Heritability and repeatability of resistance to nematode parasites in commercial beef cattle

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Abstract

Faecal egg count (FEC) is used commonly as a guide to nematode parasite burdens in animals *in vivo*. The objective of this study was to estimate the heritability and repeatability of FEC in commercial beef calves, along with breeding values for FEC in the calves and their sires, for future quantitative and molecular analyses. In 2008–2011, faecal samples from 4,621 weaned beef calves were obtained for FEC1 from 11 herds (mainly Angus or Hereford). FEC1 represented the first sample after weaning (generally between May and July); a second sample (for FEC2) was taken by September from all calves in some herds, with FEC1 and FEC2 samplings separated by an effective anthelmintic drench. Calves were sired by a total of 325 and 57 separate Angus and Hereford sires, respectively. Heritability estimates for $\log_e$(FEC+50) in Angus at Times 1 and 2 were 0.28 ± 0.05 (standard error) and 0.11 ± 0.09, respectively, with a genetic correlation of 0.89 ± 0.22 between them. Treating FEC1 and FEC2 as repeated measurements of the same trait, the repeatability estimate for $\log_e$(FEC+50) was 0.38 ± 0.04. The parameters estimated for $\log_e$(FEC+50) in weaned beef calves under commercial grazing conditions were similar to those from experimental beef calves.

Keywords: resistance; nematode; parasite; phenotyping; cattle

Introduction

Nematode parasitism is a major problem in young growing cattle in New Zealand before natural immunity develops (Bisset, 1994). If left untreated, it can result in poor production or even death. Using effective anthelmintic drenches may be a short-term solution to parasite control. However, one of the longer-term solutions is to breed nematode-resistant animals. The New Zealand beef cattle industry requires details on how this may be achieved.

Faecal egg count (FEC) is used commonly as a guide to nematode parasite burdens in animals *in vivo*. Host resistance to nematode parasites under pasture challenge , that is a low FEC level, is known to be a heritable trait in sheep (Morris et al. 1997), and a breeding approach has generated lines of sheep which are more resistant than the controls (Morris et al. 2000). We have demonstrated that FEC is heritable in beef calves managed under experimental conditions, and genetic variation in FEC is detectable under those conditions (Morris et al. 2003). However, questions remain about the practicality of sampling weaned beef calves for FEC in commercial herds, at a time when variation in FEC can still be observed. A one-generation experiment on a commercial property in Australia, where sires were phenotypically selected for a lower mean FEC, has demonstrated that genetic selection can achieve a lower FEC in progeny (Esdale et al. 1986).

Animal-to-animal variation in nematode parasite resistance is an expensive characteristic to estimate, because of animal-sampling costs and sample-measuring costs. A more convenient method of ranking animals for host resistance to nematode parasites, such as a DNA test, could be useful to bull breeders. To find such a test, a three-year Ministry of Agriculture and Forestry (MAF)-funded 'Sustainable Farming Fund' study was carried out to evaluate FEC data in beef calves under commercial conditions, for future quantitative and molecular analyses. FEC phenotypes and DNA samples were obtained in the MAF study. This report summarises the quantitative FEC data from weaned beef calves grazing under commercial conditions, including estimates of heritability and repeatability.

Materials and methods

Ethics

Faecal and blood sample collections for this study were carried out with the approval of the Ruakura Animal Ethics Committee, Hamilton, New Zealand.

Animals

The objective was to collect faecal samples for FEC from spring-born beef calves after weaning, but before the calves became naturally immune. The window of opportunity was generally from about seven to 14+ months of age, except for periods of three to four weeks after any effective anthelmintic drench treatment. The window was compromised, and reduced, if any grazing group, or mob, was moved onto crop for part of their winter feeding period. In order to determine whether any mob was parasitised to a level suitable for phenotyping by faecal sampling and FEC counting, a random subgroup of at least six animals per mob was faecal-sampled and a mean FEC determined for the sampled animals. If the monitor group mean FEC reached a threshold, generally >150 eggs/g and preferably 300–400 eggs/g, all calves in the mob were faecal-sampled. In this paper the term 'FEC1' refers to the first occasion after weaning when all the calves in a mob were faecal-sampled. In some

mobs, there was also an opportunity to collect a second faecal sample from all animals later in the season. This is termed 'FEC2'. Collection of this second sample depended on labour availability and access by the calves to pasture rather than crop. In order that independent samples were obtained from the same individuals, the trial design was that FEC1 and FEC2 were separated in time by at least one effective anthelmintic drench per animal. Calves were also blood-sampled once post-weaning for future DNA analyses.

It was generally believed in the beef industry that if a monitor group-mean FEC for weaned calves exceeded 100-150 eggs/g, the whole mob needed a drench. In order to investigate this belief, the relationship was tested here between the actual mean FEC1 for all animals in a mob and the percentage of the mob having a phenotype of zero eggs/g. For phenotypes of zero, a distinction needs to be made, particularly for genetic analyses, between a resistant animal and one which is zero because it has not experienced a sufficient parasitic challenge.

