System Dynamic Modelling Of Microbes: Simulating Farm Management Options

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EXTENDED ABSTRACT

Intensification of land use and urbanisation in New Zealand are compromising the quality of surface waters. Managing the environmental load of microbes from diffuse sources, such as agriculture, is particularly challenging. Microbial contamination of water is a complex area of environmental management, and our understanding of the subject is incomplete. Many different stakeholders are involved in the management of surface waters, each with their own perspective about who is responsible for its quality and what should be done about it.

We utilised system dynamic modelling to explore the microbial loading to water from farming activities with the intention of informing management practices. We have integrated these multiple perspectives into conceptual models and simulated components of these models. This has led to new understandings as to the potential efficacy of certain best management practices (BMPs) with respect to specific microorganisms found in the faeces of livestock.

Microbes display different survival characteristics in faeces – some die rapidly once they are deposited into the environment, whereas others are longer lived and may even multiply. We have modelled two microorganisms, *Campylobacter* a zoonotic pathogen, and *Escherichia coli* an indicator organism. These models highlight how microbial characteristics combined with agricultural practice can influence the spatial and temporal distribution of faecal microbes on a farm scale.

Modelling the different mechanisms by which microbes can be delivered to waterways has highlighted the differences between the behaviour of these two organisms. Therefore, behavioural differences among organisms need to be considered before implementing a monitoring programme to assess the effect of farm management practices on human health.

Excluding livestock from waterways may reduce the microbial load of short-lived microorganisms in waterways, but some microorganisms are more robust, they can survive in the environment for considerable periods of time, and in some cases they can multiply. A proportion of these microorganisms can subsequently be mobilised, primarily through the actions of water, and move from paddock to waterways. In this case, other BMPs are required to mitigate the effects of runoff.

Some of the BMPs used to manage sediment and nutrient loading to water also impact on the microbial loading of the environment from agriculture. This modelling work has revealed one significant area that needs to be addressed, that is, whether *any* BMPs can influence the amount of microbes shed by livestock into the environment, particularly zoonotic microbes.

1. INTRODUCTION

An ever growing body of evidence relates water quality to human activity, for example, Monaghan et al. (2007) discusses the links in terms of agriculture. The quality of fresh water can be defined in a number of ways. For example, faecal indicator organisms such as *Escherichia coli* are often used as surrogates to gauge microbial water quality. While indicator organisms tend not to be harmful to human health, their presence indicates faecal contamination and hence the presence of faecal pathogens organisms in the water. Some microrganisms, known as zoonoses are carried by animals and can cause illness in humans and it is these which we would like to manage.

In New Zealand, Scarsbrook (2006) showed a positive correlation between the level of indicator bacteria in river water and the proportion of catchments under pastoral agriculture. Collins (2002) demonstrated links between stock density and water quality. These issues are not unique to New Zealand, indeed Kay et al. (2007) discuss policy developments in the USA and Europe in response to issues around water quality and faecal indicators.

The New Zealand Parliamentary Commissioner for the Environment highlighted the environmental challenges associated with intensification of agriculture (PCE 2004). The economic success of the dairy farming industry meant that from 1980–2005 there was a 70% increase in the number of dairy cattle in New Zealand (MAF 2006), and in 2006, dairy exports accounted for 18% of the country’s total exports (Statistics New Zealand 2006). Linking agriculture, in particular dairying, with water quality, has raised a considerable amount of debate, including the awareness-raising campaign “Dirty Dairying” led by Fish and Game. The dairy sector has responded with policies such as the “Clean Streams Accord” (Crowie et al. 2006).

This project undertook to develop models to assist with the design and testing of farm management policy options to assist farmers manage zoonotic contamination of waterways from farming.

Figure 1. Conceptual map of the whole system of factors which relate to microbial loading of the environment from agriculture and potential consequences. The nodes in orange refer to the areas which were simulated in the study.

The challenge in developing models of this type is that there is a plurality of beliefs as to what the issues are, as well as a high degree of technical complexity and degree of uncertainty about the nature of the problem situation (Daellenbach and McNickle, 2005). For example, while we know livestock carry zoonotic organisms and these organisms can be found in water, it is not known how much of the human disease burden can be attributed to contamination of water caused by pastoral agricultural practices.

