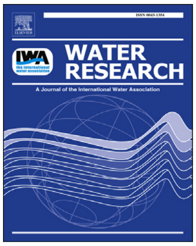
WATER RESEARCH 60 (2014) 278–288

Available online at www.sciencedirect.com

ScienceDirect

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



Baseline and storm event monitoring of *Bacteroidales* marker concentrations and enteric pathogen presence in a rural Canadian watershed

C.M. Ridley[a], R.C. Jamieson[a,*], L. Truelstrup Hansen[a], C.K. Yost[b], G.S. Bezanson[c]

[a] Department of Process Engineering and Applied Science, Dalhousie University, 1360 Barrington Street, Halifax, NS, Canada B3H 4R2
[b] Department of Biology, University of Regina, LB 244, 3737 Wascana Parkway, Regina, SK, Canada S4S 0A2
[c] Agriculture and Agri-Food Canada, Atlantic Food and Horticulture Research Centre, 32 Main Street, Kentville, NS, Canada B4N 1J5

ARTICLE INFO

Article history:
Received 11 September 2013
Received in revised form
14 April 2014
Accepted 19 April 2014
Available online 1 May 2014

Keywords:
Microbial source tracking (MST)
Bacteroidales
Host-specific markers
Rural agricultural watershed
Campylobacter

ABSTRACT

Bacteroidales 16S rRNA gene markers were evaluated for their use as a microbial source tracking tool in a well characterized 750 ha agricultural watershed in Nova Scotia, Canada. Water quality monitoring was conducted following the validation of host-specific and universal *Bacteroidales* (AllBac) markers for their proficiency in this particular geographic region, which provided further evidence that these markers are geographically stable. Increasing *Escherichia coli* concentrations were positively correlated ($p < 0.01$) with concentrations of the AllBac marker in water samples, suggesting that this universal marker is more suited as a positive DNA control rather than as an indicator of recent fecal contamination. Ruminant (BacR) and bovine (CowM2) specific marker detection was associated with increased runoff due to precipitation in sub-watersheds putatively impacted by cattle farming, demonstrating that the BacR and CowM2 markers can be used to detect the recent introduction of fecal matter from cattle farming activities during rainfall events. However, the human associated marker (BacH) was only detected once in spite of numerous on-site residential wastewater treatment systems in the watershed, suggesting that this assay is not sensitive enough to detect this type of human sewage source. *E. coli* O157:H7 and *Salmonella* spp. DNA was not detected in any of the 149 watershed samples; however, 114 (76.5%) of those samples tested positive for *Campylobacter* spp. No significant correlation ($p > 0.05$) was found between *Campylobacter* spp. presence and either *E. coli* or AllBac marker levels. Further studies should be conducted to assess the origins of *Campylobacter* spp. in these types of watersheds, and to quantify pathogen cell numbers to allow for a human health risk assessment.

---

* *Corresponding author.*
E-mail address: jamiesrc@dal.ca (R.C. Jamieson).

http://dx.doi.org/10.1016/j.watres.2014.04.039

1. Introduction

The hydrology and sources of microbial pollution in rural and agriculturally dominated watersheds are different from those in urbanized areas. Within agricultural landscapes, there are many factors to consider, including fertilization practices, drainage systems, the intensity and management of livestock operations, and subsequent manure management practices. Residential waste treatment in rural areas is also often different than that applied in cities. Septic systems are used for wastewater treatment and can have a diffuse impact on water quality (Peed et al., 2011). Conventional water quality monitoring tools, exemplified by fecal indicator organisms (FIOs) such as *Escherichia coli*, may not be adequate for assessing public health risks and identifying sources of pollution in these complex watershed systems. These limitations are largely due to issues related to the environmental persistence of some *E. coli* strains and an inability to differentiate between *E. coli* from separate hosts (Kon et al., 2009).

