Genetic relationships between dagginess, breech bareness, and wool traits in New Zealand dual-purpose sheep

N. K. Pickering,*†2 H. T. Blair,† R. E. Hickson,† K. G. Dodds,* P. L. Johnson,* and J. C. McEwan*

*AgResearch, Invermay Agricultural Centre, Mosgiel, New Zealand; and †Institute of Veterinary, Animal and Biomedical Sciences, Massey University, Palmerston North, New Zealand

ABSTRACT: Genetic and phenotypic parameters were estimated for dagginess, breech, wool, and fiber traits from approximately 29,500 progeny born in 2009 and 2010 in New Zealand dual-purpose ram breeding sheep flocks. Dagginess is adherence of fecal matter to the wool, and this study investigates the genetic and phenotypic correlations between dagginess and breech and wool traits. Estimates for heritability were moderate (0.21 to 0.44) for the following traits: dag score at 3 and 8 mo (DAG3, DAG8), breech bareness, wool length, wool bulk (BULK), mean fiber diameter, mean fiber diameter SD, mean fiber diameter CV, curvature (CURV), weaning weight at 3 mo, and autumn BW. Heritability estimates for fleece weight at 12 mo and proportion of medullated fibers were high (0.49 and 0.53, respectively). Dag score at 3 mo and DAG8 had low genetic and phenotypic correlations with all traits. Breech bareness had positive genetic and phenotypic correlations with CURV and BULK and mostly negative genetic correlations with all other wool traits. In summary the quantity and attributes of wool were not primary causative factors in fecal accumulation, leaving fecal consistency and composition as the major factors.

Key words: breech bareness, dagginess, heritability, wool

INTRODUCTION

Dagginess, or fecal soiling, is known to be associated with flystrike (Greeff and Karlsson, 2009; Smith et al., 2009). With the majority of strike occurring in the breech in New Zealand sheep (Heath and Bishop, 1995), a reduction in dagginess could have an effect on reducing flystrike. For the prevention of flystrike, a detailed understanding of the causes of dagginess is required.

Dagginess can arise from factors affecting consistency of the feces and factors affecting adherence to the breech (Wall et al., 2000; Broughan and Wall, 2007). Factors affecting consistency can be due to worm burden, immune response, feed composition, or intestine function (Ruckebusch and Fioramonti, 1980; Powanall et al., 1993; Leathwick and Atkinson, 1995; Bisset et al., 1996; Larsen et al., 1999; Bedrich and Ehrlein, 2001; Ramirez-Restrepo et al., 2004; Davidson et al., 2006). Factors affecting adherence have been shown to be related to breech bareness and wool length and type in some studies (French et al., 1998; Scobie et al., 2008).

It has already been shown that there was no genetic or phenotypic correlation between dagginess and fecal egg counts in New Zealand dual-purpose sheep (Pickering et al., 2012). A study on digestibility and intestinal activity would involve in-depth and potentially invasive measurement techniques, which is not feasible on the large numbers of animals needed for the accurate estimation of genetic parameters collected in this study. This leaves breech bareness, wool type, and related wool traits to be investigated for their genetic and phenotypic association with dagginess. The concentration on wool traits also had the added benefit that several wool traits have also been independently implicated in flystrike susceptibility (McGuirk et al., 1978; Rathie et al., 1994; Greeff and Karlsson, 2009; Smith et al., 2009).

This study aimed to collect measurements on dagginess, breech, fiber, fleece, and BW traits using a progeny test design in the New Zealand dual-purpose sheep industry. The data were used to calculate heritabilities and
Dagginess in New Zealand sheep

Dagginess in New Zealand sheep

4579

genetic and phenotypic correlations. The New Zealand dual-purpose sheep industry is dominated by Romney, Coopworth, Perendale, Texel, and composite crosses of these breeds.

MATERIALS AND METHODS

Animal ethics approval for this experiment was obtained from the AgResearch Animal Ethics Committee.

Experimental Design

A progeny test design was used for this study. Twenty-one sheep breeders, with a total of 35 recorded flocks, were recruited into the study, with all flocks linked by common sires. Progeny (n = 29,419) born in 2009 and 2010 were assessed, representing approximately 700 sires. Progeny were measured for dag score, breech bareness, wool length, and wool bulk; a proportion (~10%) of animals also had wool samples collected (as described in the Measurements section). The progeny were measured once for the above traits, between weaning and weighing at 8 mo, during the 2009/2010 and 2010/2011 seasons. All progeny measured as part of the progeny test, across all farms, were measured by the same person. Additional pedigree and performance information was obtained from Sheep Improvement Limited (SIL).

Experimental Sites

Farms (n = 21) were located across New Zealand and involved sheep breeders registered on SIL (Supplemental Figure S1; see online version of article at www.journalofanimalscience.org). In the North Island 5 farms were located in the Waikato and Hawkes Bay regions. In the South Island the majority of farms (n = 9) were from the Southland region. One farm was also involved from each of the Otago and Canterbury regions. The majority of flocks were of Romney base; however, there were 4 Perendale, 2 Texel, 1 Coopworth, and 1 Dorset breed-based flocks.

Measurements

At weaning (3 mo of age) and postweaning (BW at 6 or 8 mo of age), measurements were taken on the progeny. The measurements taken in the field were dag score (DAG3 at weaning, DAG8 at postweaning; Pickering et al., 2012), breech bareness score (BBREECH; Scobie et al., 2007), wool length (LENGTH), and hand-assessed wool bulk (BULK). Dag score was subjectively assessed on a 0 (no dags) to 5 (complete dags over the tail, under the crutch, and down the legs) scale (Fig. 1). Breech bareness was subjectively assessed on a 1 (wool up to and covering the anus) to 5 (no wool around the breech and down the leg) scale (Fig. 2). Wool length was measured in millimeters and reflects the relaxed length of the staple under no tension on the spine, above the last rib. Wool bulk was subjectively hand assessed, the wool was compressed, and the level of resistance scored from 1 (no structure, no resistance) to 4 (wool is hard to compress, strong resistance).