Parasite analyses

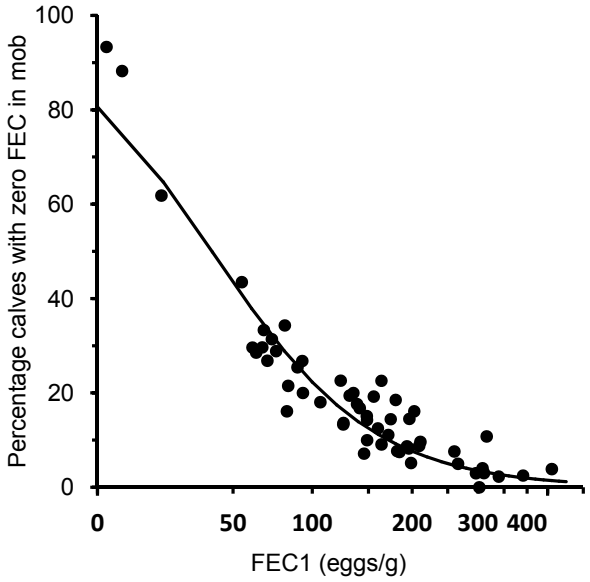
Nematode eggs were counted for FEC in faecal samples by a modified McMaster technique, in which each egg counted represented 50 eggs per g of faeces (Whitlock 1948).

Bulked faecal cultures were taken from all FEC-positive animals in five calf mobs, sourced from three herds, and incubated at 27°C for seven to ten days, to assess the composition of nematode genera present. The resulting larvae were identified, mainly by genus, as *Haemonchus*, *Teladorsagia*, *Trichostrongylus*, *Cooperia oncophora*, *Cooperia* short-tailed larvae, *Oesophagostomum*/*Chabertia*, other strongyles, and *Nematodirus.*

Data analyses

All FEC data were transformed to logarithms as $\log_e$(FEC+50), to approximate a normal distribution. Using FEC1 data (n=4,621, over all breeds), the unadjusted mean $\log_e$(FEC1+50) of each mob was plotted against the percentage of animals with a phenotype of zero eggs/g. Thereafter, minimal thresholds of 150 and 250 eggs/g were used to select mobs of data for analysis. As much pedigree information as possible was obtained on all animals sampled, and on their sires. A SAS (1995) statistical package was applied to $\log_e$(FEC+50) to find the most appropriate model for genetic analyses by breed, examining fixed effects for mob and calf sire, and age of calf as a covariate expressed as a deviation from the contemporary group. Restricted maximum likelihood (REML) procedures (Gilmour et al. 2009) were then employed with the above fixed effects, to obtain repeatability and heritability estimates, with a full pedigree matrix and a repeated-animal model. The calf's sire was excluded from the fixed effects in the REML analyses because sire was accounted for in the pedigree matrix.

Figure 1 Effects of size of measured parasite challenge (FEC1, eggs/g) on percentage of Angus calves per management group (mob) with zero faecal egg count (FEC).



Results

Parasite genera present

The genera in this study observed from larval bulk cultures were predominantly *Cooperia*. On average they comprised 73% of the worms in culture. They were followed by *Teladorsagia* at 16%. Other minor species found included: *Cooperia* (short tails), *Oesophagostomum*/ *Chabertia*, *Haemonchus.*

Lower threshold for analysis

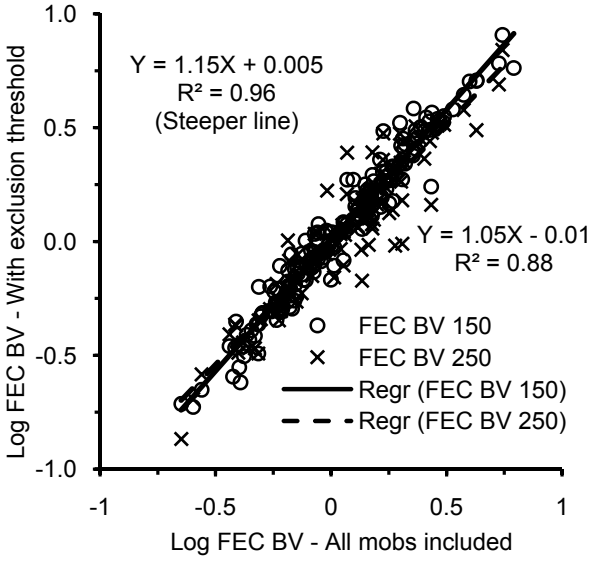
Firstly an acceptable lower limit was sought for the mean FEC1 in a mob. Fig. 1 shows the relationship for weaned Angus calves, between mean $\log_e$(FEC1+50) of the mob, and the percentage of animals in the mob with a FEC1 phenotype of zero. The equation was described by:

$$Y = 100 / (1 + \exp(2.43 (X - 4.50)))$$

so that an increasing mean FEC1 was associated with a reducing percentage of animals in the mob with a FEC1 phenotype of zero. From the equation, means of 150 and 250 eggs/g were equivalent to expectations of 12% and 5% animals with a zero egg count, respectively.

