GENETIC VARIATION IN SUSCEPTIBILITY TO FACIAL ECZEMA IN DAIRY CATTLE IN NEW ZEALAND

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SUMMARY

Facial eczema is a disease of ruminant animals, caused by a fungal toxin that grows on pastures and causes liver damage. The objective of this study was to investigate the genetic variation for susceptibility to facial eczema (FE) in dairy cattle using phenotypes collected under on-farm conditions. Weekly vat milk samples from progeny test herds were monitored for a marker of liver damage, to identify when to blood sample cows in the herd. Gamma-glutamyltransferase (GGT) enzyme concentrations in blood were used as the proxy to measure response to the fungal toxin on the animals. Log transformation (logGGT) and Box-Cox transformation (boxGGT) were applied to GGT before running the genetic analysis. The highest heritability found was for the logGGT (0.26). Genetic correlations between logGGT and production traits were all weak and positive, ranging from 0.02 to 0.12 indicating that, the trait is almost independent from production and selection for tolerance to FE could be performed without compromising milk production. The moderate heritability for logGGT indicates that 26% of the total variation of tolerance to FE among animals was attributable to genetic variance breeding values for this trait could be predicted with accuracy, enabling the identification of sires with tolerance to FE to be used in the breeding program in dairy cattle in New Zealand.

INTRODUCTION

Facial eczema (FE) is caused by the ingestion of the spores of the fungus *Psuedopithomyces chartarum* (Di Menna *et al*. 2009; Ariyawansa *et al*. 2015). The mycotoxin sporidesmin A causes damage to the liver (Smith and Towers 2002). Affected animals have reduced milk production (Mason *et al*. 2022); the worst affected animals may die or require euthanasia. Diagnosis of FE is typically via measurement of gamma glutymyltransferase (GGT) in the serum (Towers and Stratton 1978). The disease has been reported in grazing systems in Australia, South Africa, Brazil and parts of Europe (Di Menna *et al*. 2009). FE has traditionally been a problem on farms located in the North Island of New Zealand.

Genetic variation in susceptibility to sporidesmin has been demonstrated in sheep and cattle (Mcrae *et al*. 2016; Morris *et al*. 2013). In sheep, the Ramguard programme, dosing rams with sporidesmin and measuring the GGT response, is used to identify resistant sires (Amyes *et al.* 2018). However, this is not feasible for dairy sires with greater value than an individual ram. Nor acceptable to public. Previous research in cattle has demonstrated that blood sampling herds that have experienced a 'natural challenge' can be used to gather data for the estimation of genetic parameters. However, given the primarily subclinical nature of the disease, it is not easy to identify herds that have been exposed. A biomarker that can be used to screen herds that have liver damage has been identified. The aim of this work was to use the biomarker as a screening technique to identify herds where there has been a natural FE challenge and confirm that these phenotypes can be used to estimate genetic parameters.

MATERIALS AND METHODS

This work was carried out with the approval of the AgResearch Animal Ethics Committee, approval numbers 15236 and 15576. Herds were identified via screening the bulk tank milk for what, or by veterinarians volunteering herds for the study. Blood samples were collected from 9,866 animals from 34 commercial dairy herds that were naturally challenged by FE between April 2021

and May 2022. Tolerance to FE was evaluated based on gamma-glutamyltransferase (GGT) enzyme concentrations in blood as evidence of liver damage caused by sporidesmin. Genetic analysis in the present study applied to the raw GGT measurements, log-transformed GGT (logGGT) and Box-Cox transformed GGT (boxGGT) (Box and Cox 1964).

To estimate the genetic correlations between tolerance to FE and production traits, average first lactation 305-d test days yield deviations for milk, fat, and protein were extracted from the animal evaluation database after adjusting for the lactation stage included in the analysis. Descriptive statistics of each trait are summarised in Table 1.

Table 1: Mean, standard deviation, minimum, and maximum of all traits in the present study

Trait	Mean	SD	Min	Max
GGT (IU/L)	402.5	831.26	2.0	5352
logGGT (IU/L)	3.98	2.066	0.69	8.59
boxGGT	2.88	1.13	0.66	4.97
Milk (litre)	12.5	3.49	2.99	34.12
Fat (kg)	6.16	1.48	0.88	12.48
Protein (kg)	4.96	1.26	1.27	14.95

Genetic analyses were performed with AI-REML algorithm in ASReml-R v4 statistical package (Butler *et al*. 2017). A univariate animal model was performed to estimate variance components and heritability for each trait separately, whereas bivariate model was performed to estimate genetic correlations among traits. The following animal model was used for the analysis:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e},$$

where **y** is the vector of phenotypes, **X** is the matrix relating fixed effects to phenotypes, **b** is the vector of fixed effects, **Z** is the matrix relating phenotypes to animals, and **a** is the polygenic random additive genetic effect which was assumed to be normally distributed following var(a) ~N(0, Aσ_a^2), where σ_a^2 is the additive genetic variance and A is the average numerator relationship matrix (Wright 1922), and e is the vector of random residual, ~ND (0, I σ_e^2), where I is the identity matrix and σ_e^2 is the residual variance. The fixed effects in the model include cow age category, contemporary groups (herd-year-month of blood sampling), cow breed proportions (proportion of cow's breed ancestry that was Jersey, Holstein, Friesian, Ayrshire), heterosis effects (Friesian × Jersey, Jersey × Ayrshire, Jersey × Holstein) and cow's inbreeding coefficients. The genetic correlations between traits (r_a) were estimated as: $r_a = \frac{\sigma_{a_1 a_2}}{\sqrt{\sigma_{a_1}^2 \sigma_{a_2}^2}}$where $\sigma_{a_1 a_2}$ is the additive genetic covariance among traits; and $\sigma_{a_1}^2$ and $\sigma_{a_2}^2$ are the additive genetic variances.

