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Evaluating the feasibility of developing a model to better manage nematode infections of sheep

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Abstract

This study evaluates the feasibility of developing (or accessing) a sheep nematode epidemiology model for Australian conditions. Following consultation with animal health experts, such a model would need to predict the impact of integrated parasite control strategies (nutrition, grazing management, anthelmintic treatment strategies and selective breeding for resistance) upon productive traits, parasitological traits and the emergence of anthelmintic resistance. Seven existing nematode epidemiology models were reviewed to evaluate their suitability for Australian conditions in their current form, or after customisation. Whilst individually these models were found to be incapable of evaluating integrated parasite control strategies, a composite of these models could achieve this aim. The best functions from the models reviewed were identified and the initial outline of a composite model is consequently proposed. Access to such a model for industry advice, educational or research purposes can be facilitated via its inclusion in the WormBoss website following development of a user friendly interface. Further, providing open-access to the model source code will inform researchers of underlying assumptions, allow for thorough review, remove reliance upon an individual, and facilitate further development. Finally, the potential pathway and cost of developing a validated sheep nematode epidemiology model and advice tool is considered.

Executive summary

A mathematical model of the epidemiology of sheep nematodes would provide a valuable tool for the Australian sheep industry and has previously been identified as an industry priority. Such a tool would be especially useful for understanding the interactions between parasite control options and their impact upon productive traits and the emergence of anthelmintic resistance. Whilst a number of nematode epidemiology models have previously been developed, these currently remain inaccessible to the Australian sheep industry. Thus, this study evaluates the feasibility of developing (or accessing) a nematode epidemiology model for Australian conditions.

The objectives of this study were to:

- Review existing nematode epidemiology models in Australia and abroad and report on their suitability for Australian conditions in their current form, or after customisation (if possible).
- Report on the availability and accessibility of data for the input variables by the models.
- Propose a pathway to the development/customisation of a sheep nematode epidemiology model and management advice tools for industry.
- Describe the proposed outputs from such a model and industry advice tools.
- Provide recommendations on the need, feasibility and potential cost of developing a sheep nematode epidemiology model and advice tools.

A total of seven existing nematode prediction models were reviewed from available literature to determine their suitability for Australian conditions in their current form, or after customisation (if possible). The models were assessed for their ability to simulate the main parasite (nematode) control strategies currently utilised. Specifically, these are identified as the nutritional control of host immunity, grazing management to prepare low worm-risk pastures, anthelmintic treatment strategies aimed at providing adequate parasite control whilst reducing the rate at which anthelmintic resistance emerges, and selective (genetic) breeding for host resistance. These models are given as those described by:

1. Singleton *et al*., de Cisneros *et al.*
2. Leathwick *et al*.
3. Learmount *et al*.
4. Barnes *et al*., Barnes & Dobson, Dobson *et al*.
5. Laurenson *et al*.
6. Grenfell *et al*., Smith *et al*.
7. Callinan *et al*., White *et al*.

A detailed set of notes were drafted for each model. These outlined the functions, assumptions and parameter values available from the existing publications of each model, and were subsequently sent to the original authors for clarification. Further, a consultation (online survey) amongst animal health experts was carried out within the ParaBoss forum to determine the industry requirements (outputs) of a nematode epidemiology model.

Following a review of the existing nematode epidemiology models it was determined that individually these models (in their current form) are incapable of simulating integrated parasite control strategies under Australian conditions. This review also identified further issues with these models:

- The dichotomy of model development focussed on production or parasitology.
- The differing complexity of model functions.
- Minimal validation of the predictive accuracy of all models.
- The use of models to investigate scenarios for which they were not designed.

Whilst individually the models reviewed are not appropriate for use in evaluating integrated parasite control strategies in Australia, a composite would be capable of achieving this aim. As such, the best functions available from the reviewed models were identified and are proposed to constitute the initial outline for a composite model. Some of these functions, especially those relating to the free-living stages of parasitic nematodes, require further evaluation against existing literature and experimental data which may not have been available at the time the models were constructed.

Consideration was given to the accessibility and usability of the potential composite model. In order to provide a useable model/tool for industry, research and educational purposes a good user-interface is essential. As such an appropriate outline of a user-interface is detailed which attempts to strike a balance between the requirements for expert user input and predefined scenarios. The proposed outputs of this model/tool will provide an illustration of pasture infectivity, worm burdens, anthelmintic drench resistance and the productive and financial consequences arising from the combination of various options for parasite control. Access to this tool is proposed to be facilitated via its inclusion into the WormBoss website which provides an existing route to market.

Notably, the existing nematode epidemiology models reviewed were not completely transparent making a thorough review difficult. This lack of transparency has meant that the underlying assumptions contained within these models are only known by the individuals who developed these models, and not completely understood by those viewing the consequent outputs. The absence of an open source code for these models has resulted in reliance upon the individual developers, and in some cases has prevented these models from being updated once new experimental data have become available. As such, it is suggested that the source code for the proposed composite model (along with detailed literature) should be made openly available. This would serve to inform researchers of underlying assumptions, allow for thorough review, remove reliance upon an individual and facilitate further development.

The pathway for implementing the development of a composite model and output tools is detailed. Previous nematode epidemiology models have only validated certain components under specific scenarios, whilst the predictions arising from the entirety of these models have remained un-validated. As such, options are provided for field validation which would generate confidence in the model predictions. The potential cost of developing a validated sheep nematode epidemiology model for Australian conditions is subsequently detailed.

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1. Background

Nematodiasis is one of the most pervasive challenges to the health and welfare of ruminants, and has been estimated to cost the Australian sheep industry in excess of $369 million per year[1]. The cost of nematodiasis has continued to increase since the mid 2000s[2] as has the prevalence and severity of anthelmintic resistance[3]. Effective control of nematode infections continues to move towards a holistic approach which incorporates selective breeding, grazing management, nutrition and effective anthelmintic drugs. These control programs must deliver efficacious control while minimising negative effects on anthelmintic resistance in a manner that meets the risk profile of sheep producers and the welfare concerns of consumers. WormBoss regional control programs have been developed to satisfy these aims but these programs would be improved if supported by mathematical models of the epidemiology of nematode infection. While this support would be especially useful for understanding the interactions among control options (especially grazing management and anthelmintic use) so as to avoid unintended negative effects on efficacy of control and anthelmintic resistance, it could also incorporate recent advances in the understanding of nematode ecology as part of predictive tools that could be used by industry. Such models and tools would therefore improve regional control programs and support the development of farm-specific programs.

There have been a number of mathematical models used to simulate nematode epidemiology around the world, but within Australia, the WormWorld model developed by Barnes and Dobson (1990) is best known. Despite the industry support provided for the development and proofing of this model, it remains inaccessible for researchers and animal health advisors and instead is serviced by R.J. Dobson (one of the original authors). Recently, the WormWorld model was transformed into an EXCEL® format with support from a pharmaceutical company, however, this too remains inaccessible for researchers and animal health advisors.

It is time for the Australian sheep industry to have access to a model of nematode epidemiology in order to better manage the trade-offs between production and anthelmintic resistance and exploit known ecological barriers in nematode development. Given the background of previous modelling attempts in Australia and the existence of other models around the world, the first step would be to conduct a scoping study to evaluate the technical feasibility of developing (or accessing) a model and predictive advice tools to better manage nematode infections of sheep.

2. Project objectives

The objectives of this study were to:

- Review existing nematode epidemiology models in Australia and abroad and report on their suitability for Australian conditions in their current form, or after customisation (if possible).
- Report on the availability and accessibility of data for the input variables by the models.
- Propose a pathway to the development/customisation of a sheep nematode epidemiology model and management advice tools for industry.
- Describe the proposed outputs from such a model and industry advice tools.
- Provide recommendations on the need, feasibility and potential cost of developing a sheep nematode epidemiology model and advice tools.

3. Methodology

A total of seven existing nematode prediction models were reviewed from available literature. These models are given as those described by:

1. Singleton *et al*.[4], de Cisneros *et al.*[5]
2. Leathwick *et al*.[6,7,8,9]
3. Learmount *et al*.[10]
4. Barnes *et al*.[11,12], Barnes & Dobson[13,14], Dobson *et al*.[15,16]
5. Laurenson *et al*.[17,18,19,20,21]
6. Grenfell *et al*.[22,23], Smith *et al*.[24,25]
7. Callinan *et al*.[26], White *et al*.[27]

Two points of note should be acknowledged. Firstly, model 6 describes infection in cattle rather than sheep; however, functions used within this model may still inform construction of a sheep nematode epidemiology model. Secondly, in model 7, Callinan *et al.*[26] specified the adaptation of a model of a self-replacing Merino ewe flock from the unpublished PhD thesis of White (1975). The inaccessibility of this thesis therefore necessitated the use of the model later published by White *et al*.[27]

A detailed set of notes were drafted for each model. These outlined the functions, assumptions and parameter values available from the existing publications of each model, and were subsequently sent to the original authors for clarification.

A consultation (online survey) amongst animal health experts was carried out within the ParaBoss forum to determine the industry requirements (outputs) of a nematode epidemiology model which simulates integrated parasite control strategies, and each model (in their current form) was assessed to determine whether they could meet these needs.

4. Results and discussion

4.1 Review summary

Table 1 provides a summary of the attributes of the nematode models reviewed. However, it should be noted that each model differs in the relationships and parameters describing each component of the nematode life cycle, the host and host-parasite interactions. These differences (detailed in subsequent sections) represent the availability of experimental data to the model authors at the time of model construction, and the parameterisation of each model to specific nematode species, hosts and agro-climatic regions.

The functions and parameters used to describe each of the model components given in Table 1 are outlined below. The outline of each component is followed by individual discussion sections and where appropriate provides further literature for consideration.

Table 1. Summary of the seven existing nematode models reviewed

Model	1	2	3	4	5	6	7
Nematode species	1	1	3	3	1	1	2
Meteorological data	-	-	i	i	-	i	i
Pasture							
Herbage quality	-	-	-	-	i	-	r
Herbage growth	-	-	-	-	c	-	r
Herbage availability	c	i	c	c	r	-	r
Free-living larval stages							
Ewe egg contribution	r	r	r	-	r	-	-
Mortality of pre-infective larvae	c	i	r	r	c	r	r
Mortality of infective larvae	c	c	r	r	c	c	r
Duration: egg to infective larvae	c	i	r	r	c	r	r
Larval availability for ingestion	r	r	r	r	r	r	r
Host							
Nutritional requirements	-	-	-	-	r	-	r
Herbage Intake	r	r	r	r	r	-	r
Parasite-induced anorexia	-	-	-	r	r	-	r
Constrained food Intake	-	-	-	-	r	-	r
Infective larval Intake	r	r	r	r	r	r	r
Digestion	-	-	-	-	r	-	r
Nutrient allocation	-	-	-	-	r	-	r
Metabolism/catabolism	-	-	-	-	c	-	r
Live weight	r	-	-	-	r	r	r
Weight loss from parasitism	-	r	-	-	r	-	r
Wool growth	-	-	-	-	r	-	r
Host mortality	-	-	-	r	r	-	r
Faecal output	r	r	c	r	r	r	r
Between animal variation	r	-	-	-	r	-	-
Parasitic nematode stages							
Nematode pre-patent period	c	-	c	-	c	c	c
Arrested development	-	-	-	r	-	r	-
Establishment	r	r	r	r	r	r	-
Mortality of adult nematodes	c	r	c	r	r	r	r
Worm Burden	r	r	r	r	r	r	r
Fecundity	r	c	r	r	r	r	r
Faecal Egg Count	r	r	r	r	r	r	r
Anthelmintic treatment							
Efficacy	c	i	i	i	i	c	c
Genetic mechanism for resistance	-	r	r	r	r	-	-
Nematode genotype fitness	-	i	-	i	-	-	-
Allele frequencies	-	r	r	r	r	-	-

c = constant, r = relationship described in sections 4.4-4.38, i = input

4.2 Nematode species

4.2.1 Nematode species - overview

Table 2. Summary of the nematode species simulated in each model

Model	*Haemonchus contortus*	*Teladorsagia circumcincta*	*Trichostrongylus colubriformis*	*Ostertagia ostertagi*	*Generic*
1	-	✓	-	-	-
2	-	-	-	-	✓
3	✓	✓	✓	-	-
4*	✓	✓	✓	-	-
5	-	✓	-	-	-
6	-	-	-	✓	-
7	-	✓	✓	-	-

* Later versions of this model included *Trichostrongylus vitrinus* (in correspondence with R.J. Dobson); however, this inclusion has not been published.

4.2.2 Nematode species - discussion

It is important to note the specificity of the models reviewed. Generic models, such as model 2, do not refer to any particular nematode species but instead present generalisations about the dynamics of host-parasite interactions. The structure of a generic model is deliberately kept as simple as possible and thus facilitates the analysis of system behaviour and obviates the possibility that extraneous biological detail may obscure the more important processes. Notably, a generic model framework with suitably adjusted parameter values can satisfactorily represent almost all nematode and host species, as well as agro-climatic region. Thus, whilst the model described by Leathwick *et al*.[6,7,8,9] (model 2) remains generic in regards to nematode species, the host (sheep) and agro-climatic region (New Zealand) are specified.

Specific models are designed to address particular questions about the dynamics or control of a specific nematode species in a specific host and/or agro-climatic region. In terms of nematode species, models are usually parameterised to the most abundant and/or economically important nematode species within the agro-climatic region being considered and/or for which the greatest amount of experimental data exists. The models described by Laurenson *et al*.[17,18,19,20,21] (model 5) and Singleton *et al*.[4] (model 1) are therefore specific to *Teladorsagia circumcincta* infections in Scottish Blackface sheep within the Scottish Lowlands. However, it should be noted that these models are designed to address different questions. Whilst model 6 is specific to *Ostertagia ostertagi* infections in cattle, climatic variables were included to allow for the simulation of the prevalence of this nematode species within the differing agro-climatic regions of the US. However, other models have aimed to address the prevalence of numerous nematode species across a range of agro-climatic regions. This goal required the addition of considerable complexity to the respective models. Not only do they need to consider the interaction between variable climatic conditions and each nematode species, but also potentially any interactions between nematode species. The model described by Learmount *et al*.[10] (model 3) simulates the population dynamics and epidemiology of three major species of parasitic nematodes of sheep (*Teladorsagia*, *Trichostrongylus* and *Haemonchus*) across 10 agro-climatic regions of the UK. Similarly, the model described by Callinan *et al*.[26] (model 7) simulates the population dynamics and epidemiology of the *Teladorsagia* and *Trichostrongylus* species across differing agro-climatic regions of the state of Victoria in Australia. These models consider the impact of climatic variables on the free-living stages of these nematode species, however, no interaction between species was considered. The inclusion of the relationship between

climatic variables and the free-living stages of the nematode life-cycle will be discussed in a later section. Model 4 simulates concurrent populations of *Trichostrongylus colubriformis*, *Haemonchus contortus* and *Teladorsagia circumcincta* in sheep under Australian grazing systems. This includes the impact of climatic variables on the free-living parasitic stages but also incorporates species interactions within the host. Dobson *et al*.[16] identified previous experimental studies which found a major interaction between the presence of *Teladorsagia circumcincta* and the establishment of *Haemonchus contortus* within the host (see section 4.29). However, it should be noted that other density-dependent species interactions may also exist (e.g. density-dependent parasite fecundity) which have not yet been incorporated into any model.

Since the initial construction of the multi-species model outlined by Dobson *et al*.[16], *Trichostrongylus vitrinus* was also identified as an important species prevalent within southern Australia which is substantially different from *Trichostrongylus colubriformis*. As such, *Trichostrongylus vitrinus* was included in the EXCEL® version of WormWorld funded by Novartis.

It is clear given the wide range of agro-climatic regions within Australia that any model constructed to simulate the variety of Australian conditions must include *Trichostrongylus colubriformis*, *Trichostrongylus vitrinus*, *Teladorsagia circumcincta* and *Haemonchus contortus*.

4.3 Meteorological data

4.3.1 Meteorological data - overview

Table 3. Summary of the models which require the input of meteorological data

Model	Input
1	-
2	-
3	✓
4	✓
5	-
6	✓
7	✓

4.3.2 Meteorological data - inputs required (by model)

3. User-interface choice from 10 UK meteorological office regions, defines daily average temperatures (°C) and rainfall (mm)[10].
4. User input required for daily maximum and minimum air temperature (°C), rainfall (mm) and evaporation (mm)[16].
6. User input required for daily average temperature (°K), and specified start and end dates for periods of drought or heavy rainfall[23].
7. User input required for daily average temperatures (°C) and rainfall (mm)[27].

4.3.3 Meteorological data - discussion

Meteorological input data, such as temperature and rainfall, are required to define the differences between agro-climatic regions. Further, the differences between the meteorological conditions of these regions are not static, but exhibit seasonal variation.

Given that environmental factors affect the development success and duration of the free-living stages of the nematode life cycle, regional and seasonal variation in climatic conditions may be considered to be necessary for any model wishing to simulate the population dynamics and epidemiology of any nematode species. Further, the optimal environmental conditions for development success differ between nematode species. Accounting for this interaction will create regional and seasonal variation in the prevalence of the differing nematode species. This may also be considered an important requirement when consideration needs to be given to the timing of any parasite control strategies.

The inclusion of meteorological data represents a considerable hurdle in generating a truly predictive model. Meteorological prediction is an intrinsically uncertain science, and thus the inclusion of meteorological predictions within a nematode epidemiology model may be considered undesirable. Historical data on the environmental conditions at a particular location in a particular year may potentially allow us to reproduce experimental studies for qualitative validation. Learmount *et al*.[10] (model 3) used temperature data from 2004 for each of its UK regions. Notably, Callinan *et al*.[26] carried out a quantitative validation of their model (model 7) using weather data recorded at an experimental site in Hamilton, Victoria from 1975 to 1977 and reported a significant correlation ($R > 0.5$) between observed and predicted larval contamination of pasture. However, other quantitative validation studies have been less successful. Whilst it is possible to describe the responses of the free-living stages in the parasitic life cycle to changes in temperature and moisture in a laboratory setting, there is currently no way of reliably linking conventional weather data to the detailed microclimate actually experienced by the free-living stages on the pasture surface. Thus, reproducing experimental data via modelling for quantitative validation may be considered an insurmountable task, especially given the amount of detail required for predictions at an individual farm level. Further, meteorological data for any specific year may be unrepresentative of the typical climatic conditions of a region. Leathwick *et al*.[6] does not include meteorological data as an input, however, parameters affected by environmental conditions follow a general seasonal pattern. Thus, this model remains generic in regards to the specificity of year. Constructing meteorological data as a daily average of historical records may provide a more representative illustration of the climatic conditions of a particular region. Whilst this constrains the ability to carry out quantitative validations of the model, by establishing 'typical' environmental conditions we can qualitatively represent the population dynamics of the free-living stages of the nematode life-cycle.

Historical climatic data is available from the Australian government's Bureau of Meteorology (www.bom.au/climate/data/) and is provided in a number of formats from regional averages to daily weather station specific data given from first installation to current measurements.

4.4 Pasture: herbage quality

4.4.1 Pasture: herbage quality - overview

Table 4. Summary of the models which include functions to describe herbage quality or require the input of information regarding herbage quality

Model	Included
1	-
2	-
3	-
4	-
5	✓
6	-
7	✓

4.4.2 Pasture: herbage quality – functions & inputs (by model)

5. User input for crude protein, metabolisable energy, fermentable metabolisable energy, rumen degradable protein, undegradable protein and digestible undegradable protein. These remain constant across the simulated period[17].
7. For Australian conditions the digestibility of consumed green herbage (*DG*) is given as[27]:

$$DG = 0.82 \cdot e^{-0.0557 \cdot \left(\frac{AG}{2000}\right)^2} \cdot e^{-0.1 \cdot \left(\frac{NG}{45 - TOB}\right)^2}$$ from January until August

$$DG = 0.82 \cdot e^{-0.15 \cdot \left(\frac{NG}{45 - TOB}\right)^2}$$ from September until December

where *AG* is the available green herbage (kg ha^{-1}), *NG* is the weeks since germination, and *TOB* is the week of autumn break.

4.4.3 Pasture: herbage quality - discussion

Herbage quality is an important aspect to consider when constructing a mathematical model for the epidemiology of nematodes. The nutritional content of herbage may be expected to impact upon the host's food intake, infective larval intake, growth and ability to mount an effective immune response. Notably, those models which do not include herbage quality either do not include the impact of nutritional content on the host's food intake, growth and immunity and/or do not model host growth at all. As such, these models are incapable of assessing the impact of using nutritional supplementation as a parasite control strategy (e.g. protein supplementation for host immune acquisition), and may not be capable of assessing the productive benefits of any parasite control strategy. Of the models reviewed, only two consider herbage quality. The model described by Laurenson *et al*.[17] (model 5) allows for the input of the nutritional content of herbage, however, this remains constant across the simulated period. The model described by White *et al*.[27] (model 7) includes the calculation of herbage digestibility (as a variable on pasture), and whilst energy content is mentioned (White *et al*.[27] page 167) no relationship is detailed, however, energy supplementation to meet host maintenance requirements are described.

As a minimum a nematode epidemiology model should simulate both the protein and energy content of herbage. Whilst growth is predominantly driven by energy retention, the immune response is predominantly driven by protein which is not considered in the model of White *et al*.[27] (model 7). Further, all traits describing the pasture quality (crude protein content, metabolisable energy content, and digestibility) exhibit time/climate dependent variation and thus, the model described by Laurenson *et al*.[17,18] (model 5) is not capable of simulating regional and seasonal variation in herbage quality. One option to account for regional and seasonal variation in herbage quality may be to construct relationships based on those described by various State Departments of Agriculture in Australia.

4.5 Pasture: herbage growth

4.5.1 Pasture: herbage growth - overview

Table 5. Summary of the models which describe herbage growth

Model	Included
1	-
2	-
3	-
4	-
5	✓
6	-
7	✓

4.5.2 Pasture: herbage growth – functions (by model)

5. Constant growth rate of 60 kg DM ha^{-1} day^{-1}.[18]
7. Herbage growth rate (*GR*, kg ha^{-1} day^{-1}) is given as[27]:

$$GR = \frac{PG \cdot e^{1}}{350 + 33 \cdot PG} \cdot e^{-\frac{1}{350+33 \cdot PG} \cdot AG} \cdot \frac{AET}{PET}$$

where *PG* is potential growth rate (kg ha^{-1} day^{-1}), *AG* is the quantity of green herbage available (kg ha^{-1}), AET is the actual evapo-transpiration (mm day^{-1}), and PET is the potential evapo-transpiration (mm day^{-1}).

4.5.3 Pasture: herbage growth - discussion

Both herbage consumption by the grazing population and herbage growth are an important consideration when determining herbage availability. The constant herbage growth implemented by Laurenson *et al*.[18] (model 5) does not account for regional and seasonal variation in herbage growth as a consequence of climatic conditions. White *et al*.[27] (model 7) considers the impact of rainfall and evaporation on herbage growth resulting in variable herbage growth. This function may be validated or altered using data regarding herbage growth which is accessible via the Australian Government's Department of Agriculture and ABARES. The 'Rainfall to Pasture Growth Outlook Tool' provides annual growth patterns and specific growth data for 3308 locations in Australia (http://rainfal.mla.com.au/Station/AllLocations).

4.6 Pasture: herbage availability

4.6.1 Pasture: herbage availability - overview

Table 6. Summary of the models which describe herbage availability

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	-
7	✓

4.6.2 Pasture: herbage availability – functions (by model)

1. Constant herbage density of 1,200 kg DM ha^{-1}.[4]
2. Herbage availability for consumption is given as half herbage density (kg DM ha^{-1}), which follows a defined seasonal pattern given in Figure 1 and is given as representative of New Zealand conditions.[6]

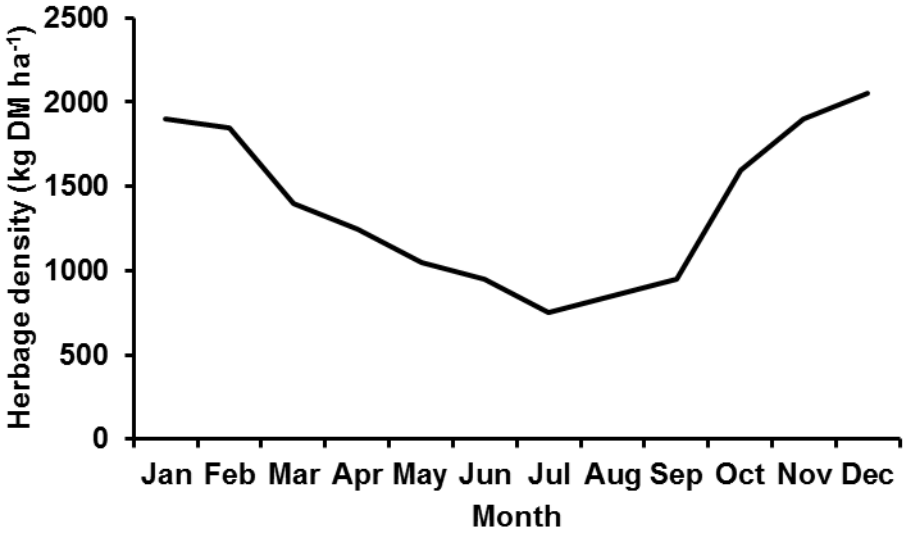

Figure 1. Herbage density (kg DM ha^{-1}) across a single year used as a representation of New Zealand conditions in Leathwick *et al*.[6]

3. Constant herbage density of 1,797 kg DM ha^{-1}.[10]
4. Constant herbage density of 0.1411125 kg DM m^{-2}. (In correspondence with R.J. Dobson, 16th July 2014)

5. Initial input required for initial herbage density (*IHD*) given as 1,500 kg DM ha^{-1}. On day 1 of simulation the herbage availability (*AH*, kg DM) is given as[18]:

$$AH_1 = IHD \cdot H$$

This is updated daily such that:

$$AH_t = \left(AH_{t-1} - \sum HI_{t-1}\right) + \left(H \cdot GR\right)$$

where *t* is the day, ∑*HI* is the total herbage intake of grazing population, *H* is the number of hectares, *GR* is grass growth (kg DM ha^{-1} day^{-1}).

