Land-use change and emerging public health risks in New Zealand: assessing Giardia risks

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Abstract

Agriculture is key to New Zealand’s economy with land-use conversions in response to market forces occurring regularly, like that of recent dairy intensification throughout the country. However, land-use conversion can occasionally result in unexpected and significant consequences for public health that need to be accurately estimated and subsequently managed accordingly. For example, dairy cattle have high Giardia prevalence in New Zealand and identical strains from infected humans and cattle located in the same geographical region have recently been reported.

Thus, the high rates of human infections in New Zealand compared to similar socioeconomic countries caused by the waterborne pathogen Giardia are particularly concerning given the increasing dairy cattle populations on the landscape. However, the ability of traditional, evidence-based, epidemiological approaches to detect such causal relationships between land-use and Giardia infections is limited given the many possible indirect links between the two, in turn highlighting the need to develop appropriate risk assessment techniques. As such, the general requirements for and development of risk assessment frameworks to evaluate the likelihood of public health risks from waterborne pathogens are introduced and explored using Giardia in New Zealand as an example.

Specifically, the importance of recent advances in Giardia-based knowledge, the incorporation of such data into existing risk assessment frameworks and the influence of remaining research gaps are each discussed for expanding currently available risk assessment tools. Not surprisingly, the availability of appropriate risk assessment tools for agencies responsible for public health and environmental management would ensure the public health risks for Giardia resulting from land-use change could be quantified holistically and strategies subsequently developed through active agency communication to minimise such risks.

Throughout history, diseases have emerged and re-emerged in the human population as conditions came about that were favourable to pathogens. Not surprisingly, human-induced land-use changes have been important drivers of significant infectious disease outbreaks and of the more than 1,400 species of organisms known to cause human infections, roughly 60% are zoonotic and transmissible between non-human and human hosts. Thus, land-use changes that alter the type and number of animals across the landscape can result in novel opportunities for disease to occur in local human populations. The significant conversion and intensification of land to dairy farming in New Zealand may be one such example creating opportunities for infectious diseases to emerge and increase in humans.
The recent intensification of existing dairy farms and the conversion to dairy farming from lower density sheep and beef farming in New Zealand is causing concern, with reports of declines in water quality coincident with such land-use change.\textsuperscript{4} Not surprisingly, this shift has resulted in considerable physical alterations to the landscape, in addition to a range of significant direct and indirect environmental, social, economic and political consequences. However, an important, yet often overlooked, consequence of changing land use to dairy farming is an increased risk to public health,\textsuperscript{5} by the transport of potentially pathogenic microorganisms from animal hosts to humans via surface waters.\textsuperscript{6}

Resulting from both point (direct) and non-point (diffuse) sources,\textsuperscript{7,8} the contamination of waterways with microorganisms present in manure that can potentially cause human infections is particularly concerning given the sheer volume of manure produced daily.\textsuperscript{9} For example, the average dairy cow produces twenty-five kilograms of faecal matter per day and preferentially defecates when crossing streams.\textsuperscript{10,11} Furthermore, it is reasonable to assume that faeces excreted onto farm fields by cattle could be transported via farm-field surface runoff to surrounding waterways.

Given the higher stocking densities typical of dairy farming (ranging upwards from 17.5 stock units per hectare) compared with those on beef and sheep farms in New Zealand (on average 10.5 stock units per hectare\textsuperscript{12}), microbial contamination can be increased substantially by dairy conversion. The possibility also exists for a concomitant increase in the risk of pathogen transmission to humans through the contact with, and consumption of, contaminated water.\textsuperscript{9} Consequently, potential public health risks need to be evaluated in areas experiencing rapid increases in cattle densities using risk assessment models.\textsuperscript{4}

**The limitations of epidemiology**

Epidemiology is an evidenced-based, scientific approach for studying disease-associated risk factors within populations\textsuperscript{13} and is the cornerstone of preventative medicine and the advancement of public health.\textsuperscript{14}

Identifying direct links between animal sources of pathogens and subsequent human recipients using epidemiological approaches can be relatively straightforward to detect, such as the transmission of genetically identical organisms to humans that have handled sick animals.\textsuperscript{15} However, establishing causal relationships between sources of waterborne pathogenic organisms and infections in humans using epidemiology can often prove difficult owing to the frequently complex, and often multiple, transmission pathways linking the two.\textsuperscript{16} Nevertheless, there have been reports of indirect transmission in regions containing large livestock populations.\textsuperscript{17}

A comprehensive analysis of waterborne infectious disease outbreaks that occurred globally between 1990 and 2005 found the presence of livestock in the catchment, coupled with rainfall, was a substantial contributing factor in 19 of 61 outbreaks evaluated.\textsuperscript{18} Thus, while epidemiology can play an important role in determining the implications of land-use change for human disease, its power at unravelling cause and effect relationships that result in changes in disease frequency can be limited. Accordingly, the development of microbial disease risk assessment strategies to tease
apart potential public health risks as a result of significant land-use changes would be particularly useful.