The need for enhanced monitoring approaches when assessing fecal pollution has given rise to new microbial source tracking (MST) technologies, which aim not only to

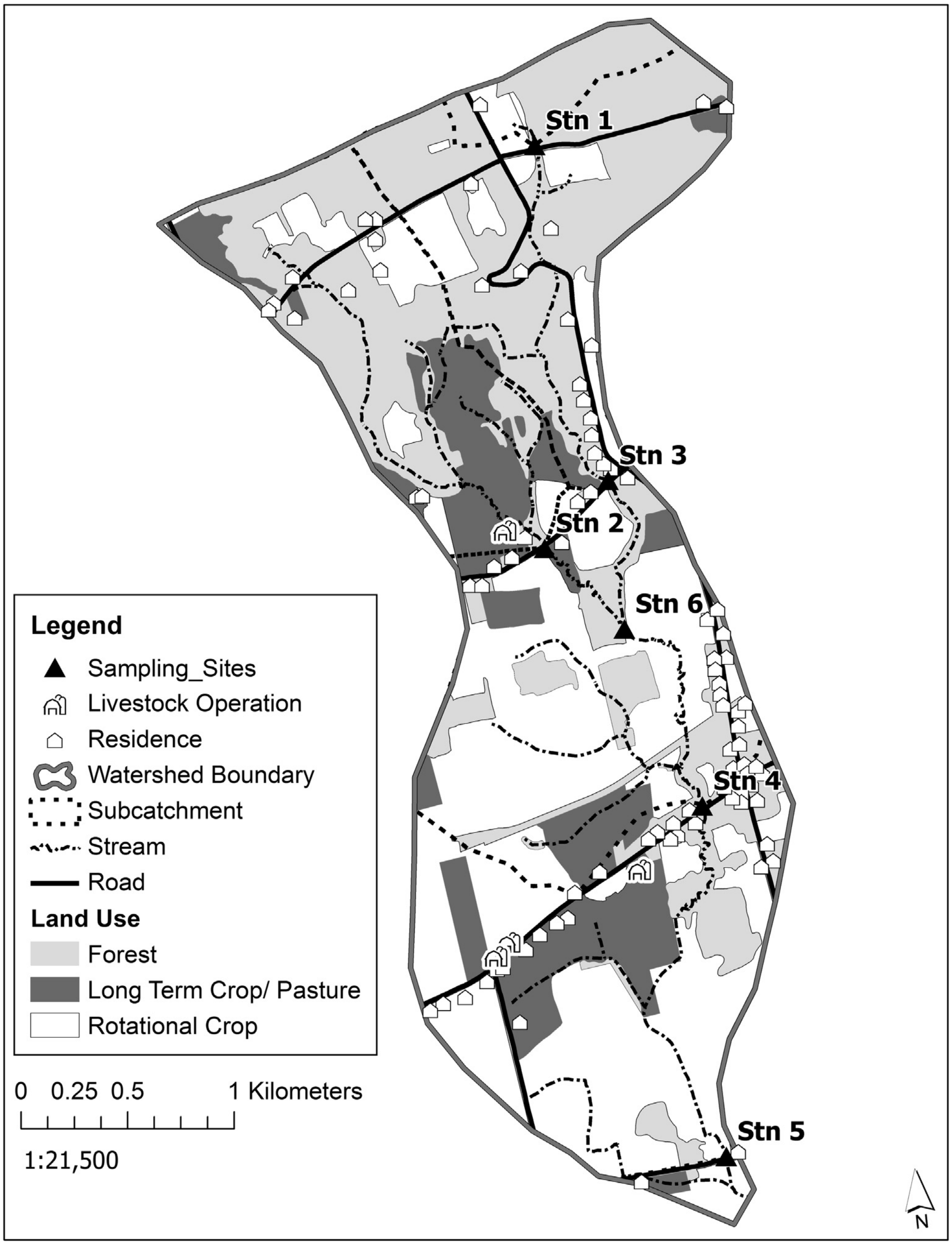


Fig. 1 – Land usage of TBW in relation to sampling stations. Stn-1 (headwater) has minimal anthropological activity; Stn-2 and Stn-4 each are downstream of cattle operations; Stn-3 is situated in a residential cluster; Stn-5 is at the watershed outlet; and Stn-6 is adjacent to a rotational crop that receives liquid dairy manure as fertilizer.