Supplementary Material for: Benefits of including methane measurements in selection strategies

D.L. Robinson¹ and V.H. Oddy

NSW Department of Primary Industries, Beef Industry Centre, University of New England, Armidale, NSW 2351, Australia

Sources and justifications of estimates of genetic (rg) and phenotypic (rp) correlations, numbered by rows in the matrix (Table 5, overleaf)

1. Correlations with weight at slaughter (SltWt)

SltWt, DFI: For cattle, weighted mean estimates from the 6 studies cited by Arthur and Herd (2008) and Crowley et al. (2010) are: rg = 0.72, rp = 0.61, for weight (during a feed efficiency test) with DFI measured over at least 50 days. Genetic correlations of weight with DFI in lambs are similar (rg = 0.85, François et al., 2007; rg = 0.71 ± 0.11, Snowden and Van Vleck, 2003, rg = 0.71, rp = 0.29, Lee et al., 2002) but lower for adults (rg = 0.34 ± 0.22, rp = 0.35 ± 0.03, Lee et al., 2002; rg = 0.20 ± 0.09, rp = 0.12 ± 0.03 for digestible DFI in Merino ewes, measured by chromium sesquioxide capsules and expressed as a ratio of the estimate for each ewe to the mean of the contemporary group, Fogarty et al., 2009; rg = 0.23 ± 0.10, rp = 0.15 ± 0.02 for correlations of same trait with post-weaning weight in crossbred ewes, Fogarty et al., 2006).

In this evaluation, slaughter weight was considered a proxy for meat production, so correlations for non-mature animals were considered the most relevant. After ‘bending’ to make the correlation matrices positive definite, the values used in the evaluation were: \( rg = 0.63 \), \( rp = 0.59 \).

SltWt, DMP: The table shows estimates of rg and rp from studies in Australia using RC and PAC. The RC protocol of restricted feeding based on a function of liveweight is likely to result in higher estimates of the correlation between weight and DMP than expected under commercial conditions when animals have ad lib access to feed. Therefore, the estimates from PAC of \( rg = 0.67 \) and \( rp = 0.47 \) were considered the most appropriate. After ‘bending’ to make the correlation matrices positive definite, a slightly lower value of \( rg = 0.64 \) was used in the final analysis.

SltWt, MPadgWt: rp should be 0 because of the adjustment for weight. There is no evidence that rg differs from 0, so the values used were: \( rp = 0 \), \( rg = 0 \).

<table>
<thead>
<tr>
<th>rg</th>
<th>rp</th>
<th>Data source for correlations of DMP and Wt (as an indicator of SltWt)</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.79</td>
<td>0.56</td>
<td>Australian cattle, RC (Donoghue et al., 2015)</td>
</tr>
<tr>
<td>0.67</td>
<td>0.49</td>
<td>Australian sheep, PAC (unpublished result, from data analyzed by Robinson et al., 2014)</td>
</tr>
<tr>
<td>0.45</td>
<td></td>
<td>Australian sheep, PAC (unpublished result, data analyzed by Robinson et al., 2015)</td>
</tr>
</tbody>
</table>

SltWt, MY: In studies that report them, genetic correlations were low, e.g. \( rg = -0.10 \) ± 0.18 for test weight, and 0.05 ± 0.17 for final weight in cattle (Donoghue et al., 2015); 0.06 ± 0.12, 0.06 ± 0.13 for weaning and 8-month weight in sheep (Pinares-Patiño et al., 2013). Given the relatively large SE, the best estimate is \( rg = 0 \). Phenotypic correlations with liveweight had lower SE and were all positive, \( rp = .04 \) ± 0.04 for test weight, \( rp = .10 \) ± .04 for final weight in cattle (Donoghue et al., 2015), \( rp = 0.01 \) ± 0.02, 0.03 ± 0.03 for weaning and 8-month weight in sheep (Pinares-Patiño et al., 2013). The pooled estimate (used in Table 5) is \( rp = 0.03 \) ± 0.01.

