

GENETIC EVALUATION AND RELATIONSHIP ACROSS AGES FOR DAG SCORE IN MATERNAL SHEEP

A.J. McMillan, S.F. Walkom and D.J. Brown

Animal Genetics & Breeding Unit*, University of New England, Armidale, NSW, 2351 Australia

SUMMARY

Daginess in sheep is an undesirable trait with both economic and welfare implications. While the trait has been investigated in Merino sheep, this is not the case for maternal sheep. With sufficient records now available from industry and research flocks via Sheep Genetics the genetic parameters for dag score can now be estimated. The heritability of dag score ranged from 0.13 (± 0.01) to 0.38 (± 0.02) across age stages with the highest heritability occurring at the yearling stage. Given the heritability it should be possible for breeders to make genetic progress towards less daggy maternal sheep, which as an indirect selection tool will potentially assist to reduce labour costs, wool losses and flystrike incidence. Positive moderate genetic correlations between age classes (0.08 to 0.83) indicate that selection based on phenotypes recorded at any age will lead to reduced dag score across investigated stages. The results suggest that breeders should be focussed on recording dag score when the environmental conditions promote the greatest expression of genetic merit, than scoring at a specific age class. However, in maternal sheep the greatest phenotypic variation in dag score appears to occur in yearling sheep.

INTRODUCTION

Dag (measured by dag score) is the accumulation of faecal matter in wool around the breech of the animal, which is associated with increased flystrike incidence within the Australian sheep population. Previous studies have indicated that flystrike is costing \$280m dollars annually (Sacket *et al.* 2006) as a result of sheep losses, cost of treatment and loss of wool as well as carcass production and value. In response to public concern and desire for management practices such as mulesing to be phased out sheep breeders are utilising indicator traits like dag score to reduce flystrike incidence (Brown *et al.* 2010). Dag score (scouring) has been shown to be related to flystrike in previous studies (James 2008; Greeff and Karlsson 2009; Smith *et al.* 2009) there are also costs associated with loss of production as well as crutching costs (Sacket *et al.* 2006).

The genetic evaluation of dag score has previously been reported in the Australian Merino population (Brown *et al.* 2010), however, the growth of maternal cross merino ewe flocks and self-replacing maternal flocks has influenced the interest within maternal stud breeders to utilise dag score in their breeding programs. The heritability of dag score has been shown to be moderate in Australian Merino sheep (0.20-0.26, Brown *et al.* 2010), (0.37-0.63, Greeff *et al.* 2013) and in another study where it ranged from 0.07 to 0.32 for animals recorded at 30 day intervals from weaning to hogget stage (Pollot *et al.* 2004).

The recent increase in dag score recording by maternal sheep breeders and records from the Information Nucleus and resource flocks (Fogarty *et al.* 2007) has led to an increase in dag score phenotype submission to Sheep Genetics, the paper investigates the genetic parameters for dag score within the maternal population and the relationship of dag score in the Weaning (Wdag), Post-weaning (Pdag), Yearling (Ydag) and Hogget (Hdag). The effect of modelling genetic groups and sire x flock effects were also explored.

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MATERIALS AND METHODS

Data. Pedigree and performance were extracted from the Sheep Genetics LAMBPLAN (Maternal) database (Brown *et al.* 2007). This database stores pedigree and performance records submitted by ram breeders that are used for LAMBPLAN (Maternal) national genetic evaluations.

A summary of records from the maternal database are presented in Table 1. Currently there are 22 flocks who have submitted 39,035 dag phenotypes across the 4 age stages investigated. The most popular stage for dag score recording was at weaning with almost 18,519 records with yearling records and post weaning records combined made up the majority of the remaining records. Most flocks who recorded dag score had records from a number of stages across different years in this dataset. There were 6,301 animals which had records across multiple stages.

The dag score phenotype are visually scored from 1-5 with a score 1 having no dags in the breech area up to a score of 5 which has an accumulation of dags in breech area and down the legs of the animal (AWI. 2013). With increasing age the dag score phenotypes showed both an increase in score but also an increase in the variation for score.

Table 1. Summary of dag score phenotypes submitted to Sheep Genetics by maternal sheep breeders across age classes.ncg; number of contemporary groups, ngg; number of genetic groups

Trait	Records	Mean	sd	Pedigree	Sires	Dams	Flocks	Ncg	ngg
Wdag	18519	1.40	0.67	39321	4696	19506	12	213	35
Pdag	7762	1.64	0.85	28283	4843	16765	10	70	38
Ydag	11784	1.83	0.93	36222	5445	20448	11	159	42
Hdag	970	1.98	0.87	11243	3300	7058	9	21	21

Statistical Analysis. Parameters were estimated in bivariate analyses for each trait combination, ASREml (Gilmour *et al.* 2015) was used fitting an animal model. The model included direct genetic, dam permanent environment effects. Fixed effects of age of animal and age of dam were fitted as covariates with both linear and quadratic effects for dam age. Birth and rearing effects were treated as non-interacting fixed effects ranging from 1-4. Flock, year of birth, sex, the date of measurement and breeder management group were used to define contemporary group.