7. Herbage availability for consumption is given as[27]:

$$AH = AG + AD$$

where *AG* is the quantity of green herbage available (kg ha^{-1}), and *AD* is the quantity of dead herbage available (kg ha^{-1}).

4.6.3 Pasture: herbage availability - discussion

The amount of herbage available for consumption by a grazing population may impact upon animal growth, but importantly may also be considered as having a dilution effect on the infective larval contamination of pasture, as this is consistently given as infective larvae kg^{-1} DM across all models (except model 6). It should be noted that, whilst discussed, herbage availability is not included in model 6[22,23,24,25] which, by calculating infection rate as a constant proportion of the total infective larval population on pasture, removes the necessity to include herbage availability or the host's herbage intake.

Models 1[4], 3[10] and 4 (In correspondence with R.J. Dobson, 16th July 2014) include herbage availability as a constant, and thus whilst the infective larval contamination of pasture (infective larvae kg^{-1} DM) may vary due to egg deposition and environmental conditions, variation in herbage availability due to the consumption of herbage by the grazing population and herbage growth is not included. Whilst Leathwick *et al*.[6] (model 2) follows the seasonal patterns of herbage availability given by Vlassoff[28], this is an input which is unaffected by model functions. In contrast, Laurenson *et al*.[18] (model 5) considers herbage availability as a function of the initial input of herbage density, the total herbage intake of the host population and herbage growth. However, herbage growth is given as a constant daily rate irrespective of climatic conditions. White *et al*.[27] (model 7) includes herbage growth as a function of rainfall and evaporation and therefore provides the best description of herbage availability from the models reviewed.

4.7 Free-living nematode stages: ewe egg contribution

4.7.1 Free-living nematode stages: ewe egg contribution - overview

Table 7. Summary of the models describing the ewe egg contribution

Model	Included
1	✓
2	✓
3	✓
4	-
5	✓
6	-
7	-

4.7.2 Free-living nematode stages: ewe egg contribution – functions (by model)

1. The ewe egg contribution (*EE*, eggs ewe^{-1} day^{-1}) is given as[4] (for *EE* > 0):

$$EE_t = (250000 \cdot a) - \frac{250000 \cdot a}{84} t$$

where *a* is number of lambs ewe^{-1} (assumed to be 2), and *t* is lamb age (days). Figure 2 provides an illustration of this function.

2. Assumed constant baseline for ewe faecal worm egg count (FEC_{EWE}) set at a minimum ($minFEC_{EWE}$) of 100 eggs g^{-1}. During lactation FEC_{EWE} 'is assumed to follow a normal distribution with respect to time, with a maximum value ($maxFEC_{EWE}$ = 1000 eggs g^{-1}) occurring 4-6 weeks after lambing.' Egg contribution per ewe is given by multiplying FEC_{EWE} by ewe faecal output[7]. Figure 2 provides an illustration of this function.
3. Ewes are explicitly simulated, thus ewe egg contribution is given as[10]:

$$EE(t) = \lambda_{EWE}(t) \cdot WB_{EWE}(t)$$

where λ_{EWE} is the fecundity of adult nematodes within the ewe, *WB* is the parasitic (worm) burden within the ewe, and *t* is the day.

5. Simulation starts at weaning, with the initial egg contamination of pasture being modelled 'such that the number of infective larvae developing on pasture was equal to the number of larvae consumed by the lamb population for the first 7 days.'[18]

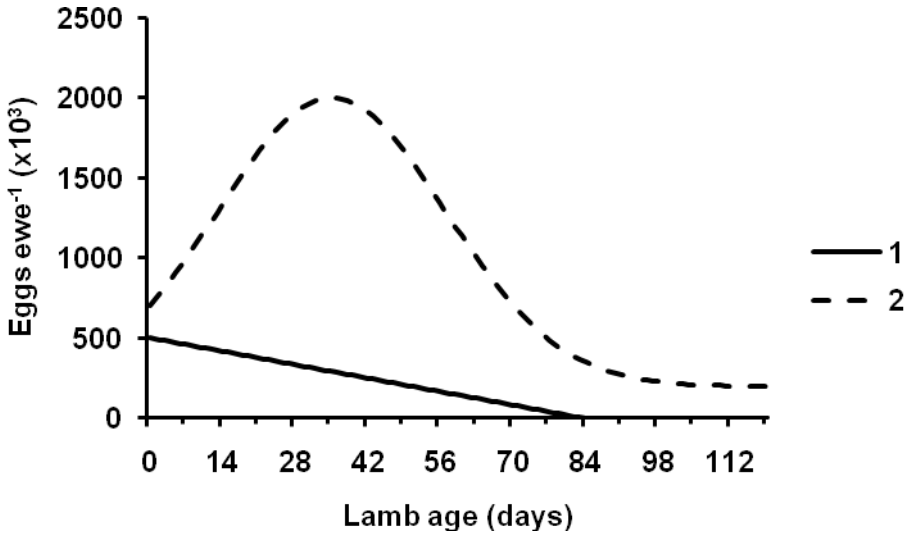

Figure 2. Egg contribution to pasture ewe^{-1} for the models described by Singleton *et al*.[4] (model 1) and Leathwick *et al*.[7] (model 2).

4.7.3 Free-living nematode stages: ewe egg contribution - discussion

The egg deposition of ewes and consequent infective larval contamination of pasture is an important aspect when considering the initial exposure to infective larvae experienced by lambs following weaning. Further, consideration needs to be given to management practices such as the separation of lambs and ewes at weaning. The egg deposition of dams is not considered in the sheep model 4 (In correspondence with R.J. Dobson, 16th July 2014) and model 7[26], or the cattle model 6[22,23,24,25]. However, the peri-parturient breakdown of immunity during pregnancy and lactation results in an increased egg output which may be expected to impact upon the infective larval contamination of pasture.

Further to the functions described by models 1[4], 2[7], 3[10] and 5[18], parasite control strategies and management practices aimed at the ewe population need to be considered. Models 2[7] and 3[10] allow for the simulation of anthelmintic treatments administered to the ewes during the peri-parturient breakdown in immunity. The underlying assumption of model 5[18] is that ewes are removed at lamb weaning, and thus the anthelmintic treatment of ewes is not considered, however, this highlights the further potential of incorporating such management practices. However, no other parasite control strategies aimed at the ewe population are considered within the models reviewed. For example a number of experimental studies have focussed on the impact of protein supplementation on the peri-parturient rise in egg counts (e.g. Houdijk *et al*.[29]). A further 16 publications were found relating the rise in faecal egg counts of ewes to body condition, nutrition and immune response to *Haemonchus contortus*, *Trichostrongylus colubriformis* and *Teladorsagia circumcincta* infections[30-45]. These may further inform the construction of appropriate functions to describe such interactions.

Exploring potential control strategies aimed at the ewe population would require for the ewes to be explicitly modelled to the same level of detail deemed necessary for the simulation of parasite control strategies aimed at lambs, such as in model 3[10], rather than just accounting for the egg deposition of ewes. However, model 3[10] is incapable of simulating the effects of protein supplementation on the peri-parturient relaxation of immunity. As such it is suggested that an alternative approach would be to add the nutrient requirements for pregnancy and lactation (AFRC[46]) to the framework described for model 5[17], assuming that immunity is initially fully acquired in ewes prior to pregnancy and that resources are allocated to these functions before the maintenance of immunity. As such a relaxation in immunity would result in a peri-parturient rise in egg counts.

4.8 Free-living nematode stages: mortality of pre-infective larvae

4.8.1 Free-living nematode stages: mortality of pre-infective larvae - overview

Table 8. Summary of the models describing the mortality of pre-infective larvae

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	✓
7	✓

4.8.2 Free-living nematode stages: mortality of pre-infective larvae – functions (by model)

1. Constant proportional mortality rate of 0.23 day^{-1}.[4]
2. % survival follows a defined seasonal pattern given in Figure 3 and is given as representative of New Zealand conditions[6].

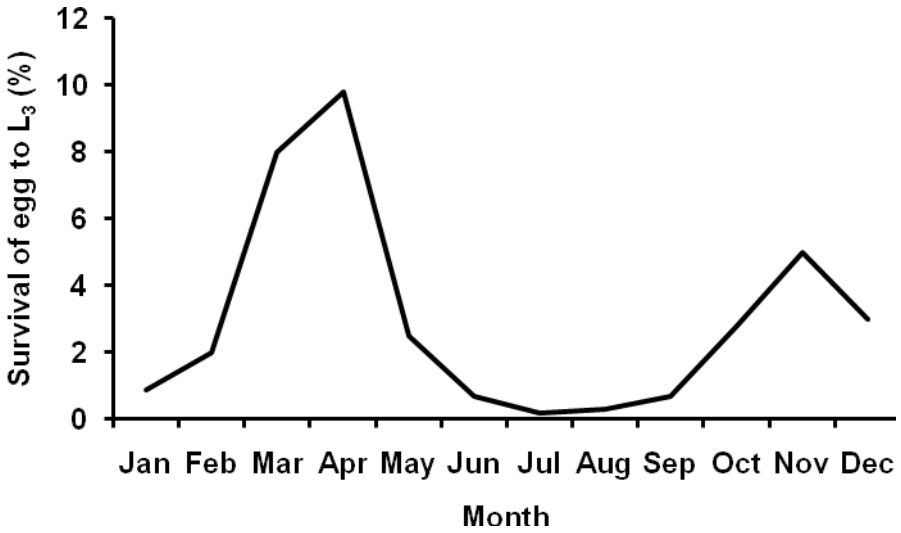

Figure 3. The survival of pre-infective larvae (%) across a single year used as a representation of New Zealand conditions in Leathwick *et al*.[6]

3. The mortality rate of pre-infective stages (μ_1) for each nematode species is dependent on the average temperature (°C) on a given day (t) such that[10]:

$\mu_1(t) = \alpha$ if °C(t) < *threshold*
$\mu_1(t) = \beta$ if °C(t) > *threshold*

where *threshold* is a constant specific to each nematode species ($threshold_{Teladorsagia}$ = 4°C, $threshold_{Trichostrongylus}$ = 10°C, $threshold_{Haemonchus}$ = 10°C); and α & β are constant mortality rates (proportion day^{-1}) specific to each nematode species ($\alpha_{Teladorsagia}$ = 0.002, $\alpha_{Trichostrongylus}$ = 0.008, $\alpha_{Haemonchus}$ = 0.014, $\beta_{Teladorsagia}$ = 0.23, $\beta_{Trichostrongylus}$ = 0.13, $\beta_{Haemonchus}$ = 0.11). These relationships are illustrated in Figure 4.

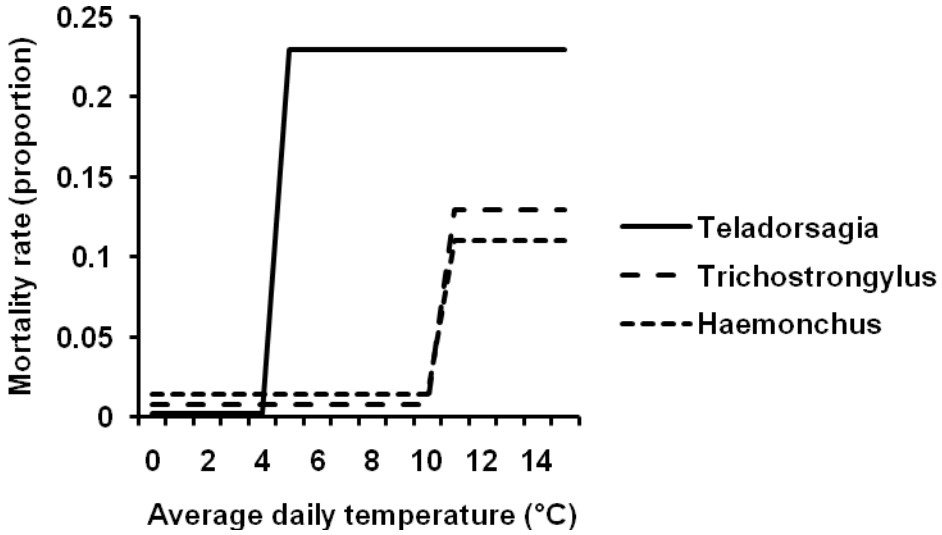

Figure 4. The relationship between average daily temperature and the mortality rates of pre-infective larvae for *Teladorsagia*, *Trichostrongylus* and *Haemonchus* as described by Learmount *et al*.[10]

4. Mortality rate is intrinsic to the calculation of the probability an egg develops to an infective larva and migrates to herbage (p) given for each nematode species as[11,16]:

$$p_{Trichostrongylus} \,\&\, p_{Telaodorsagia} = \left(\sin\left(0.103 - 0.00309 \cdot d_2 - 0.00395 \cdot n*\right)\right)^2$$
$$\text{for } 0.103 - 0.00309 \cdot d_2 - 0.00395 \cdot n* > 0$$

$$p_{Trichostrongylus} \,\&\, p_{Telaodorsagia} = 0$$
$$\text{for } 0.103 - 0.00309 \cdot d_2 - 0.00395 \cdot n* \le 0$$

$$p_{Haemonchus} = 0.000075 \quad \text{for } d_2 > -2.5$$
$$p_{Haemonchus} = 0.000095 \quad \text{for } d_2 \le -2.5 \,\&\, T_3 < 16$$
$$p_{Haemonchus} = 0.00094 \quad \text{for } d_2 \le -2.5 \,\&\, T_3 \ge 16$$

where d_2 is the sum of evaporation (mm) – rainfall (mm) for the first two days after faeces were deposited on pasture, $n*$ is the number of weeks until cumulative rain over 7 days or less exceeds 16mm, and T_3 is the mean maximum air temperature (°C) for the first 3 weeks after eggs were deposited on pasture.

5. Constant proportion of eggs develop to infective larvae (0.11 day^{-1}).[18]

6. The mortality rate of pre-infective free-living stages (μ_1) is dependent on the average temperature (°K) on day *t*, such that (for $\mu_1 < 1$)[23]:

$$\mu_1(t) = e^{\alpha_1 + \alpha_2 \cdot K(t)}$$

Where α_1 is -69.09 for Temperate conditions & -70.24 for Mediterranean conditions, α_2 is 0.2288 for Temperate conditions & 0.2346 for Mediterranean conditions. Figure 5 provides an illustration of the relationship between daily average temperature and the mortality rate of pre-infective larvae under temperate and Mediterranean conditions.

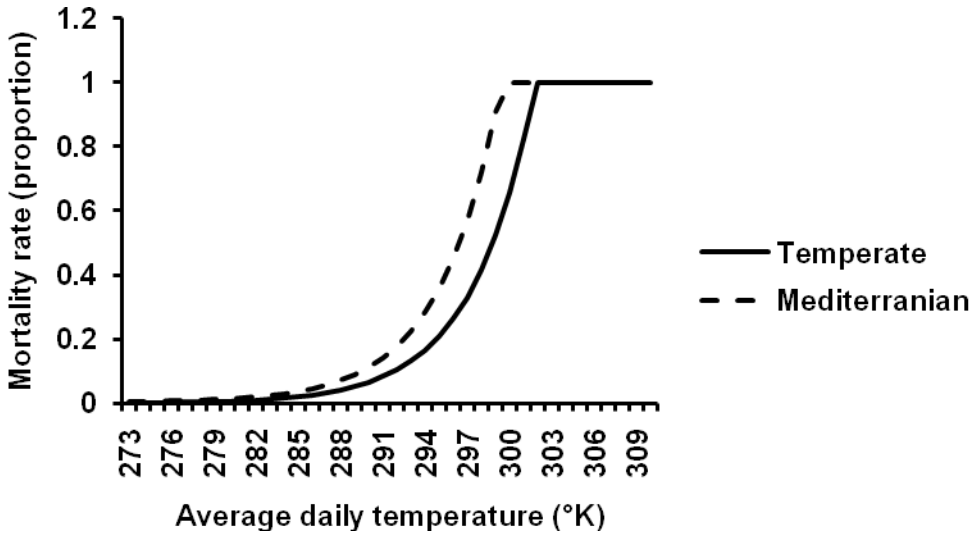

Figure 5. The relationship between daily average temperature and the mortality rate of pre-infective larvae under Temperate and Mediterranean conditions, as given by Grenfell *et al*.[23]

7. Reference is made to unpublished work (Callinan, Morley and White) relating survival to daily weather data. 'The rate parameters are expressed as transition probabilities. Transition matrices of these probabilities are accessed each day according to mean air temperature and soil moisture status … random numbers from a uniform distribution determine the transition to be made, depending on whether they are less than the cumulative probabilities for remaining in a particular stage, developing to the next stage or dying.' This would infer that a cumulative probability function is calculated from look-up tables for temperature and soil moisture, and the event (e.g. mortality) is determined by comparison to a random number.

4.9 Free-living nematode stages: mortality of infective larvae

4.9.1 Free-living nematode stages: mortality of infective larvae - overview

Table 9. Summary of the models describing the mortality of infective larvae

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	✓
7	✓

4.9.2 Free-living nematode stages: mortality of infective larvae – functions (by model)

1. Constant proportional mortality rate of 0.008 day^{-1}.[4]
2. Constant proportional survival rate of 0.977 day^{-1}.[6]
3. The mortality rate of infective stages (μ_2) for each nematode species is dependent on the average temperature (°C) on a given day (t) such that[10]:

$$\mu_2(t) = \gamma \qquad \text{if°C}(t) < threshold$$
$$\mu_2(t) = \delta \qquad \text{if°C}(t) > threshold$$

where *threshold* is a constant specific to each nematode species ($threshold_{Teladorsagia}$ = 4°C, $threshold_{Trichostrongylus}$ = 10°C, $threshold_{Haemonchus}$ = 10°C); and γ & δ are constant mortality rates (proportion day^{-1}) specific to each nematode species ($\gamma_{Teladorsagia}$ = 0.00094, $\gamma_{Trichostrongylus}$ = 0.023, $\gamma_{Haemonchus}$ = 0.027, $\delta_{Teladorsagia}$ = 0.0085, $\delta_{Trichostrongylus}$ = 0.043, $\delta_{Haemonchus}$ = 0.12). These relationships are illustrated in Figure 6.

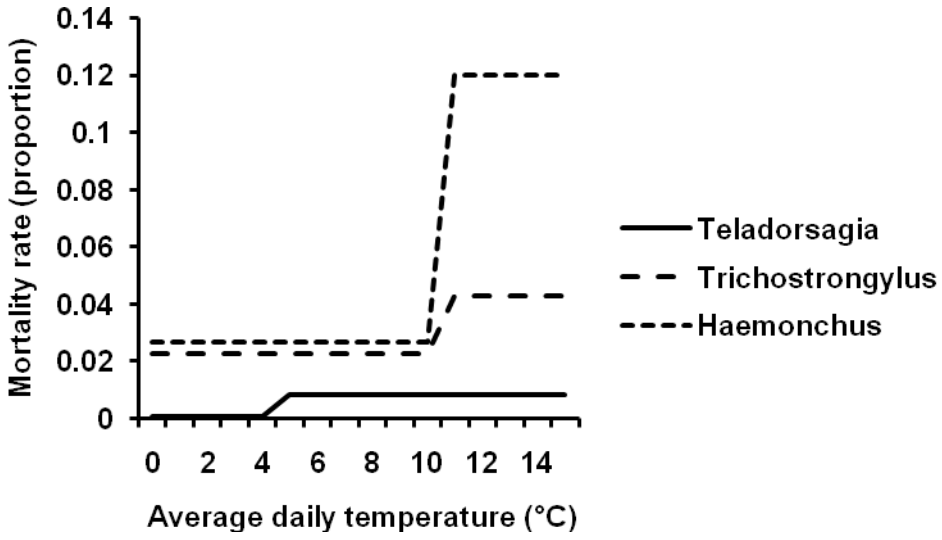

Figure 6. The relationship between average daily temperature and the mortality rates of the infective larvae of *Teladorsagia*, *Trichostrongylus* and *Haemonchus* as described by Learmount *et al*.[10]

Further, the daily mortality rate of infective larvae (μ_2) for each nematode species is assumed to be dependent on rainfall. If the average rainfall in a given month is less than 50mm then daily mortality rates are assumed to double.

4. The average lifetime (Φ_2, weeks) of an infective larva (for all nematode species) on herbage is given as (for $\phi_2 > 0$)[11,16]:

$$\phi_2 = 32.2 - 0.238 \cdot \sum_{i=7}^{10} twi - 1.04 \cdot \ln\left(1 + \sum_{i=7}^{10} rwi\right)$$

where *twi* is the average daily maximum air temperature (°C) in the i^{th} week after faeces were deposited on pasture, *rwi* is the total rain (mm) in the i^{th} week after faeces were deposited on pasture.

5. Constant proportional mortality rate of 0.035 day^{-1}.[18]
6. Constant proportional mortality rates of 0.0284 day^{-1} for infective larvae in faeces, and 0.00887 day^{-1} for infective larvae on herbage under temperate conditions.[23]
7. Reference is made to unpublished work (Callinan, Morley and White) relating survival to daily weather data. 'The rate parameters are expressed as transition probabilities. Transition matrices of these probabilities are accessed each day according to mean air temperature and soil moisture status … random numbers from a uniform distribution determine the transition to be made, depending on whether they are less than the cumulative probabilities for remaining in a particular stage, developing to the next stage or dying.' This would infer that a cumulative probability function is calculated from look-up tables for temperature and soil moisture, and the event (e.g. mortality) is determined by comparison to a random number.

4.10 Free-living nematode stages: duration of egg to infective larvae

4.10.1 Free-living nematode stages: duration of egg to infective larvae - overview

Table 10. Summary of the models describing the duration of egg development to infective larvae

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	✓
7	✓

4.10.2 Free-living nematode stages: duration of egg to infective larvae – functions (by model)

1. Constant duration of 21 days.[4]

2. The duration of eggs to infective larvae (days) follows a defined seasonal pattern given in Figure 7 and is given as representative of New Zealand conditions[6].

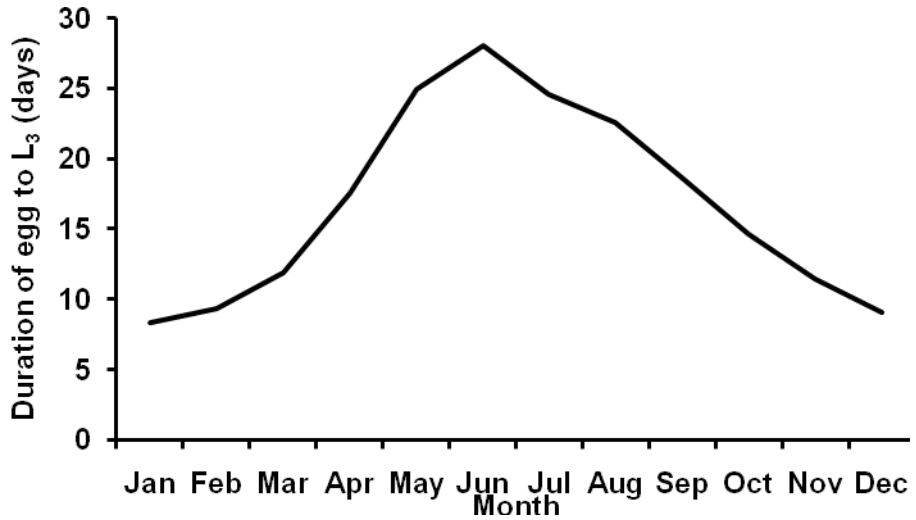

Figure 7. The duration of egg development to infective (days) across a single year used as a representation of New Zealand conditions in Leathwick *et al*.[6]

3. The duration of eggs to infective larvae is determined by a cumulative probability function (p) on day t after deposition for each nematode species such that[10]:

$$p(t) = p(t-1) \quad \text{for } °C(t) < threshold$$

$$p(t)_{Teladorsagia} = p(t-1)_{Teladorsagia} + \frac{1}{132 \cdot °C(t)^{-1.1018}} \quad \text{for } °C(t) > threshold_{Teladorsagia}$$

$$p(t)_{Trichostrongylus} = p(t-1)_{Trichostrongylus} + \frac{1}{436 \cdot °C(t)^{-1.432}} \quad \text{for } °C(t) > threshold_{Trichostrongylus}$$

$$p(t)_{Haemonchus} = p(t-1)_{Haemonchus} + \frac{1}{e^{6.82-(1.75 \cdot \ln(°C(t)))}} \quad \text{for } °C(t) > threshold_{Haemonchus}$$

where *threshold* is a constant specific to each nematode species ($threshold_{Teladorsagia}$ = 4°C, $threshold_{Trichostrongylus}$ = 10°C, $threshold_{Haemonchus}$ = 10°C), °C(t) is the average temperature on day t.