SltWt, RFI: rp should be 0 because RFI is a measure of feed intake adjusted for weight and weight gain. The weighted average of estimates from the studies cited in Arthur and Herd (2008) and Crowley et al. (2010) was very low: \( rg = -0.06 \) ± 0.05. Although this is close to zero, the pooled value was considered preferable to simply rounding the average to zero because of the possibility that the genetic correlation differs according to environment. In one study (Morris et al., 2014), low-RFI heifers (progeny of 4 low-RFI sires, range –0.82 to -1.16 kg/day) had faster weight gains than the progeny of 4 high-RFI sires (range 1.0 to 1.14 kg/day), suggesting a possible negative correlation between RFI and weight. However, this particular study did not provide information on EBVs for 400-day or final weight, so the results could simply reflect the differences in sire EBV for weight. After bending

¹ Corresponding author: D L Robinson. E-mail: Dorothy.Robinson@dpi.nsw.gov.au
to ensure the correlation matrices were positive definite, a slightly lower value of \( rg = -0.04 \) was used (Table 5).

2. Correlations with DFI

DFI, DMP: DMP is highly correlated with DFI, but only a few studies report estimates of the correlation. For beef cattle, Donoghue et al. (2015) provided estimates of: \( rg = 0.84 \pm 0.06 \), \( rp = 0.71 \pm 0.02 \). The phenotypic correlation of 0.71 is for measurements in the same 2-day session. Based on an expected correlation of 0.54 between a single day’s measurements and the mean of 30 other measurements for DFI (using the repeatability estimate of 0.31 for feed intake of beef cattle on non-consecutive days, Robinson and Oddy, 2001), a plausible value for the phenotypic correlation between DMP and DFI average DFI over a period of at least 30 days is: \( rp = 0.45 \).

DFI, MPadjWt: The compiled estimates of the genetic correlations in Table 5 (discussed above) are 0.84 for DFI with DMP and 0.63 for DFI with weight. Assume the breeding value for DFI, bvi, can be decomposed into bvi = bviw + bvir, where bviw is the component associated with weight (accounting for 0.63 * 0.63 = 40% of the variation); the remainder, bvir, therefore accounts for 60% of the variation. If the genetic correlation of bvir (the proportion not associated with weight) and MPadjWt (the proportion of MP not associated with weight) is similar to the genetic correlation of DFI and DMP (0.84), a plausible estimate of the genetic correlation of DFI with MPadjWt is 0.84 * sqrt(0.6) = 0.65, which was reduced to \( rg = 0.57 \) to ensure a positive definite matrix (Table 5). This value is consistent with the expectation of a similar, but slightly lower genetic correlation between DFI and MPadjWt than between DFI and RFI (0.73, see below). The phenotypic correlation is expected to be substantially lower because MPadjWt is affected by feed intake on the day of measurements and previous two days, so subject to additional variability from day to day variation in feed intake. A plausible value is therefore \( rp = 0.25 \).

DFI, MY: Not all studies report correlations for DFI and MY. Estimates from Donoghue et al. (2015) are: \( rg = -0.04 \pm 0.18 \), \( rp = -0.01 \pm 0.04 \) for DFI over the period that MY was measured. The phenotypic correlation in Table 5 is for DFI measured over 30+ days, which is expected to have a lower correlation than for the period over which MY is measured, so the value rounded down to \( rp = 0 \).

DFI, RFI: Pooled estimates from the 6 studies cited by Arthur and Herd (2008) and Crowley et al. (2010), weighted by the variances of estimates (rg) or numbers of animals (rp) are: \( rg = 0.73 \); \( rp = 0.62 \). RFI was included as the last row and column of Table 5, to provide an indication of the correlated response to selection. The economic weight was zero (so its inclusion should not affect the results for other traits). This last row was subject to a large amount of ‘bending’ to ensure positive definite matrices, after which the estimates were: \( rg = 0.44 \), \( rp = 0.52 \).

