# **Bacteria and Parasite Source Identification in the Kiskatinaw Watershed near Dawson Creek, B.C.**

#### 2004-2007



Prepared by Gabi Matscha Ministry of Environment (MOE) Omineca-Peace Region

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#### **EXECUTIVE SUMMARY**

#### Introduction

Under the B.C. Water Act and Environmental Management Act, the British Columbia Ministry of Environment (MOE) is responsible for regulating activities in watersheds that have a potential to affect water quality. Accordingly, the Ministry takes an active role in protecting drinking water quality at its source. In order to accomplish this task, drinking water supplies were prioritized for water quality monitoring and contaminant source identification based on risk to users and existing water quality issues. The Kiskatinaw Watershed is the first drinking water source in the Omineca-Peace Region that is being assessed in detail under this program.

The Kiskatinaw Watershed provides the sole domestic source of drinking water for residents of Dawson Creek and Pouce Coupe, as well as six schools and a large number of residences in the surrounding areas. The total number of users is estimated at about 20,000 (Rod Harmon per. com.). Sections of the Kiskatinaw River and some of its tributaries are deeply entrenched into a highly erodable landscape, resulting in sloughing banks and naturally high turbidity levels, which may impede water treatment. In addition, the watershed has a high land use density and bears a high pressure for future development. Main land use activities include agriculture, forestry, oil and gas, mining and rural residences. In an effort to increase source water protection an integrated Watershed Management Plan was developed in 1991, which is currently being updated.

Previous studies in the watershed concluded that contaminant concentrations of parasites, bacteria, organic carbon, suspended solids and turbidity in Dawson Creek's community source water are high enough to cause a risk to human health, should treatment ever be insufficient.

#### **Project Objective**

The objective of this contaminant source identification study is to identify the stream sections and land use sector activities from which these and other water borne contaminants originate. This information is then being used to recommend most effective management of raw water quality to reduce drinking water risk in a multi-barrier approach.

#### **Project Description**

The program uses water, sediment, and scat sampling methods and employs a variety of analysis approaches to identify contamination levels in the water column, to determine host species of bacteria and parasites, and to confirm the presence of strains that are infectious to humans. The project started in 2004 with the first year focusing on broad source sector identification by sampling a wide range of biological, chemical and physical parameters. The second year focused on parameters and areas of concern as identified during the first year, i.e. bacteria and parasites in the Kiskatinaw River, Brassey Creek and Halfmoon Watershed. 2004/2005 results are summarized in Matscha et al. (2006), while 2006/2007 results are analyzed and reported in this report.

#### Results and Discussion

Highest fecal indicator concentrations (fecal coliforms, *E.coli*, fecal *Streptococci*, and *Enterococci*) occurred in the water column mainly during summer sample events with moderate counts during freshet, while counts of important human health relevant parasite cysts/oocysts (*Giardia* and *Cryptosporidium*) peaked in conjunction with runoff events in mostly turbid water.

The City of Dawson Creek's treatment system, which includes settling, coagulation, filtration, chlorination, and UV treatment, is equipped to eliminate bacteria and parasites successfully; however, Health Canada recommends additional source water management to reduce numbers of infectious agents in case of treatment system ineffectiveness, particular if *Giardia* and *Cryptosporidium* cysts/oocysts have been detected in the source water (http://www.hc-sc.gc.ca/ewh-semt/pubs/water-eau/protozoa/index-eng.php).

The parasite contamination in the water column was mainly due to *Giardia* contamination. *Giardia* cysts were detected in 69% of the tested samples, while *Cryptosporidium* oocysts occurred in only 29%. In addition to the higher prevalence of *Giardia* cysts in collected water samples, their

concentrations per sample also substantially exceeded those for *Cryptosporidium* oocysts. Highest *Giardia* cyst counts were detected at the community intake after a heavy rain event in the summer of 2007 (3914 cysts/100 L). An opposite relationship was identified in collected scat, from which no *Giardia* cysts could be isolated, while *Cryptosporidium* oocysts were found in 8 of the 31 collected fecal samples (26%). It is suspected that the absence of *Giardia* cysts may be due to seasonal conditions, e.g. the dryness of the collected fecal material and the long hot summer. Of the tested scat from nine species/animal groups, only moose, deer, and cattle feces revealed *Cryptosporidium* oocysts. A repeat of the scat sampling portion of the program in cooler, wetter years is recommended to account for annual variations.

