SELECTION FOR LEAN MEAT PRODUCTION IN SHEEP: A SIMULATION STUDY

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SUMMARY

The effects of selection on carcass composition on rates of genetic progress and inbreeding were evaluated by Monte Carlo simulation. Comparisons are made between selection on individual index and on estimated breeding values calculated from BLUP in closed flocks with normal reproduction and embryo transfer.

INTRODUCTION

Consumer demands require a reappraisal of selection objectives for production of sheep meat and the development of new breeding strategies to improve carcass composition (Parrat and Simm, 1987). On the one hand diverse selection indices for terminal sire sheep breeds with the use of new techniques (B mode scanners, X-ray Computer Tomography, Nuclear Magnetic Resonance) for in vivo measurement of carcass composition have been recently examined (Simm and Dingwall, 1989). On the other hand the use of embryo transfer in nucleus breeding units has also been proposed in order to obtain higher rates of genetic progress exploiting increased selection among females (Smith, 1986).

The purpose of this study was to assess by computer simulation some of these breeding schemes with the additional employment of BLUP methodology for breeding value estimation.

MATERIALS AND METHODS

The selection goal of the schemes examined includes carcass lean weight and carcass fat weight measured at constant age, with relative economic values (REVs) of +3 and -1 per Kg respectively.

Three methods of genetic evaluation were compared: a) Individual index based on liveweight (LW), ultrasonic muscle depth (UMD) and ultrasonic fat depth (UFD) (Simm and Dingwall, 1989), b) Multi trait animal model for the same three traits: LW, UMD and UFD and c) Multi trait animal model combining liveweight (LW) and measurements of lean and fat weight obtained with perfect accuracy from in vivo techniques such as X-ray CT. Heritabilities for these traits and phenotypic and genetic correlations among them have been previously published (Simm and Dingwall, 1989).

In order to facilitate the simulations a 144-ewe flock was assumed with normal reproduction and the following structure: a) 6 males mated at 7 months of age and for one year only, b) females mated first at 19 months of age and for three years, c) 6 males and 48 females selected per year from 72 animals of each sex available and performance tested at 150 days of age. In consequence generation intervals were one year in males and three years in females and the value of the ratio average selection intensity/average generation interval was i/L =0.60.

A second flock of 32 donor ewes with reproduction by MOET was also considered, assuming 4 progenies per donor and year and 9 males and 12 females annually selected from 72 animals of each sex available for selection. Other
rules of flock management being identical, the corresponding value of the ratio $i/L$ being 0.79. Both flocks would have a similar annual rate of inbreeding per year in absence of selection (0.6%).

An additive, infinitesimal model was assumed. The vector of phenotypic values of all traits for the individual $i$ was generated as

$$y_i = \mu + \frac{1}{2} a_i S + \frac{1}{2} a_i D + \frac{1}{2} \sqrt{(1-F_S) L_i S + \frac{1}{2} (1-F_D) L_i D + R_i}$$

where $\mu$ is the vector of general means, $a_i S$ and $a_i D$ are vector of breeding values of the sire and the dam respectively who have inbreeding coefficient of $F_S$ and $F_D$; $S$, $D$ and $R_i$ are vectors of random deviates and $L$ and $R$ are lower triangular matrices from Cholesky decomposition of the genetic variance-covariance and the environmental variance-covariance matrix respectively.

The mean values assumed for the different traits are presented in Table 1, the phenotypic standard deviations being 5.31 Kg (LW), 2.08 mm (UMD), 1.25 mm (UFD), 1.8 Kg (lean) and 2.2 Kg (fat).

The mixed linear model adjusted to analyze the results was

$$y_{ijk} = p_j + a_{ijk} + e_{ijk}$$

Figure 1. Average genetic values in carcass lean and fat weights of progeny by year of selection on different methods (REV5 +3: -1).
where \( y_{jk} \) is the phenotypic record of the \( k \)-trait of the individual \( j \) in the period \( i \), \( p \) is the effect of the \( i \)-year period, \( a \) the additive genetic value and \( e \) the environmental effect. A separate, independent BLUP was run for each trait taking advantage of the canonical transformation. The number of replicates was 20.