The probability on a given day of an egg developing to an infective larva in relation to average daily temperature (°C) is given in Figure 8.

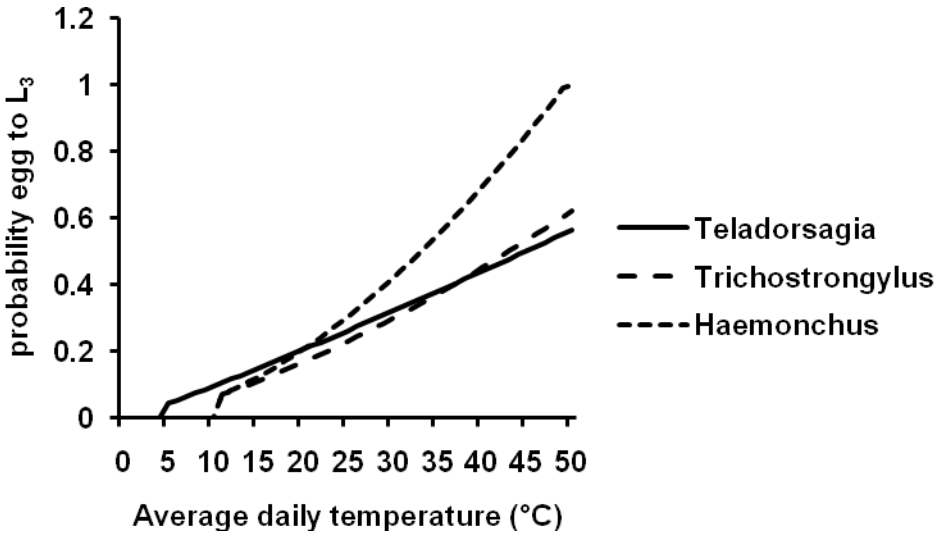

Figure 8. The relationship between average daily temperature and the probability that an egg develops to an infective larva for *Teladorsagia*, *Trichostrongylus* and *Haemonchus* as described by Learmount *et al*.[10]

4. The average time (Φ_1, weeks) for larval development and migration to herbage is given as[11,16]:

$\phi_1 = 1$	for *T.circumcincta*
$\phi_1 = 0.5$	for *H.contortus*
$\phi_1 = 3.58 - 0.138 \cdot T_1 + 0.281 \cdot n*$	for *T.colubriformis* (for $\phi_1 > 0$)

where T_1 is the average daily minimum air temperature (°C) in the first week after egg deposition on pasture, $n*$ is the number of weeks until cumulative rainfall over 7 days or less exceeds 16mm.

5. Constant duration of 7 days.[18]

6. The duration of development of eggs to infective larvae (t_h, days) is given such that[23]:

$$\sum_{i=t}^{t+t_h} e^{41.51-1268\cdot\left(K(i)^{-1}\right)} \geq 1$$

where K is the average temperature (°K) on day t.

7. Reference is made to unpublished work (Callinan, Morley and White) relating duration of development to daily weather data. 'The rate parameters are expressed as transition probabilities. Transition matrices of these probabilities are accessed each day according to mean air temperature and soil moisture status … random numbers from a uniform distribution determine the transition to be made, depending on whether they are less than the cumulative probabilities for remaining in a particular stage, developing to the next stage or dying.' This would infer that a cumulative probability function is calculated from look-up tables for temperature and soil moisture, and the duration of development is determined by comparison to a random number.

4.11 Free-living nematode stages: population dynamics - discussion

The free-living stages of the nematode life cycle contain the larger fraction of the nematode population (across all stages). Further, the free-living stages represent a large *refugia* pool of anthelmintic susceptible alleles when considering the development of anthelmintic resistance. Whilst host-parasite interactions may be expected to impact on the number of free-living stages present (via egg deposition and removal of infective larvae by herbage consumption), the greatest factor affecting the dynamics of the free-living stages is considered to be environmental conditions. The impact of climatic variables on the prevalence/abundance of nematode species is assumed to account for the differences observed between agro-climatic regions. Notably, of the models reviewed, model 1[4] and model 5[18] utilise constants for the mortality of pre-infective larvae, the duration of egg development to infective larvae and the mortality rate of infective larvae. Thus, they do not account for any interaction with climatic variables. Whilst model 2[6] does not explicitly include relationships between meteorological data and the survival of pre-infective nematode stages and the duration of egg development to infective larvae, observed seasonal patterns described by Vlassoff[28] are used.

Model 3[10] relies on stringent temperature and rainfall thresholds rather than variable functions to determine mortality rates for pre-infective larvae and infective larvae as well as the duration of development from egg to infective larva. This necessitates a sensitivity analysis to identify the limitations and implications of this methodology, however, thus far no sensitivity analysis has been carried out in regards to these temperature and rainfall thresholds.

Model 4[11,16] uses functions describing the probability and duration that an egg develops to an infective larva and migrates onto herbage, and the average lifespan of infective larvae on herbage. These functions are fit into the function described by Tallis and Donald[47]. However, the parameters and factors affecting the dynamics of differing nematode species are inconsistently given as either relationships or constants. Further, the model fit to the data used for parameterisation is given as R^2 = 0.39, and an independent validation resulted in R^2 = 0.11. These, poor correlations may be due to the absolute differences between meteorological data and microclimatic conditions. However, a notable flaw in the functions given above is that they assume a prior knowledge of maximum air temperature, rainfall and evaporation (i.e. development is dependent on conditions that eggs have not yet experienced).

Model 6[23] defines the impact of daily average temperature on the development from egg to infective larvae and the mortality rate of pre-infective and infective larvae for a Temperate and Mediterranean climate. However, no sensitivity analysis has been carried out on the constants used within the functions described above. Further, no quantitative validation study was carried out and no indication of the correlation between observed and predicted nematode life cycle stage populations are provided. To add to this the necessity to specify a Temperate or Mediterranean climate would indicate a lack of confidence in the relationship described, possibly due to a lack of the inclusion of the impact of humidity.

As the functions describing the relationship between climatic variables and the mortality of pre-infective larvae were not provided for Model 7[26] it is not considered further in this section.

Currently, none of the models reviewed satisfactorily describes the impact of climatic variables on the dynamics of the free-living stages of the nematode life-cycle. As such, further data and literature need to be used in order to formulate better relationships. Data illustrating the role of moisture and temperature in regulating the development of

Haemonchus contortus and *Trichostrongylus colubriformis* are available at the University of New England (UNE) and arose from the experimental studies of three PhD students. Further, a literature search identified 45 experimental studies and reviews[48-91] relating the impact of climatic variables to the dynamics of the free-living stages of the nematode life-cycle for *Haemonchus contortus*, *Trichostrongylus axei*, *Teladorsagia circumcincta*, *Trichostrongylus colubriformis*, *Trichostrongylus rugatus* and *Trichostrongylus vitrinus*. Further consideration may also be needed to relate meteorological data to microclimatic conditions.

4.12 Free-living nematode stages: larval availability for ingestion

4.12.1 Free-living nematode stages: larval availability for ingestion - overview

Table 11. Summary of the models describing larval availability for ingestion

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	✓
7	✓

4.12.2 Free-living nematode stages: larval availability for ingestion – functions (by model)

1. Initial larval availability for ingestion (at day 0) is defined as an input parameter (10,000 infective larvae lamb^{-1}). Larval availability (L, infective larvae lamb^{-1}) on day t is subsequently given as[4]:

$$L_t = L_{t-1} \cdot (1-\mu_2) + (EE_{t-u} + WB_{t-u} \cdot f_{t-u}) \cdot (1-\mu_1)$$

where μ_1 is the mortality rate of pre-infective larvae (constant, 0.23 day^{-1}), μ_2 is the mortality rate of infective larvae (constant, 0.008 day^{-1}), EE is the ewe egg contribution (eggs ewe^{-1} day^{-1}), WB is the average parasitic (worm) burden within the lamb population (nematodes lamb^{-1}), f is the density-dependent worm fecundity (eggs nematode^{-1} day^{-1}), u is the duration from egg to infective larvae (constant, 21 days).

2. The percentage of total infective larvae available to lambs for ingestion (pL_a) is given as[6]:

$$pL_a = e^{\frac{AH}{463}}$$

where AH is the herbage available for ingestion (kg DM ha^{-1}). As herbage density (kg DM ha^{-1}) is defined, and available herbage is given as half herbage density, the proportion of the total larval population available for ingestion in given in Figure 9.

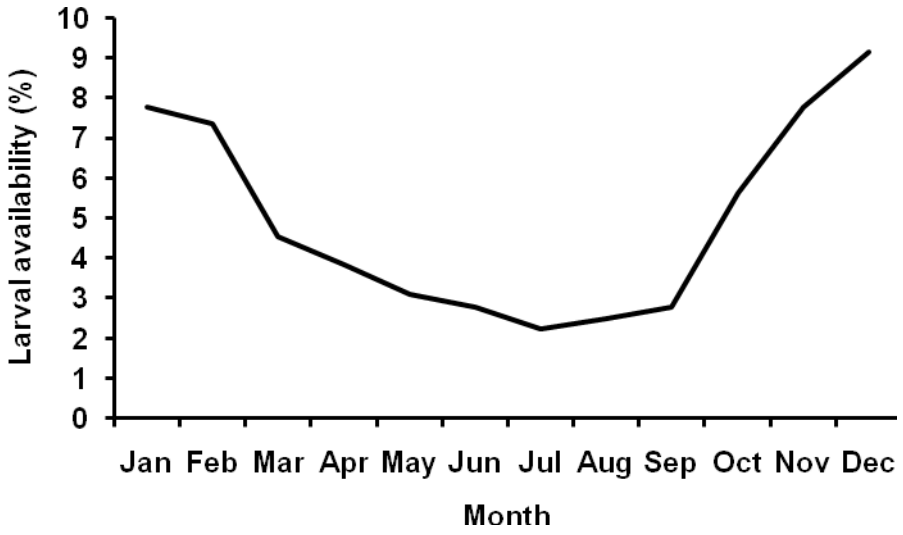

Figure 9. The percentage of the infective larval population available for ingestion (%) across a single year used as a representation of New Zealand conditions in Leathwick *et al*.[6]

3. The initial larval availability for ingestion (infective larvae kg DM^{-1}) is given as an input. Larval availability on day *t* (*L*(*t*), total infective larvae) is subsequently given as[10]:

$$L(t) = \left(L(t-1) + newL(t) - \left(\sum LI_{EWE}(t-1) + \sum LI_{LAMB}(t-1)\right)\right) \cdot (1-\mu_2)$$

where *newL* is the infective larvae arising from the pre-infective stages, LI_{EWE} and LI_{LAMB} is the larval intake of ewes and lambs, and μ_2 is the mortality rate of infective larvae.

4. Larval availability given as total infective larval population of pasture[11].
5. The initial larval availability for ingestion (infective larvae kg DM^{-1}) is given as an input. Larval availability on day *t* (L(*t*), total infective larvae) is subsequently given as[18]:

$$L_t = \left(\left(L_{t-1} - \sum LI_{t-1}\right) \cdot (1-\mu_2)\right) + \left(\sum E_{t-u} \cdot PEI\right)$$

where *LI* is the larval intake of lambs, μ_2 is the mortality rate of infective larvae (constant, 0.035), *E* is eggs deposited on pasture, *PEI* is the proportion of eggs developing to infective larvae (constant, 0.11), and *u* is the duration of development from egg to infective larvae (constant, 7 days).

6. Larval availability given as total infective larval population of pasture[23].
7. The proportion of the larval population on pasture at sward heights of 0-1cm and 1-3cm at a specific relative humidity (%) and temperature (°C) was given by a look-up table. Grazing height is assumed to be half pasture height (*HT*, cm) given as[26]:

$$HT = -0.777 + 0.00419 \cdot AG$$

where *AG* is the quantity of green herbage available (kg ha^{-1}).

4.12.3 Free-living nematode stages: larval availability for ingestion – discussion

The availability of infective larvae for ingestion is an important factor determining the infection rate of hosts. Models 1[4], 3[10], 4[16], 5[18] and 6[23] all assume that the migration of infective larvae on pasture is accounted for within the calculation of the population of infective larvae on pasture. However, Model 2[6] and 7[26] also consider the vertical migration/distribution of infective larvae on pasture. Model 2[6] assumes an exponential relationship for the vertical distribution of larvae on herbage (Vlassoff[28]), with grazing height arbitrarily set at half that of the herbage and thereby calculates the percentage of infective larvae available for ingestion. Model 7[26] determined a relationship between pasture height and herbage density, assuming grazing height was normally distributed with the mean and standard deviation being half the pasture height. Infective larvae were only available for ingestion if the grazing height was less than 3 cm and the proportion of infective larvae available for ingestion being given by a look-up table from Rees[92] which details the proportions of infective larvae of *Haemochus contortus* on herbage at heights of 0-1 cm and 1-3 cm under differing temperatures and humidities. Whilst model 7[26] does not simulate *Haemonchus contortus* infections, the distribution of *Trichostrongylus colubriformis* and *Teladorsagia circumcincta* are assumed to be the same as *Haemonchus contortus*.

The vertical distribution of larvae on pasture may significantly impact upon the larval availability for host consumption, however, the simplistic nature of the functions describing the vertical distribution of infective larvae and the grazing height of the host population in models 2[6] and 7[26] may require further attention. Reappraisal of these functions and assumptions may be informed by available literature on the vertical distribution of infective larvae on pasture[133-141] and the host's bite-depth[142-150].

In regards to the spatial/horizontal distribution of infective larvae across pasture, all the models reviewed assumed the infective larvae were distributed equally across the pasture. Previous modelling work has been carried out to look at simulating a Poisson distribution, however, when also assuming that sheep graze randomly across pasture the effect was equal to assuming equal distribution across pasture. Thus, the simpler option was preferred.

4.13 Host: nutritional requirements

4.13.1 Host: nutritional requirements - overview

Table 12. Summary of the models describing the nutritional requirements of the host.

Model	Included
1	-
2	-
3	-
4	-
5	✓
6	-
7	✓

4.13.2 Host: nutritional requirements – functions (by model)

5. The protein requirements for maintenance (PR_{MAINT}, kg day-*1*), growth (PR_{GROWTH}, kg day^{-1}), wool (PR_{WOOL}, kg day^{-1}) and immunity (PR_{IMM}, kg day^{-1}) are given as[17]:

$$PR_{MAINT} = 0.004 \cdot \left(\frac{P}{P_m} \right)^{-0.185}$$

$$PR_{GROWTH} = \frac{\Delta PG_{\max}}{ep}$$

$$PR_{WOOL} = \frac{\Delta PWool_{\max}}{ew}$$

$$PR_{IMM} = \frac{\left(0.2 \cdot PR_{MAINT}\right) \cdot \dfrac{\ln\left(\dfrac{0.0001}{\left(3 - \dfrac{LI}{5000}\right) \cdot \left(\dfrac{LI}{1 \cdot 10^6}\right)^2} \right)}{\ln(0.01)}}{ei}$$

Where P is the current body protein mass (kg), P_m is the body protein content at maturity (kg), ΔPG_{max} is the expected maximum daily body protein growth (kg day^{-1}), $\Delta PWool_{max}$ is the expected maximum daily wool growth (kg day^{-1}), ep is the efficiency of protein preposition (0.26),ew is the efficiency of protein use for wool (0.59), LI is larval intake, ei is the efficiency of protein use for immunity (0.59).

The energy requirements for maintenance (ER_{MAINT}, kg day^{-1}), growth (ER_{GROWTH}, kg day^{-1}) and wool (ER_{WOOL}, kg day^{-1}) are given as[17]:

$$ER_{MAINT} = 1.63 \cdot \left(\frac{P}{P_m^{\,0.27}} \right)$$

$$ER_{GROWTH} = \left(bl \cdot \Delta L_{des}\right) + \left(bp \cdot \Delta PG_{\max}\right)$$

$$ER_{WOOL} = bp \cdot \Delta PWool_{\max}$$

where P is the current body protein mass (kg), P_m is the body protein content at maturity (kg), ΔL_{des} is the desired lipid growth (kg day^{-1}), ΔPG_{max} is the expected maximum daily body protein growth (kg day^{-1}), $\Delta PWool_{max}$ is the expected maximum daily wool growth (kg day^{-1}), bl is energetic cost of lipid deposition (56 MJ kg^{-1}), and bp is the energetic cost of protein deposition (50 MJ kg^{-1}).

Total protein requirements (PR) and energy requirements (ER) are the sum of the individual requirements for maintenance, growth and wool.

7. The energy requirements for maintenance (ER_{MAINT}, MJ day^{-1}), pregnancy (ER_{PREG}, MJ day^{-1}), and lactation (ER_{LACT}, MJ day^{-1}) are given as[27]:

$$ER_{MAINT} = \frac{\left(0.23 + \dfrac{0.017}{0.048 + \left(AGE + 0.2\right)^3}\right) \cdot W^{0.75} \cdot \left(1.3 - 0.1 \cdot SIN\left(\left(t + 130\right) \cdot \left(2 \cdot \dfrac{\pi}{365}\right)\right)\right)}{0.546 + 0.244 \cdot DH}$$

$$ER_{PREG} = 0.38 \cdot FW + FG$$

$$ER_{LACT} = 7 \cdot MILK_{POT}$$

where *AGE* is the age of the sheep (years), *W* is the live weight (kg), *t* is the day of the year, *DH* is digestibility of herbage, *FW* is foetus weight (kg), *FG* is foetal growth (energy retention, kg), and $MILK_{POT}$ is the potential milk yield (kg day^{-1}).

4.13.3 Host: nutritional requirements - discussion

The nutritional requirements of the host are important when considering host growth, relating desired herbage intake to herbage quality, and accounting for the impact of herbage quality and supplementation on immunological responses. Of the models reviewed, only model 5[17-21] and model 7[26,27] considered the nutritional requirements of the host. Model 7[26,27] considers the energy requirements for maintenance, pregnancy and lactation with growth being given as the retention of remaining energy. Whilst, herbage intake is predominantly driven by the metabolisable energy content of herbage, the protein requirements of the host also need consideration due to the impact of parasitism and the acquisition of immunity. Model 5[17-21] considers both the protein and energy requirements for maintenance, body growth, wool growth and immunity. Thus, all these traits can be affected by the nutritional content of herbage, the effects of parasitism on herbage intake, and the availability of resources for allocation to differing processes. However, the protein and energy requirements for pregnancy and lactation are not yet included in model 5[17]. The development of functions describing protein and energy requirements may be initially based on the functions outlined for models 5[17] and 7[26], and further informed by publications detailing and investigating the protein and energy requirements for maintenance, growth, immunity, pregnancy and lactation. A search of literature identified a total of 24 publications[93-116] specifically relating to sheep. All these publications either directly used or compared experimental results against one of five models used to determine protein and energy requirements for the formulation of feeding systems. Namely, those devised by the USA National Research Council (NRC), Institut National de la Recherche Agronomique (INRA), Commonwealth Scientific and Industrial Research Organisation (CSIRO), Agricultural and Food Research Council (AFRC), and Cornell Net Carbohydrate and Protein System (CNCPS). These models are extensively reviewed and compared by Tedeschi *et al*.[114]

4.14 Host: herbage intake

4.14.1 Host: herbage intake - overview

Table 13. Summary of the models describing the herbage intake of the host

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	-
7	✓

4.14.2 Host: herbage intake – functions (by model)

1. Herbage intake (*HI*, kg DM lamb^{-1}) at age *t* (days) is given as[4]:

   $$HI_t = 0.109 \cdot (W_t - 10.18)$$ See Figure 10.

   where *W* is live weight (kg).

2. Herbage intake (*HI*, kg DM lamb^{-1}) at age *t* (days) is assumed to be zero for the first 14 days after birth, after which it is given as[6]:

   $$HI_t = 1.45 \cdot \frac{(t-14)^2}{3600 + (t-14)^2}$$ See Figure 10.

3. The herbage intake of ewes is a constant (2.3 kg DM day^{-1}), whereas the herbage intake of lambs (*HI*, kg DM lamb^{-1}) at day *t* after weaning is given as[10]:

   $$HI_t = 1.5 + t \cdot \left(\frac{0.8}{364}\right)$$ See Figure 10.

4. Herbage intake (*HI*, kg DM lamb^{-1}) at age *t* (days) is given as[14]:

   $HI_t = 0$ for $t \leq 42$

   $HI_t = (t - 42) \cdot \left(\frac{1}{154}\right)$ for $196 < t > 42$ See Figure 10.

   $HI_t = 1$ for $t \geq 196$

5. The desired herbage intake for meeting energy requirements (HI_{ENERGY}, kg DM day^{-1}) is given as[17]:

   $$HI_{ENERGY} = \frac{ER}{1.15 \cdot ME - 3.84 - 4.67 \cdot (0.9 \cdot CP - 0.032)}$$

   where *ER* is the energy requirements (kg day^{-1}), *ME* is the metabolisable energy content of herbage (MJ kg^{-1} DM), and *CP* is the crude protein content of the herbage (g kg^{-1} DM).

   The desired herbage intake for meeting protein requirements ($HI_{PROTEIN}$, kg DM day^{-1}) is given as[17]:

   $$HI_{PROTEIN} = \frac{PR}{MP}$$

   where *PR* is the protein requirements (kg day^{-1}), and *MP* is the metabolisable protein content of herbage (calculated according to the AFRC digestion model[46]).

   Herbage intake (*HI*, kg DM day^{-1}) is then given as the greater of HI_{ENERGY} and $HI_{PROTEIN}$.

7. Herbage intake (*HI*, g day^{-1}) is given as[27]:

$$HI = HI_{\max} \cdot \left(FG \cdot DG + FD \cdot \left(1 - FG\right) \cdot DD\right)$$

where HI_{max} is the maximum herbage intake (g day^{-1}), *FG* is the proportion of green herbage consumed, *FD* is the proportion of dead herbage consumed, *DG* is the digestibility of green herbage, *DD* is the digestibility of dead herbage, *t* is the animal age (days), *AG* is the available green herbage (kg), and *AD* is the available dead herbage (kg).

$$HI_{\max} = 280 + 30 \cdot \left(50 - 45 \cdot e^{-0.005t}\right) - 0.00007 \cdot \left(50 - 45 \cdot e^{-0.005t}\right)^4$$

$$FG = \left(1 - e^{-0.000002AG^2}\right) \cdot e^{-3 \cdot (DG - 0.85)^2}$$

$$FD = \left(1 - e^{-0.000002AD^2}\right) \cdot e^{-3 \cdot (DD - 0.85)^2}$$

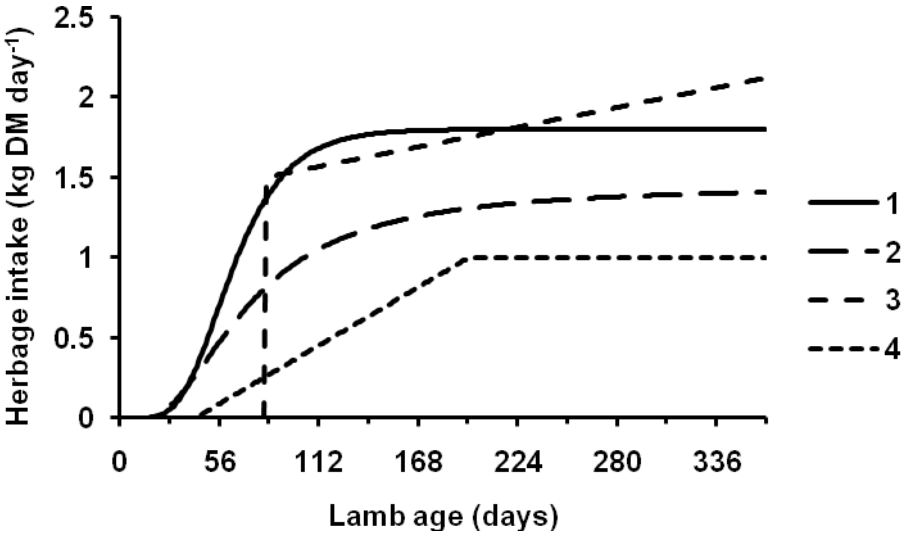

Figure 10. Herbage intake (kg DM day^{-1}) as described by Singleton *et al*.[4] (model 1), Leathwick *et al*.[6] (model 2), Learmount *et al*.[10] (model 3), and Barnes & Dobson[14] (model 4).