3. Correlations with DMP (not adjusted for weight or DFI) in normal production conditions

DFI, MPadjWt: The pooled estimate of \( rg \) for DMP and Wt (0.64, after bending, Table 5) implies that weight explains 41% of the genetic variation, i.e. \( MP = \beta wt + e \), where \( e \) (representing MPadjWt) has 59% of the variation. An estimate of the genetic correlation is therefore \( \frac{\text{var}(e)}{\sqrt{\text{var}(e)\text{var}(MP)}} = \sqrt{\text{var}(e)/\text{var}(MP)} = \sqrt{0.59} \), i.e. \( rg = 0.77 \). When MP and MPadjWt are recorded on separate occasions, \( rp \) is expected to be much lower (because each is subject to different measurement errors), so a value of \( rp = 0.40 \) was used.

DFI, MY: Estimated genetic correlations ranged from \( rg = 0.5 \) (Donoghue et al., 2015, for simultaneous RC measurements of DMP and MY in beef cattle to \( rg = 0.1 \), estimated from correlations between sire means (adjusted for fixed effects) of PAC measurements of sheep in Western Australia (with and without adjustment for liveweight) and MY measurements of offspring of the same sires in New South Wales (Dominik, personal communication). The average value of these two values, \( rg = 0.30 \) was chosen as the most plausible estimate based on currently available information.

For simultaneous measurements based on the same RC data, phenotypic correlations varied from \( rp = 0.68 \) (Donoghue et al., 2015)

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Table 5. Plausible estimates of genetic (below diagonal) and phenotypic (above) correlations

<table>
<thead>
<tr>
<th></th>
<th>SltWt</th>
<th>DMI</th>
<th>DMP</th>
<th>MPadjWt</th>
<th>MY</th>
<th>RFI</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 SltWt</td>
<td>1</td>
<td>0.59</td>
<td>0.47</td>
<td>0.00</td>
<td>0.03</td>
<td>0</td>
</tr>
<tr>
<td>2 DMI</td>
<td>0.63</td>
<td>1</td>
<td>0.45</td>
<td>0.25</td>
<td>0.00</td>
<td>0.52</td>
</tr>
<tr>
<td>3 DMP</td>
<td>0.64</td>
<td>0.84</td>
<td>1</td>
<td>0.40</td>
<td>0.20</td>
<td>0.24</td>
</tr>
<tr>
<td>4 MPadjWt</td>
<td>0.00</td>
<td>0.57</td>
<td>0.77</td>
<td>1</td>
<td>0.15</td>
<td>0.28</td>
</tr>
<tr>
<td>5 MY</td>
<td>0.00</td>
<td>-0.04</td>
<td>0.30</td>
<td>0.35</td>
<td>1</td>
<td>-0.08</td>
</tr>
<tr>
<td>6 RFI</td>
<td>-0.04</td>
<td>0.44</td>
<td>0.41</td>
<td>0.52</td>
<td>-0.08</td>
<td>1</td>
</tr>
</tbody>
</table>

SltWt = weight at slaughter; DMP = daily methane production; MPadjWt = methane production adjusted for weight; MY = methane yield; RFI = Residual Feed Intake
to $rp = 0.23$ for the dataset considered by Robinson et al. (2014), in which the sheep the fed at 20 g/kg, so methane emissions were related to liveweight ($r = 0.68$) and strongly related to an index of feed intake in the RC and two previous days ($FII, r = 0.84$); in this dataset, DMP was more highly correlated ($rp = 0.45$) with MY calculated by dividing DMP by FII. The lowest estimate of the phenotypic correlation, an average of 0.10 was for MP measured in PAC and RC measurements of MP adjusted for feed intake in the RC and previous two days (calculated from the data discussed by Robinson et al., 2015). Phenotypic correlations based on simultaneous estimates from the same dataset are likely to over-estimate the true value, which is unlikely to be greater than the repeatability of DMP (0.27 in beef cattle), so a value of $rp = 0.20$ was used, being less than the repeatability of DMP in beef cattle but higher than the phenotypic correlation of MY in the RC and DMP in PAC for sheep.