For eight *Giardia* cyst samples, collected from the water column, a species and strain analysis was conducted. Four of these samples tested positive for *Giardia lamblia* Assemblage B, a strain that is infectious to humans. A similar analysis of scat samples was unsuccessful due to interference of fecal material in the analysis process. However, the above results for waterborne *Giardia* indicate a high risk of infection, should water treatment become ineffective. Potential host species for Assemblage B (humans, cattle, beavers, muskrats, coyotes, and rabbits) should be considered for future parasite source tracking efforts.

It should also be noted that data show *E.coli* and *Enterococci* guideline exceedances for water uses other than drinking water in the Kiskatinaw River, including general livestock watering, as well as recommended chronic concentrations for irrigation of crops eaten raw and for primary contact recreation (swimming). Highest frequency of exceedances occurred in Brassey Creek, the Halfmoon Watershed and Kiskatinaw River downstream of these tributaries.

A bacteria source tracking method, using the 16-S ribosomal genomic DNA of *Bacteroides*, a strictly anaerobic intestinal bacterium, was used to identify host species of fecal contamination. It identified human and ruminant waste indicators in 80% of the samples collected at the community intake. *Bacteroides* of these two host species were distributed widely throughout the watershed (including just downstream of the East-West-Arm confluence), but were not detected at control samples in the Brassey Creek headwaters, suggesting main ruminant and human fecal contamination from pasture land and rural residential septic systems.

#### Recommendations

- We recommend continuing the bacteria source tracking project to further confirm hosts within
  agricultural areas and to identify sources upstream of the East-West-Arm confluence. Latter should
  focus on the East Kiskatinaw, where a number of potential sewage and animal waste sources
  exist. Former should include water fowl and beaver (or at least rodents as a group) as soon as
  Bacteroides markers have been identified for these host animal groups.
- A repeat of the scat sampling program is recommended to determine whether 2006 sample results
  were representative and to include beaver and muskrat scat. Beaver may be an important
  contributor of *Giardia lamblia*, Assemblage B, which was detected in the river. The identification of
  host species for the highly infectious *Giardia* and *Cryptosporidium* parasites in the water column is
  important in finding most effective management options.
- A watershed management process should consider the outcome of this study and its continuation and should focus mitigation efforts on septic system upgrades and development of livestock watering holes away from the Kiskatinaw River and tributary creeks.

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#### 1 Introduction

#### 1.1 Background

The Province's *Drinking Water Protection Act*, enacted in October 2002, places the responsibility for drinking water quality protection with the B.C. Ministry of Health and local water purveyors. However, the Action Plan for Safe Drinking Water in British Columbia (2002) as well as the Memorandum of Understanding between 13 Ministries regarding Inter-agency Accountability and Coordination on Drinking Water Protection (2006) state the Ministry of Environment's responsibility for the development of water quality standards, monitoring, compliance and enforcement, and the protection of drinking water sources. Under the B.C. *Water Act* and *Environmental Management Act*, the British Columbia Ministry of Environment (MOE) is responsible for regulating activities in watersheds that have a potential to affect water quality. Accordingly, the Ministry takes an active role in protecting drinking water quality at its source.

MOE implemented a raw water quality and stream sediment monitoring program at selected communities in the Omineca-Peace Region in 2002. Results of this one year monitoring program are summarized in Jacklin et al. (2003). The study concluded that contaminant concentrations in Dawson Creek's community source water, the upper portion of the Kiskatinaw River watershed, are high enough to cause a risk to human health, should treatment ever be insufficient. The program indicates significant concentrations of parasites, bacteria, organic carbon, suspended solids and turbidity. Results of previous monitoring programs conducted by MOE and the City of Dawson Creek in the 1970s, the 1980s and 1990s (Matscha et al, 2003) confirm recent findings.