4.14.3 Host: herbage intake – discussion

Whilst herbage intake may be expected to impact upon host productive traits, the principle function of modelling herbage intake when simulating the epidemiology of nematodes is to determine the infection rate (i.e. the number of infective larvae ingested by the host). Notably, model 6[22-25] removed the necessity to model herbage intake for this purpose by assuming that a constant proportion of the infective larvae on pasture are ingested on any given day. However, this may prove to be an inappropriate assumption given that herbage intake does not remain constant but rather varies with herbage quality, host requirements for maintenance, growth, pregnancy and lactation, as well as the impact of parasite-induced anorexia (see section 4.15).

Models 1[4], 2[6], 3[10] and 4[14] assumed a defined relationship between herbage intake and lamb age, and do not consider host requirements or herbage quality. Thus, herbage intake is unaffected by herbage quality or the impact of parasitism upon fulfilling host requirements. As such these functions are unsuitable for simulating nutritional control strategies.

Model 7[27] assumed that herbage intake is related to the availability and digestibility of herbage and is not associated with host condition or host requirements. In contrast, model

5[17] assumed that the lamb would attempt to ingest sufficient nutrients to meet the protein and energy requirements for maintenance, immunity, growth and wool production. Herbage intake is consequently a function of the herbage quality, host requirements, host digestion and host metabolism. However, the herbage intake predictions based on model 5[17] still require validation. In regards to this, there is a plethora of publications detailing experimental studies which recorded the food intake of penned ruminants due to the technical difficulties of accurately recording food intake in grazing animals. However, for the purposes of modelling herbage intake, its relation to factors such as herbage quality and the host's nutritional requirements need to be considered. After specifying the requirement to relate the food intake of sheep to such factors, a total of 14 reviews, mathematical models and books were identified[117-130]. Some of the earlier publications informed the food intake models incorporated into the GRAZPLAN, GRAZFEED and AUSFARM models/tools developed by CSIRO. However, the functions described in these models may require reappraisal in light of more recent experimental studies and current research being carried out using smart-tags to record food intake in grazing sheep as part of a collaborative project between DPI (NSW) and CSIRO.

4.15 Host: parasite-induced anorexia

4.15.1 Host: parasite-induced anorexia - overview

Table 14. Summary of the models describing parasite-induced anorexia

Model	Included
1	-
2	-
3	-
4	✓
5	✓
6	-
7	✓

4.15.2 Host: parasite-induced anorexia – functions (by model)

4. The *Trichostrongylus colubriformis* parasitic burden (WB_{Trich}) is assumed to cause a reduction in herbage intake (HI_{RED}, kg DM day^{-1}), such that[14] (see Figure 11):

$$HI_{RED} = 0 \qquad \text{for } WB_{Trich} \leq 1000$$

$$HI_{RED} = 1 - \left(2.048 - 0.3493 \cdot \log_{10}(WB)\right) \qquad \text{for } 1000 < WB_{Trich} > 81000$$

$$HI_{RED} = 0.67 \qquad \text{for } WB_{Trich} \geq 81000$$

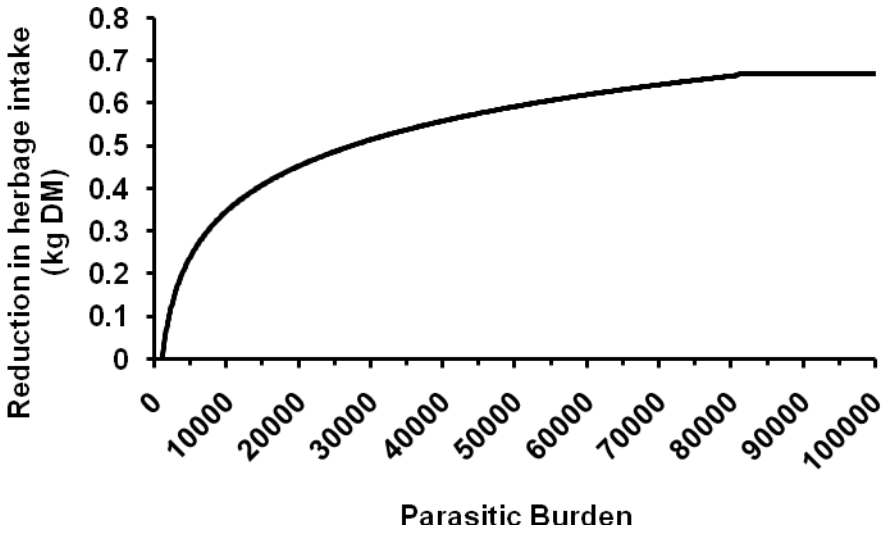

Figure 11. Proportional reduction in herbage intake as a function of parasitic burden, as detailed by Barnes & Dobson[14]

5. Parasite-induced anorexia was modelled as a direct function of the rates (i.e. 1st derivatives) of immune response acquisition, such that[17]:

$$HI = HI \cdot \left(1 - HI_{RED}\right) \text{ (kg DM day}^{-1}\text{)}$$

$$HI_{RED} = 2.5 \cdot \left(\frac{d\varepsilon}{dx} + \frac{d\mu}{dx} + \frac{df}{dx} \right)$$

where *HI* is herbage intake (kg DM day^{-1}), ε is establishment, *f* is fecundity, and μ is mortality.

7. Parasite-induced anorexia was modelled as a function of infection rate, such that[27] (see Figure 12):

$$HI = HI \cdot \left(1 - HI_{RED}\right)$$

$$HI_{RED} = -0.078 + 0.0000605 \cdot LI$$

where *HI* is herbage intake (g day^{-1}), and *LI* is the infective larval intake (ingestion).

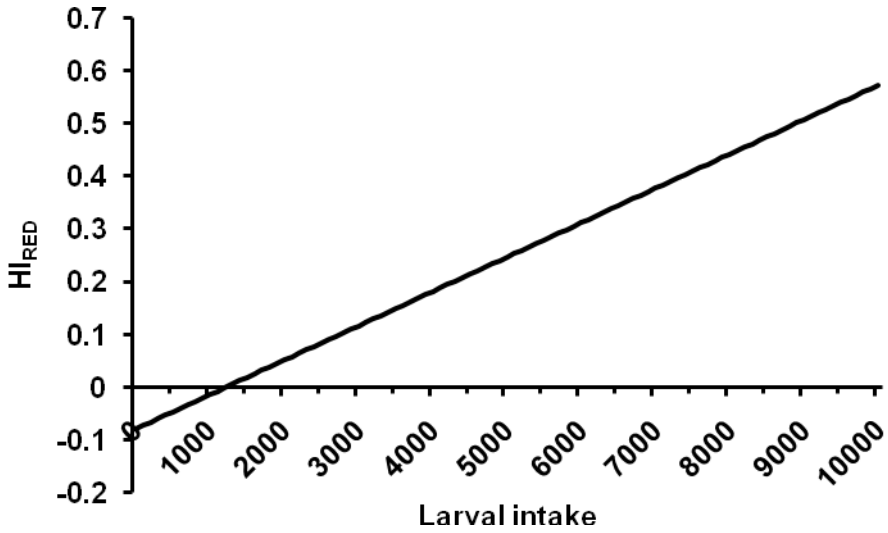

Figure 12. Proportional reduction in herbage intake as a function of larval intake as detailed by Callinan *et al*.[27]

4.15.3 Host: parasite-induced anorexia – discussion

Experimental studies have previously reported a reduction in food intake associated with infection rate in sheep (Coop *et al*.[131]). However, only three of the reviewed models account for the observed parasite-induced reduction in food intake. Model 4[14] incorporates a reduction in herbage intake related to the worm burden of *Trichostrongylus colubriformis*, but does not consider the impact of other nematode species (in correspondence with R.J. Dobson, 16th July 2014). However, it is important to note that the experiment detailed by Coop *et al*.[131] reported a reduction in food intake as a consequence of infection rate rather than worm burden. In line with this, model 7[27] utilises a linear relationship between the reduction in food intake and infection rate. In the later experimental study of Greer *et al*.[132], immune-suppressed lambs were shown to not exhibit reductions in food intake when challenged with *Teladorsagia circumcincta*. This suggested that the observed reductions in food intake were not a consequence of worm burden but rather caused by the development of an immune response. Model 5[17] therefore modelled the reduction in herbage intake as a function of the acquisition of immunity. The link between herbage intake and immunological response provides the potential to determine immunological responses from previous experimental studies (generally single species trickle challenge studies), which have not previously been exploited for this purpose. Thus, the results of such experimental studies may be reanalysed in light of recent findings and information derived from immunological studies. Further, as these studies are carried out for single species infections it is possible to determine differences in immune recognition for differing nematode species from experimental data. These studies also include growth data and therefore by determining the growth reduction due to reductions in herbage intake, the remaining reductions in growth may be attributed to direct (i.e. worm burden) losses due to parasitism.

4.16 Host: constrained herbage intake

4.16.1 Host: constrained herbage intake - overview

Table 15. Summary of the models describing constrained herbage intake.

Model	Included
1	-
2	-
3	-
4	-
5	✓
6	-
7	✓

4.16.2 Host: constrained herbage intake – functions (by model)

5. Constrained food intake (CFI, kg DM day^{-1}) is given as[17]:

$$CFI = \frac{CAP}{0.93 - \left(\frac{ME}{15.58}\right)}$$

where *CAP* is the capacity of the animal for daily indigestible organic matter (kg DM), and *ME* is the metabolisable energy content of the herbage (MJ kg^{-1} DM).

CAP is estimated as the lesser of:

$$CAP = 0.0223 \cdot W$$

or

$$CAP = 0.0223 \cdot 0.51 \cdot W_m$$

where *W* is the current live weight of the lamb (kg), and W_m is the body weight of the lamb at maturity (kg).

7. The maximum herbage intake (HI_{max}, g day^{-1}) is given as[27] (see Figure 13):

$$HI_{\max} = 280 + 30 \cdot \left(50 - 45 \cdot e^{-0.005t}\right) - 0.00007 \cdot \left(50 - 45 \cdot e^{-0.005t}\right)^4$$

where *t* is the animal age (days).

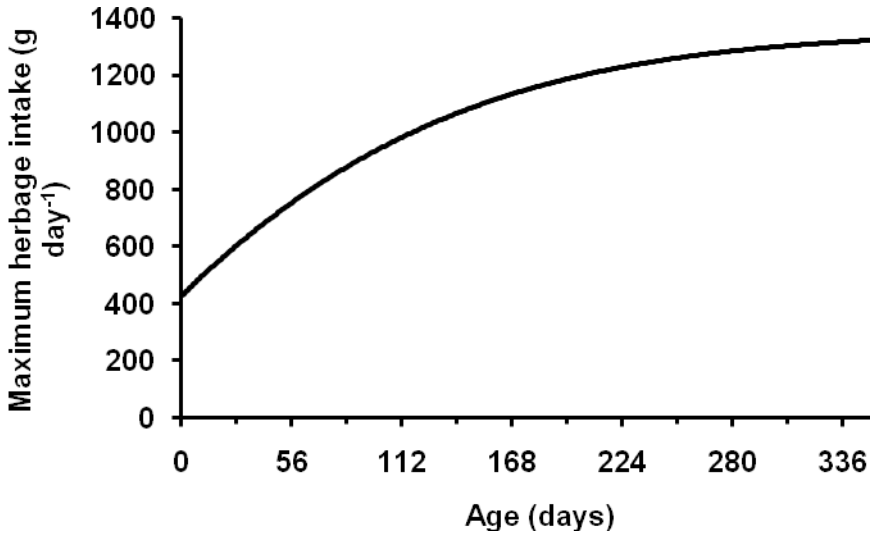

Figure 13. Maximum herbage intake as described by White *et al*.[27]

4.16.3 Host: constrained herbage intake – discussion

A number of factors can result in a host ingesting insufficient nutrients to meet it requirements for maintenance, growth, pregnancy, lactation and immunity. One such constraint is parasite-induced anorexia (see section 4.15), however, other factors may also constrain the host herbage intake. Both models 5[17] and 7[27] assume that there is a maximum intake capacity. Model 5[17] assumes this to be a function of live weight and herbage digestibility (related to metabolisable energy content). Model 7[27] assumes that the maximum intake capacity is a function of live weight, growth rate and age. However, neither model considers that the quantity of available herbage may be insufficient to allow *ad libitum* feeding. As this is an important consideration for Australian conditions (especially in times of drought), such a constraint will need to be included in a nematode epidemiology model as this would impact upon the ingestion of infective larvae and host mortality.

4.17 Host: infective larval intake

4.17.1 Host: infective larval intake - overview

Table 16. Summary of the models describing infective larval intake

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	✓
7	✓

4.17.2 Host: infective larval intake – functions (by model)

1. The larval intake (*LI*, infective larvae lamb^{-1} day^{-1}) on day *t* is given as[4]:

$$LI_t = \frac{L_t \cdot HI_t \cdot D}{AH}$$

where *L* is the larval availability for ingestion (infective larvae lamb^{-1}), *HI* is the herbage intake (kg DM lamb^{-1}), *D* is the stocking density of lambs (lambs ha^{-1}), and *AH* is the available herbage (1200 kg DM ha^{-1}).

2. The larval intake (*LI*, infective larvae lamb^{-1} day^{-1}) on day *t* is given as[6]:

$$LI_t = HI_t \cdot L_t \cdot \left(\frac{pL_a}{100} \right)$$

where *HI* is herbage intake (kg DM lamb^{-1}), *L* is the infective larvae population of the pasture (infective larvae kg^{-1} DM), and pL_a is the percentage of the infective larvae available for ingestion.

3. The larval intake (*LI*, infective larvae sheep^{-1} day^{-1}) on day *t* is given as[10]:

$$LI_t = HI_t \cdot \left(\frac{L_t}{AH \cdot ha} \right)$$

where *HI* is herbage intake(kg DM), *L* is the total infective larvae population on pasture, *AH* is the available herbage (1,797 kg DM ha^{-1}), and *ha* is the pasture size in hectares.

4. The larval intake (*LI*, infective larvae sheep^{-1} day^{-1}) on day *t* is given as (in correspondence with R.J. Dobson):

$$LI_t = HI_t \cdot \left(\frac{L_t}{AH \cdot ha} \right)$$

where *HI* is herbage intake (kg DM), *L* is the total infective larvae population on pasture, *AH* is the available herbage (0.141125 kg DM/m^2), and *ha* is the pasture size in m^2.

5. The larval intake (*LI*, infective larvae sheep^{-1} day^{-1}) on day *t* is given as[18]:

$$LI_t = HI_t \cdot \left(\frac{L_t}{AH} \right)$$

where *HI* is herbage intake (kg DM), *L* is the total infective larvae population on pasture, and *AH* is the total available herbage (kg DM).

6. The larval intake (*LI*, infective larvae calf^{-1} day^{-1}) on day *t* is given as[23]:

$$LI_t = 0.001 \cdot L_t$$

where *L* is the total infective larvae population on pasture.

7. The larval intake (*LI*, infective larvae sheep^{-1} day^{-1}) on day *t* is given as[26]:

$$LI_t = HI_t \cdot L_t$$

where *HI* is herbage intake (g), and *L* is the infective larvae population on pasture available for ingestion (infective larvae g^{-1}).

4.17.3 Host: infective larval intake – discussion

The ingestion of infective larvae by the host population may be expected to be affected by the herbage density, the infective larval population on pasture and herbage intake. However, model 6[23] does not simulate herbage density or herbage intake and thus infective larval intake is given as a constant proportion of the infective larval population on pasture. All the other models reviewed assumed that the infective larval population on pasture were equally horizontally/spatially distributed. Thus, infective larval intake was related to herbage intake by considering the number of infective larvae per kg of herbage calculated as a function of herbage density and pasture size. To add to this, models 2[6] and 7[27] also considered the vertical distribution of the infective larval population and the grazing height of the ruminant population (see section 4.12).

Further, variation in the grazing behaviour of the sheep population (and correlations to resistance traits) could be represented by including a genetic control component to infective larval intake, thus between animal variation could be included to account for the avoidance grazing of parasite resistant sheep.

4.18 Host: digestion

4.18.1 Host: digestion - overview

Table 17. Summary of the models describing digestion

Model	Included
1	-
2	-
3	-
4	-
5	✓
6	-
7	✓

4.18.2 Host: digestion – functions (by model)

5. The ‘efficiency of digestion, accounting for level of feeding, rumen outflow rate and current state of the lamb, and hence metabolisable protein available to the animal, were calculated using the equations described by the Agricultural and Food Research Council (AFRC)[46].’
7. Digestibility is given as a trait of herbage age (see section 4.4)[27].

4.18.3 Host: digestion – discussion

Digestion is an important factor in determining the herbage intake in model 5[17], and the digestibility of herbage is important in determining the availability of resources for allocation to the various processes in model 7[27]. The digestion of sheep was the focus of many studies from the 1950s through to the 1990s. However, more recently it is notable that this topic has received less attention due to general consensus. Digestion is known to be affected by feed quality and animal status/condition. Whilst model 5[17] considers herbage quality and host traits such as the level of feeding, rumen outflow rate and the current state of the lamb; model 7[27] only considers digestibility as a trait of the herbage.

Whilst a detailed model for digestion has not currently been developed, digestive models at the level required for a nematode epidemiology model are available and have previously been incorporated into predictive systems such as that described by AFRC[46]. However, currently no models for nematode infections have considered the impact of infection upon digestive processes. A number of experimental studies have previously investigated the impact of nematode infections on digestive and metabolic processes (some of which were conducted at UNE), and may be used to account for the impact of parasitism in a future model.

4.19 Host: nutrient allocation

4.19.1 Host: nutrient allocation - overview

Table 18. Summary of the models describing nutrient allocation

Model	Included
1	-
2	-
3	-
4	-
5	✓
6	-
7	✓

4.19.2 Host: nutrient allocation – functions (by model)

5. It was 'assumed that the maintenance needs of the lamb will be satisfied first.' … 'Nutrients remaining after allocation to maintenance are allocated to immunity and production (body and wool growth) in proportion to their requirements.' Protein allocated to growth (PAC_{GROWTH}, kg day^{-1}) and immunity (PAC_{IMM}, kg day^{-1}) are given as[17]:

$$PAC_{GROWTH} = \left(P_{AVAIL} - PR_{MAINT} - P_{LOSS}\right) \cdot \left(\frac{PR_{GROWTH}}{PR_{GROWTH} + PR_{IMM}}\right)$$

$$PAC_{IMM} = \left(P_{AVAIL} - PR_{MAINT} - P_{LOSS}\right) \cdot \left(\frac{PR_{IMM}}{PR_{GROWTH} + PR_{IMM}}\right)$$

where P_{AVAIL} is the total protein available from the herbage intake (kg), PR_{MAINT} is the protein requirements for maintenance (kg), and P_{LOSS} is the protein lost due to parasitism.
Daily lipid deposition ($\Delta Lipid$, kg day^{-1}) is given as[17]:

$$\Delta Lipid = \frac{\left(\left(HI \cdot \left(1.15 \cdot ME - 3.84 - 4.67 \cdot \left(0.9 \cdot CP - 0.032\right)\right)\right) - ER_{MAINT} - E_{PROTEIN}\right)}{bl}$$

where HI is herbage intake (kg DM), ME is the metabolisable energy content of the herbage (MJ kg^{-1}), CP is the crude protein content of the herbage (g kg^{-1}), ER_{MAINT} is the energy required for maintenance (MJ), $E_{PROTEIN}$ is the energy required for protein deposition (MJ), and bl is the energetic cost of lipid deposition (56 MJ kg^{-1}).

7. Energy arising from herbage intake is first allocated to meet requirements for maintenance, pregnancy and lactation, remaining energy is then allocated to energy retention (growth) and wool production[27].

4.19.3 Host: nutrient allocation – discussion

Model 7[27] considers the allocation of energy to maintenance, pregnancy, lactation, growth and wool production, however, in considering immunological responses to nematode infections the allocation of protein must also be included. Model 5[17] considers the allocation of energy and protein to maintenance, growth, wool production and immunity. However, as this model was only used to simulate lambs, pregnancy and lactation were not included. The allocation of available nutrients to meet requirements for maintenance, growth, immunity, pregnancy and lactation is the focus of a number of nutritional studies (supplementation and differing feeds). The allocation to various processes under normal conditions (i.e. non-parasitised) is generally accepted with maintenance requirements being met first, followed by pregnancy and lactation and remaining nutrients then partitioned towards growth functions. However, differences in opinion occur when an immune response is considered, where immunity is either allocated resources as part of maintenance requirements or proportionally to growth. This concept has previously been explored in a modelling study by Doeschl-Wilson *et al*.[151], and further simulation studies may be required to adjust the hierarchy of nutrient allocation so that predictions meet expectations and fit the results of experimental studies.

4.20 Host: metabolism/catabolism

4.20.1 Host: metabolism/catabolism - overview

Table 19. Summary of the models describing metabolism and catabolism

Model	Included
1	-
2	-
3	-
4	-
5	✓
6	-
7	✓

4.20.2 Host: metabolism/catabolism – functions (by model)

5. Constant efficiencies and energetic costs for the utilisation of available resources or the catabolism of body reserves are used, given as[17]:

   bl = 56 MJ kg^{-1}
   bl_c = 39 MJ kg^{-1}
   bp = 50 MJ kg^{-1}
   ei = 0.59
   ep = 0.26
   ew = 0.59

   where bl is the energetic cost of lipid deposition, bl_c is the heat combustion of lipid (i.e. catabolism), bp is the energetic cost of protein deposition, ei is the efficiency of protein use for immunity, ep is the efficiency of protein deposition for growth, and ew is the efficiency of protein use for wool.

7. The efficiency of utilisation of metabolisable energy is given as[27] (see Figure 14):

   $$em = 0.546 + 0.244 \cdot DF$$
   $$eg = 0.03 + 0.664 \cdot DF$$

   where em is the efficiency of utilisation of metabolisable energy for maintenance, eg is the efficiency of utilisation of metabolisable energy for growth and fattening, and DF is the digestibility of the energy of the herbage.

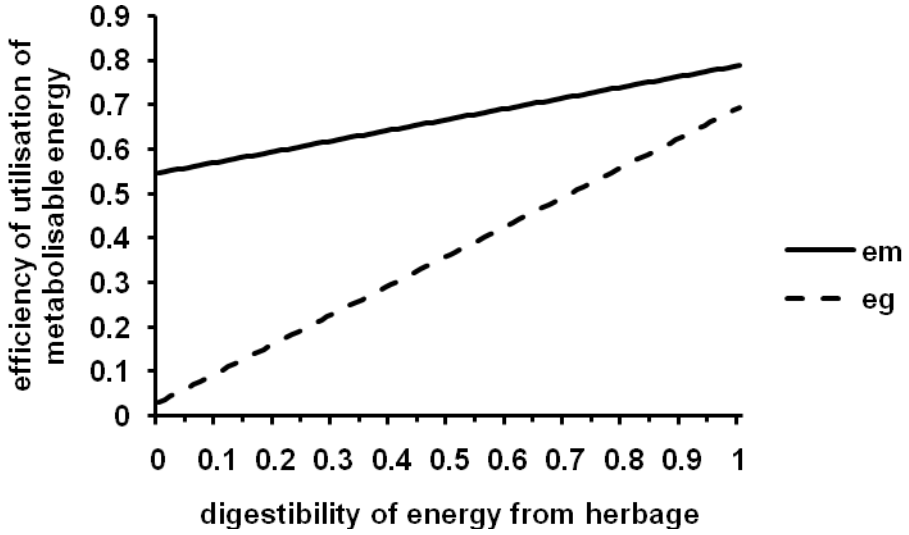

Figure 14. The efficiency of the utilisation of metabolisable energy for maintenance (em) and for growth (eg) as described by White et al.[27]

Further, the efficiency of utilisation of metabolisable energy for growth and fattening (*eg*) is reduced as a function of infection rate, such that[26] (see Figure 15):

$$eg = eg \cdot (1 - eg_{RED})$$
$$eg_{RED} = -0.135 + 0.000162 \cdot LI$$

where *LI* is the infective larval intake (ingestion).

