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BRIEF COMMUNICATION: An update on genetic parameters for facial eczema tolerance in sheep

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Introduction

Facial Eczema (FE) is a metabolic disease resulting from liver and bile-duct damage, caused by ingestion of the mycotoxin sporidesmin A, found in the spores of the fungus *Pithomyces chartarum*. Risk of FE is associated with temperature, humidity and dead leaf matter (Mitchell et al. 1959; Brook 1963; Di Menna & Bailey 1973). While FE is predominantly prevalent in the North Island of New Zealand, climatic change projections indicate that there will be an increase in the geographical spread of the fungus and associated sporidesmin, resulting in FE spreading to regions that are currently unaffected (Dennis et al. 2014).

Clinical FE is characterised by photosensitisation due to liver injury; however, reduced production (Smith 2000) and reproduction (Moore et al. 1983; Mcmillan et al. 1988; Morris et al. 1991) is also observed in both clinically and sub-clinically affected animals. The heritability of liver damage at slaughter post-sporidesmin challenge was estimated to be 0.42 ± 0.09 (Campbell et al. 1981). In the live animal, serum gamma glutamyltransferase (GGT) collected 2 to 3 weeks after sporidesmin challenge can be used as a measure of liver damage (Towers & Stratton 1978). Romney FE selection lines, initially selected for resistance or susceptibility on the basis of liver damage, were established in 1975 (Campbell et al. 1981). The estimated heritability of serum GGT at 21 days after a measured sporidesmin challenge using data from these selection lines was 0.45 ± 0.03 (Morris et al. 1995). Genetic correlations between FE and production traits have also been estimated using these animals, with a significant, though small, negative genetic correlation between log GGT and yearling fleece weight (Morris et al. 1999).

In the mid-1980s a commercial testing programme (Ramguard) was developed, which allows ram breeders to generate breeding value estimates for tested and related animals, with GGT levels measured 21 days (GGT21) after a measured sporidesmin dose (Amyes & Hawkes 2014). The Ramguard service now has 60 clients dosing a total of 800 to 1,100 rams each year. This provided an opportunity to re-estimate genetic correlations of FE with production traits, using a larger multi-flock and breed dataset.

Materials and methods

The Ramguard dataset was used to re-estimate genetic parameters for FE tolerance. The dataset consisted of approximately 20,000 animals from 111 flocks, born between 1981 and 2014, which had been tested through the Ramguard programme. Data were obtained from Sheep Improvement Limited (SIL) for GGT levels 21 days after a measured sporidesmin challenge (GGT21), weaning weight (WWT), live weight at eight and 12 months (LW8 and LW12), and fleece weight at 12 months (FW12). The genetic correlation between tolerance to FE and reproduction traits (number of lambs born) was unable to be examined due to the low number of females with recorded GGT21 values (n = 599).

To be included in the analysis, flocks needed a minimum of 45 animals with recorded GGT21, and any given contemporary group (flock:year:sex:mob, where mob accounted for different dose rates) needed to contain at least four animals, and exhibit 30% animals with elevated GGT21 (GGT21 > 70). Animals with no recorded sire were also removed. The resulting dataset consisted of 14,081 animals with GGT21 records from 57 flocks (Table 1).

Table 1 Descriptive statistics for GGT levels at 21 days after challenge (GGT21), elevated GGT21 (GGT21 > 70, presented as a binary trait), weaning weight (WWT), live weight at 8 and 12 months (LW8 and LW12), and fleece weight at 12 months (FW12) in a subset of New Zealand sheep tested by the Ramguard service

| Trait | | Descriptive statistics | | Final model | |
	N	Mean ± SD	Range	Fixed effects[1]	Random effects
GGT21	14,081	244.3 ± 338.8	5 - 2286	cg	animal
Elevated GGT21	14,081	0.57 ± 0.5	0 - 1	cg	animal
WWT	13,366	32.1 ± 5.4	12.8 - 63.1	brr aod bdev cg	animal, maternal
LW8	10,639	44.8 ± 5.4	20.9 - 68.4	brr aod bdev cg	animal
LW12	5,859	51.5 ± 5.4	30.9 - 77.6	brr aod bdev cg	animal
FW12	9,008	3.7 ± 0.6	1.7 - 8.6	brr aod bdev cg	animal

[1]cg: contemporary group; brr: birth rearing rank; aod: age of dam; bdev: birth date deviation.

The majority of animals were purebred Romneys (63%), however the dataset also included Coopworth (11%) and Perendale (6%), and dual-purpose composite animals (15%), along with a small number of other breeds (5%).