Additional data were obtained from SIL, including data from contemporaries of the animals measured from the flocks and birth years involved in this study. These data included parentage, birth and rearing rank, age of...
dam, birth date, and grazing mob history, as well as weaning weight at 3 mo (WWT), BW at 6 and 8 mo (LW6, LW8), and fleece weight at 12 mo (FW12). Dag score at 3 and 8 mo were also included so as to incorporate any dag measurements recorded by the breeder on other mobs or at a different time from when data collection took place. It is to be noted that all lambs are crutched, removing dags and wool from the breech, within a month of weaning, thus resetting the dag score back to 0 before measurement of DAG8. A summary of raw data available for the 2009- and 2010-born progeny is shown in Table 1.

From model fitting, the maternal effect was significant for WWT and autumn BW (generated from LW6 and LW8 data; see below). Dam information was needed to correctly estimate maternal effects. Maniatis and Pollott (2003) showed that genetic parameters became less biased as the proportion of maternal pedigree records increased. Thus, to estimate the maternal effects, additional pedigree and performance data on the dams and their contemporaries were obtained from SIL.

**Data Cleaning**

Data were subjected to quality checks to ensure that subjectively assessed trait values were within the ranges expected, measurements had been undertaken on the correct scale, measurements had been collected at the correct age, there were more than 5 measures for the contemporary group, and sex was correctly recorded. Traits were scaled as appropriate to homogenize the variance (Brown et al., 2005). To homogenize the variance, 3 transforming methods were tested, and the most suitable method was chosen for each trait: log<sub>10</sub>, scaled to the mean of contemporary group, or arcsin on the score divided by the maximum score. For each transformation tested, the mean was plotted against the SD for each contemporary group (flock by birth year by sex); a flat distribution indicated the data were homogeneous. A reduced variation was identified for contemporary groups (DAG3: flock by birth year by sex by DAG3mob, DAG8: flock by birth year by sex by DAG8mob) having dag scores below a certain threshold. To mitigate this, log and arcsin transformations were tested; however, the best method to homogenize the variance was to delete dag observations from those contemporary groups with mean dag score below 0.5 for DAG3 and 0.25 for DAG8. This discarded mobs that had little variation in dag score at time of measurement. For the dag score trait to be fully expressed there is a requirement for the animals to undergo an environmental challenge. Independent queries to the breeders concerned had already identified that contemporary groups with low means were the result of insufficient environmental challenge. To determine if deleting records from contemporary groups with low means, as a method of discarding groups with insufficient environmental challenge, affected heritability estimates, univariate runs were performed using the models determined below (see Statistical Analysis section). No significant changes were observed (data not shown). For DAG3 23% and for DAG8 25% of the data were removed from the final data set.

For BBREECH, contemporary groups (flock by birth year by sex by BBREECHmob) with a low mean had little variation. Thus, as with DAG3 and DAG8, contemporary groups with mean BBREECH score less than 1.2 had their BBREECH data deleted. This excluded 1 purebred Romney flock, which had no variation in their flock for this trait. For LENGTH, data were scaled via means of the contemporary group (flock by birth year by sex by LENGTHmob) to the overall mean of the data set. For BULK no scaling was applied.

### Table 1. Summary of 2009/2010 progeny data set before data cleaning, transformation, and addition of dam information

<table>
<thead>
<tr>
<th>Trait</th>
<th>n</th>
<th>Mean</th>
<th>SD</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>DAG3</td>
<td>17,215</td>
<td>1.1</td>
<td>1.2</td>
<td>0</td>
<td>5</td>
</tr>
<tr>
<td>DAG8</td>
<td>25,498</td>
<td>1.1</td>
<td>1.4</td>
<td>0</td>
<td>5</td>
</tr>
<tr>
<td>BBREECH</td>
<td>28,814</td>
<td>1.9</td>
<td>0.9</td>
<td>1</td>
<td>5</td>
</tr>
<tr>
<td>LENGTH, mm</td>
<td>25,420</td>
<td>57.7</td>
<td>16.3</td>
<td>25</td>
<td>145</td>
</tr>
<tr>
<td>BULK</td>
<td>25,406</td>
<td>2.4</td>
<td>1.0</td>
<td>1</td>
<td>4</td>
</tr>
<tr>
<td>MFD, µm</td>
<td>1623</td>
<td>33.4</td>
<td>3.8</td>
<td>24.2</td>
<td>48.5</td>
</tr>
<tr>
<td>FDSD, µm</td>
<td>1452</td>
<td>8.6</td>
<td>1.3</td>
<td>5.2</td>
<td>15.4</td>
</tr>
<tr>
<td>FDCV, %</td>
<td>1452</td>
<td>26.8</td>
<td>6.7</td>
<td>15.8</td>
<td>78.2</td>
</tr>
<tr>
<td>MED%</td>
<td>1378</td>
<td>8.1</td>
<td>11</td>
<td>0.1</td>
<td>63.9</td>
</tr>
<tr>
<td>CURV, deg/mm</td>
<td>1452</td>
<td>48.2</td>
<td>9.9</td>
<td>21.3</td>
<td>90.1</td>
</tr>
<tr>
<td>WWT, kg</td>
<td>70,763</td>
<td>27.7</td>
<td>5.8</td>
<td>6.6</td>
<td>54</td>
</tr>
<tr>
<td>LW6, kg</td>
<td>36,823</td>
<td>41.0</td>
<td>7.8</td>
<td>11.5</td>
<td>76</td>
</tr>
<tr>
<td>LW8, kg</td>
<td>16,096</td>
<td>40.1</td>
<td>6.4</td>
<td>11.2</td>
<td>74.8</td>
</tr>
<tr>
<td>FW12, kg</td>
<td>8105</td>
<td>3.1</td>
<td>1.1</td>
<td>0.74</td>
<td>6.9</td>
</tr>
</tbody>
</table>

1DAG3, DAG8 = dag score at 3 and 8 mo; BBREECH = breech bareness; LENGTH = length of relaxed wool staple on spine; BULK = wool bulk; MFD = mean fiber diam.; FDSD = SD of MFD; FDCV = CV of MFD; MED% = proportion of medullated fiber; CURV = curvature; WWT = weaning weight at 3 mo; LW6, LW8 = BW at 6 and 8 mo; FW12 = fleece weight at 12 mo.
For the wool fiber traits; MFD, FDSD, and MED% were all scaled via means of the contemporary groups (flock by birth year by sex by MFDmob) to the overall average of the data set. For MED%, observations from contemporary groups with a mean MED% score greater than 20 were deleted as they were outliers. The wool fiber traits of FDCV and CURV were not scaled.

