Contents lists available at ScienceDirect



Environmental Toxicology and Pharmacology

journal homepage: www.elsevier.com/locate/etap

Modelling the impact of targeted anthelmintic treatment of cattle on dung fauna



Andrew S. Cooke^{a,c}, Eric R. Morgan^{a,b}, Jennifer A.J. Dungait^{c,*}

^a School of Veterinary Sciences, University of Bristol, Bristol Life Sciences Building, 24 Tyndall Avenue, Bristol, BS8 1TQ, United Kingdom

^b Institute for Global Food Security, Queen's University Belfast, University Road, Belfast, BT7 1NN, United Kingdom

^c Sustainable Agriculture Sciences, Rothamsted Research, North Wyke, Okehampton, Devon, EX20 2SB, United Kingdom

ARTICLE INFO

Keywords: Anthelmintic resistance Helminth Antiparasitic Targeted selective treatment Refugia Agriculture Environment

ABSTRACT

The insecticidal properties of many anthelmintics pose a risk to dung fauna through the effects of drug residues in dung on the activity, oviposition and development of dung-dwelling invertebrates. Reductions in dung fauna numbers can inhibit dung degradation, which may impact biodiversity and nutrient cycling on farms. A simulation model was created to predict the impact of antiparasitic drugs on cattle dung fauna, and calibrated using published data on the dung-breeding fly *Scathophaga stercoraria*. This model was then tested under different effective dung drug concentrations (EC) and proportions of treated cattle (PT) to determine the impact under different application regimens. EC accounted for 12.9% of the observed variation in *S. stercoraria* population size, whilst PT accounted for 54.9%. The model outputs indicate that the tendency within veterinary medicine for targeted selective treatments (TST), in order to attenuate selection for drug resistance in parasite populations, will decrease the negative impacts of treatments on dung fauna populations by providing population refugia. This provides novel evidence for the benefits of TST regimens on local food webs, relative to whole-herd treatments. The model outputs were used to create a risk graph for stakeholders to use to estimate risk of anthelminthic toxicity to dung fauna.

1. Introduction

Anthelmintic drugs are widely and routinely administered to grazing livestock to control gastrointestinal nematodes and other parasites. Anthelmintics are typically not fully metabolized within the host animal and residues of the drugs are often excreted in dung (McKellar et al., 1993) (and urine (McKellar, 1997)) and can therefore exert non-target effects on invertebrate fauna which spend part, or all, of their life cycle in dung (Floate, 1998a, 1998b; Gover and Strong, 1995; Madsen et al., 1990; Sommer et al., 1992; Sutton et al., 2014) and also on soil invertebrates (Scheffczyk et al., 2016). Such effects include inhibited motility, oviposition, emergence, and reduced dung pat colonisation (Floate, 1998a, 1998b; Gover and Strong, 1995; Suarez et al., 2003). Invertebrate dung fauna significantly contribute to the degradation of dung through physical processes and therefore reductions in the activity and populations of degradative fauna can to slow dung degradation (Madsen et al., 1990; Wall and Strong, 1987) with potential knock-on effects on important local processes., including local ecology (Beynon, 2012; Strong, 1993; et al., 2012; Wall and Beynon, 2012) and epidemiology. In recent years, the mounting resistance of gastrointestinal parasites of domestic livestock to anthelmintic drugs has led to a shift away from whole-herd treatments, and recommendations for targeted selected treatment (TST) (Charlier et al., 2014) of only part of the herd. This strategy aims to generate refugia from drug exposure among parasite populations, slowing the development of resistance. In principle, refugia from drug residues ought also to be generated for dung fauna, supporting their populations; however, to date no systematic attempts have been made to evaluate this possibility.

The ability to assess and predict the impact of anthelmintics and other routine veterinary medicines on the wider environment is essential for informed drug development and policy in agriculture. In particular, parasite control practices that slow the development of resistance to commonly administered anthelmintics are essential to sustainable livestock production systems. However, the scale and complexity of the drug-dung-fauna system is challenging to observe and quantify *in vivo* and is difficult to fully represent under controlled laboratory conditions. Modelling techniques are the best alternatives to address these issues by allowing for the manipulation of a wide range of variables specific to individual field scenarios, and rapid assessments of the potential impacts of new parasite control and other management

* Corresponding author.

E-mail address: jennifer.dungait@rothamsted.ac.uk (J.A.J. Dungait).

http://dx.doi.org/10.1016/j.etap.2017.07.012

Received 3 July 2017; Received in revised form 22 July 2017; Accepted 24 July 2017 Available online 07 August 2017

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practices on dung fauna. Boxall et al. (2007) developed a screening index for assessing the impact of veterinary medicines on dung flies. The index was simple and allowed for estimates to be calculated with relatively small amounts of data, allowing for rapid screening of multiple drugs. The index assessed impact by multiplying three variables: proportion of cattle treated, proportion of time of faunal contact with dung, and dung toxicity. A central assumption was that the three variables are equally weighted, but this assumption inadvertently creates a potential mathematical ceiling to drug toxicity. Vale and Grant (2002) took a different approach in their development of a model to assess the impact of insecticide-contaminated dung on dung fauna. The model considered a broad and novel range of variables including the response to distinct adverse ecological events on insect life cycle stages and dung-insect interactions which aided the understanding of the importance of refugia for the ecology different species of invertebrates.