**Microbial risk assessment strategies**

When waterborne pathogens are presumed to be present in the environment it is necessary to assess the potential transmission risk of those organisms to humans, even in the absence of current disease outbreaks. However, while it is important to monitor municipal water supplies and recreational waterways for pathogens, several factors limit their ability to accurately detect such risks. These include poor correspondence between pathogen presence and microbial indicators or pathogens and turbidity (also used as an indicator), time lags between sampling and pathogen identification, the occurrence of false negatives and positives, the patchiness of pathogens in the tested substrate and the issue of appropriately-timed sampling schedules. Therefore, appropriate and accurate risk assessment strategies, in addition to traditional monitoring procedures, should be developed to minimise the likelihood of significant disease outbreaks.

Risk assessment strategies model the likelihood environmental sources of waterborne pathogens capable of causing disease in local human populations will do so given a particular set of variables. To accurately predict health risks, multiple models that link through a risk assessment framework are required to account for the complex transmission pathway of the organism from its source to human infections. For example, such a framework may comprise multiple models that represent five general steps of microbial transmission from farm animals to infected humans, as outlined in Figure 1.

**Figure 1. A generalised risk assessment framework for modelling the transmission of a waterborne pathogen from an environmental source through to subsequently infecting humans**

While several risk assessment model structures exist, with each requiring different types of input parameters, quantitative models are the ideal approach owing to the high level of accurate quantitative information employed. However, alternative models like semi-quantitative and qualitative models can also provide effective risk analyses when accurate quantitative information is limited. Nevertheless, regardless of the specific type of individual model utilised in the risk assessment framework, it is important the models are fully interchangeable, such that as new information becomes available it can be incorporated into the framework, improving the overall accuracy. For example, until recently microbial risk assessments were based on static models developed for chemical risk assessment, despite fundamental differences in the processes underlying microbial and chemical risks, including transmission mechanisms, exposure risks, incubation periods and immune status. Fortunately, an
increased awareness of disease risks from agricultural sources, as well as an improved understanding of the mechanisms surrounding microbial risks, has led to the development of dynamic models specifically for microbial risk assessment.

Significant information exists for the development of risk assessment frameworks to model the transmission risks of infectious organisms from their source to infected humans (Table 1). Not surprisingly though, the power of a risk assessment framework to accurately predict reality depends on the quality of the individual model components used to develop the overall framework, including their assumptions. Thus, when a number of key parameters remain unknown or unaccounted for in individual models, the overall accuracy of a risk assessment framework that incorporates those models is compromised. For example, in their model of the fate and transport of Cryptosporidium from dairy cattle to waterways in New York State, Walker & Stedinger (1999) assumed the pathogen moved in an identical manner to water. While the accuracy of the authors predictions was compromised by their disregard for surface entrapment and filtration processes, overall the dynamic model was an improvement on the static chemical-based models previously employed.

Table 1. Currently available quantitative information for developing a microbial risk assessment framework

<table>
<thead>
<tr>
<th>Framework step</th>
<th>Published data</th>
</tr>
</thead>
<tbody>
<tr>
<td>(a) Source of pathogen (animals)</td>
<td>Microbial release from faeces</td>
</tr>
<tr>
<td>(b) Genetic characterisation</td>
<td>See Table 2</td>
</tr>
<tr>
<td>(c) Movement of pathogen in runoff</td>
<td>Soil erosion</td>
</tr>
<tr>
<td></td>
<td>Grassed waterways</td>
</tr>
<tr>
<td></td>
<td>Experimental columns</td>
</tr>
<tr>
<td></td>
<td>Transport state of pathogen</td>
</tr>
<tr>
<td></td>
<td>Transport mechanisms and fate</td>
</tr>
<tr>
<td></td>
<td>Overland flow—soil box</td>
</tr>
<tr>
<td></td>
<td>Georeferenced estimate of runoff</td>
</tr>
<tr>
<td>(d) Pathogen characteristics in water</td>
<td>Sedimentation of free and attached (oo)cysts</td>
</tr>
<tr>
<td>(e) Disease capabilities of pathogen</td>
<td>Human exposure to pathogens</td>
</tr>
<tr>
<td></td>
<td>Modes of transmission</td>
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<td></td>
<td>Disease outbreak detection</td>
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</tbody>
</table>

