Heritability of Dags and its Genetic Relationship with Fleece Traits and Live Weights

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Introduction

Dagginess, or the accumulation of faecal material around the perineum region of sheep, is a trait of interest to New Zealand sheep breeders/farmers. The four major reasons are; firstly, dagginess is recognised as having a positive genetic (0.86± 0.17) and phenotypic correlation (0.23) with flystrike (Greeff and Karlsson, 2009). The arrival of *Lucillia cuprina* ("Aussie blowfly") to New Zealand in the 1990s has also markedly increased the incidence of, and losses due to flystrike. Flystrike is an animal welfare issue in New Zealand, the presence of dags is a major contributing factor to the sheep's degree of susceptibility to flystrike. Secondly, there are severe penalties for presenting daggy sheep for slaughter and the quality thresholds are being driven higher by the shift from frozen to chilled meat. Thirdly, the number of stock units managed per labour unit has increased by 20.8% from 1819 (1980/81) to 2198 (2007/08) (Anon. 2009). Finally the costs of activities such as dagging and dipping have increased substantially. Since year 2000 shearing expenditure has increased by 74.1%, and animal health expenses have increased by 87.2% (Anon. 2009).

The long term aim of the current work is to develop genomic selection in New Zealand maternal sheep breeds for both dagginess and host resistance to flystrike. As a prerequisite to doing this, detailed knowledge of suitable fixed effect models and genetic and phenotypic parameters between these traits and beneficial production traits in recorded New Zealand industry flocks is required. Currently, the New Zealand industry consists of Romney, Coopworth, Perendale, Texel and composite crosses which are merging to form a single gene pool. These animals are genetically evaluated within a single analysis in Sheep Improvement Limited (SIL) called SIL ACE (Young and Newman, 2009).

Materials and Methods

Data. Data for weaning weight (WWT), liveweight at 6 months and 8 months (LW6, LW8), fleece weight at 12 months (FW12) and dag score at 3 months and 8 months (DAG3, DAG8) were obtained from the SIL database for animals born between 1990 and 2008. Dags are scored on a 6 point scale; 0 (no dags) to 5 (complete coverage of the breech and down the legs by faecal material). The SIL database holds records on research and breeder flocks in New Zealand and performs across flock evaluations (Young and Newman, 2009). Flocks used in this analysis are involved in Ovita-funded genomic selection research programmes. The dataset contained over 2 million records with pedigree information, and covered a range of breeds, predominantly Romney, Coopworth, Perendale, Texel, and some composite breeds.

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Statistical analyses. Fixed effects models were initially determined using the general linear model procedure (SAS, 2004). The models fitted included fixed effects of sex (F or M), birth-rearing rank (born single, twin, or triplet, reared single, twin, or triplet), and trait grazing group or birth year-traitgroup-wwtgroup cohort. Birthday scaled to mean (see below), and age of dam in linear and quadratic forms were fitted as covariates. Interactions between these effects were tested and discarded from the final model if not significant via backwards elimination. Traits were then fitted in bi-variate analyses with ASReml (Gilmour *et al*, 2009) using full animal random effects as well as the previously determined fixed effects model in order to estimate genetic parameters. Maternal random effects were fitted for WWT, DAG3 and DAG8 in a uni-variate analysis. However, estimates for DAG3 and DAG8 changed by less than 0.05, so were dropped from the final analysis. Maternal random effects were not fitted for LW8 and FW12, as published estimates are small.

Data models were configured for each trait separately. For DAG3 and DAG8, data was first screened to ensure age at measurement fell within stated bounds. Log and arcsin transformations were then tested, but these did not improve the fit to normality or homoscedasticity. It was noticeable that most of the deviation from normality was due to contemporary groups with low mean dag score. In order to address this mean dag score for each contemporary group of year, flock and grazing group were calculated. Means of 0.5 and 0.25 respectively for DAG3 and DAG8 were set as thresholds. Contemporary groups with values below these means were discarded.

For WWT, data were scaled via means of contemporary group assigned as flock, year, sex, and wwt grazing group (wwtmob). For LW8 and LW6, the data were combined to generate an autumn live weight with the maximum amount of information. This was based on the number of animals for each contemporary group assigned as flock, year, sex, lw8mob, lw6mob, and wwtmob. The new autumn LW8 values were then scaled via means of its new contemporary group (flock, year, sex, new lw8mob, wwtmob). For FW12, data were scaled via means of contemporary group assigned as flock, year, sex, fw12mob, lw8mob, and wwtmob. Final models developed are shown in table 1.

Two birthday deviations were applied. For DAG3 and DAG8, the birthday minus the mean birthday for all animals in the dataset (bdaya) was used. For the last three traits the birthday minus its mean for the WWT contemporary group (bdev) was used. Animals with a bdev less than -40 and greater than 40 were discarded. Table 2 shows the number of records in the dataset before cleaning and the number of records kept for the ASReml analyses.