During the research design phase we applied a systems dynamics methodology (Forester 1994; Maani and Cavana 2000) to enable people to be solution focused in complex situations. This paper discusses how the information was modelled and the outcomes of this modelling work rather than detailing the identification of stakeholders and capturing their perspectives.

2. WORKSHOP OUTCOMES

The outcome of a number of workshops and interviews with stakeholders was a conceptual overview of the whole system (Figure 1). This described the possible relationship between agriculture and human health, including feedback mechanisms that highlighted the interaction between the perception of human health and agricultural practice.

This is a highly complex model. A number of the variables were either “soft variables” and unquantifiable or “hard variable”. In addition, the relationships between several of the variables could be described at best as uncertain. Though the qualitative model proved useful to gaining an understanding the situation (Coyle 2000), choices were made about what aspects of the model would be useful to simulate.

3. MODEL DEVELOPMENT

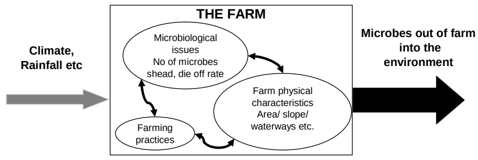

Figure 2. Defining the narrow system of interest. The system focused on issues in the farm and the key system inputs and outputs.

In response to the initial conceptual work, a narrower system of interest was defined (Figure 2). This focused on issues on a farm scale and dairy farms in particular, where farmers may have some control and where there was some empirical evidence and knowledge to enable potential management options to be evaluated. This frame was taken as it supported the project aim of testing out policies or BMPs that could be applied on farm to manage microbial loading of the environment.

A number of modelling studies have looked at microbial loading of the environment from agriculture. Jamieson et al. (2004) notes that these types of studies have three essential components: characterisation of the production and distribution of microbes; simulation of transport of microbes from land surface to water; and the transportation route through the stream network. The model developed in this project focuses on the first two and excludes transportation through the stream network. So we focused on the orange nodes in Figure 1. The approach differs somewhat from Walker et al. (1990) and Collins and Rutherford (2004) who also considered the effectiveness of agricultural management practices, but did not address the spatial distribution of microbes in detail. This work provides an approach to estimate the temporal and spatial variation in microbial loading on paddocks, and it also considers multiple microbes, not just one indicator organism.

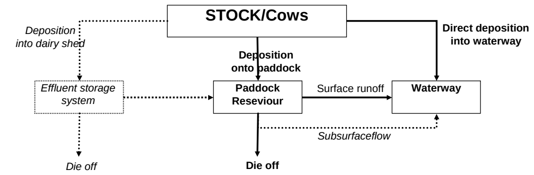

Figure 3. Key microbial reservoirs and flows in the simulation model. The reservoirs and flows illustrated by solid line are modelled in this paper.

Faeces are deposited onto paddocks, in the dairy shed and/or directly into waterways (Figure 3). Faecal material moves from the paddock to waterways through overland flow or subsurface drainage, or from the dairy shed onto the paddock through effluent irrigation. For simplicity we will focus on the direct deposition of faeces into waterways and transportation by overland flow from paddock into waterways. The work also excludes point sources such as untreated direct discharges to waterways from effluent ponds as this activity is not permitted under New Zealand’s Resource Management Act, 1991.

4. MICROBIAL TRANSPORT

Microbial transportation of faecal material from paddocks to waterways is facilitated by water, either due to rainfall and/or (effluent) irrigation. Under certain circumstances overland flow can transport microbes to rivers. In this work we have utilised the SCS Curve Number (USDA 1986) method combined with rainfall data to assess the amount of runoff during rain and or irrigation events.

On a small scale Muirhead et al. (2005; 2006) showed that the concentration of microbes in runoff relates to the concentration of microbes in the cow pats. On a larger, paddock scale, Collins et al. (2005) found an inverse relationship between the time since grazing and the concentration of microbes in surface runoff. This suggests that the amount of microbes transported to waterways is at least in part, a function of the size of the microbial reservoir. The age of the faecal material may impact on the mobility of microbes from the pats (Close et al. 2007) as cow pats dehydrate after deposition and this may influence the mobility of microbes.