For WWT, data were scaled via means of the contemporary group (flock by birth year by sex by WWTmob) to the overall average of the data set. Either LW6 or LW8 was used as the autumn BW (LWAU), taking the weight with the maximum amount of data for the contemporary group (flock by birth year by sex by LW8mob by LW6mob by WWTmob). The new LWAU were then scaled via means of the new contemporary group (flock by birth year by sex by LWAUmob by WWTmob) to the overall average of the data set. For FW12, data were scaled via means of the contemporary group (flock by birth year by sex by FW12mob by LWAUmob by WWTmob) to the overall average of the data set. To offset the differences in age at measurement, birth date deviation from the mean of the contemporary group was used as a covariate for all traits analyzed.

Statistical Analysis

For each trait these processes were followed to derive the final analytical model. Fixed-effect models were initially determined using the general linear model procedure (SAS Inst. Inc., Cary, NC). Fixed effects fitted included flock (flk), sex (F or M), birth-rearing rank (brr, born single, twin, or triplet, reared as single, twin, or triplet), site of OFDA100 measurement (NZWTA or Massey University), and grazing mob (trait mob) or contemporary group (mainly flk by birth year by sex by traitmob). Birth date deviation (bdev) from the mean of contemporary group (flock by birth year by sex by WWTmob) and age of dam as linear (aod) and quadratic (aod^2) effects were fitted as covariates. Interactions between these effects were tested and discarded from the final model via backward elimination if not significant. Regression coefficients and fixed-effect contrasts were obtained from the final model retained.

To assess the significance of maternal (random) and breed (covariate) effects, they were fitted in univariate models for each trait using ASREML (Gilmour et al., 2009). Breed effect consisted of 4 covariates (romperc, coopperc, perenperc, texelperc) each calculating the proportion of a breed (Romney, Coopworth, Perendale, and Texel, respectively) in the animal. A maternal genetic effect was retained only for WWT and LWAU. Breed covariates were discarded for all traits except FW12 as they influenced genetic variance estimates by less than 2% Traits were then fitted in bivariate analyses with ASReml using full animal random effects as well as maternal effects where appropriate. Genetic and phenotypic parameter estimates and their SE were obtained by averaging across all relevant bivariate runs.

Selection Response

The selection response for DAG3 and DAG8 in scenario 1 (selection on DAG3 and DAG8) was 0.59 and 0.47 SD per unit of selection intensity, respectively. For scenario 2 (selection on BBREECH wool and fiber traits) the selection response was 0.32 and 0.08 for DAG3 and DAG8, respectively. For scenario 3 (selection on 10 traits) the response was 0.65 and 0.47 for DAG3 and DAG8, respectively.

RESULTS

Measurements

Table 1 shows a summary of the traits measured, before data cleaning, for both the 2009- and 2010-born progeny. The final number of LWAU measurements (which were generated from LW6 and LW8 data; see above) was 46,212 (average: 41 kg, SD: 7.3). For WWT and LWAU, which have maternal components, measurements and pedigree information for the dams and their contemporaries were included. This brought the total number of WWT and LWAU measurements to 287,247 and 191,109, respectively.

Model Fitting

Table 2 describes the final linear models applied for each characteristic. Table 3 shows means and an ANOVA summary for the traits examined. No fixed effects were significant for MED%. Age of dam (both linear and quadratic) was significant for production and visual traits, WWT, LWAU, FW12, DAG3, DAG8, BBREECH, and BULK (P < 0.05 to P < 0.001). Birth date deviation was significant for all traits except DAG8 and FDCV. Birth-rearing rank was significant for each trait except LENGTH. Each level of birth-rearing rank was compared against lambs born and reared as triplets. The traits WWT and LWAU were affected by birth-rearing rank (P < 0.001). However, for all other traits birth-rearing rank was not significant (P > 0.05) for most comparisons. Contemporary group fixed effects (mainly flk by birth year by traitmob) were significant for all traits except for MFD, FDCV, and MED%.

Breed percentage was fitted as a covariate for all traits; however, it was only significant for FW12. Heritability for fleece weight changed from 0.52 to 0.46 when breed was omitted from the univariate run. Heritability estimates varied by less than 2%, depending on whether breed was fitted or not, for traits other than FW12, and thus, breed was discarded from the model for these traits.
Genetic Parameters

Heritabilities, correlations, and phenotypic SD are presented in Table 4. The traits WWT and LWAU have moderate (range 0.21 to 0.23) heritabilities. Maternal heritability estimates for these traits were 0.23 ± 0.005 and 0.13 ± 0.005, respectively. The genetic correlation between the direct and maternal effects for WWT was -0.45 ± 0.01 and between direct and maternal effects for LWAU was -0.28 ± 0.02. High heritabilities were estimated for FW12 and MED% (0.49 ± 0.05 and 0.53 ± 0.11, respectively), and the remaining traits had moderate heritabilities between 0.23 ± 0.09 and 0.44 ± 0.02.

