<td>0.42 ± 0.16</td>
<td>0.22 ± 0.05</td>
</tr>
</tbody>
</table>

1Heritabilities are presented in bold with phenotypic and genetic correlations above and below the diagonal, respectively.

A favourable and moderate positive genetic correlation of 0.38 ± 0.05 between HCWT and PWWT suggests that current selection for higher PWWT should lead to a beneficial increase in HCWT. Ultrasound measurements are taken infrequently in the Canadian sheep population, but are advantageous for selection as they are measured at an earlier age and can also be measured directly on selection candidates. Hot carcass weight was found to have a strong genetic correlation with EMDUS (0.71 ± 0.19), while FATGR and FATUS had a moderate positive genetic correlation (0.49 ± 0.14). These results support the use of selection on ultrasound traits to improve carcass characteristics. Interestingly, CONF, which is used as a measure of muscularity (Les Éleveurs d'ovins du Québec, 2017), did not have a significant genetic correlation with HCWT or EMDUS but was found to be unfavourably positively correlated with FATGR (0.48 ± 0.05). This indicates that alternative and more objective measures of muscularity are needed to increase lean meat yield...
(Einarsson et al., 2015). A weak positive genetic correlation of 0.15 ± 0.07 was found between HCWT and FATGR. This unfavourable genetic correlation was smaller than some literature estimates (e.g., Brito et al., 2017), but emphasizes the importance of index selection to avoid unfavourable increases in carcass fatness.

Conclusions

This study presents the first genetic parameter estimates for carcass traits in Canadian heavy lambs. Carcass traits were found to be moderately heritable (0.17 to 0.32), indicating that there is potential to improve carcass traits in the Canadian heavy lamb population through selection. Correlations between post-weaning growth or ultrasound traits and carcass traits were generally favourable, however, unfavourable correlations among carcass traits underscore the importance of using index selection for balanced genetic improvement. Future research will focus on the inclusion of carcass traits into terminal sire selection indexes to improve lamb production efficiency and carcass quality.

Acknowledgements

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List of references