Our understanding of microbial transport and the factors that influence it is incomplete, though there have been a number of studies including Collins et al (2002), that found run off flow rate to be a key factor in the transport of microbes. The efficacy of a number of BMPs also appears to decrease with increasing flow rates when presumably total microbial transport is at its highest. Even though there is considerable uncertainty surrounding microbial transport, many modellers have considered the issues of microbial transport in their work, including Walker et al. (1990), Tian et al. (2002) and Collins and Rutherford (2004). All of these authors considered distance and the volume of runoff as important factors in determining the extent of microbial transport, though most did not consider rainfall intensity in their work. It is not surprising to find that when analysing these models there are differences of over two orders of magnitude in these estimates of microbial transportation over distances less than 100 m.

5. FAECAL MICROBIAL RESERVOIRS

It was assumed that the primary reservoir of the microbes was within the faecal material, though it is possible that soil may also act as a reservoir.

Knowing the survival curve (Sinton pers com) see Figure 4, concentration of microbes in fresh faeces (Moriarty pers com) and the faecal production rate, enables the estimation of the size of the reservoir at a particular time and location. It is clear that the prevalence and concentration of zoonotic microbes such as *Campylobacter* within dairy herd faecal matter varies over time (Stanley et al. 1998). This is an important issue as the level of microbes within the faecal matter determines the amount that enters the environment and there is a possibility that management practices may influence this level. Simulating prevalence and related issues can be handled using the Susceptible Infected and Recovered models (SIR) of Kermack and Kendrick (1927). This was not undertaken due to the lack of data available to parameterise the model. If it had been done it would have been doubtful that the results would have been robust and defensible in the eyes of the project stakeholders.

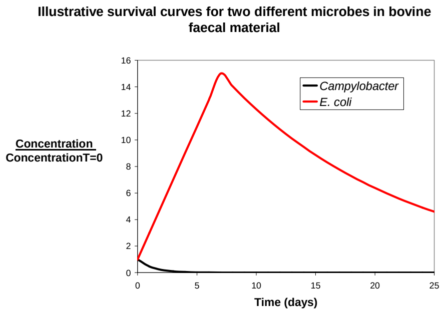

Figure 4. Illustrative survival curves for two microbes. The exact form is climate dependent, however it appears *Campylobacter* under all conditions is less robust than *E .coli* in the environment.

Pastoral agricultural systems, as practiced in New Zealand, require that stock is rotated around the farm, to make optimal use of grass production. The precise details depend on the agricultural system employed, time of year and weather. The outcome of this is that the density of faecal material and the microbes contained within it are expected to vary around the farm.

iThink^{TM} system dynamics software, from isee^{TM} systems provides very simple and accessible tools for modelling growth and die-off in populations, especially delays which are an important aspect of the situation. Using these tools, models of microbial density were created. They show that the density of *Campylobacter* peaks immediately following stock removal from a paddock (Figure 5). Conversely, *E. coli* tends to peak sometime after the stock is removed. This is due to the growth of *E. coli* within the faecal material after deposition, before it dies off – this is much slower for *E. coli* than for *Campylobacter*. The combination of different growth and die off rates means that the average loading of *E. coli* on a paddock tends to be much higher than *Campylobacter* when expressed in terms relative to the concentrations of these microbes in fresh faeces. The variation in on-farm concentrations tends to be much greater for *Campylobacter* than for more resilient microbes even when the observed variation in the concentration of *Campylobacter* in fresh bovine faecal matter is excluded.

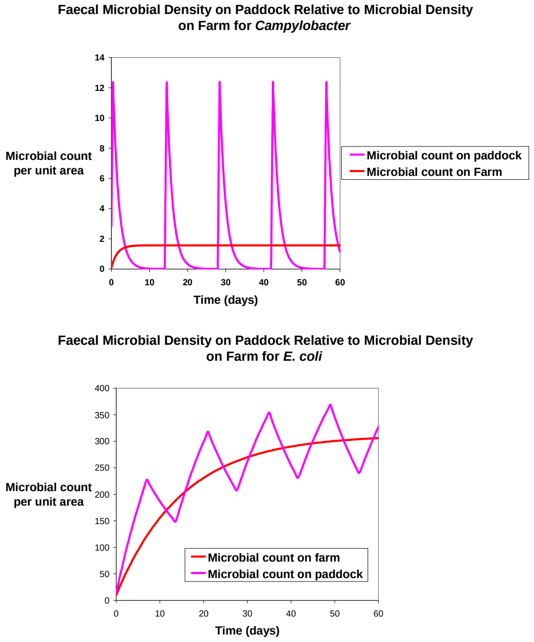

Figure 5. The faecal microbial density of the farm and a paddock for two microorganisms. The model assumes an input of 1 unit per day and that stock remain on the paddock for 0.5 days every 14 days Note the much greater the accumulation of *E. coli* compared with *Campylobacter*.

