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BRIEF COMMUNICATION: Estimates of genetic parameters for flystrike in New Zealand Romney and Romney cross sheep

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Introduction

Myiasis, or flystrike, is a major animal welfare problem for sheep that causes significant production losses and potentially death. It is estimated that the prevalence of flystrike is 3-5% in the national flock (Heath & Bishop 1995) and is estimated to cost the New Zealand industry $40 to $50 million annually (Beef + Lamb New Zealand 1999). These costs accrue via production losses through reduced wool and body growth, morbidity, and control strategy costs including insecticide, lamb shearing and crutching.

An alternative and more permanent approach is to breed for sheep that are genetically resistant to flystrike. As current prevention techniques have been successful over the last several decades, there has been little research into host resistance to flystrike in New Zealand (Brandsma & Blair 1997; Scobie & O'Connell 2010). A number of research projects have been undertaken in Australian Merinos (McGuirk et al. 1978; Rathie et al. 1994; Greeff & Karlsson 2009; Smith et al. 2009). Although these studies have limited relevance to New Zealand dual-purpose sheep, they do suggest potential indirect prediction traits that could be used in a selection programme. These traits include dagginess, breech bareness, and wool fibre traits such as mean fibre diameter, standard deviation of mean fibre diameter and coefficient variation of mean fibre diameter. Dagginess and breech bareness have been confirmed as potential indirect indicators in a New Zealand easy-care sheep resource flock (Scobie et al. 2007; Scobie & O'Connell 2010). The objective of this study is to investigate the association of these traits with flystrike, with the aim of assessing their potential as indirect indicators for flystrike.

Materials and methods

This work was carried out with the approval of the AgResearch Invermay Animal Ethics Committee.

Field measurements and sample collections

The flystrike "season" runs from October to April, peaking during February and March (Heath & Bishop 2006). Lambs from 11 properties over two flystrike seasons, 2009/10 and 2010/11, were assessed for flystrike. There were nine North Island, and two South Island properties. All flocks were genetically linked, with six of the properties carrying Sheep Improvement Limited (SIL) recorded flocks. The animals were primarily Romney or Romney cross. A variety of husbandry measures were used to reduce flystrike incidence including lamb shearing and crutching all animals.

Flystrike cases were recorded and ear tissue and wool samples collected throughout the season by the farmers. Measurements, ear tissue and wool samples from the control (non-affected) animals were collected at the end of the season. Controls were matched to cases by flock, year, sex and mob. Tissue and blood samples from all potential sires were collected by the farmer or a qualified person for paternity parentage testing.

Measurements were taken on the date of flystrike observation, flystrike anatomical location, dag score, breech bareness score, and the following wool fibre traits: mean fibre diameter (MFD), standard deviation of fibre diameter (FDSD), coefficient of variation of fibre diameter (FDCV), proportion of medullation (MED%), and mean fibre curvature (CURV). The anatomical location of flystrike was classed into six regions: breech, body, belly/pizzle, shoulders, head and feet (modified from French et al., 1995). Dag score was recorded on a 0 (No dags) to 5 (Complete dags over the tail, under the crutch, and down the legs) scale. Breech bareness was recorded on a 1 (Wool up to and covering the anus) to 5 (No wool around the breech and continues down the leg) scale. Wool fibre traits were measured on an OFDA100 (IWTO 1998). Additional information was available for lambs sourced from SIL recorded flocks, including: parentage, age of dam, birth and rearing rank, birthday and grazing mob.

Genetic estimates

Flystrike was scored as a binomial trait (0 = No flystrike, 1 = Presence of flystrike). Results were scaled to the mean incidence rate of the within year contemporary group using the equation Scaled flystrike score = Flystrike score / $\sqrt{(p \times (1 - p))}$ where p = the incidence rate. The scaled flystrike score was then log transformed as $\log_{10}$ (Scaled flystrike score + 1). Statistical models were pre-determined for dag score, and breech bareness by Pickering et al. (2011). Fixed effect models were initially determined for wool traits and the transformed relative flystrike score using the general linear model procedure (SAS 2004). The model for

Table 1 Summary statistics for traits measured on flystrike cases and controls including number of observations (n), mean, standard deviation (SD), minimum (Min) and maximum (Max) for dag score, breech bareness score (Breech score), mean fibre diameter (Diameter), fibre diameter standard deviation (FDSD), fibre diameter coefficient of variation (FDCV), proportion of medullation, and mean fibre curvature (Curvature).