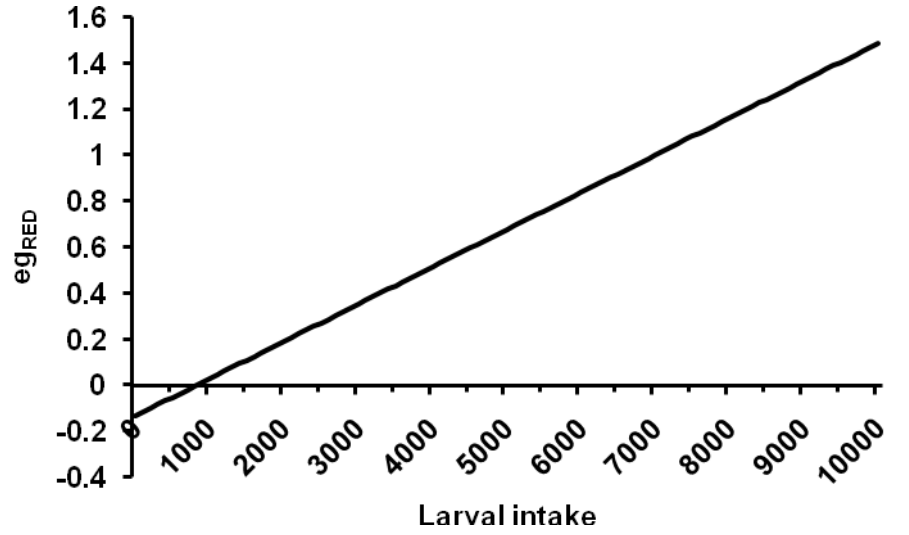

Figure 15. Reduction in the efficiency of the utilisation of metabolisable energy for growth as described by Callinan *et al*.[26]

4.20.3 Host: metabolism/catabolism – discussion

Metabolism (the efficiency of protein and lipid deposition) is known to be variable. Further, nematode infections have previously been shown to impact upon metabolic processes. As such, the functions described in model 7[26] may be preferential to the constants used in model 5[17]. However, experimental studies conducted at UNE regarding the impact of nematode infection metabolic processes may also aid in the construction of suitable functions to describe the dynamics of metabolism.

4.21 Host: live weight

4.21.1 Host: live weight - overview

Table 20. Summary of the models describing the host live weight.

Model	Included
1	✓
2	-
3	-
4	-
5	✓
6	✓
7	✓

4.21.2 Host: live weight – functions (by model)

1. Lamb live weight (*W*, kg) at age *t* (days) is given as[4] (see Figure 16):

$$W_t = 10.18 + 0.000036 \cdot e^{\frac{0.614\left(1-e^{-0.0471t}\right)}{0.0471}}$$

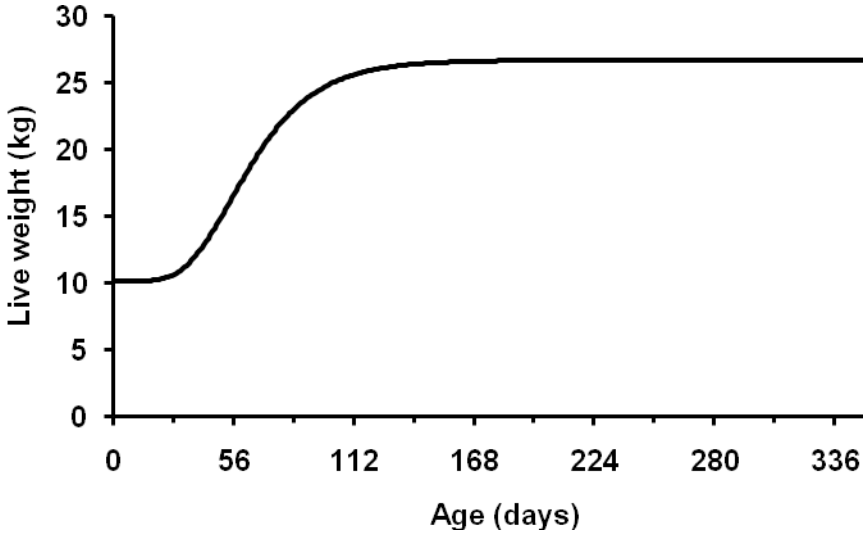

Figure 16. Lamb live weight (kg) as described by Singleton *et al*.[4]

5. Lamb live weight was calculated as the sum of protein, lipid, ash, water, wool and gut fill. Observed live weight is a result of desired growth for each component reduced according to constraints/reductions in herbage intake and direct losses due to parasitism (damage and repair). Functions describing the desired growth for each component and for gut fill were given as[17]:

$$\Delta PG_{\max} = P \cdot \frac{0.023}{P_m^{0.27}} \cdot \ln\left(\frac{P_m}{P}\right)$$

$$\Delta L_{des} = \Delta PG_{\max} \cdot \left(\frac{L_m}{P_m}\right) \cdot \left(1.46 \cdot \left(\frac{L_m}{P_m}\right)^{0.23}\right) \cdot \left(\frac{P}{P_m}\right)^{\left(\left(1.46 \cdot \left(\frac{L_m}{P_m}\right)^{0.23}\right)-1\right)}$$

$$\Delta Ash = 0.211 \cdot \Delta PG$$

$$\Delta Water = 2.65 \cdot \Delta PG \cdot \left(\frac{P}{P_m}\right)^{-0.185}$$

$$\Delta Wool_{\max} = \left(\frac{0.0009 \cdot P}{P_m^{0.27}}\right) + \left(0.16 \cdot \Delta PG_{\max}\right)$$

$$GF = HI \cdot \left(11 - \left(\frac{7 \cdot ME}{15}\right)\right)$$

where ΔPG_{max} is the maximum protein growth (kg day^{-1}), P is the current protein mass (kg), P_m is the protein mass at maturity (kg), ΔL_{des} is the desired lipid growth (kg day^{-1}), L_m is the lipid mass at maturity (kg), ΔPG is actual protein growth (kg), ΔAsh is the accretion of ash (kg day^{-1}), $\Delta Water$ is the accretion of water (kg), $\Delta Wool_{max}$ is the maximum wool growth (kg day^{-1}), GF is the gut fill (kg), HI is herbage intake (kg DM), and ME is the metabolisable energy content of the herbage (MJ kg^{-1} DM).

6. Calf live weight (W, kg) on day t of simulation is given as[24] (see Figure 17):

$$W_t = 66.41 \cdot e^{0.0041t}$$

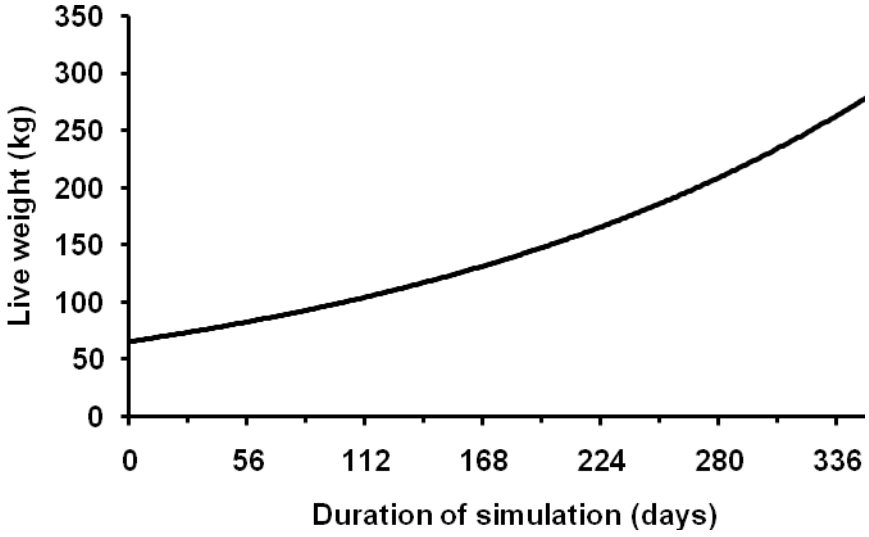

Figure 17. Calf live weight (kg) as described by Smith *et al*.[24]

7. Weight change (ΔW, kg day^{-1}) was given as[27]:

$$\Delta W = \frac{eg \cdot \left(\left(HI \cdot ME \right) - ER_{MAINT} - ER_{PREG} - ER_{LACT} \right)}{3.8 + 0.52 \cdot W}$$

where *eg* is the efficiency of utilisation of metabolisable energy for growth and fattening, *HI* is herbage intake (g day^{-1}), *ME* is the metabolisable energy content of herbage (MJ g^{-1}), ER_{MAINT} is the energy requirements for maintenance (MJ day^{-1}), ER_{PREG} is the energy requirements for pregnancy (MJ day^{-1}), ER_{LACT} is the energy requirements for lactation (MJ day^{-1}), and *W* is the current weight (kg).

4.21.2 Host: live weight – discussion

Sheep growth models have been and continue to be an important aspect of productive models used as tools for industry. Thus, this topic has received a lot of attention resulting in numerous models being developed and available for use. More recently however, experimental studies have focussed on genetic variation in growth traits (see section 4.26) as part of selective breeding programs for productive traits. As such, any growth model used as part of a nematode prediction model will need to incorporate the ability to satisfactorily account for variation via alterations to input parameters. Of the models reviewed, live weight predictions in models 1[4] and 6[24] are unaffected by herbage quality, herbage intake or parasitism, whilst models 5[17] and 7[27] are influenced by herbage quality, herbage intake, digestion, metabolism and parasitism. However, model 7[27] only considers energy retention, whilst model 5[17] considers the accretion of protein, lipid, ash and water.

4.22 Host: weight loss from parasitism

4.22.1 Host: weight loss from parasitism - overview

Table 21. Summary of the models describing the host weight loss due to parasitism

Model	Included
1	-
2	✓
3	-
4	-
5	✓
6	-
7	✓

4.22.2 Host: weight loss from parasitism – functions (by model)

2. Loss of live weight (W_{LOSS}, kg) due to parasitism is given as[6]:

$$W_{LOSS} = \left(\left(2.54 \cdot 10^{6} \right) \cdot \sum WB \right) + \left(\left(\left(3.21 \cdot 10^{5} \right) \cdot \sum LI \right) \cdot \left(1 - \left(\frac{\sum WB}{\alpha} \right) \right) \right)$$

where $\sum WB$ is cumulative worm burden, $\sum LI$ is cumulative larval intake, and α is a constant (value not published).

5. Reductions in weight gain were a result of reductions in herbage intake and protein losses due to parasitism (P_{LOSS}) given as[17]:

$$P_{LOSS} = \left(0.03 - \left(\left(1.6\cdot10^{-6}\right)\cdot WB\cdot f\cdot\left(\frac{WB}{2500}\right)^{-0.25}\right)\right)\cdot\left(\left(8\cdot10^{-5}\right)\cdot WB\cdot f\cdot\left(\frac{WB}{2500}\right)^{-0.25}\right)^{2}$$

where *WB* is worm burden, and *f* is fecundity (eggs worm^{-1}).

7. Reductions in weight gain were a result of reductions in herbage intake and the utilisation of metabolisable energy for growth[26,27]

4.22.3 Host: weight loss from parasitism – discussion

Of the models reviewed, only three included the impact of parasitism on weight gain. As such, the other models could not be used to evaluate the productive implications of parasitism or the impact of parasite control strategies on productive losses. Whilst model 1[4,5] does not currently include reductions in weight gain, future development has been proposed to relate the expression of immunity to reductions in growth rate (in correspondence with M.J. Stear, 18th August 2014). Whilst model 2[6] does not simulate live weight, the losses due to the impact of parasitism on growth rate are included and are given as a function of both infection rate and worm burden. Model 7[27] does not include a direct impact of parasitism but rather assumes that reductions in weight gain solely arise from reductions in herbage intake and metabolism. Model 5[17] assumes that reductions in weight gain occur as a result of reductions in herbage intake, however, it also includes a direct protein loss caused by the parasitic burden via damage and repair to the gastrointestinal lining and plasma leakage. Whilst currently this model does not include host genetic control in this function, the inclusion of between animal variation may allow for the simulation of host resilience to parasitism.

4.23 Host: wool growth

4.23.1 Host: wool growth - overview

Table 22. Summary of the models describing wool growth

Model	Included
1	-
2	-
3	-
4	-
5	✓
6	-
7	✓

4.23.2 Host: wool growth – functions (by model)

5. The maximum potential wool growth ($\Delta Wool_{max}$, kg day^{-1}) is given as[17]:

$$\Delta Wool_{\max} = \left(\frac{0.0009 \cdot P}{P_m^{\,0.27}} \right) + \left(0.16 \cdot \Delta PG_{\max} \right)$$

where ΔPG_{max} is the maximum protein growth (kg day^{-1}), P is the current protein mass (kg), and P_m is the protein mass at maturity (kg).

Actual wool growth is the result of the maximum potential wool growth and reductions in available resources for allocation to wool growth.

7. Wool growth ($\Delta WOOL$, kg week^{-1}) is given as[27]:

$$\Delta WOOL = \left(\frac{PF}{52} \right) \cdot \left(1 + 0.08 \cdot SIN\left(\left(D - 80 \right) \cdot \frac{2\pi}{365} \right) \right) \cdot 0.2 + 0.8 \cdot \left(\frac{\left(HI \cdot ME \right) - ER_{MAINT} - ER_{PREG} - ER_{LACT}}{HI_{\max} \cdot ME} \right)$$

where PF is the potential clean fleece weight (kg, undefined input parameter), D is the day of the calendar year, HI is the herbage intake (g day^{-1}), HI_{max} is the maximum herbage intake (g day^{-1}), ME is the metabolisable energy content of the herbage (MJ kg^{-1}), ER_{MAINT} is the energy requirements for maintenance (MJ day^{-1}), ER_{PREG} is the energy requirements for pregnancy (MJ day^{-1}), and ER_{LACT} is the energy requirements for lactation (MJ day^{-1}).

4.23.3 Host: wool growth – discussion

Both models 5[17] and 7[27] consider wool growth as a consequence of potential wool growth and the availability of resources. Model 5[17] assumes that the potential wool growth per day is a function of the protein attributes of each animal (current mass, mature mass and growth). In contrast, model 7[27] assumes that the potential wool growth per week follows a defined seasonal pattern (utilising a SIN curve). In regards to the impact of allocation of resources towards wool growth, model 5[17] considers the availability of protein and the energetic cost of protein deposition for wool growth, whilst model 7[27] only considers the availability of energy. A combination of model 5 (animal protein status, and protein and energy availability) and model 7 (seasonal wool growth) may be desirable for a potential future model.

4.24 Host: mortality

4.24.1 Host: mortality - overview

Table 23. Summary of the models describing host mortality

Model	Included
1	-
2	-
3	-
4	✓
5	✓
6	-
7	✓

4.24.2 Host: mortality – functions (by model)

4. The adult worm burden (*WB*) considered lethal to the host differs for each nematode species (LWB_{Trich}, LWB_{Tela}, LWB_{Haem}). For mixed infections host death is assumed to occur if[16]:

$$WB_{Trich} + \left(\frac{LWB_{Trich}}{LWB_{Tela}} \cdot WB_{Tela} \right) + \left(\frac{LWB_{Trich}}{LWB_{Haem}} \cdot WB_{Haem} \right) \geq LWB_{Trich}$$

where LWB_{Trich} = 25000, LWB_{Tela} = 50000, and LWB_{Haem} = 15000.

5. Host mortality would occur if insufficient resources were available to meet the protein and energy requirements for maintenance, and the host was unable to catabolise sufficient resources from reserves. The total protein available for catabolism (P_{LABILE}, kg) is given as[17]:

$$P_{LABILE} = 0.2 \cdot P_{\max}$$

where *P* is the maximum achieved body protein content (kg).

Further, the minimum lipid content (L_{BASE}, kg) is given as[17]:

$$L_{BASE} = 0.2 \cdot P$$

where *P* is the current protein content (kg).

7. Lamb mortality (*LM*) is not predicted as a consequence of parasitism, but rather as a function of environmental conditions such that[27]:

$$LM = \left(\left(1 - PLS \right) \cdot TLF \cdot RLF \cdot \left(1 - RS \right) \right) + \left(\left(TLF - 0.9 \right) \cdot \left(RLF - 0.8 \right) \cdot \left(0.2 \cdot n \right) \right)$$

where *PLS* is the probability of lambs surviving to weaning (undefined input parameter), *RS* is an undefined input parameter to allow for wind, *n* is the total number of lambs, and *TLF* and *RLF* are functions of temperature (*T*, °C) and rainfall (*R*, mm) given as[27]:

$$TLF = 0.2 + 0.1 \cdot ABS\left(T - 18 \right)$$
$$RLF = 0.8 + 0.015 \cdot \left(R_t + R_{t+1} \right)$$

where *t* is the week of birth.

4.24.3 Host: mortality – discussion

The mortality of sheep as a consequence of parasitism is of particular importance and represents large productive losses. Whilst model 7[27] includes host mortality, this is given as a function of climatic conditions and parasitism is not considered. Model 5[17] assumes that mortality would occur if insufficient resources were available to meet the protein and energy requirements for maintenance, and the host was unable to catabolise sufficient resources from reserves. Whilst this is sufficient to describe mortality due to *Trichostrongylus* and *Teladorsagia* nematodes, *Haemonchus contortus* is known to have a much higher pathogenicity due to blood feeding. Model 4[16] assumes threshold worm burdens for each nematode species considered lethal to the host. Whilst this approach may overly simplistic and require threshold values to be specified, it may be the most appropriate method for determining host mortality due to *Haemonchus contortus* infections.

4.25 Host: faecal output

4.25.1 Host: faecal output - overview

Table 24. Summary of the models describing the faecal output of the host

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	✓
7	✓

4.25.2 Host: faecal output – functions (by model)

1. Faecal output (g day^{-1} lamb^{-1}) is given as[4]:

   $$FO_t = W_t \cdot 20$$

   where W_t is the live weight (kg) on day t.

2. Faecal output (*FO*, kg lamb^{-1}) at age *t* (days) is assumed to be zero for the first 14 days after birth, after which it is given as[6] (see Figure 18):

   $$FO_t = 1.4 \cdot \frac{(t-14)^2}{3600 + (t-14)^2}$$

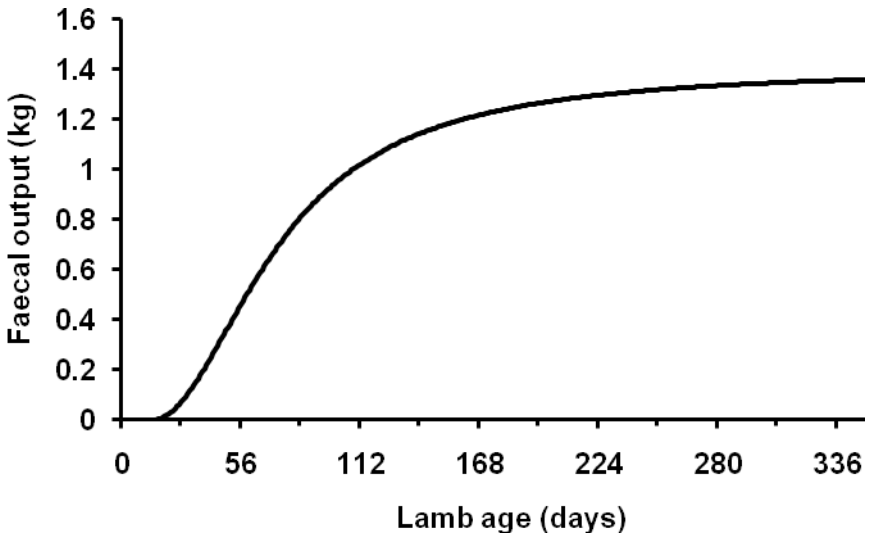

Figure 18. Faecal output (kg lamb^{-1}) as described by Leathwick *et al*.[6]

3. Constant faecal outputs of 2kg day^{-1} for lambs and 2.3kg day^{-1} for ewes[10].
4. Faecal output (kg DM lamb^{-1}day^{-1}) is equal to the herbage intake (kg DM day^{-1}). In correspondence with R.J. Dobson, 16th July 2014.

5. Faecal output on day *t* (FO_t, kg DM lamb^{-1} day^{-1}) is given as[17]:

$$FO_t = HI_t \cdot (1 - DMD)$$

where *HI* is the herbage intake, and *DMD* is the dry matter digestibility of the herbage (calculated according to equations outlined by AFRC[46]).

6. Faecal output on day *t* (FO_t, kg calf^{-1} day^{-1}) is given as[24] (see Figure 19):

$$FO_t = 0.23 \cdot W_t^{0.8}$$

where W_t is the calf live weight (kg) on day *t*.

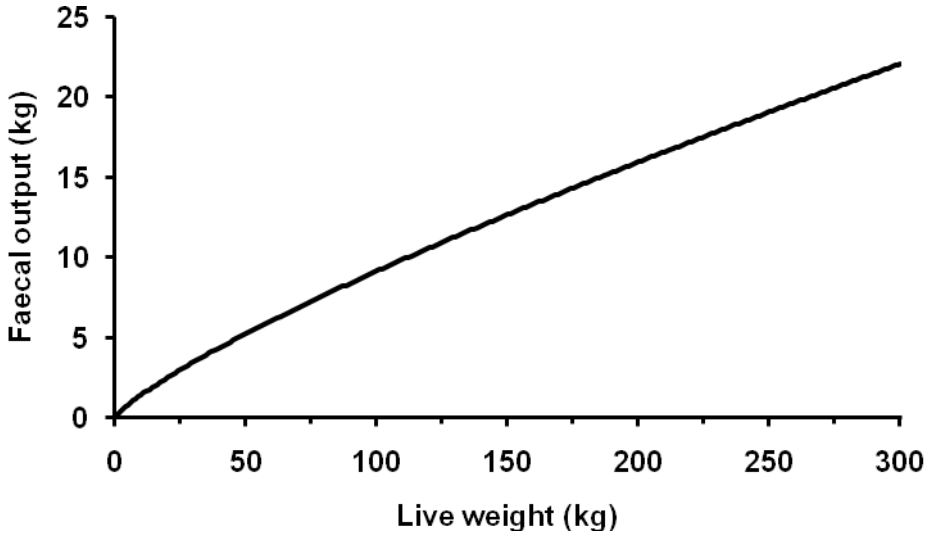

Figure 19. Faecal output (kg calf^{-1} day^{-1}) as described by Smith *et al*.[24]

7. Faecal egg counts are presented and discussed, however, the calculation for faecal output is not detailed[26]

4.25.3 Host: faecal output – discussion

The inclusion of faecal output is important for the prediction of faecal egg counts. Simplistic assumptions about faecal output may cause poor correlation between observed and predicted faecal egg counts when validating any model. As such, careful consideration needs to be given to the simulation of faecal output. Faecal output is related to both herbage quality and the impact of sheep status/condition on digestion, therefore it is suggested that faecal output should be predicted as a consequence of herbage intake and digestion as described in model 5[17].

4.26 Host: between animal variation

4.26.1 Host: between animal variation - overview

Table 25. Summary of the models describing between animal variation

Model	Included
1	✓
2	-
3	-
4	-
5	✓
6	-
7	-

4.26.2 Host: between animal variation – functions (by model)

1. Between animal variation was assumed to occur in 2 parameters representing the rate at which immunity acquires and impacts upon establishment and fecundity. Lamb phenotypes for these parameters were generated as[5]:

$$P_i = G_i + E_i$$

where G_i is the additive genetic component of the i^{th} individual sampled from a normal distribution $N(\mu,h^2\sigma^2_p)$, and E_i is the environmental component of the i^{th} individual sampled from a normal distribution $N(0,(1-h^2)\sigma^2_p)$. The mean trait values (μ), heritabilities (h^2) and phenotypic variances (σ^2_p) are given as input traits.

5. Between animal variation was assumed to occur in 12 parameters describing growth (initial empty body weight, protein content at maturity, and lipid content at maturity), maintenance (protein and energy requirements) and resistance (minimum, maximum, and rate of acquisition for establishment, mortality and fecundity).

   The lamb population (10000 lambs) arose from 5000 dams and 250 sires within a pre-determined mating structure. Parental breeding values for each trait (A_i) were sampled from a normal distribution of $N(0,h^2\sigma^2_p)$, where h^2 is defined as an input heritability for each trait and σ^2_p is defined as an input phenotypic variance for each trait. Genetic correlations between traits were also included for immune functions (r = 0.5) and were resolved using a Cholesky decomposition. Phenotypes (P) for each lamb ($_i$) were generated as[18]:

$$P_i = \mu + A_i + E_i$$

where μ is the population mean for each trait, A_i is the average additive genetic deviation for the parents of the i^{th} individual, and E_i is the environmental deviation sampled from a normal distribution $N(0,\sigma^2_p(1-h^2))$.