The Kiskatinaw Watershed provides the sole domestic source of drinking water for residents of Dawson Creek and Pouce Coupe, as well as six schools and a large number of residences in the surrounding areas. Rod Harmon, the City of Dawson Creek's Water Resource Manager, estimates the total number of water users to be 20,000. Alternative water supplies were considered, but rejected based on the high cost for these options (Rod Harmon verbal communication, July 2006). In addition, the watershed has a high land use density and bears a high pressure for future development. In an effort to increase source water protection an Integrated Watershed Management Plan was developed for the Kiskatinaw Watershed in 1991. In 2001 the City of Dawson Creek initiated a series of stakeholder meetings resulting in an updated Kiskatinaw River Watershed Management Plan (Dobson, Urban Systems, 2003). The Plan, which is currently being updated, calls for a number of protective measures, among them water quality monitoring and source identification.

#### 1.2 Purpose and Objectives

In response to the 2002/2003 MOE study results and the City of Dawson Creek's interest in managing the watershed, MOE designed a contaminant source identification program for the Kiskatinaw watershed upstream of the community water intake. The project commenced in the fall of 2004. The purpose of the project is to identify sources of critical contaminants in the watershed.

Source identification is the second phase of a water quality management process. During this phase, the main land use sectors are identified and a monitoring program designed to determine the relative effects of these sectors. This phase also provides a baseline from which to identify the effects of future developments, and information on contamination, timing and location for use in the next stage of a watershed management process.

The typical phases of a water quality management process include:

#### 1st: Baseline monitoring and problem identification

In the Kiskatinaw, this phase included previous monitoring efforts at the community water intake in the 1970s, 1980s and 1990s (Matscha et al, 2003), the 2002/2003 MOE study (Jacklin et al, 2003), and MOE data, collected under an MOE watershed characterisation program 2002-2004 (unpublished, see Appendix in Matscha et al, 2006).

#### 2nd: Source identification of water quality impacts

The results of this phase are described in this document.

#### 3rd: Source management, where required

This phase will be directed by the final results of the 2<sup>nd</sup> phase.

#### 4th: Performance monitoring and plan adjustment

Effective watershed management requires attainment monitoring to guide plan adjustment.

#### 1.3 Previous Project Reporting

An interim report (Matscha et al, 2006) described the project and summarized and interpreted analysis results for >70 parameters in water and sediment collected at 14 sites up and downstream of various land use sectors during 2004-2005. The above document found that high bacteria, parasite, organic carbon, turbidity and TSS levels have a potential to impact drinking water quality and/or treatment. It also identified the Brassey Creek Watershed and the Kiskatinaw Section below Brassey Creek as main contamination areas for high bacterial and parasite concentrations at the pump house; however, significant contamination with the parasite *Giardia* is more widely distributed throughout the watershed than bacterial contamination. The report recommended additional investigation of sources for high parasite cyst/oocyst and bacteria concentrations and their health risk.

In 2006 and 2007, the study was continued in partnership with the B.C. Centre for Disease Control and support from the City of Dawson Creek and Northern Health. It focussed on bacteria and parasites as recommended above. Results were presented to residents in the Brassey Creek Watershed on May 10, 2007 as well as to the Watershed Planning Stakeholder group on December 12, 2007.

#### 1.4 Purpose of this Report

This report summarizes the results of the contaminant source identification phase (2004 to 2007). It focuses on bacteria and parasites as one of the main issues in the watershed. Since all collected water chemistry data under this project have been discussed in detail in the above document (Matscha et al, 2006), their inclusion into this report will be limited to a brief summary of results as a means to set the context.

For risk assessment purposes, results are compared to B.C. Water Quality Guidelines (Nagpal et al, 2001) and the Summary of Guidelines for Canadian Drinking Water (Federal–Provincial–Territorial Committee on Drinking Water, 2003), which provide the benchmarks for judging acceptability to users. The report will conclude with recommendations for watershed management. It also identifies knowledge gaps and suggests additional work to fill these gaps.

