The genetics of lamb survival is different across different birth types

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Summary

Lamb survival significantly impacts the productivity of the Australian sheep industry, with twin and multiple-born lambs suffering greater mortality rates than single-born lambs. Using data from the Sheep CRC Information Nucleus and MLA Resource Flock, genetic parameters for lamb survival to weaning and birth weight across different birth types were estimated. The additive genetic and maternal variances (maternal genetic and permanent environmental components) for survival to weaning were significantly higher for twin and multiple born lambs than for single born lambs. The direct heritability for survival to weaning was also higher in twin-born (0.06) than in single lambs (0.04) but not for multiples (0.04). Birthweight was weakly negatively correlated genetically to survival in single born lambs (-0.10) but positively correlated for twins (0.20), and multiples (0.29). The results of this study demonstrate that the genetic relationship between birthweight and survival is different across different types of birth, therefore selecting for overall birthweight to improve lamb survival will not be beneficial for survival across different birth types. Splitting lamb survival for type of birth may be more beneficial but challenging to implement in commercial breeding programs.

Keywords: lamb survival, birth weight, genetic evaluation

Introduction

Poor lamb survival is the main cause of reproductive inefficiency in sheep world-wide and is a looming animal welfare issue (Dwyer et al. 2016). Under extensive grazing in Australia, lamb survival from birth to weaning varies considerably and is often less than 80%, with losses in twin lambs typically 2-2.5 times that of singles in the same flock (Hinch and Brien 2014). Compared to reducing other sources of reproductive inefficiency, improving twin lamb survival is predicted to yield the largest economic return under Australian conditions (Young et al. 2014).

The prospects for genetic improvement of lamb survival have generally been regarded as poor, mainly due to low heritability estimates, however, genetic gains of 0.52% a year have been reported in a flock selected for multiple-rearing ability (Cloete et al. 2009) and New Zealand industry flocks have been achieving small but positive genetic trends for lamb survival since 2001 (Brien and Young 2016).

The relationship between birth weight and lamb survival is complex and at a phenotypic level has been described as negative quadratic in nature by Hatcher et al. (2009) and different between singles, twins, and multiples. Therefore, attempts to select for higher birthweight to
improve twin and multiple-born lamb survival may potentially result in a reduction in lamb survival of singles due to dystocia.

In this paper we explore the potential for targeting the genetic improvement of lamb survival by birth type, given the greater economic benefit and scope for improving the survival of twins under Australian conditions. In a preliminary study, Kelly et al. (2016) suggested that early lamb survival of singles, twins and multiples be treated as separate traits, on the basis of analyses using a sire model. Herein, we have used a similar approach on a larger dataset to genetically analyse lamb survival to weaning and birth weight.

Material and methods

Sources of data and records collected
A total of 36, 615 lambs from the Information Nucleus (IN) of the Sheep Co-operative Research Centre (Sheep CRC) and the Meat and Livestock Australia’s (MLA) Resource Flock contributed data to the study. Records of lamb survival to weaning and birth weight from 23, 617 lambs from the Sheep CRC’s IN, from eight locations across Australia from 2007 to 2011, were utilised. The flocks contained Merino and crossbred ewes (9,501 dams) that were inseminated annually to Merino, maternal and terminal breed rams (480 sires). Further details on the design, data collection and management of the IN have been reported by Fogarty et al. (2007) and Brien et al. (2010).

The MLA Resource Flock began as the IN. In 2012, approximately 620 former IN base flock ewes, plus 2,384 additional ewes were mated by AI at 2 research farm sites, ‘Kirby’ at Armidale, New South Wales and at Katanning in Western Australia. Data from 12, 998 lambs born from annual matings from 2012 to 2015 were used in this study. Management of the MLA Resource Flock followed a similar protocol to the IN Flock, however, pedigrees were verified by DNA analysis from a blood/tissue sample collected from each lamb.

Data analysis
The data were analysed using an animal model in ASReml (Gilmour et al. 2009). Lamb survival to weaning (LS), although a binary trait, was assumed to be distributed normally for these analyses and has been treated as a trait of the lamb. Lamb survival (LS) and birth weight (BW) data were split into single born lambs (LS_S and BW_S = 13, 738), twin born (LS_T and BW_T = 19, 237) and multiple, triplets and above (LS_M and BW_M = 3, 640). The univariate model for both traits included age of dam, flock, year, sex, type of birth, day of birth and any significant two-way interactions. Genetic groups (180) were also included in the model as fixed effects and were derived from the pedigree. Random effects of dam (combined maternal and permanent environmental) and animal were also included. The bivariate models included all significant fixed and random effects.

Results
The phenotypic and additive genetic variances for lamb survival were highest for twin and multiple born lambs (Table 1). Heritability of twins was higher than that of multiple and single born lambs. The separate maternal additive and permanent environmental variances were not estimable, however, the proportion of the total variance explained by the maternal component was almost four times higher in twins (0.15) and multiples (0.14) compared to singles. Similarly the proportion of the total variance explained by the maternal component of
birth weight was significantly higher in twin and multiple lambs.