**Giardia in New Zealand**

Giardia is a common protozoan parasite capable of causing infections in a wide range of mammalian hosts. Originally thought to show host specificity, substantial evidence suggests Giardia duodenalis (synonyms Giardia intestinalis and Giardia lamblia) is better considered a species complex, as multiple and genetically distinct assemblages have been characterised. Seven assemblages are currently recognised for G. duodenalis: A and B, the only assemblages capable of causing disease in humans but also identified from a wide range of other mammalian hosts including cattle, C and D isolated from dogs, E isolated from livestock (cattle, sheep and pigs), F isolated from felines, and G isolated from rats.

Worldwide G. duodenalis is one of the most frequently identified protozoan parasites causing gastro-intestinal disease (termed giardiasis) in humans. In New Zealand,
giardiasis is the third most common notifiable human disease caused by a microbial agent\(^2\) and occurs at higher rates than in other socioeconomically similar countries. For example, during the past 5 years rates have ranged in New Zealand between 29 and 42 cases per 100,000 population compared to 15 and 8 per 100,000 for Canada and the USA, respectively.\(^42-45\) Yet in spite of the high rate of human giardiasis in New Zealand, few studies have investigated the likely causes.

Table 2. A comparison of the prevalence rate of *Giardia duodenalis* in cattle and the genetic characterisation of isolates from humans and cattle worldwide between 2000 and 2008 (chronological order). Modified from Winkworth et al (2008)\(^46\)

<table>
<thead>
<tr>
<th>Area</th>
<th>Number of <em>Giardia</em> positive hosts in study</th>
<th>Prevalence rate in cattle</th>
<th>Assemblage in humans</th>
<th>Assemblage in calves</th>
</tr>
</thead>
<tbody>
<tr>
<td>New Zealand—North Island(^47)</td>
<td>15 calves</td>
<td>41%</td>
<td>A 73%</td>
<td>B 27%</td>
</tr>
<tr>
<td>Italy(^48)</td>
<td>30 humans</td>
<td></td>
<td>A 80%</td>
<td>B 20%</td>
</tr>
<tr>
<td>New Zealand—North Island(^49)</td>
<td>26 calves</td>
<td>10%</td>
<td>A 50%</td>
<td>B 50%</td>
</tr>
<tr>
<td>Australia(^50)</td>
<td>31 calves</td>
<td>89%</td>
<td>A 55%</td>
<td>B 45%</td>
</tr>
<tr>
<td>Italy(^51)</td>
<td>24 calves, 37 humans</td>
<td>Not reported</td>
<td>A 45%</td>
<td>B 41%</td>
</tr>
<tr>
<td>USA—East Coast(^52)</td>
<td>237 calves</td>
<td>52%</td>
<td>A 50%</td>
<td>B 21%</td>
</tr>
<tr>
<td>USA—East Coast(^53)</td>
<td>204 calves</td>
<td>36%</td>
<td>A 13%</td>
<td>E 87%</td>
</tr>
<tr>
<td>Ethiopia(^54)</td>
<td>59 humans</td>
<td></td>
<td>A 14%</td>
<td>B 7%</td>
</tr>
<tr>
<td>Portugal(^55)</td>
<td>14 calves</td>
<td>14%</td>
<td>A 14%</td>
<td>E 79%</td>
</tr>
<tr>
<td>New Zealand—South Island(^56)</td>
<td>40 calves, 30 humans</td>
<td>31%</td>
<td>A 77%</td>
<td>B 23%</td>
</tr>
</tbody>
</table>

Since the identification of *Giardia* from dairy cattle during the early 1980’s\(^56\) high prevalences have been described in newborn calves (ranging from 10-89% prevalence worldwide), while adults have shown low yet persistent levels.\(^50,52,57,58\) In New Zealand, recent studies focussing on dairy cattle have reported between 31% and 41% *Giardia* prevalence in calves\(^47,59\) and 5% prevalence in adults.\(^48\) No correlations between faecal morphology and the presence of *Giardia* in dairy cattle have been observed in New Zealand.\(^59\) However, despite an apparent lack of clinical symptoms, cattle excrete wide-ranging concentrations of *Giardia*, indicating active infections.\(^60\)
Until recently livestock were not considered a source of *G. duodenalis* strains capable of causing human disease, as historically they were reported to only harbour livestock-specific strains (Assemblage E).