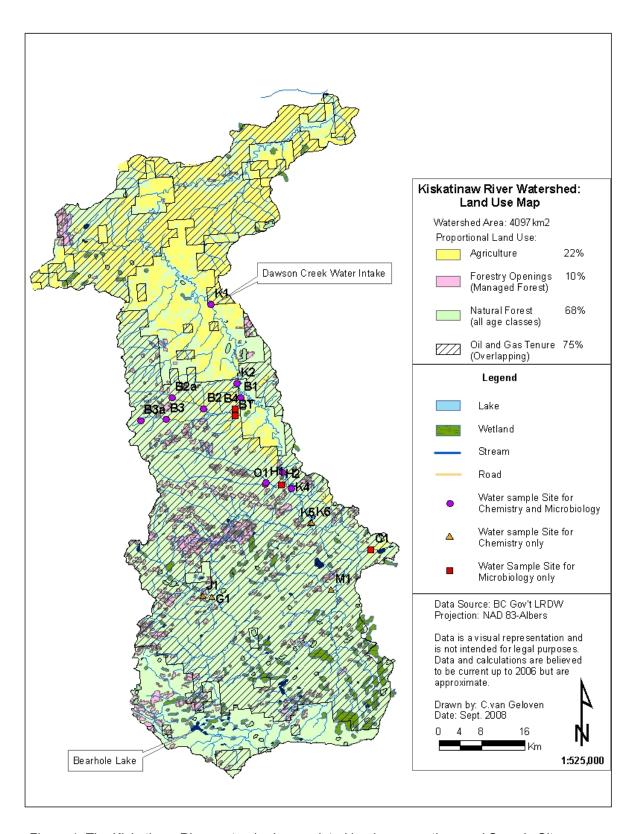


Figure 1: The Kiskatinaw River watershed, associated land-use practices and Sample Sites

Table 1: Sample Sites and their Markers in Figure 1.

Sample Site	Site Marker in Figure 1
Kiskatinaw mainstem at the community intake	K1
Kiskatinaw mainstem downstream of Brassey Creek	K2
Kiskatinaw mainstem downstream of Halfmoon and Oetata, upstream of Brassey Creek	K3
Kiskatinaw mainstem upstream of Halfmoon and Oetata, downstream of E-W-Arm Junction	K4
West Kiskatinaw Arm just upstream of the confluence with East Kiskatinaw	K5
East Kiskatinaw Arm just upstream of the confluence with West Kiskatinaw	K6
Brassey Creek near the mouth	B1
Brassey Creek 1km upstream of Cutbank road crossing	B4
Brassey Creek Headwaters North Arm u/s of Hwy crossing	B2
Brassey Creek Headwaters North Arm above all grazing at oil and gas road crossing	B2A
Brassey Creek Headwaters South Arm u/s of Hwy crossing	B3
Brassey Creek Headwaters South Arm above all grazing accessible by helicopter only	B3A
Tributary into lower Brassey Creek	BT
Oetata Creek just upstream of confluence with Halfmoon	01
Halfmoon Creek just upstream of confluence with Oetata Creek	H1
Halfmoon Creek downstream of confluence with Oetata Creek	H2
Jackpine Creek just upstream of confluence with Hourglass	J1
Hourglass Creek just upstream of confluence with Jackpine Creek	G1
Ministik Creek near the mouth	M1

#### 2 Site Description

#### 2.1 Overview

The Kiskatinaw River originates in the foothills of the Rocky Mountains near Tumbler Ridge and flows approximately 200 km north before joining the Peace River at the Alberta border in Northeast British Columbia. The main stem is formed from the convergence of two branches: the West Kiskatinaw River and the slightly longer East Kiskatinaw River, which drains Bearhole Lake. The watershed consists of nineteen major sub-basins (Berry, 1995) and drains 4,098 km² (Rex, 2003).

The river is situated in the Boreal White and Black Spruce biogeoclimatic zone, which is characterized by rolling topography, long and cold winters and a landscape composed of black spruce bogs intermixed with stands of white spruce and trembling aspen at higher elevations (Ministry of Forests, 1998). While the watershed topography is generally low-gradient, sections of the channel are deeply entrenched into a highly erodable landscape. Exposed sloughing banks are common, suggesting that landscape characteristics have the potential to affect water quality.

Land use activities within the watershed include agriculture (including range), forestry, oil, gas, residential development, roads, and mineral exploration, with agriculture and range use concentrating downstream of the confluence of the East and West Kiskatinaw arms (Figure 1).

No major waste disposal permits have been issued for the Kiskatinaw River basin. A small landfill permit exists at Fellers Heights and several sewage disposal (to ground) permits for private residences and industrial camps have been issued by the Peace Liard Community Health Unit. The Northern Health Authority identified approximately 220 sewage lagoons in the watershed (Sheila Withrow personal communication April 2002). Lagoons are by far the most common means of sewage treatment in the drainage.