Table 1. Variance component estimates for phenotypic (σ²_P), additive genetic (σ²_A), and maternal (σ²_M), and heritability estimates for lamb survival and birth weight.

<table>
<thead>
<tr>
<th>Trait</th>
<th>σ²_P</th>
<th>σ²_A</th>
<th>σ²_M</th>
<th>h²</th>
<th>σ²_M/σ²_P</th>
</tr>
</thead>
<tbody>
<tr>
<td>LS</td>
<td>0.120</td>
<td>0.005</td>
<td>0.009</td>
<td>0.039±0.009</td>
<td>0.074±0.006</td>
</tr>
<tr>
<td>LS_S</td>
<td>0.083</td>
<td>0.003</td>
<td>0.003</td>
<td>0.040±0.013</td>
<td>0.036±0.008</td>
</tr>
<tr>
<td>LS_T</td>
<td>0.129</td>
<td>0.008</td>
<td>0.019</td>
<td>0.059±0.013</td>
<td>0.145±0.009</td>
</tr>
<tr>
<td>LS_M</td>
<td>0.220</td>
<td>0.008</td>
<td>0.030</td>
<td>0.036±0.052</td>
<td>0.137±0.020</td>
</tr>
<tr>
<td>BW</td>
<td>0.760</td>
<td>0.235</td>
<td>0.214</td>
<td>0.309±0.020</td>
<td>0.282±0.007</td>
</tr>
<tr>
<td>BW_S</td>
<td>0.859</td>
<td>0.277</td>
<td>0.130</td>
<td>0.322±0.029</td>
<td>0.152±0.014</td>
</tr>
<tr>
<td>BW_T</td>
<td>0.667</td>
<td>0.177</td>
<td>0.253</td>
<td>0.265±0.026</td>
<td>0.380±0.009</td>
</tr>
<tr>
<td>BW_M</td>
<td>0.714</td>
<td>0.155</td>
<td>0.187</td>
<td>0.217±0.082</td>
<td>0.262±0.025</td>
</tr>
</tbody>
</table>

The overall genetic correlation between BW and LS was positive but negligible (0.11 ± 0.09). When each trait was split by type of birth the genetic correlation was still negligible but negative for singles (-0.10 ± 0.13), however it was low and positive for twins (0.20 ± 0.11) and multiples (0.29 ± 0.31; Table 2). It should be noted that the standard errors for the multiple born lambs were high as a result of the low numbers in this category.

Table 2. Phenotypic and genetic correlations between birth weight and lamb survival.

<table>
<thead>
<tr>
<th></th>
<th>Overall</th>
<th>Singles</th>
<th>Twins</th>
<th>Multiples</th>
</tr>
</thead>
<tbody>
<tr>
<td>R_P</td>
<td>0.39 ± 0.03</td>
<td>0.10 ± 0.01</td>
<td>0.28 ± 0.05</td>
<td>0.35 ± 0.04</td>
</tr>
<tr>
<td>R_G</td>
<td>0.11 ± 0.09</td>
<td>-0.10 ± 0.13</td>
<td>0.20 ± 0.11</td>
<td>0.29 ± 0.31</td>
</tr>
</tbody>
</table>

Discussion

The additive genetic variance of survival to weaning in twin and multiple-born lambs is more than twice that of those born as singles. However, the heritability of survival is only 50% higher in twins and no higher in multiple born lambs than in singles, due to higher residual variation, particularly in the latter case. In a similar approach to the study herein Hatcher et al. (2014) concluded that maternal additive variance, permanent environmental variance and maternal heritability were all higher in dams of twins than dams of singles, but unlike in our study, there was little difference in additive genetic variance for lamb survival across a range of ages from 1 day after birth up till weaning.

Although we were unable to partition maternal variance into genetic and environmental components, the results for maternal variance are nonetheless of considerable interest and are broadly in line with the conclusions of Hatcher et al. (2014), and Kleemann et al. (2016) who reported repeatabilities of 0.28 vs 0.11 for survival in multiple-reared and single-reared lambs, respectively. Bunter et al. (2017), also found evidence for differences in maternal variances and maternal heritability of lamb survival between single-born and twin-born Merino lambs, but concluded that through the scaling of variances, genetic evaluation of rearing ability could be satisfactorily performed by defining the one trait for lamb survival, regardless of birth type.

Whilst there was little overall genetic relationship between birthweight and survival, the relationship varied for different types of birth, with the genetic correlation for singles being weakly negative and twins and multiples lowly positive. Hence, indirect selection for survival
based on birthweight would be inefficient.

In conclusion, considering lamb survival separately for singles, twins and multiples would appear to be more effective than treating it as one trait regardless of birth type. However utilising the genetic relationship between birth weight and survival for different birth types may be difficult to implement in practice.

Acknowledgements

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