Of the visually assessed traits there was a high positive genetic correlation between DAG3 and DAG8 (0.74 ± 0.04) and between BBREECH and BULK (0.66 ± 0.03). There was a moderate and high negative correlation between BBREECH and LENGTH and between WWT and LWAU. High heritabilities were estimated for FW12 and MED% (0.49 ± 0.05 and 0.53 ± 0.11, respectively), and the remaining traits had moderate heritabilities between 0.23 ± 0.09 and 0.44 ± 0.02.

There were moderate to high genetic correlations between wool fiber traits, MFD, FDSD, FDCV, and MED%. Curvature had negative correlations with the wool fiber traits except with MED%, which was close to 0. There were moderately negative correlations between wool fiber traits and BBREECH except for CURV, where the correlation had a high positive correlation. Correlations of wool fiber traits were positive with LENGTH, except for CURV, which had a high negative correlation. Genetic correlations were low or negative with BULK, DAG3, and DAG8, except for CURV, which had a high positive correlation with bulk. There was also a moderate positive correlation between FDSD and DAG3.

Weaning weight and LWAU have low and negative genetic correlations with all other traits except with BULK, BBREECH, and MFD, which were moderately positive. There was a high genetic correlation between WWT and LWAU (0.64 ± 0.02). Fleece weight at 12 mo had moderate correlations with most traits except with DAG8, BBREECH, BULK, and WWT and a moderate negative correlation with CURV.

Phenotypic correlations among visually assessed traits, DAG3, DAG8, BBREECH, BULK, and WWT, were close to 0 except for a moderate positive correlation between DAG3 and DAG8 (0.41 ± 0.01) and between BBREECH and BULK (0.52 ± 0.01), a low negative correlation between BBREECH and LENGTH, and moderate negative correlation between LENGTH and BULK. Curvature had moderate positive correlation with visually assessed traits of BBREECH and BULK and a moderate negative correlation with CURV.

Phenotypic correlations among visually assessed traits, DAG3, DAG8, BBREECH, BULK, and LENGTH, and BULK, were close to 0 except for a moderate positive correlation between DAG3 and DAG8 (0.41 ± 0.01) and between BBREECH and BULK (0.52 ± 0.01), a low negative correlation between BBREECH and LENGTH, and moderate negative correlation between LENGTH and BULK. Curvature had moderate positive correlation with visually assessed traits of BBREECH and BULK and a moderate negative correlation with LENGTH. All other wool fiber traits have little to no correlation with all visually assessed traits, except moderate positive correlations between MFD and DAG8, between MFD and LENGTH, and between FDSD and LENGTH. Between the wool fiber traits there were moderate to high positive phenotypic correlations. Exceptions were between MFD and FDCV, which was low, and between CURV and all

Table 2. Final mixed models and fixed effects including contemporary groups used for individual trait analysis

<table>
<thead>
<tr>
<th>Trait</th>
<th>Fixed effects</th>
<th>Random effects</th>
<th>Contemporary group</th>
</tr>
</thead>
<tbody>
<tr>
<td>DAG3</td>
<td>sex brr aod bdev cg</td>
<td>animal</td>
<td>flk.byr.DAG3mob</td>
</tr>
<tr>
<td>DAG8</td>
<td>sex brr aod bdev cg</td>
<td>animal</td>
<td>flk.byr.DAG3mob,DAG8mob</td>
</tr>
<tr>
<td>BBREECH</td>
<td>brr aod bdev cg brr</td>
<td>animal</td>
<td>flk.byr.BBREECHmob</td>
</tr>
<tr>
<td>LENGTH</td>
<td>aod bdev cg.brr</td>
<td>animal</td>
<td>flk.byr.LENGTHHmob</td>
</tr>
<tr>
<td>BULK</td>
<td>brr aod bdev cg brr</td>
<td>animal</td>
<td>flk.byr.BULKmob</td>
</tr>
<tr>
<td>MFD</td>
<td>brr bdev ofda cg</td>
<td>animal</td>
<td>flk.byr.MFDmob</td>
</tr>
<tr>
<td>FDSD</td>
<td>brr bdev ofda cg brr</td>
<td>animal</td>
<td>flk.byr.FDSDmob</td>
</tr>
<tr>
<td>FDCV</td>
<td>brr ofda cg</td>
<td>animal</td>
<td>flk.byr.FDCVmob</td>
</tr>
<tr>
<td>MED%</td>
<td>no model</td>
<td>animal</td>
<td></td>
</tr>
<tr>
<td>CURV</td>
<td>brr bdev ofda cg</td>
<td>animal</td>
<td>flk.byr.MED%mob</td>
</tr>
<tr>
<td>WWT</td>
<td>brr aod bdev cg brr</td>
<td>animal, maternal</td>
<td>flk.byr.WWTmob</td>
</tr>
<tr>
<td>LWAU</td>
<td>brr aod bdev cg brr</td>
<td>animal, maternal</td>
<td>flk.byr.LWAUmob,WWTmob</td>
</tr>
<tr>
<td>FW12</td>
<td>brr aod bdev breed</td>
<td>animal</td>
<td>flk.byr.FW12mob,LWAUmob,WWTmob</td>
</tr>
</tbody>
</table>

1DAG3, DAG8 = dag score at 3 and 8 mo; BBREECH = breech bareness; LENGTH = length of relaxed wool staple on spine; BULK = wool bulk; MFD = mean fiber diam.; FDSD = SD of MFD; FDCV = CV of MFD; MED% = proportion of medullated fiber; CURV = curvature; WWT = weaning weight at 3 mo; LWAU = autumn BW; FW12 = fleece weight at 12 mo.
2brr = birth rearing rank; aod = age of dam as linear and quadratic; bdev = birth date deviation; ofda = site where fiber measurement done; cg = contemporary group.
3flk = flock; byr = birth year; DAG3mob = DAG3 grazing mob; DAG8mob = DAG8 grazing mob; BBREECHmob = BBREECH grazing mob; LENGTHmob = LENGTH grazing mob; BULKmob = BULK grazing mob; MFDmob = MFD grazing mob; WWTmob = WWT grazing mob; LWAUmob = LWAU grazing mob; FW12mob = FW12 grazing mob.
4Breed: romperc, coopperc, perenperc, texelperc.
other wool fiber traits. The phenotypic correlations between CURV and other wool fiber traits were moderately negative except with FDCV, which was close to 0.