Eighteen water withdrawal licences exist in the watershed, of which the City of Dawson Creek's is the largest.

#### 2.2 Hydrology

Stream flow data have been collected on a regular basis since 1966 by the Water Survey of Canada at station number 07FD001, located downstream from the community water supply pump house at the Alaska Highway crossing. This station is situated below most major tributaries and incorporates a drainage area of 3,685 km².

Average flows are lowest in late summer and during the winter months and generally highest during spring freshet. Shorter peak flows occur throughout the summer as a result of rain events and overland runoff, assisting potential impact of land use activities on water quality (Figure 2).

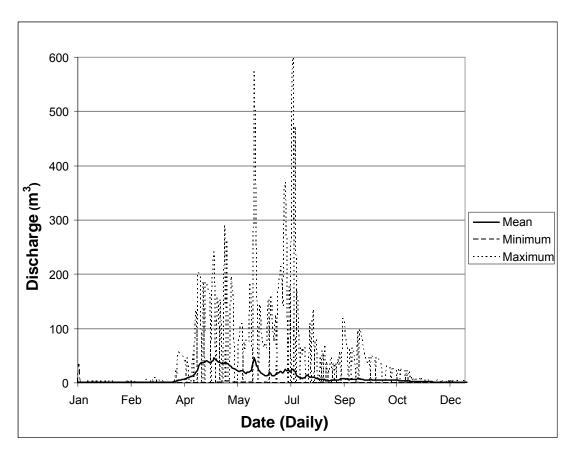


Figure 2: Lowest (bottom dashed line), average (middle solid line) and maximum (upper dashed line) daily flows observed in the Kiskatinaw River near Farmington at the Environment Canada survey station 07FD001 over the period 1944 – 2006.

#### 2.3 Community Water Treatment System

The City of Dawson Creek draws its domestic water supply directly from the Kiskatinaw River near Arras, upstream of the Highway 97 crossing. At the point of diversion, the river drains about  $2,800 \text{ km}^2$  of the watershed. From there the water is piped into a series of three settling reservoirs and later into a treatment facility, where it undergoes coagulation, filtration, chlorination (Sodium Hypo-chlorite disinfection) and UV treatment. Besides the settling reservoirs, the system includes a clean water reservoir that holds 2 Million US gallons. The total holding capacity of all four reservoirs is 200 Million US gallons, which would meet the city's demand for 67 - 80 days during high summer usage of 2.5 and 3 Million US gallons (high daily usage as per the City's website)

((http://www.dawsoncreek.ca/cityhall/departments/water/waterdemandmanagement.asp).

#### **3** Project Description

#### 3.1 General Considerations

Prince George MOE staff conducted an air photo and helicopter reconnaissance (Aug 11, 2004) to confirm the locations and extent of various land use sectors, and of suitable sampling sites in the Kiskatinaw River and its tributaries. Additional land use and water user information was collected from the sources listed in the interim report (Matscha et al, 2006).

The project consisted of two parts:

- 1. Broad source sector identification (2004/2005)
  - Consideration of all major land use activities in the watershed as potential contaminant sources.
  - A wide range of parameters were sampled at 14 sites throughout the watershed (chemical, physical, microbiological).
  - Water and Sediment samples.
- 2. Focus on sections and tributaries with high pathogen concentrations (2006/2007)
  - Consideration of natural, agricultural and residential fecal contaminant sources.
  - Sample analysis focussed on the detection and source tracking of bacterial indicators of fecal contamination and human infectious parasite groups at 12 sample sites.
  - Water and Scat samples.

Methods and results of the source sector identification are summarized and examined in Matscha et al (2006). A detailed description of methods, results and discussion of microbiological data under both parts and a short summary of water chemistry data are included below.