RESULTS AND DISCUSSION

The laboratory defined 'adequate' range for GGT is 3-47 IU/L (Gribbles Veterinary, Hamilton). Herds that were sampled had elevated GGT concentrations, averaging 402.5 IU/L across all herds sampled, indicative of liver damage. Figure 1 shows the difference of distribution between raw GGT, logGGT and boxGGT. Both logGGT and boxGGT were able to remove the skewness of the raw data so the distribution was more suitable for genetic analysis.

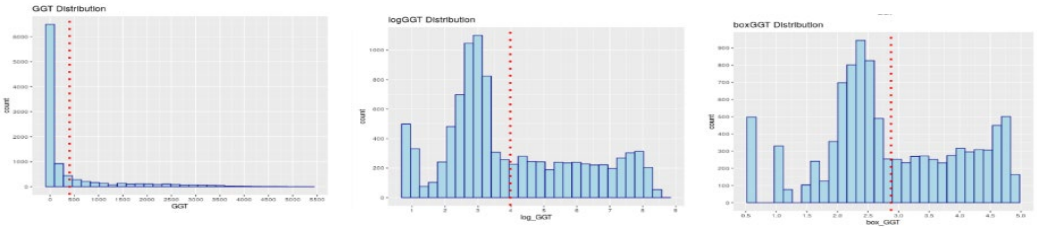

Figure 1. Distribution of raw GGT, logGGT, and boxGGT from cow blood samples with the mean represented in the dotted red line

Figure 2 shows associations between each of age (years) and breed and GGT. Average serum GGT concentrations were highest for 3-year old animals (515.6 IU/litre), and lowest for 10-year old animals (278 IU/litre) indicating that younger animals are more susceptible to FE. Holsteins and Jerseys had similar average serum GGT concentrations (approximately 48x IU/litre for each breed), but crossbred animals (Holstein x Jersey) had lower GGT (363.9 IU/litre), suggesting a possible heterosis effect on tolerance to FE.

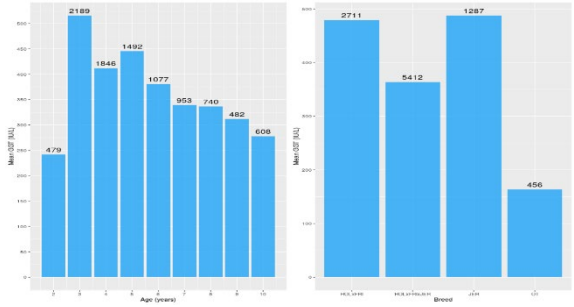

Figure 2. Associations between each of age and breed and raw GGT presented as means with the number of observations in each class annotated above the bars

Variance components and genetic parameter estimates. Variance components and heritability estimates for GGT, logGGT and boxGGT are presented in Table 2. The highest heritability estimate was for the logGGT (0.26). The raw GGT had the lowest heritability estimate (0.15). The heritability estimate for logGGT was slightly lower than previously reported heritability estimates in dairy cattle in New Zealand (Cullen *et al*. 2011; Morris *et al*. 1990; Morris *et al*. 1998), which ranged from 0.29 to 0.34. The moderate heritability for logGGT indicates that selection for tolerance to FE is possible in dairy cattle after a natural challenge from infected pasture.

Table 2. Variance components and heritability estimates with their standard errors between parentheses for raw GGT, logGGT and boxGGT

Trait	σ_a^2	σ_e^2	h^2
GGT	72026.05	408747	0.15 (0.02)
logGGT	0.76	2.21	0.26 (0.03)
boxGGT	0.24	0.70	0.25 (0.03)

Estimates of genetic correlations between production traits and logGGT are shown in Table 3. Genetic correlations between logGGT and production traits were generally weak, and positively correlated for all traits ranging from 0.02 ± 0.03 (fat) to 0.12 ± 0.03 (volume). Morris *et al*. (1990),

reported opposite results where the genetic correlations between logGGT and production were negative in Jersey cattle in New Zealand. The positive genetic correlations in the current study were unfavourable when selecting for tolerance to FE, given that the goal is to reduce logGGT. However, the estimate for fat was close to zero. Furthermore, for milk, volume and protein, these weak genetic correlations indicate that logGGT is almost independent of production traits and one could select for tolerance to FE without compromising milk production.

Table 3. **Estimates of genetic correlations (r_g) between logGGT and production traits, with their standard errors between parentheses**

Trait	r_g
Milk volume	0.12 (0.03)
Milk fat	0.03 (0.03)
Milk protein	0.09 (0.03)

CONCLUSIONS

Bulk milk screening for the biomarker was able to identify herds with elevated GGT in individual animals. Tolerance to FE in naturally challenged dairy herds is moderately heritable and genetic gain would be expected with selection for improved tolerance to FE. The genetic correlations between tolerance to FE and production traits are weak, indicating that FE tolerance is almost independent of production and selection for sires with tolerance to FE is possible without affecting milk production.

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