The traits WWT and LWAU have low to negative phenotypic correlations with all other traits, except LWAU with FW12 (0.23 ± 0.01). There was a high phenotypic correlation between WWT and LWAU (0.69 ± 0.01). Fleece weight at 12 mo had low to negative correlations with all other traits except a moderate positive correlation with MFD (0.25 ± 0.04).

**Selection Response**

The selection response for DAG3 and DAG8 in scenario 1 (selection on DAG3 and DAG8) was 0.59 and 0.47 SD per unit of selection intensity, respectively. For scenario 2 (selection on BBREECH, wool and fiber traits) the selection response for DAG3 and DAG8 was 0.32 and 0.08 SD per unit of selection intensity, respectively. For scenario 3 (selection on all 10 traits) the response for DAG3 and DAG8 was 0.65 and 0.47 SD per unit of selection intensity, respectively.

**DISCUSSION**

The potential for accumulation of feces on the breech region can arise from a number of factors affecting consistency of feces and the adherence of feces to the breech. This study investigated breech cover, wool, and fiber traits for their association with dagginess. Nearly 29,500 progeny representing approximately 700 sires were measured, and genetic and phenotypic parameter estimates were calculated.

**Table 3. Means and ANOVA summary for traits after cleaning, transformation, and addition of dam information for WWT and LWAU**

<table>
<thead>
<tr>
<th>Item</th>
<th>DAG3</th>
<th>DAG8</th>
<th>BBREECH</th>
<th>LENGTH</th>
<th>BULK</th>
<th>MFD</th>
<th>FSD</th>
<th>FDCV</th>
<th>MED%</th>
<th>CURV</th>
<th>WWT</th>
<th>LWAU</th>
<th>FW12</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. Observations</td>
<td>13,225</td>
<td>6,173</td>
<td>26,337</td>
<td>24,210</td>
<td>24,209</td>
<td>1,271</td>
<td>1,271</td>
<td>1,271</td>
<td>1,134</td>
<td>1,271</td>
<td>284,916</td>
<td>190,174</td>
<td>7,931</td>
</tr>
<tr>
<td>Mean</td>
<td>1.22</td>
<td>1.19</td>
<td>1.95</td>
<td>57.65</td>
<td>2.36</td>
<td>33.30</td>
<td>8.60</td>
<td>25.80</td>
<td>8.10</td>
<td>48.69</td>
<td>28.40</td>
<td>40.02</td>
<td>3.02</td>
</tr>
<tr>
<td>Residual SD</td>
<td>1.23</td>
<td>1.33</td>
<td>0.76</td>
<td>9.15</td>
<td>0.78</td>
<td>2.54</td>
<td>1.10</td>
<td>2.59</td>
<td>5.97</td>
<td>6.58</td>
<td>4.07</td>
<td>4.17</td>
<td>0.39</td>
</tr>
<tr>
<td>CV%</td>
<td>100.99</td>
<td>111.51</td>
<td>39.11</td>
<td>15.87</td>
<td>32.94</td>
<td>7.62</td>
<td>12.81</td>
<td>10.05</td>
<td>119.40</td>
<td>13.52</td>
<td>10.41</td>
<td>13.04</td>
<td></td>
</tr>
<tr>
<td>$R^2$</td>
<td>0.15</td>
<td>0.11</td>
<td>0.31</td>
<td>0.08</td>
<td>0.37</td>
<td>0.17</td>
<td>0.23</td>
<td>0.54</td>
<td>0.00</td>
<td>0.54</td>
<td>0.36</td>
<td>0.67</td>
<td>0.13</td>
</tr>
<tr>
<td>Fixed effects</td>
<td>0.13 $^{2}$</td>
<td>0.10 $^{2}$</td>
<td>0.09 $^{2}$</td>
<td>0.08 $^{2}$</td>
<td>0.10 $^{2}$</td>
<td>0.04 $^{2}$</td>
<td>0.33 $^{2}$</td>
<td>0.00 $^{2}$</td>
<td>0.27 $^{2}$</td>
<td>0.01 $^{2}$</td>
<td>0.12 $^{2}$</td>
<td>0.01 $^{2}$</td>
<td>0.02 $^{4}$</td>
</tr>
<tr>
<td>Contrasts $^5$</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>brr 11</td>
<td>-0.01 ns</td>
<td>0.13 ns</td>
<td>0.13 ns</td>
<td>0.23 ns</td>
<td>1.62***</td>
<td>-3.74***</td>
<td>-0.50 ns</td>
<td>-3.00 *</td>
<td>12.88***</td>
<td>7.72***</td>
<td>-0.26***</td>
<td></td>
<td></td>
</tr>
<tr>
<td>brr 12</td>
<td>1.07**</td>
<td>1.31**</td>
<td>-0.44 ns</td>
<td>-0.46 ns</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>brr 21</td>
<td>0.02 ns</td>
<td>0.03 ns</td>
<td>-0.00 ns</td>
<td>0.13 ns</td>
<td>2.09***</td>
<td>-0.01 ns</td>
<td>0.41 ns</td>
<td>-3.44**</td>
<td>8.71***</td>
<td>4.18***</td>
<td>-0.18 ns</td>
<td></td>
<td></td>
</tr>
<tr>
<td>brr 22</td>
<td>0.01 ns</td>
<td>0.06 ns</td>
<td>0.00 ns</td>
<td>0.3 ns</td>
<td>0.67*</td>
<td>-0.02 ns</td>
<td>-0.47 ns</td>
<td>-0.73 ns</td>
<td>4.41***</td>
<td>4.07***</td>
<td>0.08 ns</td>
<td></td>
<td></td>
</tr>
<tr>
<td>brr 31</td>
<td>-0.14 ns</td>
<td>-0.07 ns</td>
<td>-0.48 ns</td>
<td>-0.13 ns</td>
<td>1.61*</td>
<td>1.13 ns</td>
<td>-0.31 ns</td>
<td>-1.90 ns</td>
<td>12.18**</td>
<td>10.36*</td>
<td>0.54 ns</td>
<td></td>
<td></td>
</tr>
<tr>
<td>brr 32</td>
<td>-0.09 ns</td>
<td>-0.02 ns</td>
<td>0.20 ns</td>
<td>-0.1 ns</td>
<td>0.95*</td>
<td>-0.59 ns</td>
<td>0.16 ns</td>
<td>-1.04 ns</td>
<td>5.36***</td>
<td>3.90**</td>
<td>-0.48 ns</td>
<td></td>
<td></td>
</tr>
<tr>
<td>brr 33</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Covariates $^6$</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>bdev</td>
<td>-0.01***</td>
<td>0.00 ns</td>
<td>-0.01***</td>
<td>-0.28***</td>
<td>0.00 ***</td>
<td>-0.06***</td>
<td>-0.02***</td>
<td>0.07 **</td>
<td>-0.19***</td>
<td>-0.17***</td>
<td>-0.01***</td>
<td></td>
<td></td>
</tr>
<tr>
<td>aod</td>
<td>0.13***</td>
<td>0.13*</td>
<td>0.09***</td>
<td>0.52 ns</td>
<td>0.09 ***</td>
<td></td>
<td></td>
<td></td>
<td>1.66***</td>
<td>1.60***</td>
<td>0.05***</td>
<td></td>
<td></td>
</tr>
<tr>
<td>aodq</td>
<td>-0.01**</td>
<td>-0.01*</td>
<td>-0.01***</td>
<td>-0.06 ns</td>
<td>-0.01 ***</td>
<td></td>
<td></td>
<td></td>
<td>-0.18***</td>
<td>-0.17***</td>
<td>-0.01***</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