RESULTS AND DISCUSSION

Genetic parameter estimates and the genetic and phenotypic correlations across age classes are presented for the base model (Table 2) and the extended model which included genetic groups and the sire by flock interaction fitted as random (Table 3). These terms are used within Sheep Genetics Evaluations and improve the fit of models especially for analysing industry data structure and recording are not always balanced (Brown *et al.* 2007). The results showed that the inclusion of genetic groups and the sire x flock term within the model had no significant impact on the additive genetic variance nor the heritability.

The heritability of dag score at weaning, post-weaning, yearling and hogget stage was 0.13, 0.27, 0.38, 0.20, respectively (Table 2). These pattern are similar to that estimated by (Pollot *et al.* 2004) in Merino sheep which had a low heritability at weaning (0.07) before peaking at a moderate heritability (0.32) at 270 days and then declining to lower estimates of 0.08, 0.13 and 0.16 for 300, 330 and 360 days of age respectively. Although the heritability for these maternal animals may be higher due to industry recording likely only being undertaken when dag was more strongly expressed with the mean dag score ranging from 1.4 to 1.98 vs 0.36 to 1.50 (Pollot *et al.* 2004) although those merino animals were scored with a slightly different scoring method (Larsen *et al.* 1994).

The highest heritability estimate, 0.38, was observed for Ydag this is almost double the estimate for late dag score (ldag) (0.20) in Merinos although it should be noted that ldag includes dag score from across yearling, hogget and adult stages (Brown *et al.* 2010).

Phenotypic correlations were positive and range from low (0.19) to moderate (0.45) with stronger correlations for the later stages, environmental effects have a large impact for the trait to be expressed.

Genetic correlations were generally high and positive although there were some deviations between the base model and the extended model. The extended model showed slightly higher correlations between traits although not all of these were significant. However genetic correlations with Hdag were compromised by the small number of records at this stage leading to high standard errors. Given these correlations recording and selection for dag score at any of the stages would result in a positive impact on the other stages.

Table 2. Phenotypic variance ($\hat{\sigma}_p^2$) and direct heritability (h^2) with phenotypic correlations above the diagonal and genetic correlations below the diagonal for base model

Trait	$\hat{\sigma}_p^2$	h^2	Wdag	Pdag	Ydag	Hdag
Wdag	0.35±0.00	0.13±0.01		0.19±0.01	0.17±0.02	0.08±0.03
Pdag	0.66±0.01	0.27±0.02	0.66±0.07		0.45±0.02	0.19±0.04
Ydag	0.83±0.01	0.38±0.02	0.54±0.07	0.83±0.04		0.66±0.26
Hdag	0.55±0.02	0.20±0.04	0.75±0.16	0.08±0.18	0.60±0.15	

Table 3. Phenotypic variance ($\hat{\sigma}_p^2$) and direct heritability (h^2) with phenotypic correlations above the diagonal and genetic correlations below the diagonal for the model that included genetic groups and the sire by flock interaction

Trait	$\hat{\sigma}_p^2$	h^2	Wdag	Pdag	Ydag	Hdag
Wdag	0.35±0.00	0.13±0.01		0.19±0.01	0.18±0.02	0.08±0.03
Pdag	0.66±0.01	0.26±0.02	0.77±0.08		0.45±0.02	0.18±0.04
Ydag	0.84±0.01	0.38±0.02	0.62±0.07	0.87±0.05		0.81±0.16
Hdag	0.56±0.02	0.16±0.05	0.85±0.24	-0.12±0.23	0.63±0.21	

Given the results it appears that the extended model is appropriate for analysis of the data although the effects estimated were small especially considering the stronger genetic groups effects previously seen in Merinos. Measurements made at the weaning stage had the lowest heritability estimate and also the smallest phenotypic variances however still had strong genetic associations with dag score measured at the other stages. To improve dag score, recording could be at any of the stages with a preference for later recording. However recording would be best when trait expression is maximised regardless of stage.

The LAMBPLAN (Maternal) genetic evaluation has been following the MERINOSELECT analysis approach. Analysing early (edag) and late (ldag) traits with edag including marking and weaning stage records and late dag including records from yearling, hogget and adult records. The estimated genetic correlations are moderate-high across stages with the exception of Pdage-Hdage which particularly suffers from high standard errors due to small number of records. Given these correlations the traits could be analysed either following the MERINOSELECT model with combined late and early trait groups or as individual stage based traits.

CONCLUSIONS

It should be possible to genetically improve dag scores in maternal sheep with appropriate selection and recording as moderate heritability estimates were observed across stages with moderate- high genetic correlations between age stages. Given this visual scoring for dag score should be performed when the trait is showing its greatest expression.

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