However, several studies have identified Assemblage A and B from cattle, the same *G. duodenalis* assemblages found to cause human disease (Table 2). Of particular concern in New Zealand is that dairy cattle appear to exclusively carry Assemblage A and B strains, with the livestock Assemblage E strain undetected to date.46

**Linking land use and human giardiasis**

While multiple transmission pathways are known for *Giardia*, transmission via water may be of particular significance in areas with large numbers of dairy cattle. This is because dairy cattle are typically maintained at high densities,12 they produce large quantities of faecal waste,10,11 exhibit high *Giardia* prevalence,59 and cysts have been detected from aquatic and terrestrial environments worldwide where large cattle populations reside.61 Furthermore, the cysts excreted in their faeces are environmentally resistant, immediately infectious to susceptible hosts9 and move passively across landscapes into waterways in surface runoff.62 Therefore, it is important to understand and estimate the contamination of waterways by *Giardia* from farm surface runoff, especially as the water may subsequently be used for recreational pursuits or human consumption.

In New Zealand a number of factors support a causative relationship between the use of land for dairy farming and the high levels of giardiasis infections in humans. These include the high prevalence of *Giardia* in dairy calves,47,59 the detection of *Giardia* in aquatic environments across the country,61 the intensive use of surface water for recreational purposes and municipal drinking water supplies,63 the high human rates of giardiasis compared to other nations42 and the isolation of identical *Giardia* genotypes from humans and calves located in the same geographic region.46 However, evidence of unambiguous links between farm animal density and giardiasis infections in humans in New Zealand using traditional epidemiological approaches have proved elusive.64 This is not to say causative relationships do not exist, only that the sensitivity of the authors’ methods may have been too coarse to detect any patterns present in the available data sets. Therefore, in light of the potential for *Giardia* transmission between dairy cattle and humans in New Zealand, a microbial risk assessment framework should be developed to help evaluate such risks.

While significant information exists for the development of a risk assessment framework to specifically understand the risk of environmental sources of *Giardia* to public health (Table 3), several important information gaps remain. For example, mechanisms responsible for the release and transport of *Giardia* cysts from bovine faeces remain poorly understood and are currently unknown for flow rates above 10ml per minute.71 Accordingly, recent runoff experiments employing saturated soil overland flow rates of 2 litres per minute were restricted to the use of *Giardia* present in liquid spikes, rather than cattle faeces.62 Although it remains to be determined, it is possible faecal particles may occupy sites where biocolloid straining would otherwise remove *Giardia*, with the pathogen consequently remaining in the runoff.78 Therefore, research to elucidate the mechanisms of release of *Giardia* from faecal matter, as well as the effect of faeces on *Giardia* movement through the soil, would further improve risk assessment simulations.
Table 3 Parameters currently known for assessing the risk of environmental sources of *Giardia* to public health