$^*$ P < 0.001; ** P < 0.01; * P < 0.05; ns = not significant.

$^1$DAG3, DAG8 = dag score at 3 and 8 mo; BBREECH = breech bareness; LENGTH = length of relaxed wool staple on spine; BULK = wool bulk; MFD = mean fiber diam.; FSD = SD of MFD; FDCV = CV of MFD; MED% = proportion of medullated fiber; CURV = curvature; WWT = weaning weight at 3 mo; LWAU = autumn BW; FW12 = fleece weight at 12 mo.

$^2$Proportion of variance explained by fixed-effect contemporary group (see Table 1).

$^3$Contemporary group (flock by birth year by MFD grazing mob) shown to demonstrate no fixed effects significant for MED%.

$^4$Proportion of variance explained by fixed-effect contemporary group and brr interaction (see Table 1).

$^5$Contrasts birth rearing rank (brr) as born single (1), twin (2), or triplet (3) and reared as single, twin, or triple with born and raised as a triplet (brr33).

$^6$bdev = birth date deviation; aod, aodq = age of dam as linear and quadratic.

**Model Fitting**

The traits DAG3, DAG8, and MED% had high CV. This was also seen by Pickering et al. (2012) for DAG3 and DAG8, and they showed that deleting contemporary groups with low means was the best method to stabilize the variance across contemporary groups. In this data set the means were greater than that previously shown. One reason is that traits were allowed more time to be expressed before measurement; however, 23% and 25% of DAG3 and DAG8 measurements, respectively, were still deleted because of low contemporary group means. This stabilized the variance across contemporary groups,
as seen in Pickering et al. (2012), and therefore the data were on an appropriate scale for analysis.

Breed percentage was fitted as a covariate for all traits to account for potential effects of breed admixture in addition to the fixed effects fitted. Only for FW12 were there any significant additional effects explained by breed. For all other traits genetic estimates differed by less than 2%, depending on whether breed percentage was fitted or omitted. There is a potential for breed to be confounded with contemporary group; however, the slight difference also suggests that the breeds used were sufficiently linked through the industry, possibly by the wide uptake of composite breeds. Romney, Coopworth, Perendale, and Texel make up 93% of the total breed composition of this dual-purpose industry data set. Coopworth and Perendale are fixed interbred crosses containing 50% Romney; thus, the small change in estimates when breed was fitted as a covariate was not unexpected.

There was a negative maternal direct genetic correlation for and between WWT and LWAU. Maniatis and Pollott (2003) showed this could be the result of a data structure with limited measurements on dams and granddams. However, additional data on dams and their contemporaries were included in this analysis, especially to mitigate this bias. Both negative and positive correlations have been estimated in other studies (Clarke et al., 2000; Safari et al., 2005; Huisman et al., 2008). Allowing for a nonzero direct maternal covariance did reduce heritability and direct genetic and phenotypic correlations slightly (at the second decimal place). The correlations between the resulting estimated breeding values from the WWT- LWAU bivariate run with and without the direct maternal covariances fitted ranged between 0.93 and 0.96 for WWT, WWT maternal, LWAU, and LWAU maternal breeding values. For genetic evaluations and ranking of individuals these correlations show there is no commercially significant reranking of individuals by constraining these covariances to 0, and this may be a useful pragmatic strategy for industry evaluations.

### Comparison with Other Studies

Heritability estimates for dagginess in New Zealand dual-purpose sheep breeds range from 0.24 to 0.34 (Bisset et al., 1992; Scobie et al., 2008; Pickering et al., 2012), and those from Australian Merino flocks range from 0.09 to 0.55 (Pollott et al., 2004; Greeff and Karlsson, 2009; Smith et al., 2009). The heritability estimate for DAG3 (0.44) in this study was greater than the other New Zealand estimates; however, the DAG8 heritability estimate was similar to those previously reported from New Zealand.