To find an acceptable value of 'X' when sire summaries are required, Fig. 2 shows the relationship between sire means when all sampled progeny of the sire group were included, or only restricted mobs with means >150 eggs/g or > 250 eggs/g. At a threshold of 150 eggs/g, compared with all records included, the R^2 value was slightly reduced to 0.96, whereas many progeny records were lost at 250 eggs/g, leading to an R^2 value of 0.88 and a trade-off between progeny numbers and sire accuracy. A threshold of 150 eggs/g was selected for the sire summaries from the present data.

Figure 2 Breeding values for $\log_e$ (Faecal egg count, FEC) for Angus sires, in $\log_e$ eggs/g. Estimates for all mobs are plotted against estimates where management groups (mobs) with average counts of < 150 or < 250 eggs/g have been excluded.



Parameter estimates

The phenotypic standard deviation for $\log_e$ (FEC+50) was 0.84 $\log_e$ eggs/g. Table 1 shows the parameter estimates for $\log_e$ faecal egg count in Angus and Hereford cattle. Results are presented using either all FEC1 data or a restricted data set for the more numerous (Angus) data where minimal mean-FEC1 thresholds of 150 and 250 eggs/g were applied. That is mobs were selected whose mean $\log_e$ (FEC+50) was > 5.01 or > 5.52 $\log_e$ units. Maximal FEC1 counts per herd (eggs/g) in the Angus cattle were: 2007 calf crop (3 herds) 1,400–1,600; 2008 crop (8 herds) 450–2,550; 2009 crop (4 herds) 1,400–4,000; 2010 crop (4 herds) 1,400–3,900. Heritability estimates for log-transformed data are given for FEC1 and FEC2 samples. Repeatabilities were estimated for $\log_e$(FEC+50), given that FEC1 and FEC2 were independent samples of the same trait per animal. The standard errors of these estimates increased as the restriction reduced the numbers of qualifying records. The genetic correlation between log(FEC1+50) and log(FEC2+50) was 0.89 ± 0.22.

Discussion

The larval bulk culture data, where *Cooperia* and *Teladorsagia* were the predominant genera, were consistent with other publications on cattle parasites (Brunsdon 1964; Morris et al. 2003).

As the mean FEC for a mob increased, the percentage of contemporaries with a phenotype of zero declined (Fig. 1). This led to increasing confidence that a zero phenotype was a measured value for an animal, indicating the ability to discriminate FEC phenotypes among animals, rather than being evidence that the mob had failed to receive sufficient parasitic challenge. There was a compromise required between waiting for mean FEC to rise after weaning, and losing mobs by turning weaned calves onto a crop.

In Table 1, the parameter estimates appear to decline from the first to second sampling time. A shift over time in the nematode species could provide an explanation, but it is possible that a small number of animals sampled for FEC2 had reached immune status by that sampling time. This would have affected genetic parameter estimates particularly in numerically small progeny groups.

This study provided the opportunity to assess commercial sires for genetic merit for resistance (Fig. 2), at a range of lower FEC means. However, there was a trade-off between the restriction and the number of records remaining. A restriction of mobs with a mean of at least 150 eggs/g was chosen for the present analysis. The heritability estimates (Table 1) for transformed values of FEC1 and FEC2 were very similar to those found in sheep (Morris et al. 1997; Morris et al. 2000), and to those reported for cattle from experimental progeny (Morris et al. 2003) where low mob means were not a restriction.

Finally, the data provided an opportunity to estimate the repeatability of FEC, on the assumption that a similar trait was being measured over winter (FEC1) or early in the following spring (FEC2). Repeatability estimates were at least 0.34 (Table 1), and extended to an upper value of 0.47, with a greater standard error, when restrictions were placed on numbers of animals in a mob with zero FEC. Heritability estimates for FEC were similar in these commercial beef cattle and in experimental herds which have been investigated. The cattle data are similar to those from sheep. It is concluded that there

Table 1. Number of calves sampled, and heritability and repeatability estimates of $\log_e$(FEC + 50) assuming that FEC1 and FEC2 are the same trait sampled at different times, by breed and management group (mob), above different lower thresholds.

Breed	Restriction	Number of FEC1 records	Heritability ± standard error		Repeatability
			FEC1	FEC2	
Angus	None	4,022	0.24 ± 0.04	0.16 ± 0.09	0.34 ± 0.03
	Mobs > 150 eggs/g	3,001	0.28 ± 0.05	0.11 ± 0.09	0.38 ± 0.04
	Mobs > 250 eggs/g	1,786	0.35 ± 0.08	0.34 ± 0.16	0.47 ± 0.05
Hereford	None	599	0.17 ± 0.09	-	-

is sufficient measureable genetic variation to select for reduced FEC in commercial beef cattle, if required.

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