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Relevant studies</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cattle infection prevalence</td>
<td>Dairy cattle: calves&lt;sup&gt;77,79&lt;/sup&gt;; adults&lt;sup&gt;85&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>Beef cattle&lt;sup&gt;6&lt;/sup&gt;</td>
</tr>
<tr>
<td>Genotype present in cattle</td>
<td>Dairy cattle&lt;sup&gt;63&lt;/sup&gt;</td>
</tr>
<tr>
<td>Rate of pathogen excretion</td>
<td>Average number of cysts excreted&lt;sup&gt;20&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>Volume of faeces: calves&lt;sup&gt;67&lt;/sup&gt;; adults&lt;sup&gt;10&lt;/sup&gt;</td>
</tr>
<tr>
<td>Pathogen viability</td>
<td>Water&lt;sup&gt;68&lt;/sup&gt;; faeces&lt;sup&gt;69&lt;/sup&gt;; soil&lt;sup&gt;69&lt;/sup&gt;</td>
</tr>
<tr>
<td>Mechanism and release rate of <em>Giardia</em> from faeces</td>
<td>Limited to 10ml runoff per minute&lt;sup&gt;0.77&lt;/sup&gt;</td>
</tr>
<tr>
<td>Transported state of <em>Giardia</em> (single cysts, clumps, etc.)</td>
<td>Attachment mechanisms&lt;sup&gt;72,73&lt;/sup&gt;</td>
</tr>
<tr>
<td>Movement through experimental soil columns</td>
<td></td>
</tr>
<tr>
<td>Movement across landscape (single cysts)</td>
<td>Bare soil&lt;sup&gt;62&lt;/sup&gt;; newly vegetated&lt;sup&gt;62&lt;/sup&gt;; after one growing season&lt;sup&gt;8&lt;/sup&gt;</td>
</tr>
<tr>
<td>Heterogeneity of pathogen</td>
<td>In water&lt;sup&gt;61&lt;/sup&gt;</td>
</tr>
<tr>
<td>Sedimentation/settling rate</td>
<td>Sedimentation of free and attached cysts&lt;sup&gt;18,76&lt;/sup&gt;</td>
</tr>
<tr>
<td>Contact time/exposure risk</td>
<td>For humans&lt;sup&gt;58,77&lt;/sup&gt;</td>
</tr>
<tr>
<td>Dose ingested</td>
<td>For humans&lt;sup&gt;41&lt;/sup&gt;</td>
</tr>
</tbody>
</table>

The effect of vegetation development along waterways at reducing *Giardia* in runoff reaching the waters edge has also been determined recently. However, despite a substantial reduction in *Giardia* reaching the waterway after one year of vegetation development (98% of that applied), approximately 3500 organisms per litre still reached the water’s edge.<sup>75</sup> As the ingestion of as few as one to ten cysts has been reported to cause giardiasis in humans,<sup>41</sup> the high levels of *Giardia* remaining are concerning. Although filtering capacities may improve as the vegetation develops further,<sup>79</sup> with potentially greater rates of *Giardia* infiltration observed as more deeply-rooted species become established,<sup>75</sup> this remains to be determined. Additionally, while further vegetation growth may result in lower *Giardia* numbers in runoff, the effect (if any) for the overall disease risk is unclear.

**Conclusion**

Significant challenges surround the conversion of land to dairy farming. This paper discussed an important consequence that is often overlooked; an increased risk to public health. As water resources become increasingly scarce and variable in quality due to escalating demand, it seems likely that the indirect impact of land-use conversion on human health may also escalate. Therefore, it is crucial good communication exists between agencies responsible for public health and those responsible for environmental management, such that management responses to land-use consequences are holistic. Not surprisingly, improving the techniques available for accurately evaluating potential risks is clearly beneficial to both public health and environmental managers for identifying, developing and implementing strategies to reduce the risks.
This paper has highlighted the public health challenges New Zealand faces in relation to managing land use conversions to dairy farming. In particular, it focussed on the waterborne pathogen *Giardia*, which causes significant disease in the New Zealand population compared with similar socioeconomic countries. By incorporating the recent advances in *Giardia* knowledge outlined in this paper into a risk assessment framework, an appropriate evaluation of the public health risk of *Giardia* as a result of land-use change to dairying in New Zealand can begin to take shape. For example, the framework previously developed for *Cryptosporidium* by Walker & Stedinger (1999) could be appropriately modified to assess *Giardia* risk by substituting *Giardia*-specific information where possible.

While use of the Walker & Stedinger model would significantly advance *Giardia* risk management assessments in New Zealand, important information gaps remain. Thus, additional research is required to ensure further clarification and improvement to the overall accuracy of public health risk assessments of *Giardia* in New Zealand as a result of land-use change. While not inclusive, such gaps include a comprehensive understanding of the mechanisms responsible for the release of *Giardia* cysts from bovine faecal matter at different rainfall and surface runoff rates and in turn, the affect of dissolved faeces on *Giardia* movement through the soil, the *Giardia* cyst retention capabilities of riparian buffers older than one year and different surface runoff rates.

Clearly some uncertainty surrounding individual model components remains when assessing regional and site-specific *Giardia* risks given the practical limitations of testing all possible variations that may exist between different environments. However, while the available data may not be ideal for the particular situation being assessed, it should not preclude its inclusion in a risk assessment. Rather, the level of uncertainty inherent in the available data should be accounted for in the assessment simulations and discussed accordingly, ensuring risk evaluations are still performed and, consequently, prove informative for public health and environmental managers.

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