Heritabilities for WWT and LWAU were similar to previously published estimates (Bisset et al., 1992; Brash et al., 1994a; Conington et al., 1995; Douch et al., 1995; Pollott

<table>
<thead>
<tr>
<th>Trait</th>
<th>DAG3</th>
<th>DAG8</th>
<th>BBREECH</th>
<th>LENGTH</th>
<th>BULK</th>
<th>MFD</th>
<th>FDCV</th>
<th>MED%</th>
</tr>
</thead>
<tbody>
<tr>
<td>WWT</td>
<td>0.47</td>
<td>0.73</td>
<td>-0.09</td>
<td>0.22</td>
<td>-0.08</td>
<td>0.03</td>
<td>0.09</td>
<td>0.04</td>
</tr>
<tr>
<td>LWAU</td>
<td>0.47</td>
<td>0.73</td>
<td>-0.09</td>
<td>0.22</td>
<td>-0.08</td>
<td>0.03</td>
<td>0.09</td>
<td>0.04</td>
</tr>
<tr>
<td>FW12</td>
<td>0.47</td>
<td>0.73</td>
<td>-0.09</td>
<td>0.22</td>
<td>-0.08</td>
<td>0.03</td>
<td>0.09</td>
<td>0.04</td>
</tr>
</tbody>
</table>

**Table 4.** Estimates of heritabilities (diagonal), phenotypic (above diagonal) and genotypic (below diagonal) correlations, and phenotypic SD (σp) ± SE

**Notes:** 1. Direct genetic effect estimate from bivariate estimates; the maternal effect estimate was 0.23 ± 0.00.

---

1. Direct genetic effect estimate from bivariate estimates; the maternal effect estimate was 0.13 ± 0.00.
Dagginess in New Zealand sheep

Heritability for FW12 was a little greater than previous New Zealand estimates (Bisset et al., 1992; Wuliji et al., 2011) but was similar to Australian Merino estimates (Huisman and Brown, 2008).

Breech bareness heritability was similar to other New Zealand dual-purpose (Scobie et al., 2007, 2008) and Australian Merino estimates (Greeff and Karlsson, 2009; Smith et al., 2009; Brown et al., 2010). In this study LENGTH and BULK were subjectively assessed traits, but in other studies staple length and bulk were machine tested. However, heritability estimates were similar to those calculated by Wuliji et al. (2011) in New Zealand Romneys.

The heritability estimates for the fiber traits MFD, FDSD, FDCV, and CURV were low compared with dual-purpose and Merino estimates (Brash et al., 1994b,c; Safari et al., 2005; Sumner et al., 2007; Huisman et al., 2008; Mortimer et al., 2009; Brown et al., 2010; Wuliji et al., 2011). Heritability estimates for MED% have not been previously reported; however, a summary from the New Zealand Central Progeny Test reports an average sire mean MED% of 5.8% (Craven et al., 2010), with a range of 3.5% to 7.6%. This is comparable to mean MED% of 8.1% for this data set.

The genetic correlation between WWT and LWAU was less than that reported in a previous study (Pickering et al., 2012); however, the phenotypic correlation was similar and is consistent with previously published estimates for dual-purpose breeds (Clarke et al., 2000). Genetic correlations between DAG3 and DAG8 were similar to previous estimates by Pickering et al. (2012).

Breech bareness genetic and phenotypic correlations with DAG3 and DAG8 were lower than previous estimates by Scobie et al. (2007, 2008). Genetic correlations were also lower than estimates in Australian Merinos; however, phenotypic correlations were similar (Greeff and Karlsson, 2009; Smith et al., 2009). This could be a consequence of the breed composition of this study, with the majority of flocks (21 of 34) being Romney based. The Romney breed has only moderate breech bareness, and there is little variation in pure-bred Romneys for this trait. Romneys have traditionally been selected for wool growth, and thus, the longer wool of a Romney can counteract the benefit of a bare breech.

This was consistent with the genetic correlation between LENGTH and BBREECH (-0.48 ± 0.04), which indicates longer wool is correlated with less breech bareness. For a Romney purebred flock, Scobie et al. (2008) calculated genetic and phenotypic correlations between breech bareness and dag score at weaning of 0.89 ± 0.46 and -0.12 ± 0.05, respectively. However, combining all flocks in this study, which also included TEFRom (Texel, East Friesian, and Romney composite) and Suffolk sheep, had genetic and phenotypic correlations of -0.44 ± 0.12 and -0.18 ± 0.02, respectively.

There are no known published estimates on genetic and phenotypic correlations between dagginess and the wool traits LENGTH and BULK and the fiber traits FDSD, FDCV, MED%, and CURV. The only known published genetic correlation between late dag score (first recording at either yearling, hogget, or adult age) and mean fiber diameter was 0.07 ± 0.10 and between staple length and late dag score was -0.25 ± 0.14 (Brown et al., 2010). In this data set, it was found that dagginess at DAG3 or DAG8 had little or no genetic or phenotypic correlation with most wool or fiber traits. The exceptions were the moderate genetic correlations of DAG3 with FDSD and LENGTH, but their phenotypic correlations were close to 0. In neither case were the estimates significant. Dag score at 3 mo had a moderate genetic correlation with FW12, greater than the previous estimate by Pickering et al. (2012). However, again the phenotypic correlation was close to 0. In a case-control study in young lambs it was noted that longer fleeces with low crimp frequency accumulated more feces than short wool with tighter crimp frequency (French et al., 1998). In a more recent study looking at factors affecting fecal accumulation, wool length was only significant in 2 out of 4 inspections (Broughan and Wall, 2007).

There are no known published genetic correlation estimates of BBREECH with LENGTH, BULK, or the fiber traits. The genetic and phenotypic correlations shown here between BBREECH, LENGTH, and BULK indicate that sheep with shorter, bulkier wool will have larger bare breeches than sheep with longer, less bulky wool. As there were only low genetic and phenotypic correlations between BBREECH, wool, and fiber traits with DAG3 and DAG8, this suggests that fecal accumulation was not associated with wool length or type.

