



Cattle-derived microbial input to source water catchments: An experimental assessment of stream crossing modification



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ARTICLE INFO

Article history:

Received 15 September 2014

Received in revised form

19 March 2015

Accepted 29 March 2015

Available online 2 April 2015

Keywords:

Dairy

Livestock

Microbial pollution

Source water quality

Stream bridging

ABSTRACT

The provision of safe drinking water is a global issue, and animal production is recognized as a significant potential origin of human infectious pathogenic microorganisms within source water catchments. On-farm management can be used to mitigate livestock-derived microbial pollution in source water catchments to reduce the risk of contamination to potable water supplies. We applied a modified Before-After Control Impact (BACI) design to test if restricting the access of livestock to direct contact with streams prevented longitudinal increases in the concentrations of faecal indicator bacteria and suspended solids. Significant longitudinal increases in pollutant concentrations were detected between upstream and downstream reaches of the control crossing, whereas such increases were not detected at the treatment crossing. Therefore, while the crossing upgrade was effective in preventing cattle-derived point source pollution by between 112 and 158%, diffuse source pollution to water supplies from livestock is not ameliorated by this intervention alone. Our findings indicate that stream crossings that prevent direct contact between livestock and waterways provide a simple method for reducing pollutant loads in source water catchments, which ultimately minimises the likelihood of pathogenic microorganisms passing through source water catchments and the drinking water supply system. The efficacy of the catchment as a primary barrier to pathogenic risks to drinking water supplies would be improved with the integration of management interventions that minimise direct contact between livestock and waterways, combined with the mitigation of diffuse sources of livestock-derived faecal matter from farmland runoff to the aquatic environment.

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1. Introduction

Globally, more than one billion people do not have access to safe drinking water, and between five and ten million people become seriously ill or die each year from consuming water containing microbial pathogens (e.g. Gleick, 1998; Ashbolt, 2004; Shannon et al., 2008). Such figures are disproportionately represented in developing nations; however, outbreaks of disease caused by contaminated drinking water originating from catchments with agricultural land-use still occur in countries with sophisticated water treatment facilities (Hrudey and Hrudey, 2007; Goss and Richards, 2008). An improved understanding of the origin of

microbial contamination in source water catchments is therefore required to design and implement effective mitigation measures that minimize these human health risks.

Contamination of drinking water commonly occurs via microbial pollution entering source waters, combined with inadequate disinfection at treatment facilities or in water distribution networks (Westrell et al., 2003). Accordingly, agencies and utilities worldwide are increasingly recognizing of the importance of understanding and managing source waters as they move to implement a total quality management framework approach for drinking water safety (WHO, 2004; Davison et al., 2005; Hamilton et al., 2006; Edgar et al., 2010; NHMRC, NRMCC, 2011). However, while there is clear recognition that effective catchment management and source water protection provide an important primary barrier for the protection of drinking water quality (e.g. NHMRC, NRMCC, 2011), source water catchments are coming under increased

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pressure worldwide from anthropogenically driven changes in land-use (Postel and Thompson, 2005; Leigh et al., 2010; Emelko et al., 2011). To illustrate, a strong relationship is evident between the extent of agricultural development and the degree of microbial contamination in source water catchments (Hansen and Ongerth, 1991; Roser and Ashbolt, 2007; Goss and Richards, 2008). Livestock wastes, for example, can contain many pathogenic microorganisms infectious to humans (Becher et al., 2004; Castro-Hermida et al., 2006; Coklin et al., 2007). Consequently, microbial contamination of the aquatic environment occurs where there is direct livestock contact with water (e.g. via direct defecation and washing of contaminants from hooves and lower legs), combined with diffuse sources from runoff of livestock derived faecal material (Davies-Colley et al., 2004; Monaghan et al., 2007; Wilcock et al., 2007; Stott et al., 2011).

Changes to on-farm operations, such as maintaining vegetative buffer strips along river banks, can reduce catchment-derived microbial pollution to aquatic environments and water supply reservoirs (e.g. Kay et al., 2012; Burt et al., 2013). Livestock exclusion from waterways, such as via stream bank fencing and bridging, can also reduce microbial pollution to streams. For example, the replacement of ford crossings by bridges has been predicted to achieve a 0.62 log₁₀ reduction in the daily mean *Escherichia coli* (*E. coli*) concentration (i.e. where a 1 log₁₀ reduction denotes a 10-fold or 90% decrease in numbers of microorganisms) in New Zealand streams (Davies-Colley et al., 2004; Kay et al., 2012). Despite these predictions, there has been limited experimental testing worldwide of the performance of crossing modifications in mitigating microbial pollution as a point source, and this remains a key knowledge gap in source water protection.