7. MODELLING RESULTS

Using information about the microbial reservoir and transport enables us to simulate the situation on farm and inform debate about possible management options and responses. This section considers an example of using the model to assess the potential impact of direct deposition of faecal material in waterways, relative to transportation due to runoff.

7.1. Worked example

Consider a paddock which is stocked for 12 hours with a return every 14 days (Ross and Donnision 2006), as might be the case for a dairy farm at certain times of the year. The stock can access a water way, and 1% of faecal mater is deposited in the stream (Wilcock 2006). Direct deposition is very efficient at delivering microbes to waterways. The remaining faecal matter is deposited on the paddock. Ingress into streams by cattle can only take place when the paddock is stocked. Surface runoff, due to rainfall tends to be an infrequent event when compared with the frequency of direct deposition into waterways or the frequency of rainfall events. It is expected to be less efficient at delivering microbes to waterways than direct deposition, but it can occur at any time, mobilising faecal material even when the paddock is not stocked.

So what happens when there is a runoff event, and how important is it in terms of total microbial load when compared with direct depositions? Figure 6 shows the results of simulation using a range of feasible estimates of the fraction (efficiency) of microbial reservoir transported to waterways.

The ratio of microbes in runoff compared to direct deposition is considerably higher under all circumstances for *E. coli* than *Campylobacter*. The *Campylobacter* ratio is also sensitive to time. So we expect the ratio of *E. coli* to *Campylobacter* concentration in runoff to depend on the time that has passed since the paddock was grazed.

Runoff can deliver large loads of *E. coli* to waterways, whereas the *Campylobacter* load is proportionally lower compared with the contribution from direct deposition.

The overall interpretation of these results depends on the performance measure of the system as a whole. This needs to take into account the frequency and magnitude of runoff events.

For example, if the performance measure reduced levels of *E. coli* entering waterways and runoff was apparently an issue, it might be appropriate to focus on reducing runoff. Similar strategies have been developed to assist with the management of phosphates. In contrast, if the performance measure managed *Campylobacter*, more effort may be put into reducing stock incursions into waterways.

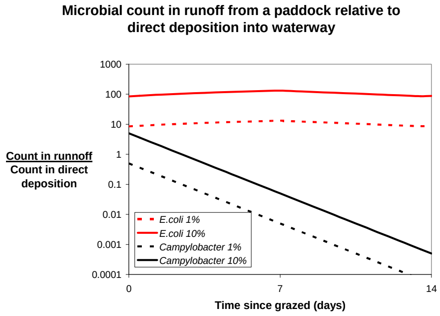

Figure 6. Counts of microbes in runoff relative to direct deposition. The percentages refer to the fraction of the microbial reservoir transported to the river during a runoff event. The differences between the two microbes are due to the size of their microbial reservoirs.

8. CONCLUSIONS

Combining information from a number of sources and integrating it using this model has identified differences which may be useful when managing microbial contamination. For example, keeping stock out of waterways may be a more effective management strategy for short-lived microbes than longer-lived microbes. These issues need to be borne in mind when considering health impacts of agricultural practices as it means that indicator microorganisms are not perfect analogies of the pathogenic microorganisms. Differences in the behaviour of indicators and pathogens need to be considered before implementing a monitoring programme to assess the effect of farm management practices on human health.

This type of modelling approach can be applied to different farming systems other than dairying. It can also address micro-organisms other than *E. coli* and *Campylobacter*

Many of the management strategies that we are considering for microbial contamination issues are common to the management of phosphate and sediment from agriculture. However these strategies tend to be end-of-pipe solutions. In the case of microbes there is *prima facie* evidence to suggest that the carriage rate of zoonotic organisms is less consistent than indicator organisms. The factors that influence many of the zoonotic pathogens are not yet fully understood.

This work supports some of the current policies which are aimed at managing water quality, such as excluding livestock from waterways. The models provide evidence of differential behaviour of microbes which can improve our interpretation of indicator organism's data when assessing microbial water quality and the potential impact from agriculture.

9. ACKNOWLEDGMENTS

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