4.26.3 Host: between animal variation – discussion

Control strategies utilising either phenotypic variation (e.g. targeted selective treatment) or genetic variation (e.g. selective breeding for resistance) can only be simulated if included within a model. Only two of the models reviewed included between animal variation. The method used is the same in both of these models. Model 1[5] only included variation in immunological traits, whilst model 5[18] also included growth traits, the computation of

correlations between traits and maternal effects. The inclusion of between animal variation in further traits may also be desirable. For example, between animal variation affecting infective larval intake and losses due to parasitism may account for grazing behaviour and resilience, respectively.

There is an abundance of literature detailing genetic parameter estimates, as well as maternal and environmental impacts upon growth, immunological and parasitological parameters for a number of breeds. Safari *et al*.[152] provides a review of these parameter estimates, and further parameter estimates for Australian conditions may be available through the Sheep CRC based at UNE.

4.27 Parasitic nematode stages: pre-patent period

4.27.1 Parasitic nematode stages: pre-patent period - overview

Table 26. Summary of the models describing the pre-patent period of parasitic nematodes

Model	Included
1	✓
2	-
3	✓
4	-
5	✓
6	✓
7	✓

4.27.2 Parasitic nematode stages: pre-patent period – functions (by model)

1. The duration of development from ingested infective larvae to adult nematode is given as a constant of 14 days.[4]
3. The duration of development from ingested infective larvae to adult nematode is given as a constant of 20 days.[10]
5. The duration of development from ingested infective larvae to adult nematode is given as a constant of 14 days.[17]
6. The duration of development from ingested infective larvae to adult nematode is given as a constant of 18 days.[23]
7. The duration of development from ingested infective larvae to adult nematode is given as a constant of 18 days.[26]

4.27.3 Parasitic nematode stages: pre-patent period – discussion

Differences in the defined pre-patent period of each model represent parameterisation to specific nematode species. This can be observed for the single nematode species models where the pre-patent period for *Teladorsagia circumcincta* is given as 14 days in models 1[4] and 5[17], and the pre-patent period for *Ostertagia ostertagi* is given as 18 days in model 6[23]. In the multi-species models (3[10] and 7[26]), the pre-patent period is given as an average across nematode species. This assumption may be expected have an impact upon on the representation of the dynamics of each nematode species. As such, where multi-species infections are to be simulated, the pre-patent period for each nematode species should be defined.

4.28 Parasitic nematode stages: arrested development

4.28.1 Parasitic nematode stages: arrested development - overview

Table 27. Summary of the models describing the arrested development of parasitic nematodes

Model	Included
1	-
2	-
3	-
4	✓
5	-
6	✓
7	-

4.28.2 Parasitic nematode stages: arrested development – functions (by model)

4. The proportion of established nematodes that become arrested (*AR*) on week (*t*) is dependent upon the nematode species such that[15,16]:

$$AR_{Trich}(t) = 0.81 - 0.76 \cdot \frac{f_{Trich}}{XCORD} \quad \text{for } f_{Trich}(t) \le XCORD$$

$$AR_{Trich}(t) = 0.05 - \left(0.05 \cdot \frac{f_{Trich} - XCORD}{1 - XCORD} \right) \quad \text{for XCORD} < f_{Trich}(t) < 1$$

$$AR_{Haem}(t) = 0 \quad \text{for } t < 3.22954$$

$$AR_{Haem}(t) = 0.613969 \cdot \left(1 - e^{-0.574918(t-3.22954)}\right) \quad \text{for } t \ge 3.22954$$

$$AR_{Tela}(t) = 0.36 \quad \text{for } LI_{Tela}(t) < 1750$$

$$AR_{Tela}(t) = 0.36 + 0.2 \cdot \left(\left(\frac{LI_{Tela}(t)}{1750} \right) - 1 \right) \quad \text{for } 1750 \le LI_{Tela}(t) \le 3500$$

$$AR_{Tela}(t) = 0.56 \quad \text{for } LI_{Tela}(t) > 3500$$

where *f* is fecundity (eggs worm^{-1}), *LI* is larval intake, *AGE* is the lamb age in weeks, and *XCORD* is given as[15,16]:

$$XCORD = 1 - \frac{3.5 \cdot (AGE - 12)}{100} \quad \text{for } 12 < AGE < 37$$

$$XCORD = 0.125 \quad \text{for } AGE \ge 37$$

6. Exponential functions describe the proportion of infective larvae developing to adult, remaining larvae are assumed to be arrested[23].

4.28.3 Parasitic nematode stages: arrested development – discussion

Only models 4[15,16] and 6[23] consider arrested development, whilst all other models consider that infective larvae which do not establish are lost. In contrast, model 6[23] assumes that there is no mortality in infective larvae failing to establish. The complexity and heavy requirement for parameterisation in model 4[15,16] may be considered undesirable, and thus a

simpler solution may be to simulate the population of infective larvae which do not establish and to impose a mortality rate equal to that described for adult nematodes (section 4.30).

4.29 Parasitic nematode stages: establishment

4.29.1 Parasitic nematode stages: establishment - overview

Table 28. Summary of the models describing the establishment of parasitic nematodes

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	✓
7	-

4.29.2 Parasitic nematode stages: establishment – functions (by model)

1. The proportion of ingested larvae which establish (*E*) as adult worm on day *t* is given as[4]:

$$E_t = E_{MIN} + \left(E_{MAX} - E_{MIN}\right) \cdot e^{-ECF_t}$$

where E_{MAX} is the nematode establishment for naïve lambs (constant, 0.4), E_{MIN} is the nematode establishment after immune acquisition (constant, 0.0), and *ECF* is the establishment control factor given as[4]:

$$ECF_t = 0.5^{1/\tau_2} \cdot ECF_{t-1} + \left(\rho_2 \cdot LI_{t-z}\right)$$

where τ_2 is the half life of establishment response (constant, 8.1 days), ρ_2 is the establishment response factor (constant, 0.0001 infective larvae^{-1}), *LI* is larval intake (infective larvae lamb^{-1}), and *z* is the time for initiation of immune response (constant, 7 days).

2. The proportion of ingested larvae which establish (*E*) as adult worms is given as[6]:

$$E = 0.466 - \left(\left(8.02 \cdot 10^{4}\right) \cdot AGE\right) - \left(\left(7.23 \cdot 10^{7}\right) \cdot \sum LI\right)$$

where *AGE* is the lamb age (days), and ∑*LI* is cumulative larval intake.

3. The proportion of ingested larvae which establish (*E*) as adult worms at lamb age (*t*) is given as[10] (see Figure 20):

$$E_t = E_{MAX} \quad \text{for } t \le 42$$

$$E_t = E_{MAX} - (t - 42) \cdot \left(\frac{E_{MAX} - (0.1 \cdot E_{MAX})}{q} \right) \quad \text{for } 42 < t < (q + 42)$$

$$E_t = 0.1 \cdot E_{MAX} \quad \text{for } t \ge (q + 42)$$

where E_{MAX} is the maximum proportion of larvae establishing (constant, 0.39), and *q* is the infection duration in days required to reach full immunity for each nematode species (q_{Tela} = 33, q_{Trich} = 123, q_{Haem} = 84).

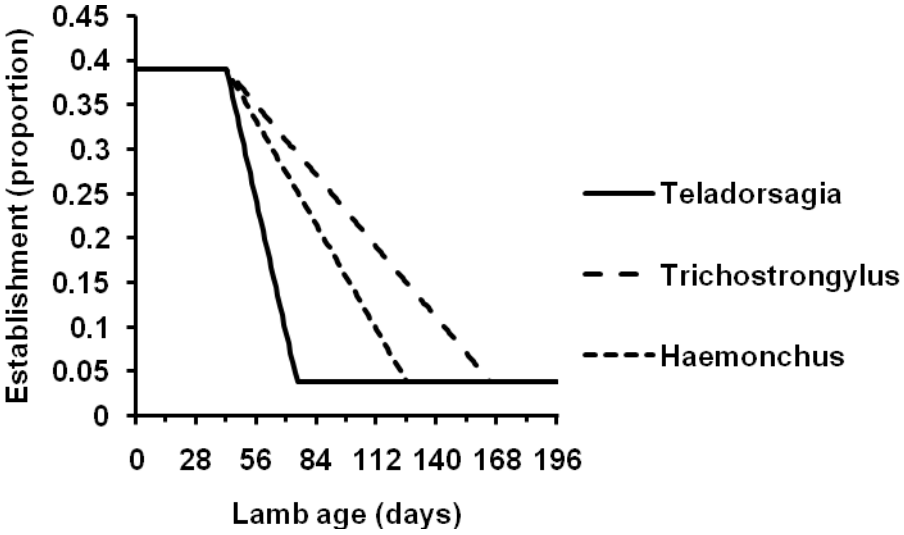

Figure 20. The relationship between lamb age (days) and the establishment rate of infective larvae for *Teladorsagia*, *Trichostrongylus* and *Haemonchus* as described by Learmount *et al*.[10]

4. The proportion of ingested *Trichostrongylus* larvae which establish (E_{Trich}) as adult worms during week (*t*) of infection given as[15]:

$$E_{Trich}(t) = \left(\frac{x}{1 + x} \right)$$

$$x = e^{\left(1.2 \cdot \frac{z}{1+z} \right) \cdot (T + ET_{50} - t)}$$

$$z = e^{0.13 \cdot (AGE - 19)}$$

$$T = \frac{3532}{LI_{Trich}(t) \cdot E_{Trich}(1) \cdot E_{Trich}(t)}$$

$$ET_{50} = 2.2 \cdot \frac{1.2}{\left(1.2 \cdot \frac{z}{1+z} \right)}$$

where *AGE* is the lamb age (weeks).

The value of E_{Trich} is adjusted for worm burden (*WB*) and larval intake (LI_{Trich}) as follows[15]:

$$E_{Trich}(t) = E_{Trick}(t-1) + \frac{0.25 - E_{Trich}(t-1)}{4.857} \quad \text{for } LI_{Trich} < 350,\ t > 6 \ \&\ WB < 400$$

$$E_{Trich}(t) = E_{Trich}(t-1) - \frac{E_{Trich}(t-1) - 0.03}{4.857} \quad \text{for } LI_{Trich} < 350,\ t > 6 \ \&\ WB > 3500$$

The proportion of ingested *Haemonchus* larvae which establish (E_{Haem}) as adult worms during week (*t*) of infection given as[16]:

$$E_{Haem}(t) = 0.01338 + \left(0.41756 \cdot \frac{x}{1+x}\right)$$

$$x = e^{4.01784(6.47627 - t)}$$

The value of E_{Haem} is adjusted for the host age (*AGE*, weeks) and the impact of species interactions as follows[16]:

$$E_{Haem}(t) = 1.864 \cdot E_{Haem}(t) \quad \text{for } AGE \le 6$$

$$E_{Haem}(t) = (2.08 - 0.036 \cdot AGE) \cdot E_{Haem}(t) \quad \text{for } 6 < AGE < 52$$

$$E_{Haem}(t) = 0.208 \cdot E_{Haem}(t) \quad \text{for } AGE \ge 52$$

$$E_{Haem}(t) = 0.45 \cdot E_{Haem}(t) \quad \text{for WB} > 3000, \text{ or } \frac{LI_{Tela}}{LI_{Tela} + LI_{Trich} + LI_{Haem}} > 0.2$$

where *WB* is the worm burden (non-species specific), and *LI* is the larval intake for each nematode species.

The proportion of ingested *Teladorsagia* larvae which establish (E_{Tela}) as adult worms during week (*t*) of infection given as[16]:

$$E_{Tela}(t) = 0.35 - \frac{0.05 \cdot t}{4} \quad \text{for } 0 \le t \le 4 \ \underline{\&}\ LI_{Tela} > 350$$

$$E_{Tela}(t) = 0.3 - \frac{0.23 \cdot (t-4)}{4} \quad \text{for } 4 < t \le 8 \ \underline{\&}\ LI_{Tela} > 350$$

$$E_{Tela}(t) = 0.07 - \frac{0.04 \cdot (t-8)}{4} \quad \text{for } 8 < t \le 12 \ \underline{\&}\ LI_{Tela} > 350$$

$$E_{Tela}(t) = 0.03 \quad \text{for } t > 12 \ \underline{\&}\ LI_{Tela} > 350$$

$$E_{Tela}(t) = E_{Tela}(t-1) + \frac{0.25 - E_{Tela}(t-1)}{4.857} \quad \text{for } LI_{Tela} < 350 \ \underline{\&}\ WB < 400$$

$$E_{Tela}(t) = E_{Tela}(t-1) \quad \text{for } LI_{Tela} < 350 \ \underline{\&}\ 400 \le WB \le 2000$$

$$E_{Tela}(t) = E_{Tela}(t-1) - \frac{E_{Tela}(t-1) - 0.03}{4.857} \quad \text{for } LI_{Tela} < 350 \ \underline{\&}\ WB > 2000$$

where LI_{Tela} is the *Teladorsagia* larval intake, and *WB* is the worm burden (non-species specific)

5. The proportion of ingested larvae which establish per day (*E*) as adult worms is given as[18] (see Figure 21):

$$E = \left(\frac{E_{MAX} \cdot a^3}{a^3 + \left(\sum LP\right)^3} \right) + E_{MIN}$$

where *a* is a rate constant, E_{MAX} is the maximum proportion of larvae establishing, E_{MIN} is the minimum proportion of larvae establishing (0.06), and $\sum LP$ is the cumulative larval population resident within the host. *a* and E_{MAX} are assumed to be under genetic control of the host are determined when the population is constructed (to include between-animal variation).Population means are given as *a* = 190000 and E_{MAX} = 0.7.

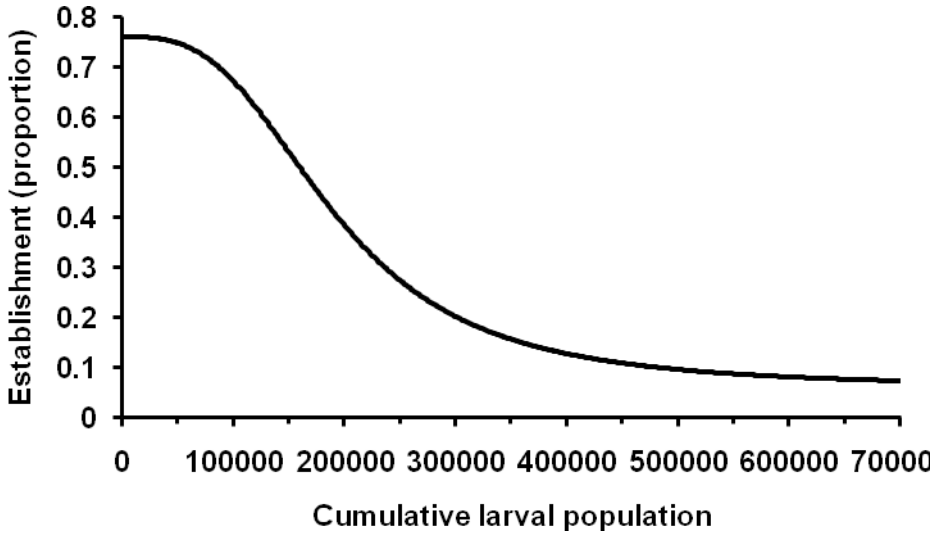

Figure 21. The relationship between cumulative larval population resident within the host and the proportion of infective larvae establishing as described by Laurenson *et al*.[18]

6. The proportion of ingested larvae which establish (*E*) as adult worms is given as[22] (see Figure 22):

$$E(t) = e^{-0.00863t}$$

where *t* is the duration of infection (days).

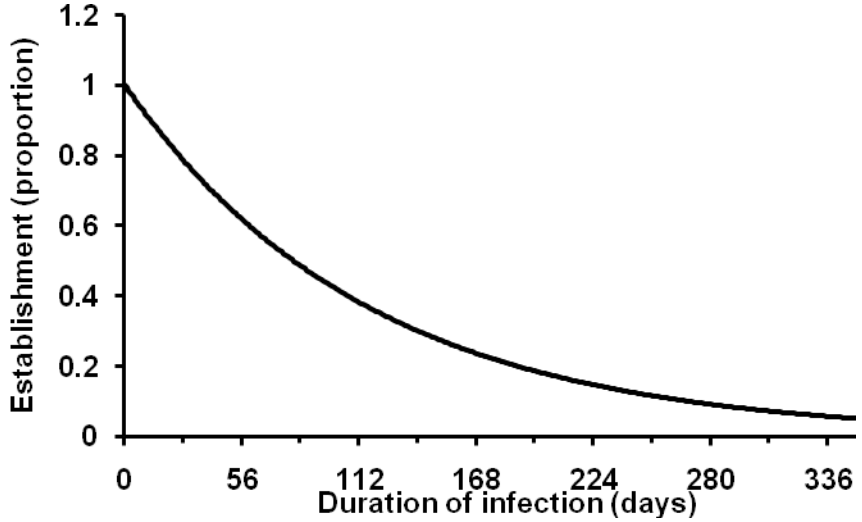

Figure 22. Relationship between the duration of infection and the proportion of infective larvae establishing within the host as described by Grenfell *et al*.[22]

4.30 Parasitic nematode stages: mortality

4.30.1 Parasitic nematode stages: mortality - overview

Table 29. Summary of the models describing the mortality of parasitic nematodes

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	✓
7	✓

4.30.2 Parasitic nematode stages: mortality – functions (by model)

1. The mortality rate of adult nematodes is a constant of 0.0307 day^{-1}.[4]
2. The survival rate of adult nematodes (μ) is given as[6] (see Figure 23):

$$\mu = 0.9993 - \left(\left(5.603 \cdot 10^{-8}\right) \cdot \sum LI\right)$$

where $\sum LI$ is cumulative larval intake.

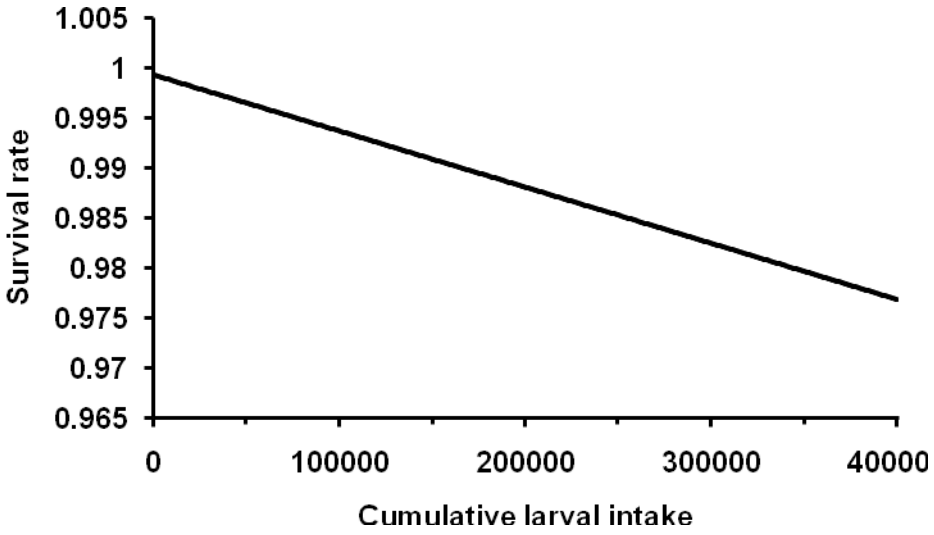

Figure 23. The relationship between cumulative larval intake and survival rate described by Leathwick *et al*.[6]

3. The mortality rate of adult nematodes is a constant of 0.07 day^{-1}.[10]

4. The mortality rate of adult *Trichostrongylus* nematodes per week (μ_{Trich}) is given as[15]:

$$\mu_{Trich}(t) = 0 \qquad \text{for } t \le t_0$$

$$\mu_{Trich}(t) = \frac{1}{t_0 + 9 - t} \qquad \text{for } t_0 < t < (t_0 + 9)$$

$$\mu_{Trich}(t) = 1 \qquad \text{for } t \ge (t_0 + 9)$$

where t is the duration of continuous infection (weeks), and t_0 is the number of weeks until the establishment of ingested larvae first falls below 0.01.

The mortality rate of adult *Haemonchus* nematodes per week (μ_{Haem}) is given as[16]:

$$\mu_{Haem} = 0.0054 \qquad \text{for } WB \le 4613$$

$$\mu_{Haem} = 0.0530 \qquad \text{for } WB > 4613$$

where *WB* is the worm burden (non-species specific).

The mortality rate of adult *Teladorsagia* nematodes per week (μ_{Tela}) is given as[16]:

$$\mu_{Tela}(t) = 0.041 \qquad \text{for } t > min \ \underline{\&} \ LI_{Tela} < 1750$$

$$\mu_{Tela}(t) = 0.041 - 0.012 \cdot \left(\frac{LI_{Tela}}{1750} - 1 \right) \qquad \text{for } t > min \ \underline{\&} \ 1750 < LI_{Tela} < 3500$$

$$\mu_{Tela}(t) = 0.041 - 0.012 \cdot \left(\frac{LI_{Tela}}{3500} - 1 \right) \qquad \text{for } t > min \ \underline{\&} \ 3500 \le LI_{Tela} < 7000$$

$$\mu_{Tela}(t) = 0.020 \qquad \text{for } t > min \ \underline{\&} \ LI_{Tela} > 7000$$

where LI_{Tela} is the *Teladorsagia* larval intake, t is the duration of continuous infection (weeks), and *min* is the number of weeks of exposure required to cause an increase in mortality, such that[16]:

$$\min = 14.714 \qquad \text{for } LI_{Tela} < 1750$$

$$\min = 14.714 - 3.429 \cdot \left(\frac{LI_{Tela}}{1750} - 1 \right) \quad \text{for } 1750 \leq LI_{Tela} < 3500$$

$$\min = 11.286 - \left(\frac{LI_{Tela}}{3500} - 1 \right) \quad \text{for } 3500 \leq LI_{Tela} < 7000$$

$$\min = 10.286 \quad \text{for } LI_{Tela} > 7000$$

5. The mortality rate of adult nematodes per day (μ) is given as[18] (see Figure 24):

$$\mu = \left(\frac{\mu_{MAX} \cdot \left(\sum LP \right)^3}{b^3 + \left(\sum LP \right)^3} \right) + \mu_{MIN}$$

where b is a rate constant, μ_{MAX} is the maximum mortality rate, μ_{MIN} is the minimum mortality rate, and $\sum LP$ is the cumulative larval population resident within the host. b, μ_{MIN} and μ_{MAX} are all assumed to be under genetic control of the host are determined when the population is constructed (to include between-animal variation). Population means are given as b = 650000, μ_{MIN} = 0.01 and μ_{MAX} = 0.11.

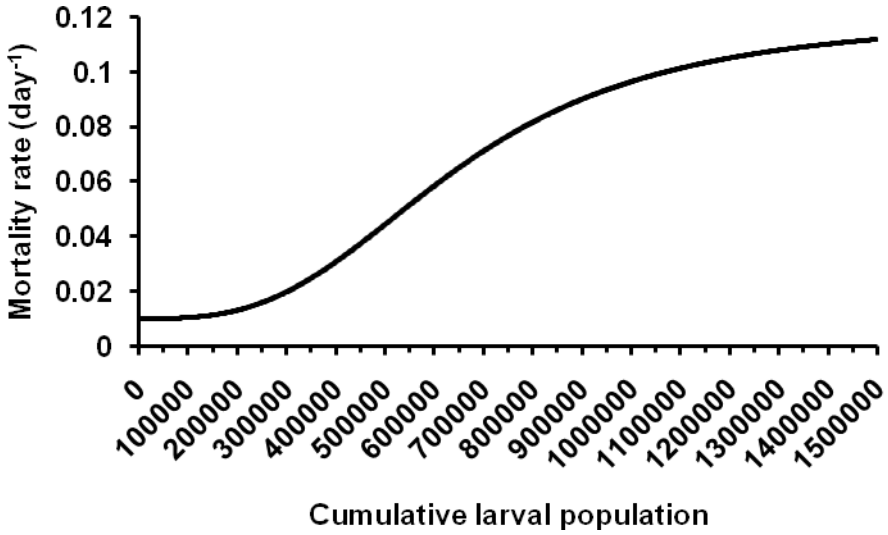

Figure 24. The relationship between cumulative larval population resident within the host and the mortality rate of adult nematodes as described by Laurenson *et al*.[18]

6. The mortality rate of adult nematodes per day (μ) is given as[22] (see Figure 25):

$$\mu = 0.01713 + \left(\left(3.82 \cdot 10^{-8} \right) \cdot \sum LI \right)$$

where $\sum LI$ is the cumulative larval intake.