Table 1: Animal models for each of the five traits.

Trait	Fixed effects	Random effects
DAG3	brr, sex, aod, aod2, bdaya, flk*yr*dag3mob	Animal
DAG8	brr, sex, aod, aod2, bdaya, flk*yr*dag8mob	Animal
WWT	brr, aod, aod2, bdev, flk.yr*wwtmob.sex	Animal, Maternal
LW8	brr, aod, aod2, bdev, flk.yr*lw8mob.sex	Animal
FW12	brr, aod, aod2, bdev, flk.yr*fw12mob.sex	Animal

Table 2. Number of records (N) held for each trait before data cleaning and finally used for the ASReml analysis.

	DAG3	DAG8	WWT	LW6	LW8	FW12
N before	64,832	45,858	1,825,042	436,660	644,662	808,745
N analysis	48,022	45,332	1,754,303	-	1,015,626*	771,370

* This is the adjusted autumn LW8 after combining LW6 and LW8 data.

Results and discussion

Estimates of heritabilities, genetic and phenotypic correlations between traits are shown in table 3. All traits had moderate heritability, WWT maternal heritability was 0.204 (0.001). DAG3 and DAG8 have moderate heritabilities with a high genetic correlation. Scobie *et al* (2008) estimated DAG3 heritabilities of 0.31 and 0.34 for a Romney and Perendale flock respectively. DAG3 and DAG8 also had positive genetic correlations with FW12. This is as expected due to longer wool more easily accumulating faecal material. However, the relationship is low and the phenotypic correlation, between DAG3 and FW12, is not significant. DAG3 has a generally low and negative genetic correlation with LW8. This suggests faster growing animals will have less dags. WWT and LW8 have a high positive correlation as expected, and both WWT and LW8 have a low correlation with FW12.

Table 3: Heritability estimates, genetic and phenotypic correlations between weaning weight direct (WWTd), live weight at 8 months (LW8), fleece weight at 12 months (FW12), dag score at 3 months (DAG3), and at 8 months (DAG8)[*], and phenotypic standard deviations (last row).

Traits	WWTd	LW8	FW12	DAG3	DAG8
WWTd	**0.181(0.002)**	0.726(0.001)	0.206(0.001)	-0.157(0.005)	-0.017(0.005)
LW8	0.913(0.002)	**0.363(0.002)**	0.361(0.001)	-0.088(0.007)	-0.050(0.006)
FW12	0.189(0.008)	0.207(0.006)	**0.368(0.003)**	0.001(0.008)	-0.029(0.007)
DAG3	-0.056(0.038)	-0.100(0.027)	0.069(0.027)	**0.340(0.012)**	0.405(0.008)
DAG8	-0.013(0.033)	-0.010(0.027)	0.089(0.028)	0.712(0.025)	**0.308(0.012)**
σp	4.069	4.583	0.422	1.247	1.431

[*]Genetic correlations between traits are displayed below the diagonal and phenotypic correlations above the diagonal. Heritability estimates are displayed in bold on the diagonal with s.e. in brackets.

An alternative model fitting breed percentage as covariates for Romney, Coopworth, Perendale, and Texel (these account for greater than 93% of the total breed composition present in the analysis) was also investigated to account for potential effects of breed admixture. However, estimates changed by less than 0.01, so unadjusted estimates are presented here. This is perhaps not unexpected given that both Coopworths and Perendales are fixed interbred crosses consisting of 50% Romney. Sires from this resource are now being genotyped with the Illumina OvineSNP50 BeadChip with 520 genotyped to date and more than 500 planned over each of the next 2 years. These results will form the basis of an appropriate methodology for developing genomic selection training and validation sets. Further analysis is required to include more traits including number of lambs born, lamb survival, ultrasound fat and muscle depths, and faecal egg counts into the current analysis.

Additional data is being collected in these flocks on dags, breech bareness (lack of wool cover around the perineum), wool length, bulk, and flystrike, along with those traits indicated above over the next two years. One immediate benefit from this work is that the current parameters and fixed effects models used in SIL and SIL-ACE can be updated.

Conclusion

The current industry data set has provided accurate estimates of the genetic parameters of the New Zealand industry. However, appropriate criteria for screening dagginess records required development. The traits of interest DAG3 and DAG8 have moderate heritability with low negative and positive genetic relationships with liveweight and fleeceweight respectively. This augurs well for industry selection for decreased dagginess and increased flystrike resistance. As New Zealand maternal sheep breeds are merging into a single gene pool, this analysis is a useful initial exploration of the parameters and models required to estimate breeding values for this composite breed mix. Future work will explore the genetic relationship of dagginess with flystrike resistance and lead to implementation of genomic selection in New Zealand maternal sheep breeds.

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