The majority of estimated parameters for genetic and phenotypic correlations between fiber traits were based on Australian Merinos (Taylor et al., 1999; Safari et al., 2005; Huisman and Brown, 2008), with a few studies on New Zealand Romneys (Wuliji et al., 2011), Perendales (Sumner et al., 2007), and Australian Coopworths (Brash et al., 1994b). There are no known parameter estimates for MED%. The genetic and phenotypic correlations reported here between fiber traits and subjectively assessed traits of LENGTH and BULK were similar or less than those reported previously. Of interest was the high genetic correlation between BULK and CURV (0.86 ± 0.11) and between BBREECH and CURV (0.76 ± 0.10) and the negative genetic correlation between LENGTH and CURV (-0.71 ± 0.10) and the corresponding moderate phenotypic correlations of 0.33 ± 0.03, 0.22 ± 0.03, and -0.37 ± 0.03, respectively. Compression of the fleece is dependent on the geometry of the fiber such that CURV and MFD account for 85% of the variation seen in core bulk (Sumner et al., 2007). In this study the high cor-
relation between hand-assessed BULK and CURV suggests that hand-assessed BULK was an effective estimate of core bulk. Additionally, the genetic and phenotypic correlations of BULK and CURV with LENGTH and BBREECH were similar. The low negative genetic correlation between BULK and MFD indicates selecting for bulky fleeces may give slightly lower MFD.

There are few known published genetic parameter estimates between fiber traits (CURV, MED%, FDSD, FDCV) and WWT and LWAU in dual-purpose sheep. Genetic and phenotypic correlations between WWT and wool traits (MFD, staple length, and CURV) reported by Huisman and Brown (2008) in Australian Merinos were similar to those reported here. For postweaning BW their phenotypic correlations were similar, but their genetic estimates were greater than those reported in this study. Genetic and phenotypic correlations between WWT and wool traits (MFD, staple length, and BULK) in New Zealand Romneys were reported by Wuliji et al. (1998, 2011). These estimates were similar to those reported here except for a greater estimate for genetic correlation between WWT and MFD and a smaller phenotypic correlation between WWT and BULK. Combining the results from this study and those from Wuliji et al. (1998, 2011) selecting for fiber traits should have no impact on WWT or LWAU, except selecting for decreased MFD may decrease WWT and LWAU.

The correlations of FW12 with fiber traits were either smaller than or similar to other estimates published in New Zealand and Australia (Wuliji et al., 1998; Taylor et al., 1999; Safari et al., 2005; Sumner et al., 2007; Wuliji et al., 2011). Heavier fleeces were correlated with longer wool staples, greater MFD, greater FDSD, and less CURV; however, genetic and phenotypic correlations with BULK were close to 0. Thus, using any of the fiber traits as indirect indicators for flystrike will not have a detrimental effect on FW12.

**How Much Response in Dagginess**

**Do the Wool and Fiber Traits Explain?**

To examine the effectiveness of direct vs. indirect selection for dagginess, the genetic parameters estimated in this study for DAG3, DAG8, BBREECH, and fiber and wool traits (LENGTH, BULK, MFD, FDSD, FDCV, MED%, CURV) were used in a selection index tool (van der Werf, 2006) with the sole objective being to reduce dagginess through DAG3 and/or DAG8. Approximately 47% of the genetic response achieved by direct selection for DAG3 was achieved by indirect selection on BBREECH, fiber, and wool traits, but only 17% of the direct genetic response in DAG8 was achieved. Thus, for both dagginess traits BBREECH, fiber, and wool traits provided little or no additional predictive power to measuring dagginess directly. The difference between DAG3 and DAG8 results was mostly likely due to animals measured at DAG8 being either crutched or shorn soon after weaning, thus reducing the predictive ability of the wool traits. It would appear from these results that a considerable proportion of the genetic variation in dagginess was independent of wool weight, fiber traits, and BBREECH.

Given the above observations, the likely additional factors affecting the genetic variation in dagginess are pasture quality, composition, and quantity offered. These factors can affect incidence of dag formation of groups of animals; however, to affect individuals, they would have to respond differently to the ingested feed or alternatively act via diet selection. Including the result from Pickering et al. (2012), which shows dagginess was not associated with fecal egg count or nematodirus egg count, this leaves factors affecting fecal consistency as the likely cause for fecal accumulation. Previous studies have shown moderate to high genetic and phenotypic correlations between fecal consistency score and dag score in New Zealand Romneys (McEwan et al., 1992; Douch et al., 1995) and Australian Merinos (Pollott et al., 2004). Differences in fecal consistency have been attributed to pasture composition and NDF levels (Leathwick and Atkinson, 1995; Davidson et al., 2006), immune response to larvae (Larsen et al., 1999) and fungal endophytes (Pownall et al., 1993; Fletcher et al., 1999), and large intestine function (Ruckebusch and Fioramonti, 1980; Bedrich and Ehrlein, 2001). The traits DAG3 and DAG8 were moderately heritable. Thus, there would likely be a genetic component underlying the factors listed above.

**Conclusions**

Dagginess at 3 and 8 mo of age in New Zealand dual-purpose sheep shows little to no genetic and phenotypic correlations with breech bareness or wool or fiber traits. When all wool traits and BBREECH are combined together in an index, they can only achieve a minor fraction of the genetic gain observed when selecting on dags alone. As a previous study (Pickering et al., 2012) shows, there was no correlation with fecal egg counts; this then leaves internal processes such as intestinal function, immune response, and feed composition as potential causes underlying dagginess. It is well known that dagginess is a major factor in flystrike susceptibility; therefore, any studies into the above factors that might elucidate the major causes for dagginess and develop strategies to reduce dagginess and thus flystrike would be beneficial.
LITERATURE CITED