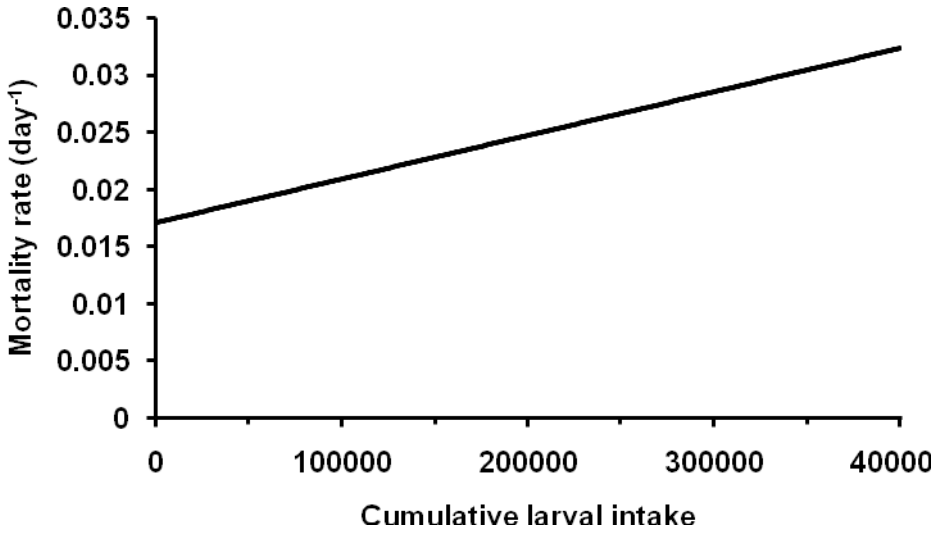

Figure 25. The relationship between cumulative larval intake and the mortality rate of adult nematodes as described by Grenfell *et al*.[22]

7. The mortality rate of adult *Teladorsagia* nematodes per day (μ_{Tela}), and adult *Trichostrongylus* nematodes per day (μ_{Trich}) are given as[26]:

$$\mu_{Tela}(t) = \left(LI \cdot \left(1.27 \cdot 10^{-4}\right)\right) + \left(\left(1.32 \cdot 10^{-3}\right) \cdot t\right)$$
$$\mu_{Trich}(t) = \left(LI \cdot \left(7.5 \cdot 10^{-5}\right)\right) + \left(\left(9.4 \cdot 10^{-5}\right) \cdot t\right)$$

where *LI* is the larval intake (non-species specific).

4.31 Parasitic nematode stages: worm burden

4.31.1 Parasitic nematode stages: worm burden - overview

Table 30. Summary of the models describing the parasitic worm burden

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	✓
7	✓

4.31.2 Parasitic nematode stages: worm burden – functions (by model)

1. Worm burden (*WB*) is given as[4]:

$$WB_t = WB_{t-1} \cdot (1-\mu) + \left(E_t \cdot LI_{t-j}\right)$$

where *t* is lamb age (days), μ is the mortality rate of adult worms (constant, 0.0307 day^{-1}), *LI* is larval intake, *E* is the proportion on ingested larvae which establish as adult worms, and *j* is the pre-patent period (constant, 14 days).

2. Worm burden (*WB*) is given as[6]:

$$WB_t = WB_{t-1} \cdot (1 - \mu_t) + (E_t \cdot LI_t)$$

where *t* is lamb age (days), μ is the mortality rate of adult worms, *LI* is larval intake, and *E* is the proportion on ingested larvae which establish as adult worms.

3. Worm burden (*WB*) is given as[10]:

$$WB_t = WB_{t-1} \cdot (1 - \mu) + E_t \cdot (LI_{t-j} \cdot (1 - \mu))$$

where *t* is lamb age (days), μ is the mortality rate of infective larvae and adult worms (constant, 0.07 day^{-1}), *LI* is larval intake, *E* is the proportion on ingested larvae which establish as adult worms, and *j* is the pre-patent period (constant, 20 days).

4. Worm burden (*WB*) is given as[15]:

$$WB_t = (WB_{t-1} + E_t \cdot LI_t) \cdot (1 - \mu_t)$$

where *t* is lamb age (days), μ is the mortality rate of infective adult worms, *LI* is larval intake, and *E* is the proportion on ingested larvae which establish as adult worms.

5. Worm burden (*WB*) is given as[17]:

$$WB_t = WB_{t-1} \cdot (1 - \mu_t) + (E_t \cdot LI_{t-j})$$

where *t* is the current duration of simulation (days), μ is the mortality rate of adult worms, *LI* is larval intake, *E* is the proportion on ingested larvae which establish as adult worms, and *j* is the pre-patent period (constant, 14 days).

6. Worm burden (*WB*) is given as[23]:

$$WB_t = WB_{t-1} \cdot (1 - \mu_t) + (E_t \cdot LI_{t-j})$$

where *t* is the current duration of simulation (days), μ is the mortality rate of adult worms, *LI* is larval intake, *E* is the proportion on ingested larvae which establish as adult worms, and *j* is the pre-patent period (constant, 18 days).

7. The calculation of worm burden is discussed but not detailed[26].

4.32 Parasitic nematode stages: fecundity

4.32.1 Parasitic nematode stages: fecundity - overview

Table 31. Summary of the models describing nematode fecundity

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	✓
7	✓

4.32.2 Parasitic nematode stages: fecundity – functions (by model)

1. The density-dependent fecundity of adult nematodes (*F*, eggs worm^{-1} day^{-1}) is given as[4]:

$$F_t = \left(96.516 \cdot l_t^{4.7452}\right) - 1$$

where *t* is lamb age (days), and *l* is worm length (cm) given as[4]:

$$l_t = 1.0103 - \left(0.4536 \cdot \log_{10}\left(IgA_t + 1\right)\right) - \left(0.0310 \cdot \log_{10}\left(WB_t + 1\right)\right)$$

where *WB* is the adult worm burden (worms lamb^{-1}), and *IgA* is immunoglobulin A activity (optical density units) given as[4]:

$$IgA_t = \left(0.5^{1/\tau_1} \cdot IgA_{t-1}\right) + \left(\left(8.61 \cdot 10^{-6}\right) \cdot LI_{t-z}\right)$$

where τ_1 is the half-life of IgA activity (8.1 days), *LI* is larval intake, and *z* is the time for initiation of immune response (7 days).

2. The fecundity of adult nematodes is constant (450 eggs female worm^{-1} day^{-1}) assuming a 1:1 gender ratio[6].

3. The fecundity of adult nematodes (*F*, eggs worm^{-1} day^{-1}) is given as[10] (see Figure 26):

$$F\left(t\right) = F_{MAX} \qquad \text{for } t \le 42$$

$$F\left(t\right) = F_{MAX} - \left(t - 42\right) \cdot \left(\frac{0.5 \cdot F_{MAX}}{q}\right) \qquad \text{for } 42 < t < (q + 42)$$

$$F\left(t\right) = 0.5 \cdot F_{MAX} \qquad \text{for } t \ge (q + 42)$$

where *t* is lamb age (days), q is the infection duration in days required to reach full immunity for each nematode species (q_{Tela} = 33, q_{Trich} = 123, q_{Haem} = 84), and F_{MAX} is the maximum fecundity for each nematode specis (*Teladorsagia* = 152, *Trichostrongylus* = 207, *Haemonchus* = 3436).

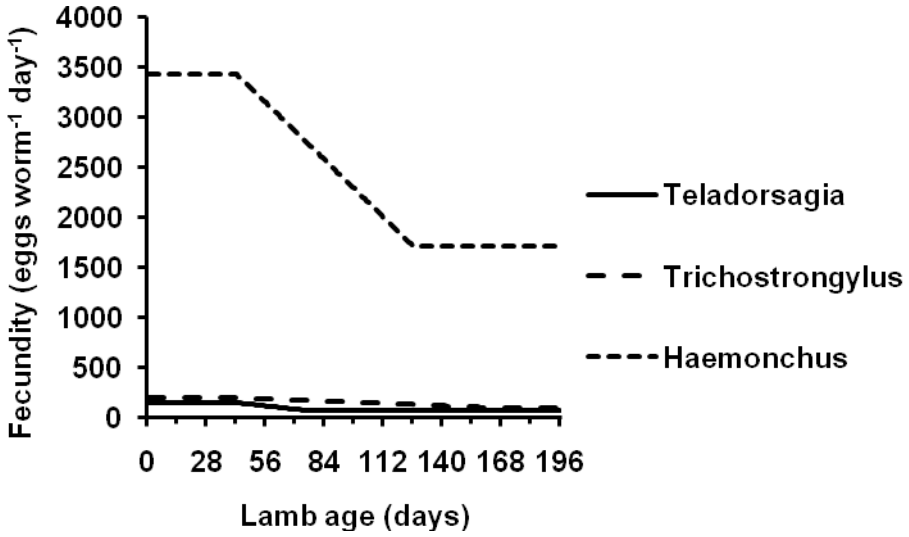

Figure 26. The relationship between lamb age (days) and the fecundity of adult nematodes for *Teladorsagia*, *Trichostrongylus* and *Haemonchus* as described by Learmount *et al*.[10]

4. The fecundity of adult *Trichostrongylus* nematodes (F_{Trich}, eggs female nematode^{-1} week^{-1}), assuming a 1:1 gender ratio, is given as[13]:

$$F_{Trich} = F_{MAX} \cdot \alpha \cdot \beta$$

where F_{MAX} is the maximum fecundity (4900 eggs^{-1} female nematode^{-1} week^{-1}), and α & β are given as[13]:

$\alpha = 0$	for $0 \le i \le 2$
$\alpha = i - 2$	for $2 < i < 3$
$\alpha = 1$	for $i \ge 3$
$\beta = e^{-0.41 \cdot (t-2.4)}$	for $WB > 2921$ & $t > 2.4$
$\beta = 1$	for $WB \le 2921$ or $t \le 2.4$

where i is worm age (weeks), WB is worm burden (non-species specific), and t is time (weeks) since WB exceeded 2921.

5. The fecundity of adult nematodes (F, eggs worm^{-1} day^{-1}) is given as[18] (see Figure 27):

$$F = \left(\frac{F_{MAX} \cdot c^3}{c^3 + \left(\sum LP \right)^3} \right) + F_{MIN}$$

where c is a rate constant, F_{MAX} is the maximum fecundity, F_{MIN} is the minimum fecundity (5), and $\sum LP$ is the cumulative larval population resident within the host. c and F_{MAX} are assumed to be under genetic control of the host are determined when the population is constructed (to include between-animal variation). Population means are given as c = 210000 and F_{MAX} = 20.

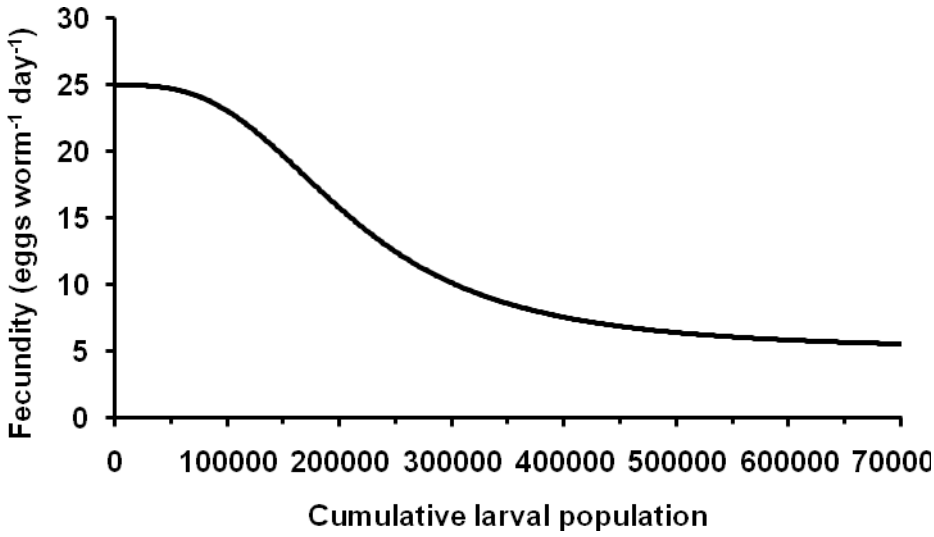

Figure 27. The relationship between cumulative larval population resident within the host and the fecundity of adult nematodes as described by Laurenson *et al*.[18]

6. The fecundity of adult nematodes (*F*, eggs female nematode^{-1} day^{-1}), assuming a 1:1 gender ratio, is given as[24]:

$$F_t = 356 \cdot e^{-0.993 \cdot WB \cdot (t-18)}$$

where *WB* is worm burden, and *t* is the duration of infection (days).

7. Fecundity is given by an undefined function described as 'a cumulative distribution function of egg output per female nematode per day'. Differences between species are accounted for such that 'the ratio of eggs per faecal pellet to total nematode count for *Teladorsagia* was 1:1.8 and that for *Trichostrongylus* was 1:5.1'.[26]

4.33 Parasitic nematode stages: faecal egg count

4.33.1 Parasitic nematode stages: faecal egg count - overview

Table 32. Summary of the models describing faecal egg counts

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	✓
7	✓

4.33.2 Parasitic nematode stages: faecal egg count – functions (by model)

1. Faecal egg count (*FEC*, eggs g^{-1}) is given as[4]:

$$FEC_t = \frac{F_t \cdot WB_t}{FO_t}$$

where *t* is lamb age (days), *F* is fecundity (eggs $worm^{-1}$ day^{-1}), *WB* is worm burden, and *FO* is faecal output (g day^{-1} $lamb^{-1}$).

2. Faecal egg count (*FEC*, eggs g^{-1}) is given as[6]:

$$FEC_t = \frac{0.5 \cdot F \cdot WB_t}{1000 \cdot FO_t}$$

where *t* is lamb age (days), *F* is fecundity (450 eggs female $worm^{-1}$ day^{-1}), *WB* is worm burden, and *FO* is faecal output (kg day^{-1} $lamb^{-1}$).

3. Faecal egg count (*FEC*, eggs g^{-1}) is given as[10]:

$$FEC_t = \frac{F_t \cdot WB_t}{1000 \cdot FO_t}$$

where *t* is lamb age (days), *F* is fecundity (eggs $worm^{-1}$ day^{-1}), *WB* is worm burden, and *FO* is faecal output (kg day^{-1} $lamb^{-1}$).

4. Faecal egg count (*FEC*, eggs g^{-1}) for *Trichostrongylus* nematodes is given as[13]:

$$FEC_t = \frac{F_t \cdot WB_t}{1000 \cdot FO_t}$$

where *t* is lamb age (days), *F* is fecundity of *Trichostrongylus* adults (eggs $worm^{-1}$ day^{-1}), *WB* is worm burden, and *FO* is faecal output (kg day^{-1} $lamb^{-1}$).

Faecal egg count (*FEC*, eggs g^{-1}) for *Haemonchus* nematodes is given as[16]:

$$FEC = 4.57 \cdot WB_{Haem}^{\ 0.84}$$

where WB_{Haem} is the *Haemonchus* worm burden.

Faecal egg count (*FEC*, eggs g^{-1}) for *Teladorsagia* nematodes is given as[16]:

$$FEC = 0.13 \cdot WB_{Tela} \qquad \text{for } LI_{Tela} < 1750$$

$$FEC = \left(0.13 - \left(\frac{LI_{Tela} - 1750}{6250}\right)\right) \cdot WB_{Tela} \qquad \text{for } 1750 \le LI_{Tela} < 3500$$

$$FEC = \left(0.13 - \left(\frac{LI_{Tela} - 3500}{25000}\right)\right) \cdot WB_{Tela} \qquad \text{for } 3500 \le LI_{Tela} < 7000$$

$$FEC = 0.07 \cdot WB_{Tela} \qquad \text{for } LI_{Tela} > 7000$$

where WB_{Tela} is the *Teladorsagia* worm burden, and LI_{Tela} is the *Teladorsagia* larval intake.

5. Faecal egg count (*FEC*, eggs g^{-1} DM), accounting for density-dependent effects on fecundity, is given as[17]:

$$FEC_t = \frac{F_t \cdot \left(\frac{WB_t}{2500}\right)^{-0.25} \cdot WB_t}{1000 \cdot FO_t}$$

where *t* is the duration of simulation (days), *F* is fecundity (eggs $worm^{-1}$ day^{-1}), *WB* is worm burden, and *FO* is faecal output (kg DM $lamb^{-1}$ day^{-1}).

6. Faecal egg count (*FEC*, eggs g^{-1}) is given as[24]:

$$FEC_t = \frac{0.5 \cdot F_t \cdot WB_t}{1000 \cdot FO_t}$$

where *t* is duration of infection (days), *F* is fecundity (eggs female $worm^{-1}$ day^{-1}), *WB* is worm burden, and *FO* is faecal output (kg day^{-1} $calf^{-1}$).

7. Faecal egg counts are presented and discussed, however, the calculation for faecal egg count is not detailed[26].

4.34 Parasitic nematode stages – discussion

The establishment (including pre-patent period and arrested development), mortality and fecundity of parasitic nematode stages are assumed to be a function of the acquisition of immunity. However, information regarding estimates in naive animals and following the expression of acquired immunity will be required for differing nematode species. Sufficient experimental studies have already been carried out which may provide the required information. Kao *et al.*[153] carried out a survey/review of such estimates (proportions) for differing nematode species with Australia, New Zealand, France, USA, and Argentina. This review provides an extensive list of references for these values and may therefore inform the parameterisation of a nematode infection model.

In regards to the acquisition of immunity, models 1[4] and 5[18] provide the best option to describe the consequent impacts upon establishment, mortality and fecundity. Model 5[18] is the only model of those reviewed to consistently utilise the same dependent variable. Specifically, the acquisition of immunity was assumed to be a function of the cumulative infective larval population resident within the host. It should be noted that this allows for the impact of anthelmintic treatment on the larval population and thus antigen recognition, when cumulative larval intake would not. Model 1[4] explicitly simulates components of the Th2 immune response (e.g. IgA activity, see section 4.32), and also accounts for potential reductions in immune expression by incorporating half-lives. This inclusion means that in the absence of a parasitic challenge (or if there are insufficient resources for the maintenance of immunity) then immune expression would revert towards a naive state. However, both these models only simulate single species infections and therefore consideration needs to be given to the simulation of multi-species infections. One option would be to bind the functions for establishment, mortality and fecundity described in model 5[18] between 0 and 1. These can then be applied to maximum and minimum values for each nematode species. However, the infective larvae of one species may not impact upon the acquisition of immunity to the same extent as other species (differences in antigen exposure), and thus adjustments (species equivalents) may be required for differing species.

4.35 Anthelmintic treatment: efficacy

4.35.1 Anthelmintic treatment: efficacy - overview

Table 33. Summary of the models describing the efficacy of anthelmintic treatments

Model	Included
1	✓
2	✓
3	✓
4	✓
5	✓
6	✓
7	✓

4.35.2 Anthelmintic treatment: efficacy – functions (by model)

1. If simulated, anthelmintic treatment is assumed to have 100% efficacy and occur at 28 day intervals.[4]
2. The initial efficacy of an anthelmintic active can be specified for the differing anthelmintic resistance genotypes of the nematode population.[7,8]
3. The initial efficacy of an anthelmintic active was assumed to have either 100% or 0% efficacy against the differing anthelmintic resistance genotypes of the nematode population and whether resistance was dominant or recessive. The persistence of anthelmintic efficacy can also be specified.[10]
4. The initial efficacy of an anthelmintic active can be specified for differing anthelmintic resistance genotypes of the nematode population.[14]
5. The initial efficacy of anthelmintic treatment can be specified for the differing anthelmintic resistance genotypes of the nematode population.[20]
6. The efficacy and persistence of an anthelmintic treatment can be specified.[25]
7. The efficacy of an anthelmintic treatment can be specified.[26]

4.36 Anthelmintic treatment: genetic mechanism for resistance

4.36.1 Anthelmintic treatment: genetic mechanism for resistance - overview

Table 34. Summary of the models describing the genetic mechanism for anthelmintic resistance

Model	Included
1	-
2	✓
3	✓
4	✓
5	✓
6	-
7	-

4.36.2 Anthelmintic treatment: genetic mechanism for resistance – functions (by model)

2. 'The model employs 27 genotypes, representing up to three anthelmintic classes, as outlined by Barnes and Dobson (1990).' However, this model also includes the potential for side-resistance (i.e. a gene inferring resistance to more than one active).[7,8]
3. The mechanism of anthelmintic resistance was assumed to be monogenic with 2 alleles (R = resistant, S = susceptible), yielding 3 possible genotypes (RR, RS, SS) for each of 4 chemical classes (benzimidazole, levamisole, avermectin and milbemycin). Thus, model employs 81 genotypes.[10]
4. The model employs up to 27 genotypes. Three genes are modelled, each with 2 alleles (R = resistant, S = susceptible), yielding 3 possible genotypes per gene (RR, RS, SS). Thus, the model can simulate up to 3 genes determining resistance to a single active, or up to 3 actives each controlled by a single monogenic mechanism (or any combination between).[14]
5. The model employs 3 genotypes. Resistance to a single active is assumed to be monogenicwith 2 alleles (R = resistant, S = susceptible), yielding 3 possible genotypes (RR, RS, SS).[20]

4.37 Anthelmintic treatment: genotype fitness

4.37.1 Anthelmintic treatment: genotype fitness - overview

Table 35. Summary of the models describing the fitness disadvantage of anthelmintic resistant genotypes

Model	Included
1	-
2	✓
3	-
4	✓
5	-
6	-
7	-

4.37.2 Anthelmintic treatment: genotype fitness – functions (by model)

2. The relative fitness of different genotypes (in the absence of anthelmintic treatment) may be specified. This may represent differences in their ability to mate, produce eggs, survive on pasture or to establish in the host. For simplicity fitness is implemented by removing a proportion of eggs of each genotype before they are deposited on pasture. For example, the relative fitness can be set to reduce the number of homozygous resistant genotypes (RR) by 20%, while not affecting the numbers of heterozygous (RS) or homozygous susceptible (SS) eggs.[7,9]
4. The relative fitness of different genotypes (in the absence of anthelmintic treatment) may be specified and is modelled as a reduction in fecundity.[14]

4.38 Anthelmintic treatment: allele frequencies

4.38.1 Anthelmintic treatment: allele frequencies - overview

Table 36. Summary of the models describing the fitness disadvantage of anthelmintic resistant genotypes

Model	Included
1	-
2	✓
3	✓
4	✓
5	✓
6	-
7	-

4.38.2 Anthelmintic treatment: allele frequencies – functions (by model)

2. The frequency of resistant alleles of within host worm burdens (q) on each day (t) follows Hardy-Weinberg laws and is given as[7]:

$$q(t) = \frac{A_{RR}(t) + 0.5 \cdot A_{RS}(t)}{A_{RR}(t) + A_{RS}(t) + A_{SS}(t)}$$

where A is the number of adult worms of a given genotype within the host.

The frequency of resistant alleles of eggs (q_{egg}) deposited on day (t) is given as[7]:

$$q_{egg}(t) = \frac{F_{RR} \cdot q(t)^2}{F_{RR} \cdot q(t)^2 + \left(2 \cdot F_{RS} \cdot q(t) \cdot \left(1 - q(t)\right)\right) + F_{SS} \cdot \left(1 - q(t)\right)^2}$$

where q is the resistant allele frequency of the within host worm burden, and F is the fitness disadvantage of differing genotypes.

3. 'Gene frequencies for adult worms are calculated using Hardy-Weinberg laws.'[10]
4. The number of each genotype at each stage of the nematode life-cycle are simulated (e.g. eggs, infective larvae and adult worms). Thus, the frequency of alleles for resistance and susceptibility for each gene can be calculated for any stage of the life-cycle.[14]
5. 'The total population of each resistance genotype was tracked on a daily basis in hosts and on pasture, along with the frequency of the resistant allele.'[20]

4.39 Anthelmintic treatment - discussion

Knowledge on the mode of action, mode of inheritance and the genetic mechanisms for anthelmintic resistance to differing drug classes could add realism to the theoretical framework currently described by the models reviewed. This could generate a model for anthelmintic resistance which better fits the experimental data available for each anthelmintic class. A total of 60 publications[154-213] were found detailing such information.

Further, the initially low frequencies of resistant genotypes to all anthelmintic drugs has previously been proposed to be the result of a fitness disadvantage for resistant genotypes. Such a fitness disadvantage would result in a decreased rate at which resistance emerges when anthelmintics are administered and a reversion to susceptibility in their absence. A total of 23 reviews and experimental studies[214-236] were found pertaining to fitness disadvantages within *Haemonchus contortus*, *Trichostrongylus colubriformis* and *Teladorsagia circumcincta* for the anthelmintic classes of benzimidazoles, nicotinic agonists and macrolytic lactones.

5. Feasibility of developing a model for Australian conditions

Each of the models reviewed was designed to address particular questions about the dynamics or control of specific nematode species in a specific host and/or agro-climatic region. Thus, whilst each model follows a generalised framework describing the population dynamics throughout the differing stages of the nematode life cycle, certain components were only included if the authors deemed them necessary for the aim/purpose of their model. The consequence, for the purpose of simulating the impact of integrated parasite control strategies on multi-species nematode infections in sheep across differing regions of Australia, is that the models reviewed incompletely describe the nematode life cycle and are initially unsuitable in their current form.

