



A stochastic model accommodating the FAMACHA[®] system for estimating worm burdens and associated risk factors in sheep naturally infected with *Haemonchus contortus*

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ABSTRACT

A previously developed multiple regression algorithm was used as the basis of a stochastic model to simulate worm burdens in sheep naturally infected with *Haemonchus contortus* over five consecutive *Haemonchus* seasons (November to January/February) on a farm in the summer rainfall region in South Africa, although only one season is discussed. The algorithm associates haemoglobin levels with worm counts in individual animals. Variables were represented by distributions based on FAMACHA[®] scores and body weights of sheep, and Monte Carlo sampling was used to simulate worm burdens. Under conditions of high disease risk, defined as the sampling event during the worm season with the lowest relative mean haemoglobin level for a class of sheep, the model provided a distribution function for mean class *H. contortus* burdens and the probability of these occurring.

A mean *H. contortus* burden for ewes ($n = 130$ per sample) of approximately 1000 (range 51–28,768) and 2933 (range 78–44,175) for rams ($n = 120$ per sample) was predicted under these conditions. At the beginning of the worm season when the risk of disease was lowest (i.e. when both classes had their highest estimated mean haemoglobin levels), a mean worm burden of 525 (range 39–4910) for ewes and 651 (range 37–17,260) for rams was predicted. Model indications were that despite being selectively drenched according to FAMACHA[®] evaluation, 72% of the ewes would maintain their mean worm burden below an arbitrarily selected threshold of 1000 even when risk of disease was at its highest. In contrast, far fewer rams (27%) remained below this threshold, especially towards the end of the worm season.

The model was most sensitive to changes in haemoglobin value, and thus by extrapolation, the haematocrit, which is used as the gold standard for validating the FAMACHA[®] system. The mean class haemoglobin level at which there was a 50% probability of worm burdens being ≤ 1000 worms was 7.05 g/dl in ewes and 7.92 g/dl in rams.

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1. Introduction

Severe anthelmintic resistance in South Africa and elsewhere led a team of South African scientists to lay the basis for application of the principle of Targeted Selective Treatment (TST) (Malan and Van Wyk, 1992), from which

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the FAMACHA[®] system of clinical evaluation of haemonchosis was developed. The system is based on classification of the colour of the conjunctival mucous membranes of sheep and goats against a dedicated colour chart in order to identify and treat only those animals which are unable to manage unaided (i.e., without anthelmintic treatment) under severe *Haemonchus* challenge (Bath et al., 1996). While this system has potential for application under field conditions (Van Wyk and Bath, 2002), at present, labour input requirements and complexity in the face of dwindling numbers of knowledgeable advisors are serious limiting factors. This paper is part of a multi-faceted approach aimed eventually at addressing these limitations through an automated, computerised decision support system (Van Wyk and Reynecke, 2011). Risk analysis is a crucial component of this initiative, with the emphasis on, but not restricted to, stepwise retrospective analysis of clinical data collected through various methods of applying TST, for instance the FAMACHA[®] clinical test for anaemia.

Because most predictive models are at best representative of only a part of the whole system (Dobson, 1999), it is important that they should have as few assumptions about the system as possible. On the other hand, it is well accepted that it is not necessary to have complete knowledge of a system in order to develop a model that can be used to answer worthwhile questions about the system (Smith, 1994), and computer models relating parasite populations to anthelmintic resistance have effectively contradicted many of the recommendations of most conventional worm control programmes, such as routinely to drench all animals, and periodically to rotate anthelmintic classes. For example, a model by Barnes et al. (1995) indicated that irrespective of the drug rotation strategy, the endpoint, i.e. intractable resistance to each drug, would be reached more or less simultaneously whether two drugs are rotated or used in series. Their model also indicated that non-treatment of a few animals in order to preserve susceptible worms would delay selection for resistance, as has subsequently been supported by various field studies (Kenyon et al., 2009; Leathwick et al., 2006; Greer et al., 2009; Waghorn et al., 2008, 2009).

Learmount et al. (2006) developed a computer model for the United Kingdom to simulate expected egg counts (and therefore predict the timing of expected peaks in faecal egg counts) for a variety of inputs including regional weather data, stocking density, initial pasture contamination levels, parasite species proportions, as well as lambing dates, the timing of flock movements and removal of lambs. However, because the FAMACHA[®] system is effectively a test of the anaemia status of animals, and requires furthermore that the animals be evaluated often during the peak worm season (Van Wyk and Bath, 2002), data such as anaemia status and associated environmental risk factors such as rainfall and temperature are readily and frequently available directly from the point of exposure. Furthermore, the approach taken by Learmount et al. (2006) would be difficult to implement under climatic conditions in most of South Africa, where rainfall is much more limiting to this species than temperature.

With stochastic risk assessment models such as the one described in this work, inputs are in the form of mathematical distribution functions representing a pre-determined range of values, rather than a single value such as is commonly found in deterministic models (Vose, 1998, 2000), and as such they describe a continuous range of potential values that could occur according to the information known about the input parameter. Monte Carlo simulation allows the random sampling of values from within the defined input distribution functions and this occurs each time the model is run (i.e. for each iteration). The output of the model is thus also a distribution function representing the possible results that could occur and the probability of a given value occurring (Vose, 2000).

In the present work, a previously published deterministic linear regression algorithm (Roberts and Swan, 1982) was used as the basis of a stochastic simulation model, since it is based on the use of red cell parameters and body weight to estimate worm burdens in sheep. The aims of the present study were (1) to determine if the model output (i.e. the distribution for worm count in a given class of sheep) could be validated against the observed trend in FAMACHA[®] proportions and the attendant variability in body weight of sheep through a given worm season; (2) to estimate flock haemoglobin values which would have to be maintained by selective drenching in order to maintain the flock worm burden below a selected pathogenic worm threshold; and (3) to determine if the model would predict differential susceptibility to worm infection between the two classes of hoggets (namely young replacement ewes and rams) in the study.

2. Materials and methods

2.1. Origin of data

The series of trials, as well as the data used to develop the model, and the FAMACHA[®] testing procedures have been described more fully in Reynecke et al. (2011a) and Riley and Van Wyk (2009). The trials formed part of a series of trials on what was designated Farm 1 by Van Wyk (2008) and Reynecke et al. (2011a,b) to validate the FAMACHA[®] system, and to estimate heritability (Bisset et al., 2001; Riley and Van Wyk, 2009). Sampling occurred over five successive *Haemonchus* seasons and involved different groups of two classes of sheep, namely approximately 130 and 200 per season respectively of young replacement ewes (EWEREP), which annually replaced aging ewes in the flock, and rams of similar age (RAMREP). Although ten data sets comprising five each for the EWEREP and RAMREP classes of sheep over five consecutive *Haemonchus* seasons were analysed, the similarity of the results between years led to the analyses for only one of the sets being discussed in detail in this study.

2.2. Model system

A multiple regression equation (Roberts and Swan, 1982) was used to estimate the risk of haemonchosis. It allows the estimation of the worm burden of an animal by taking its haemoglobin level and body weight into account

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