Here, we test the hypothesis that the proportion of cattle treated (PT) with anthelmintics has a greater influence on *Scathophaga stercoraria* populations than the strength of drug residue in dung (EC). We build on previous theoretical and modelling approaches to create a new modelling approach to simulate the drug-dung-fauna system and evaluate the potential impacts of antiparasitic drug use in grazed cattle production systems. We use the model to consider how varying treatment regimens administered by veterinarians for the purpose of livestock health and welfare have non-target influences on dung invertebrates, and to provide a risk graph to inform stakeholders in sustainable livestock production systems.

2. Methods

2.1. Model description

A simulation model was created using NetLogo 5.0.4 (Wilensky, 1999) to estimate the impact of a hypothetical anthelmintic that expressed insecticidal properties when excreted in dung by cattle in a grazed field, upon a model dung invertebrate. A 2-dimensional virtual pasture system was created, occupied by a herd of cattle and a population of the model invertebrate. All actions and interactions presented were simulated hourly time-steps for each individual cattle or invertebrate, as appropriate.

2.2. Model components

The model simulated the interaction between a model dung invertebrate and cattle defecation behaviour, and the potential for invertebrate survival to be changed by different concentrations of anthelmintic residues in the dung.

The model invertebrate was the yellow dung fly *Scathophaga ster-coraria*. The model utilized published data (Table 1) to simulate the life cycle of *S. stercoraria* in a temperate cattle grazing system. *Scathophaga stercoraria* is a well-studied dung fauna species, for which detailed information on life cycle parameters is widely available. The species is highly abundant across the northern hemisphere, and some of its life cycle stages are dependent on dung.

The model cattle were based on published data on temperate grazing commercial beef and dairy herds (Table 1). There were two components to cattle behaviour: (1) defaecation frequency, and (2) randomized movement across a field. The cattle were treated or untreated with a hypothetical anthelmintic, producing toxic or non-toxic dung, respectively. The proportion of cattle treated (PT) ranged from 0 to 1 in increments of 0.1 and was specific as an independent variable in each simulation,

The rate of defecation of model dung by the model cattle and its mean carrying capacity for *S. stercoraria* was based on published data for temperate commercial beef and dairy systems (Table 1). The model dung were toxic or non-toxic. The strength of the toxicity, i.e. effective concentration (EC) ranged from 0 to 1 in increments of 0.1 and was

Table 1

Model variables and values used for simulations. Mean values are fixed constants other than those with a standard deviation (S.D.) which were random variables within a standard normal distribution generated by random number generator using NetLogo 5.0.4. Sources: ^{1.} Blanckenhorn, (1997), ^{2.} Blanckenhorn et al. (2010), ^{3.} Römbke et al. (2009), ^{4.} Martin et al. (2004), ^{5.} Aland et al. (2002), ^{6.} Gary et al. (1970), ^{7.} Oudshoorn et al. (2008), ^{8.} Sahara et al. (1990), ^{9.} Villettaz Robichaud et al. (2011), ^{10.} Floate (1998), ^{11.} Vale and Grant (2002), ^{12.} Geiger (2010), ^{13.} Parker (1970).

Variable ^{source}	Value
Dung fauna (<i>S. stercoraria</i>) Adult life span (emergence to death) ¹ Juvenile period (egg to emergence) ² Female:male ratio ¹ Dung preference ³ Progeny to reach adulthood ⁴	44 days 22 days 1:1 0 10.8 (2.9)
Cattle and dung Mean daily defecation rate (pats per day) ^{5–9} Dung attractive period (with drug residue) to <i>S. stercoraria</i> ^{3,10,11} Dung attractive period (no drug residue) to <i>S. stercoraria</i> ^{3,10,11} Mean dung pat carrying capacity for juveniles ¹² Season length ¹³ Number of cattle	11.2 (2.4) 5 days 5 days 4.3 6 months 20

specific as an independent variable in each simulation. The dung became unattractive for *S. stercoraria* regardless of toxicity after a simulated 120 h.

A starting population of 100 individuals of *S. stercoraria*, covering a random distribution of ages within typical life expectancy for *S. stercoraria*, were simultaneously introduced to the system. They actively sought out cattle dung in order to produce off-spring with no preference for toxic or non-toxic dung. Population fitness responses of the *S. stercoraria* to contact with toxic dung was based on the interaction between PT and the specific EC.

Primary assumptions were:

- (i) the model dung toxicity retained a constant toxicity for 120 h
- (ii) there were no sub-lethal effects of the anthelmintics upon *S. stercoraria*
- (iii) there were no other sources of mortality exist for *S. stercoraria* other than toxicosis or exceedance of life span
- (iv) the population of S. stercoraria is isolated.

No values or weightings of variables within the model were assumed or given arbitrary values.

2.3. Application of modeling approach

The model was run 605 times. Each run simulated 4380 h (6 months) using all combinations of 11 PT values and 11 EC values, totaling 121 unique sets of parameter values. There were five repeats of each set, with variable outcomes depending on values simulated from normal distributions: the mean of each set of repeats was used for statistical analyses. The Anderson-Darling normality test was conducted on residuals for the dependent variable of final population size at the end of the simulated period to ensure appropriateness for parametric testing. This was followed by Pearson's correlation analyses of final population size versus PT and EC. Multiple regression analyses were then conducted to attribute how much of the variation in final population size was due to PT and EC, respectively.

A number of individual paired simulations were run to evaluate the index created by Boxall et al. (2007). These simulations were performed in pairs in which the product of PT and EC were equal, but the individual values of PT and EC in each pair were not equal. To achieve this the values for PT and EC of pair 1 were switched to form pair 2 (Table 2). For the Boxall et al. (2007) model to agree with the presented model, there should be no significant different between pairs that meet the aforementioned assumptions. Final population numbers from

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