Following a review of the individual models, a number of issues became apparent. Firstly, there is a dichotomy between whether these models were developed with a focus on production or parasitology. Secondly, a comparison of the functions used to describe equivalent model components highlights differences in complexity. Such complexity does not necessarily infer added benefit and may in fact be detrimental due to an increased requirement for parameterisation. Thirdly, very little validation has been carried out to determine the predictive accuracy of all the models reviewed and thus do not instil user confidence in the outputs. Finally, in some instances these models have previously been used to investigate scenarios and parasite control strategies for which they were not designed to simulate.

Whilst individually the models reviewed are not appropriate for use in evaluating integrated parasite control strategies in Australia, a composite would be capable of achieving this aim. In considering the development of a composite model, the different functions used to describe equivalent components of each model can be compared and the best functions identified. These functions can then be evaluated against available literature and experimental data (identified within section 4) to assess the reliability of existing functions or to subsequently develop appropriate relationships where model components are found to be based on minimal data or poor relationships.

The best functions available from the reviewed models were identified for the purpose of predicting the impact of nutrition, grazing management, anthelmintic treatment strategies and selective breeding for resistance on production traits in sheep, parasitological traits and

the emergence of anthelmintic resistance under Australian conditions. The resultant initial composite model outline is given in section 6.

6. Initial outline for composite model structure

The following section details the selection of the best functions available for each model component following a review of existing nematode models (section 4). Model components specified as inputs are not considered. Selected model components will be subsequently evaluated against available literature and experimental data (see section 4 discussions).

6.1 Initial outline for composite model structure - summary

Table 37 provides a summary of model function selection from the seven existing nematode epidemiology models reviewed. The reason for the selection is subsequently detailed in sections 6.2-6.20.

Table 37. Summary of composite model selection.

Model component	Model selection/outline
Nematode species	4
Meteorological data	input
Pasture	
Herbage quality	input
Herbage growth	function of herbage quality & meteorological input
Herbage availability	function of initial availability, growth & consumption
Free-living larval stages	
Ewe egg contribution	model 3
Mortality of pre-infective larvae	*
Mortality of infective larvae	*
Duration: egg to infective larvae	*
Larval availability for ingestion	models 2 & 7
Host	
Nutritional requirements	models 5 & 7
Herbage Intake	model 5
Parasite-induced anorexia	model 5
Constrained food Intake	models 5 & 7
Infective larval Intake	any of models 1, 2, 3, 4, 5 or 7
Digestion	model 5
Nutrient allocation	models 5 & 7
Metabolism/catabolism	model 7
Live weight	model 5
Weight loss from parasitism	models 5 & 7
Wool growth	models 5 & 7
Host mortality	models 4 & 5
Faecal output	model 5
Between animal variation	model 5
Parasitic nematode stages	
Nematode pre-patent period	models 1 & 5
Arrested development	†
Establishment	models 1 & 5
Mortality of adult nematodes	model 5
Worm Burden	†
Fecundity	models 1 & 5
Faecal Egg Count	†
Anthelmintic treatment	
Efficacy	model 4
Genetic mechanism for resistance	model 4
Nematode genotype fitness	model 4
Allele frequencies	model 4

* Functions described the impact of climatic variables on the population dynamics of the free-living stages are to be derived from experimental data.

† Arrested development and worm burden are a consequence of infective larval intake, establishment and mortality. Faecal egg counts are a consequence of faecal output and fecundity.

6.2 Nematode species (see section 4.2)

Nematode species to be simulated:

1. *Haemonchus contortus*
2. *Teladorsagia circumcincta*
3. *Trichostrongylus colubriformis*
4. *Trichostrongylus vitrinus*

Reason:

The wide range of agro-climatic regions within Australia results in the differing prevalence/abundance of nematode species. Model 4[16] simulated concurrent populations of *Haemonchus contortus*, *Teladorsagia circumcincta* and *Trichostrongylus colubriformis*. However, the requirement to include *Trichostrongylus vitrinus* has also been previously been identified (WormWorld meeting minutes, December 2002), and requested by Paul Nilon in recent correspondence (30th July 2014).

6.3 Free-living nematode stages: ewe egg contribution (see section 4.7)

Model Selection:

- Model 3 (Learmount *et al*.[10])

Reason:

Accounting for the implication of parasite control strategies aimed at the ewe population necessitates the explicit simulation of the ewe population.

6.4 Free-living nematode stages: population dynamics (see section 4.8-4.11)

Model Selection:

- None

Reason:

Whilst model 3[10], 4[11,16], 6[23] and 7[26] attempt to describe the impact of climatic variables on the population dynamics of the free-living stages of the nematode life cycle, the functions outlined result in poor correlations with experimental data. Since construction of these models, further experimental data has become available (through experimental studies carried out at the University of New England) which can be used to generate more reliable functions.

6.5 Free-living nematode stages: larval availability for ingestion (see section 4.12)

Model Selection:

- Model 2 (Leathwick *et al*.[6])
- Model 7 (Callinan *et al*.[26])

Reason:

Whilst all models consider the total population of infective larvae on pasture, only models 2[6] and 7[26] include the vertical distribution of infective larvae and the grazing height of the host population.

6.6 Host: nutritional requirements (see section 4.13)

Model Selection:

- Model 5 (Laurenson *et al*.[17])
- Model 7 (White *et al*.[27])

Reason:
Model 5[17] considers the protein and energy requirements for host maintenance, growth, wool and immunity. Model 7[27] includes the energy requirements for pregnancy and lactation.

6.7 Host: herbage intake (see section 4.14)

Model Selection:

- Model 5 (Laurenson *et al*.[17])

Reason:
Model 5[17] considers the impact of herbage quality, host nutrient requirements, animal status/condition, and digestive and metabolic processes.

6.8 Host: parasite-induced anorexia (see section 4.15)

Model Selection:

- Model 5 (Laurenson *et al*.[17])

Reason:
Model 5[17] is the only model reviewed to link reductions in herbage intake to the immune response.

6.9 Host: constrained herbage intake (see section 4.16)

Model Selection:

- Model 5 (Laurenson *et al*.[17])
- Model 7 (White *et al*.[27])

Reason:
Both model 5[17] and 7[27] consider the maximum herbage intake of the host/animal.

6.10 Host: infective larval intake (see section 4.17)

Model Selection:

- Model 1 (Singleton *et al*.[4])
- Model 2 (Leathwick *et al*.[6])
- Model 3 (Learmount *et al*.[10])
- Model 4 (in correspondence with R.J. Dobson, 16th July 2014)
- Model 5 (Laurenson *et al*.[18])
- Model 7 (Callinan *et al*.[26])

Reason:
All these models consider the availability of infective larvae for ingestion and the herbage intake of the host.

6.11 Host: digestion (see section 4.18)

Model Selection:

- Model 5 (Laurenson *et al*.[17])

Reason:
Model 5[17] considers digestion to be a function of herbage quality and host condition/status.

6.12 Host: nutrient allocation (see section 4.19)

Model Selection:

- Model 5 (Laurenson *et al*.[17])
- Model 7 (White *et al*.[27])

Reason:
Model 5[17] considers the allocation of protein and energy towards maintenance, growth, wool productive and immunity. Model 7 also considers the allocation of energy to pregnancy and lactation.

6.13 Host: metabolism/catabolism (see section 4.20)

Model Selection:

- Model 7 (Callinan *et al*.[26])

Reason:
Model 7[26] considers the relationship between metabolism and herbage quality, and includes the impact of parasitism on metabolic processes.

6.13 Host: live weight (see section 4.21)

Model Selection:

- Model 5 (Laurenson *et al*.[17])

Reason:
Model 5[17] considers body composition (i.e. the accretion of protein, lipid, ash and water).

6.14 Host: weight loss from parasitism (see section 4.22)

Model Selection:

- Model 5 (Laurenson *et al*.[17])
- Model 7 (Callinan *et al*.[26])

Reason:
Model 5[17] includes the impact of nutrient availability and its allocation to growth, as well as direct protein losses due to parasitism. Model 7[26] also includes the impact of parasitism on metabolism.

6.15 Host: wool growth (see section 4.23)

Model Selection:

- Model 5 (Laurenson *et al*.[17])
- Model 7 (White *et al*.[27])

Reason:
Models 5[17] and 7[27] both include the impact of nutrient availability and the allocation towards wool growth.

6.16 Host: mortality (see section 4.24)

Model Selection:

- Model 4 (Dobson *et al*.[16])
- Model 5 (Laurenson *et al*.[17])

Reason:
Model 4[16] includes lethal worm burdens that may be applicable to *Haemonchus contortus* infections. Model 5[17] considers the availability of nutrients for allocation to maintenance and the catabolism of body reserves (protein and lipid) applicable to *Teladorsagia circumcincta* and *Trichostrongylus colubriformis* infections.

6.17 Host: faecal output (see section 4.25)

Model Selection:

- Model 5 (Laurenson *et al*.[17])

Reason:
Model 5[17] calculates faecal output as a consequence of herbage intake, herbage quality and digestive processes.

6.18 Host: between animal variation (see section 4.26)

Model Selection:

- Model 5 (Laurenson *et al*.[17])

Reason:
Model 5[17] includes variation in growth traits, immunological traits and the nutrient requirements for maintenance. Further, this model allows for the imputation of correlations between traits, and includes maternal effects.

6.19 Parasitic nematode stages (see sections 4.27-4.34)

Model Selection:

- Model 1 (Singleton *et al*.[4])
- Model 5 (Laurenson *et al*.[18])

Reason:
Model 1[4] explicitly model components of the Th2 immune response (e.g. IgA activity), and includes half-lives which allow for reversion to naïve status. Model 5[17] allows for the impact of anthelmintic treatment on the infective larval burden of the host and its subsequent impact

on the acquisition of immunity. Further, both these models include density-dependent effects on fecundity.

6.20 Anthelmintic treatment (see sections 4.35-4.39)

Model Selection:

- Model 4 (Barnes & Dobson[14])

Reason:
Model 4[14] allows for the simulation of monogenic or multi-genic mechanisms for anthelmintic resistance, and allows for the potential simulation genotype fitness disadvantages.

7. Accessibility and usability

Consideration was given to the accessibility and usability of the potential composite model. In order to provide a useable model/tool for industry, research and educational purposes a good user-interface is essential. As such an appropriate outline of a user-interface is detailed (section 7.1) which attempts to strike a balance between the requirements for expert user input and predefined scenarios. The proposed outputs (section 7.2) of this model/tool will provide an illustration of pasture infectivity, worm burdens, anthelmintic drench resistance and the productive and financial consequences arising from the combination of various options for parasite control. Access to this tool is proposed to be facilitated via its inclusion into the WormBoss website which provides an existing route to market.

Notably, the existing nematode epidemiology models reviewed were not completely transparent making a thorough review difficult. This lack of transparency has meant that the underlying assumptions contained within these models are only known by the individuals who developed these models, and not completely understood by those viewing the consequent outputs. The absence of an open source code for these models has resulted in reliance upon the individual developers, and in some cases has prevented these models from being updated once new experimental data has become available. As such, it is suggested that the source code for the proposed composite model (along with detailed literature) should be made openly available. This would serve to inform researchers of underlying assumptions, allow for thorough review, remove reliance upon an individual and facilitate further development.

7.2 Advice tool user-interface (for inputs)

7.2.1 Simulation scenario

- New scenario
- Saved scenario

Note: Scenarios can be saved to allow users to make adjustments rather than re-entering information for each simulation.

7.2.2 Start date

- Input start date

Note: The model will simulate 1 year from the date specified.

7.7.3 Meteorological data

- ***General*** – Select region/location
- ***Advanced*** – Input climatic data

Note: Selection specifies regional daily averages for temperature and rainfall. A figure will be included in the user interface to allow temperature and rainfall patterns to be observed.

7.7.4 Level of pasture contamination & nematode species prevalence

- ***General*** – Select low, medium or high initial level of infective larvae on pasture
- ***Advanced*** – Specify the initial number of infective larvae (kg^{-1} DM) for each nematode species

Note: Use of the general option will specify nematode species prevalence in accordance with selection of region/location (i.e. associated to meteorological data).

7.2.5 Herbage quality

- ***General*** - Select low, moderate or high quality pasture
- ***Advanced*** - Specify pasture quality (crude protein & metabolizable energy content)

Note: In conjunction with the meteorological data selection/input, the selection or specification of herbage quality will determine the quality of pasture across the year (constructed from information provided by state departments of agriculture). A figure showing the energy and protein content across the year will aid the user in selection of an appropriate quality of herbage.

7.2.6 Herbage growth

- ***General*** – Automated
- ***Advanced*** - Adjustment of automated growth calculation using a scaling factor

Note: Data regarding pasture growth is accessible via the Australian Government's Department of Agriculture and ABARES. Analysis of this data will provide simplistic relationships between meteorological data, pasture quality and pasture growth. An illustrative figure for pasture growth across the year will be included in the user interface.

7.2.7 Herbage availability

- Input initial quantity of pasture available (herbage mass, kg DM ha^{-1})

Note: Whilst the initial herbage mass is required as an input, subsequent herbage availability will be calculated as a function of this value, pasture growth, pasture decay and the herbage intake of the grazing population and will be given as a model output.

7.2.8 Paddock setup

- Specify the number of paddocks and the area of each individual paddock

7.2.9 Sheep breed

- ***General*** - Select sheep breed or 'continue selective breeding'

- ***Advanced*** - Specify average breeding values, mean trait parameters, coefficients of variance and correlations

Note: A library of parameter values for differing sheep breeds will be constructed to allow for breed selection. The advanced option will allow for alteration of these values. These will be used to construct genotypes and phenotypes for the initial parental generation (sires and dams) and the subsequent offspring (lambs). The option for selective breeding is detailed in section 7.2.13.

7.2.10 Joining/mating, peak lambing & number of lambs per ewe

- Input the date of joining/mating or peak lambing, and the number of lambs per ewe

Note: If the date of peak lambing is specified then the date of joining/mating will be back calculated to allow for the simulation of pregnancy.

7.2.11 Paddock & flock allocation

- Input the number of sheep allocated to each paddock
- Ewes, sires and lambs from any given paddock may be selected to move to another paddock on any given date
- Ewes, sires or lambs may be specified to be removed from the simulation on any given date
- A productive goal may be specified for the removal of lambs for slaughter

Note: This setup allows for the flexible simulation of farm management practices and enables weaning, paddock rotation and productive goal practices to be specified.

7.2.12 Nutritional supplementation

- Input date, quality and quantity of nutritional supplementation (protein and energy)

7.2.13 Selective breeding

- Choose whether selective breeding is to be simulated
- Specify traits and weighting for selective breeding program
- Input the percentage of the lamb population to be used in a selective breeding program

Note: Outputs for average breeding values and variance according to the specified breeding strategy will be saved at the end of the simulation. These can be selected for use in a subsequent simulation within the 'select sheep breed' section.

7.2.14 Anthelmintic treatment

- Input the number of anthelmintic actives to be simulated
- Specify the duration of action for each active
  - ***General*** - short or long acting
  - ***Advanced*** - specify duration
- Specify the efficacy of each active
  - ***General*** – total efficacy
  - ***Advanced*** - resistance genotype efficacies
- Specify which actives are to be given to which paddock on which date
- Select whether targeted selective treatment is to be simulated

- Choose determinant criteria (random or specific trait, e.g. live weight, WEC)
- Choose proportional treatment or threshold value

Note: Using the general selection for anthelmintic efficacy will result in a monogenic mechanism being used with the resistance allele being recessive (known mechanism for the benzimidazoles). Using the advanced selection for anthelmintic efficacy will allow the user to infer the dominance or neutrality of alleles for resistance and susceptibility. Each anthelmintic active is assumed to be independent.

7.2.15 Economic inputs

- Costs
  - Input the cost of an anthelmintic dose per animal
  - Input the cost of testing per animal (e.g. WEC)
- Gains
  - Input the sale price per kg of carcass or live weight
  - Input the sale price per kg of wool

Note: Animals removed from the simulation due to meeting productive goals will be included in economic calculations, however, animals removed due to mortality will not. Further, wool fibre diameter is not considered.

7.3 Advice tool outputs

7.3.1 General outputs

To determine the importance of outputs required from a nematode epidemiology model, a survey was carried out in which individuals were asked to rank the importance of six topics. Table 38 provides the results of this survey and is composed of responses from eight members of the ParaBoss forum.

Table 38. Importance of information provided by a model for worm control.

	Unimportant (score 1)	**Marginal benefit** (score 2)	**Useful** (score 3)	**Important** (score 4)	**Must have** (score 5)	**Average rating**
Pasture infectivity	0.0%	0.0%	12.5%	37.5%	50.0%	4.38
Worm burdens	0.0%	0.0%	0.0%	62.5%	37.5%	4.38
Drench resistance	0.0%	0.0%	0.0%	62.5%	37.5%	4.38
Production consequences	0.0%	0.0%	12.5%	75.0%	12.5%	4
Financial consequences	0.0%	0.0%	25.0%	62.5%	12.5%	3.88
Mortality consequences	0.0%	0.0%	25.0%	75.0%	0.0%	3.75

This survey suggested that all topics surveyed are required at a general level output. As such the tool will provide the following as general outputs:

- Plots of pasture infectivity across the year for each of the paddocks specified by the user

- Plots of average worm burdens for sheep populations grazing on each of the specified pastures across the year
- Plots for anthelmintic efficacy of each active for each paddock across the year
- Plots for the average live weight and wool growth for sheep populations grazing on each of the specified pastures across the year
- Economic values (gains – costs) for each of the specified paddocks
- The number of mortalities for each of the specified paddocks

7.3.2 Advanced outputs

All variables calculated by the model will be available.

8. Development pathway and potential cost

8.1 Background

This study evaluated the feasibility of developing (or accessing) a sheep nematode epidemiology model for Australian conditions. Seven existing nematode epidemiology models were reviewed to evaluate their suitability for Australian conditions in their current form, or after customisation. Whilst individually these models were found to be incapable of evaluating integrated parasite control strategies, a composite of these models could achieve this aim and provide a useful tool for industry, research and educational purposes. Thus, this section details the pathway for implementing the development of a composite model and output tools (section 8.2).

Further, previous nematode epidemiology models have only validated certain components under specific scenarios, whilst predictions arising from the entirety of these models have remained un-validated. As such, options are provided for field validation which would generate confidence in the model predictions (section 8.3).

The timeline and potential cost of developing a validated sheep nematode epidemiology model for Australian conditions is subsequently detailed (section 8.4).

8.2 Advice tool development pathway

1. Yan Laurenson will create the composite model, and will be guided by discussion with an industry steering group.
2. A PhD student (modeller) will work closely with Yan Laurenson on model development and sensitivity analysis. This will help in documenting the model, increase industry capabilities in mathematical modelling, and in part (along with an open source model code) prevent complete reliance upon an individual.
3. As model development proceeds, interim advice tools will be created based on the modules developed. These can inform practices on the single implementation of parasite control strategies, with the final integrated tool informing on the combination of parasite control strategies.

4. A software developer/engineer will create a C++ user interface to generate the final output tool.

8.3 Option for field validation

Field validation studies are proposed to run for two years in three locations (New South Wales, Victoria and Western Australia). These studies will provide valuable validation data for the model to ensure that it captures variation in regional climatic conditions and management practices. As the field studies will be run concurrent to model development, the data gathered will be used to validate the model during the final year of the project. Further, the field studies will also be used to inform the regional merits of targeted selective treatment (TST), which remains the most important and contentious debate among Australia's parasitology community. The proposed field study design for each site is given in section 8.3.1, and the proposed measurements are given in section 8.3.2.

8.3.1 Field study design

- Each site is to consist of 32 hectares divided into 16 plots (2 hectares each)
    - 2 treatment groups (No TST or TST)
        - Up to 4 drenching occasions per year
    - Ewes and lambs (2 groups post weaning)
    - 4 replicates

	Ewes (No TST)	Ewes (TST)	Lambs (No TST)	Lambs (TST)
1				
2				
3				
4				

Replicate

Figure 28. Overview of site setup.

- Initially 80 ewes will be allocated to the ewe plots (i.e. 10 ewes/plot)
- Lambs (80) will graze with ewes until weaning, then move to lamb plots (10 lambs/plot)
- In the second year of the experiment the lamb group will be replaced

- 6 weeks prior to each drenching occasion 3 (uninfected) sheep will be added to each plot (12 sheep per treatment and lamb or ewe group), and removed following treatment for FEC reduction test
    - 1 sheep untreated
    - 1 sheep treated with active 1
    - 1 sheep treated with active 2

8.3.2 Field study measurements

- Live weight & Body condition score
    - 160 animals
    - 26 times per year (every 2 weeks)
- Reproductive scan
    - 80 ewes
    - 1 time per year
- Meteorological data
    - Weather station
- Pasture quality & mass
    - 16 plots
    - 12 times per year (every month)
- Pasture infectivity
    - Methodology to be determined
- WEC
    - 160 animals
    - 26 times per year (every 2 weeks)
- WEC coproculture (morphological)
    - 16 plots
    - 26 times per year (every 2 weeks)
- WEC coproculture (PCR)
    - 160 animals
        - 2 times per year
    - WEC reduction test animals
        - 12 animals
            - 3 groups (untreated, active 1, active 2)
            - 2 treatments (No TST & TST)
            - 2 groups (ewes & lambs)
        - 3 times per year (initial + 2 during experiment)
- WEC reduction test
    - 208 animals
        - 16 plots
        - 10 animals per plot
        - 3 WECRT animals per plot
    - 3 times per year (initial + 2 during experiment)

8.4 Project timeline and potential cost

8.4.1 Project timeline

The timeline for developing a validated sheep nematode epidemiology model for Australian conditions is given in Figure 29.

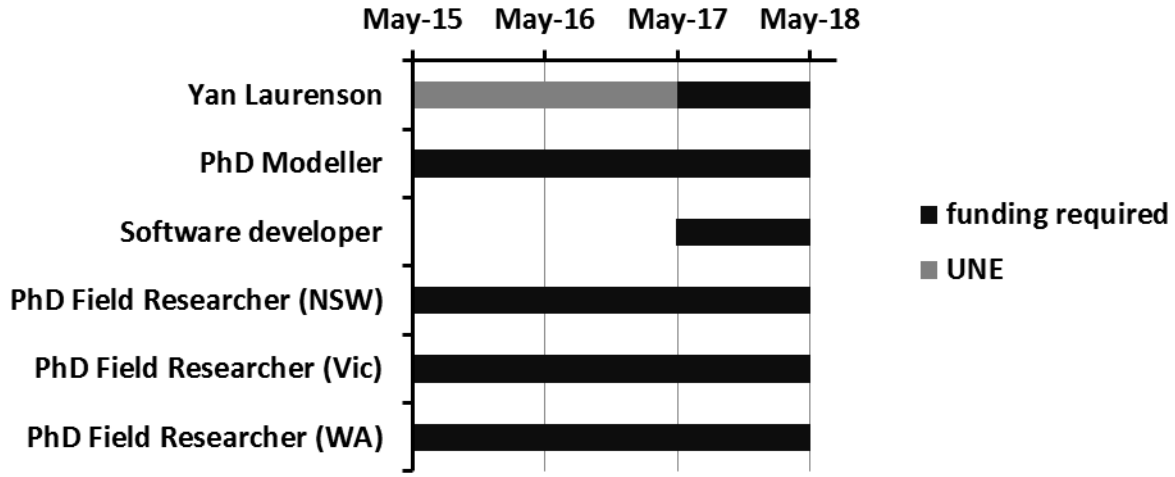

Figure 29. Time line of project activity indicating UNE-supported positions and where project funds are required.

8.4.2 Project costs

The potential project costs for developing a validated sheep nematode epidemiology model for Australian conditions is given in Table 39.

Table 39. Breakdown of the proposed project costs.

		Cost ($ yr^{-1})	Number	Duration (yrs)	Project costs ($)
Model development	**Yan Laurenson**	111,697	-	1	111,697
	PhD modeller	35,392*	1	3	106,176
	Software developer	98,363	1	1	98,363
	Operators, conferences, software	15,000	1	3	45,000
	Total				**361,236**
Field studies	**PhD field researcher**	35,392*	3	3	318,528
	Field academic supervision	25,000	3	3	225,000
	Field operating costs	61,034	3	2	366,204
	Total				**909,732**
	Model & software development				361,236 (28%)
	Field studies/validation				909,732 (72%)
	Total				**1,270,968**

* The $ cost per year for PhD students will be dependent upon application for Australian Postgraduate Awards (APA), if successful this cost will be reduced by $25,392 per year ($304,704 reduction in total project costs).

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