**DMP, RFI:** If A explains $r_1^2$ of the variation in B, and B explains $r_2^2$ of the variation in C, A might be expected to explain $r_1 r_2^2$ of the variation in C, suggesting that a rough estimate of the correlation between A & C is $r_1 r_2$. Hence, based on $rg = 0.84$ for MP and DFI (Table 5) and the pooled estimate (before ‘bending’) of $rg = 0.73$ for DFI and RFI (based on the 6 studies cited by Arthur and Herd, 2008 and estimates from Crowley et al., 2010), $rg$ is estimated as 0.84*0.73 = 0.61. Similarly, using $rp = 0.45$ for MP and DFI (Table 5) and $rp = 0.62$ for DFI and RFI (pooled estimate above, before bending), $rp$ is estimated as 0.45*0.62 = 0.28. Similar to the estimates for DFI, RFI, these estimates were subject to a large amount of ‘bending’ to ensure positive definite matrices, resulting in $rg = 0.41$, $rp = 0.23$ (used only to estimate correlated changes in RFI).

### 4. Correlations with MPadjWt

**MPadjWt, MY:** As described above, the pooled estimate of $rg$ for DMP and MY was 0.30 (Table 5). The very low to zero correlations of MY with Wt suggest that adjusting MP for Wt is likely to increase the correlation, so a value of $rg = 0.35$ was used. Phenotypic correlations from sheep RC data were quite low (0.1 for MY0 and 0.19 for MY3) as was the average correlation of 0.1 for PAC MPadjWt and RC measurements of MP adjusted for feed intake (Robinson et al., 2015), so a value of $rp = 0.15$, between the lower and upper estimates was used for PAC MPadjWt and RCMY.

**MPadjWt, RFI:** a similar genetic correlation is expected to that of MP and DFI, or perhaps somewhat lower after accounting for weight adjustment in both variables. The estimate of 0.84 for MP with DFI was therefore reduced to 0.66, and further reduced by the bending procedure to $rg = 0.53$. A relatively low value of $rp = 0.3$ was considered likely because of low repeatability of MPadjWt; this value further reduced by the bending procedure to $rp = 0.28$.

### 5. Correlation with RCMY

**MY, RFI:** some studies indicate that low-RFI (i.e. efficient) animals may have higher MY, e.g. Mercadante et al., (2015) tested 118 cattle for RFI during the growth phase then measured methane emissions on a subset of 23 males and 23 females; the low-RFI group had higher MY (25.1 vs 22.8, $P < 0.001$) than the high-RFI group. The 23 males underwent a second RFI test over the same period as their methane emissions were measured and classified by the second RFI test as 9 low and 14 high RFI animals, for which there was no significant difference in MY ($P = 0.38$). In view of these results, the correlations were assumed to be low, but negative: $rg = -0.08$, $rp = -0.08$.

**Sensitivity testing.** Additional sensitivity analyses were conducted using higher estimates of correlations for DMP and MY. The estimate of $rp$ was increased to 0.40 and $rg$ to 0.47 (close to the reported value of $rg = 0.5$ (Donoghue et al., 2015) for simultaneous measurement in RC, based on a model that did not account for the G x E effects that result in lower correlations for repeat methane measurements after 2 month interval [0.27 for DMP, 0.21 for MY] than on consecutive days [0.95 for DMP, 0.85 for MY, Donoghue et al., 2016]. To ensure the genetic covariance matrix remained positive definite, it was necessary to increase $rg$ for MY with MPadjWt (to 0.57), reduce the correlation of DMP with DMP by 1 percentage point (to 0.83); a genetic correlation of zero was also assumed for DFI with MY.

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**LITERATURE CITED**