Trait	Case					Case				
	n	Mean	SD	Min	Max	n	Mean	SD	Min	Max
Dag score	604	2.8	1.5	0.0	5.0	714	0.8	1.0	0.0	5.0
Breech score	703	1.2	0.5	1.0	4.0	682	1.2	0.4	1.0	3.0
Diameter (μm)	592	33.8	3.6	23.3	44.7	662	35.4	3.2	25.8	46.4
FDSD (μm)	592	8.3	1.3	5.1	14.1	662	8.2	1.2	5.5	12.1
FDCV (%)	592	24.6	3.1	17.4	35.6	662	23.2	2.7	16.8	36.2
Medullation (%)	592	8.1	10.6	0.0	54.6	662	6.0	8.8	0.0	79.0
Curvature (°/mm)	592	46.5	8.2	29.1	81.1	662	44.8	8.4	26.5	74.9

Table 2 Estimates of heritability (h^2) ± standard error and phenotypic standard deviation (σ_p) for the transformed relative flystrike score, dag score, breech bareness score (Breech score), mean fibre diameter (Diameter), fibre diameter standard deviation (FDSD), fibre diameter coefficient of variation (FDCV), proportion of medullation and mean fibre curvature (Curvature), and the phenotypic (r_p) and genotypic (r_g) correlations ± standard error between flystrike and the other measured traits.

Trait	Parameter			
	h^2	σ_p	r_p	r_g
$\log_{10}(FLY+1)$	0.39 ± 0.12	0.41		
Dag score	0.23 ± 0.09	1.50	0.62 ± 0.02	0.71 ± 0.14
Breech score	0.35 ± 0.11	0.43	-0.03 ± 0.03	-0.18 ± 0.21
Diameter (μm)	0.58 ± 0.14	2.99	-0.24 ± 0.03	-0.23 ± 0.18
FDSD (μm)	0.30 ± 0.12	1.18	0.00 ± 0.03	0.50 ± 0.24
FDCV (%)	0.43 ± 0.14	2.75	0.20 ± 0.03	0.72 ± 0.17
Medullation (%)	0.25 ± 0.10	10.12	0.09 ± 0.03	0.05 ± 0.24
Curvature (°/mm)	0.34 ± 0.12	7.06	0.08 ± 0.03	-0.11 ± 0.23

analysing the transformed relative flystrike code included terms for sex, within year contemporary group and their interaction. Fibre trait models included a term for birth and rearing rank for all traits, birthday deviation from mean of the within year contemporary group and within year contemporary group were fitted for MFD, FDSD and CURV. A within year contemporary group term by birth and rearing rank interaction was fitted for FDSD. No effects were fitted for MED%, as they were not significant. Traits were then fitted in bivariate analyses with ASReml (Gilmour et al. 2009) using full animal random effects.

The heritability of liability (h_l^2) to flystrike was derived from the heritability of flystrike on the observed scale (h_o^2) using Equation 23 from Lee et al. (2011).

Results and discussion

There were 836 case and 745 control samples collected over the two flystrike seasons. Incidence rates per flock and year ranged between 0.47% and 8.18%. The majority of strike occurred in the breech (89% in 2009/10 and 75% in 2010/11); strike was also recorded on the head, body, shoulders and belly/pizzle. No flystrike was recorded on the feet. A summary of the measurements are shown in Table 1.

The low incidence rate observed in this study and the design of the experiment suggests the heritability estimate derived in this study of 0.39 ± 0.12 on the observed scale, and 0.28 ± 0.06 on the liability scale, was a conservative estimate of flystrike heritability in New Zealand dual purpose sheep. The high genetic and phenotypic correlation with dag score (Table 2) and significant positive genetic correlations with FDSD and FDCV, suggest these traits as potential indirect indicators for flystrike. Using individual records, indirect selection to reduce flystrike via reducing dagginess is expected to be approximately 54% as effective as selecting directly on the flystrike trait.

During model fitting, date at which flystrike occurred was highly significant, accounting for 39% of the variation. Including date at which flystrike occurred in a survival analysis would improve estimates, but may not be a practical trait to record under commercial conditions, hence it was not used in this analysis.

Conclusions

This study has indicated that it may be possible to genetically reduce the incidence of flystrike by selection. Flystrike has moderate heritability on the observed scale, and a high genetic and phenotypic correlation with dagginess under commercial conditions. Hence, it may also be possible to use dagginess as an indirect indicator for flystrike.

Further analysis on this dataset will include genotyping all lambs and sires through 5K and 50K Ovine SNPchips respectively. A genome wide association study will be performed to see if any genomic regions are significantly associated with flystrike.

Acknowledgements

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