Testing the response of contaminants to stream crossing modification can be done using two survey approaches. The first is a “space-for-time” substitution (Pickett, 1989) to compare sites in a large number of streams that differ in livestock contact with water. Streams with bridge crossings used by livestock serve as “treatment” sites, sites downstream of ford crossings as survey controls, and/or streams where livestock have no direct access to streams as reference sites (Downes et al., 2002). Such spatially broad approaches can be completed with few sample times and can cover a wide geographic region. However, natural differences in stream physical, chemical and biological characteristics (e.g. turbidity) can limit the ability to assign differences in response variables among streams to the experimental treatment. Our approach compares longitudinal differences in response variables within individual streams and uses sites upstream and downstream of crossings as survey controls and treatments, respectively. Although such designs have a reduced spatial extent, the key advantage is that among-stream differences in response variables are reduced, and the comparison of patterns in longitudinal variation are directly linked to the experimental treatment because control and impact sites have minimal confounding factors (sensu Stewart-Oaten et al., 1986). Our confidence that the crossing modification is the mechanism regulating change is further improved when we compare longitudinal patterns in response variables before and after crossing modification in some streams while leaving others as experimental controls (see Downes et al., 2002).

In this study, we experimentally tested the effects of a stream bridging structure on downstream water quality designed to reduce direct contact between livestock and waterways. We used a modified before-after-control-impact (BACI) design to compare longitudinal changes in the concentrations of *E. coli*, Enterococci and suspended solids (TSS) within stream channels draining into a water supply reservoir. We predicted that the establishment of a bridging structure would reduce inputs of *E. coli*, Enterococci and TSS along the longitudinal stream profile when compared with a

control stream where no changes were made to an existing ford that allows cattle direct contact with the waterway. The aim of this study was to quantify reach-scale changes in microbial pollution loads in response to the establishment of bridged cattle crossings.

2. Materials and methods

2.1. Sites and sampling

This study was undertaken in the catchment of Lake Baroon (dam completed in 1989, reservoir capacity of 61,000 ML and a surface area of 3.8 km² at full supply). With a yield of 20,000 ML y⁻¹, the reservoir is the single source of raw water for an advanced water treatment plant that is the primary supply of potable water to more than 300,000 people across the Sunshine Coast region. The Lake Baroon catchment drains an area of 74 km² and has three main tributaries; Obi Obi, Bridge and Walkers Creeks. The landscape is characterized by rolling hills in the south-west with steeper slopes cut by incising waterways towards the north and north-east. The regional climate is subtropical with a mean annual rainfall of ~1700 mm, and a mean annual minimum and maximum temperature of 14 °C and 26 °C respectively (BoM, 2012). Approximately 50% of the catchment is forested, and rural activities (mostly small acreage beef, dairy, and hobby farms) and residential urban areas comprise ~40% and ~10% of the catchment area, respectively. Microbial contamination of waterways within the catchment is largely due to livestock, as animal *Bacteroides* markers are ubiquitous, and other *Bacteroides* (e.g. human, waterfowl) are either only sporadically detected or entirely absent (GHD, 2014).

Our study focuses on Daley and Obi Obi Creeks in the headwaters of the Lake Baroon catchment (Fig. 1) where both streams dissect a 1.2 km² dairy farm (400 head of dairy cattle; ~300 milkers and ~100 dry cows).

The farm is divided into upper and lower paddocks to manage grazing pressure and pasture recovery. The herd has direct access to Obi Obi Creek for watering regardless of which paddocks are open to grazing; however the herd also have direct access to Daley Creek when confined to the lower paddocks. When the grazing the lower paddocks each animal is required to cross both Obi Obi and Daley Creeks twice a day in transit between the pasture and the dairy. To reduce the physical contact between the dairy herd and the stream during daily crossing, the existing ford at Obi Obi Creek was replaced with a culvert bridge in January 2013 whereas the crossing

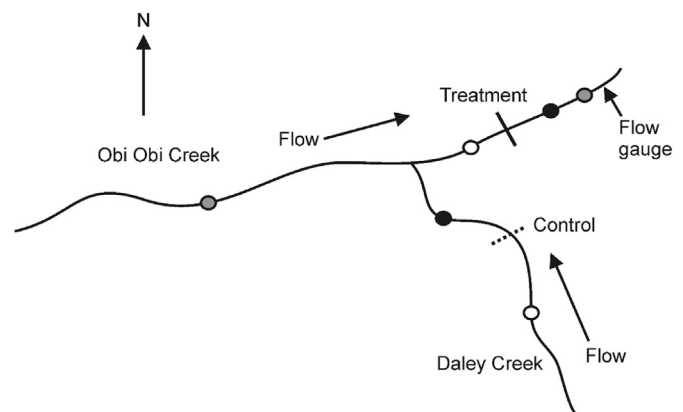


Fig. 1. Schematic diagram (not to scale) indicating the location of study sites relative to the unmodified (control) and modified (treatment) crossings. Grey circles indicate location of monthly monitoring sites (sampled between August 2011 and August 2013), whereas filled and unfilled circles indicate sites sampled four times before and four times after crossing modification as part of the experiment.

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