RESULTS AND DISCUSSION

Figure 1 presents the average genetic values in carcass lean and fat weights over years 0-10, showing the genetic progress attained with the three breeding schemes simulated: IND, BLUP, BLUP-ET and BLUP-CT (all in solid lines) together with the expected values from selection on the conventional index (EXP, in dotted line). Simulated rates of genetic change from selection on index (IND) were 164 g year\(^{-1} \) in carcass lean weight and 50 g year\(^{-1} \) in fat weight. These figures are lower than the expected values (EXP) by 16% and 28% respectively.

As expected genetic progress in both carcass traits was greater with BLUP than with individual index selection (IND), relative differences being larger for fat (68%) than for lean weight (19%). Similarly, the combined use of embryo transfer and BLUP evaluation allowed extra responses of 58% in lean and 116% in fat weight (BLUP-ET vs. IND).

BLUP evaluation combined with perfect precision of in vivo carcass evaluation (X-ray CT or NMR) may permit a very important extra annual response of 61% in lean and a small reduction (-0.06%) in fat weight (BLUP-CT vs. IND).

According to Kempster et al. (1986), the average lamb carcass in Britain in 1984 had an estimated lean: fat ratio of 2.2:1. Thus, besides the BLUP-CT scheme, any other of the three analyzed schemes should result in improvements in lean percentage at a constant age because the respective ratios between genetic progress in lean and fat were 3.3:1 (IND), 2.3:1 (BLUP) and 2.4:1 (BLUP-ET). Table 1 summarizes the average phenotypic values of criteria and objectives of selection at the 10th year. Selected animals from these schemes show higher live weight values and there will be a further indirect increase in lean percentage of progeny slaughtered at a fixed weight as usually occurs in practice.

Paradoxically, the simulated results for selection on individual index evidence a greater improvement in lean proportion at constant age than the expected one (lean:fat ratio = 2.8) because the low response in fat weight.
For the chosen relative economic weights (+3 lean, -1 fat), the use of BLUP evaluation with embryo transfer or with normal reproduction is not clearly justified in order to improve carcass composition. Simm and Dingwall (1989) indicate that no further improvement in lean proportion is expected at any relative economic weight for lean as a result of selection on indices including half-sib information. However the inclusion of family information via BLUP methodology may be advantageous at lower economic weights for lean weight. As an example, results of a simulation with different relative economic weights (2 lean, -1 fat) and individual records on LW, UMD and UFD together with BLUP evaluation showed important changes in carcass composition with rates of genetic progress of +150 g year of lean and -23 g year of fat weight.

Average inbreeding of progeny by year of selection on different methods are presented in Figure 2. In relation to selection on index (IND), rates of inbreeding increased in schemes with BLUP evaluation, particularly in combination with reproduction by embryo transfer (BLUP-ET). In this last case, the observed annual rate of inbreeding largely exceeds the convenient values in breeding schemes and a greater annual number of rams or the use of methods of minimization of inbreeding should be recommended.

Table 1. Average phenotypic values for selected traits and average inbreeding in base population and at the 10th year of selection with different methods.

<table>
<thead>
<tr>
<th>Selection method</th>
<th>LW (Kg)</th>
<th>UMD (mm)</th>
<th>UFD (mm)</th>
<th>Lean (Kg)</th>
<th>Fat (Kg)</th>
<th>H</th>
<th>S.O.(H)</th>
<th>F (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Base population</td>
<td>65.0</td>
<td>28.7</td>
<td>7.6</td>
<td>16.1</td>
<td>12.9</td>
<td>-</td>
<td>-</td>
<td>0.0</td>
</tr>
<tr>
<td>INDEX</td>
<td>69.7</td>
<td>30.5</td>
<td>7.3</td>
<td>17.9</td>
<td>13.5</td>
<td>40.2</td>
<td>0.9</td>
<td>3.8</td>
</tr>
<tr>
<td>BLUP</td>
<td>70.6</td>
<td>30.7</td>
<td>7.3</td>
<td>18.1</td>
<td>13.7</td>
<td>40.5</td>
<td>1.3</td>
<td>7.3</td>
</tr>
<tr>
<td>BLUP-ET</td>
<td>72.3</td>
<td>31.4</td>
<td>7.3</td>
<td>18.6</td>
<td>14.0</td>
<td>41.8</td>
<td>1.2</td>
<td>13.5</td>
</tr>
<tr>
<td>BLUP-CT</td>
<td>68.9</td>
<td>-</td>
<td>-</td>
<td>18.8</td>
<td>13.0</td>
<td>43.4</td>
<td>0.4</td>
<td>7.6</td>
</tr>
</tbody>
</table>

REFERENCES


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