Heritability of GGT21 was examined firstly using the reported values transformed by the natural log (log GGT21), and secondly reporting it as a binary (tolerant/susceptible) trait, so that animals with elevated GGT21 (GGT21 > 70) were categorised as susceptible. Data analysis models (Table 1) were as per those currently used for SIL analysis (S. A. Newman, pers. comm.). Variance and covariance components were estimated using restricted maximum likelihood (REML) procedures fitting an animal model using ASReml (Gilmour et al. 2009). Heritabilities were obtained by running univariate analyses on the respective traits, and genotypic and phenotypic correlations between log GGT21 and production traits were obtained by running bivariate analyses.

Results and discussion

Of the 14,081 animals with GGT21 records, 8,097 were classified as having elevated GGT. Table 2 presents the heritability estimates and genotypic and phenotypic correlations for the analysed traits. Heritability estimates (± standard error) for log GGT and elevated GGT (0/1) were 0.44 (± 0.03) and 0.28 (± 0.02) respectively. Heritability estimates for the production traits ranged between 0.18 and 0.38, with low standard errors. There were no significant genotypic or phenotypic correlations between log GGT21 and any of the production traits.

The reported heritability estimate of log GGT21 is comparable to those reported previously (Morris et al. 1995; Morris et al. 1999). While the dataset examined did include approximately 2,000 records from the FE selection lines, removing these animals only reduced the heritability of log transformed GGT21 to 0.42 (± 0.03). Both log-transformed and binary GGT21 heritability estimates are slightly higher than those reported in New Zealand dairy cattle (Cullen et al. 2011).

The lack of significant genetic correlations between log GGT and production traits indicate that selecting for FE resistance would not have a negative effect on either live weights or fleece weights. The estimates for the production traits were comparable to previously published genetic parameters for New Zealand dual-purpose sheep (Pickering et al. 2012), but lower than those published by Morris et al. (1999). As expected, genetic correlations between production traits were positive, and ranged from low, between weaning weight and fleece weight at 12 months, to high, between live weight at 8 and 12 months. The previously reported negative genetic correlation (-0.16 ± 0.07) between fleece weight at 12 months of age and log GGT (Morris et al. 1999) was not replicated in this analysis. The current study uses a larger dataset from multiple flocks, as opposed to a small sampling of animals from a selection-line research flock, which probably accounts for the observed differences. Morris et al. (1999) found that in the FE-selection line animals, resistant lambs were significantly lighter than susceptible lambs at weaning and four months of age, but that there was no significant difference between the lines at seven or 13 months of age. Resistant animals also produced heavier fleeces than their susceptible counterparts, although these differences were not reflected in the genetic correlations in that study.

Using the current dataset, the genetic correlation between tolerance to FE and reproduction traits (number of lambs born) was unable to be examined. To examine these parameters, the current dataset would need to be expanded to include records from the progeny of animals with GGT21 records. Morris et al. (1999) reported no significant difference in ewe reproduction between the resistant and susceptible selection-line animals, however, they did observe a major difference in ram fertility. Ram fertility is not routinely measured by flocks in which the current dataset was generated, and therefore, the relationship between GGT21 and ram fertility could not be examined in this study.

This dataset is now also being used in-conjunction with genomic data to identify genomic regions controlling tolerance to FE and produce genomic breeding values (gBVs). Initial results of this work have been reported by Phua et al. (2014).

Conclusions

This study utilises a large industry dataset to re-estimate genetic parameters for FE tolerance. The heritability of log GGT was estimated to be 0.44 ± 0.03. There were no significant genotypic or phenotypic correlations between log GGT21 and any of the production traits.

Table 2 Estimates of heritability (diagonal, in bold), genetic (below diagonal) and phenotypic (above diagonal) correlations (± standard errors), and residual standard deviations (RSD) for log GGT21, weaning weight (WWT), live weight at 8 and 12 months of age (LW8, LW12), and fleece weight at 12 months of age (FW12) in New Zealand sheep (n = 14,081) tested by the Ramguard service

Trait	log GGT21	WWT	LW8	LW12	FW12
log GGT21	**0.44 ± 0.03**	0.03 ± 0.02	0.03 ± 0.01	-0.02 ± 0.02	0.01 ± 0.01
WWT	0.00 ± 0.05	**0.18 ± 0.02**	0.62 ± 0.01	0.45 ± 0.01	0.12 ± 0.01
LW8	0.08 ± 0.05	0.79 ± 0.03	**0.38 ± 0.02**	0.64 ± 0.01	0.32 ± 0.01
LW12	0.02 ± 0.07	0.57 ± 0.05	0.69 ± 0.04	**0.38 ± 0.03**	0.38 ± 0.01
FW12	0.09 ± 0.05	0.15 ± 0.06	0.32 ± 0.05	0.37 ± 0.06	**0.38 ± 0.03**
RSD	0.16	0.63	0.68	0.81	0.81

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