#### 3.2 Sample Sites, Sample Frequency and Sample Matrix

During the first year of the project, sample sites (Figure 1) were selected to divide the main stem into relatively large sections where oil, gas and forestry activities were separated from agriculture. This resulted in four sample sites in the main stem (K1-K4) and one each at the mouths of the West (K5) and East Kiskatinaw (K6) Rivers. Additional sample sites were placed in tributaries with the highest density of each of the major land use activities (agriculture, oil and gas, forestry, residential, roads). These include Brassey Creek (B1-B3) (mainly agriculture and residential, some oil and gas), Oetata (O1) and Halfmoon (H1) Creeks (both forestry and range use, some oil and gas), Jackpine (J1), Hourglass (H1) and Ministik Creeks (M1) (last three: mainly oil and gas, roads, and some forestry).

The second part of the project (in 2006 and 2007) focussed on the Kiskatinaw River downstream of the East- and West-Arm confluence (K1-K4), the Brassey (B1-B3, B2-A, B3-A, B4 and TB) and Halfmoon (H2) watersheds, where concentrations of fecal contamination had been particularly high during 2004/05 sampling. A sample site in Cutbank Creek was added to identify impact from residences around Cutbank Lake and from an oil and gas camp with a history of sewage seepage into the creek. Sites for microbiological sampling are shown in red and purple in Figure 1.

Water samples were collected five times throughout the first year (August 2004 to August 2005), covering seasonal flow conditions (Matscha et al, 2006).

In 2006 and 2007 sampling effort focussed on runoff events and summer months, based on first year results that indicated highest pathogen concentrations during freshet, after storm events and/or during warm summer periods. Scat samples were collected once in September of 2006 upstream of the sample sites in the Kiskatinaw mainstem (K1-K4) and two sites in Brassey Creek (B1, B3).

#### 3.3 Water Quality Parameters

The first year water sample analysis included 70 parameters typically affected by land use sector types that are found in the Kiskatinaw watershed (for details see Matscha et al, 2006). Analysis in 2006-2007 included fecal coliforms, *E.coli*, fecal *Streptococci*, *Enterococci* and *Bacteroides*, and the parasite cyst/oocyst for *Giardia* and *Cryptosporidium*. Fecal bacteria numbers are used as an indicator for fecal contamination, while *Giardia* and *Cryptosporidium* concentrations provide information about human infectious parasites. In addition, the identification of strains/genotypes is used as a measure of risk to human health. Cyst and oocysts are dormant spores of parasites that can survive in the environment over long periods and serve to transfer them between hosts. In an effort to identify sources of fecal contamination, a bacteria source tracking (BST) method (Field et al, 2003) was applied to determine source species (human, ruminant, pig, dog, elk). For parasite source identification, genome sequencing of waterborn parasites were applied and parasite presence in scat was established.

#### 3.4 Sampling Methods

Water Samples

Parasite sampling in 2004 employed a high volume filtering method described in EPA (1995). During 2004, field filtering of 50 L sample water was conducted. In 2005, the filtering method was changed to the USEPA Method 1623. The filter used with this method was more sensitive, but had the tendency to plug up from the highly turbid Kiskatinaw water, which made lab filtration necessary. The usual 50 L filter volume became impractical. Instead 10 L water samples were collected and shipped to the lab.

MOE staff collected water samples in laboratory certified container's (sterilised polyethylene jars for bacteria and 10 L plastic containers for parasites). Representative grab samples were collected from the raw water tap at the pump house (K1) or directly from the Kiskatinaw River or its tributaries (all other sites). Prior to sampling from the raw water tap, the source was flushed for five minutes in order to minimize contamination by system piping.

10 L parasite containers were washed with soapy water, rinsed four times with tap water and three times with sample water prior to sample collection. Sterilized bacterial sample bottles were not rinsed. Samples were shipped in coolers with ice packs to arrive at the appropriate lab within 24 hours of collection.

For water chemistry and sediment sampling details, please refer to Matscha et al (2006).

#### Scat Samples

Scat sampling was undertaken by mapping all scat found within a 30 m wide and one kilometre long riparian transect upstream of selected water sampling sites. Four to five scat were selected per transect, based on their condition (preferring fresher and moister specimen) and species representation. Each scat sample was individually bagged in a sterile and sealable stool sample bag. Information on scat location in relation to the creek, scat condition and species of origin were noted.

#### 3.5 Analysis Methods

Bacteria concentrations were determined by JR Laboratories Inc. (2004/05) and Cantest (2006/07), using membrane filtration (Part 9222 Franson at al., 2005). Pacific Environmental Science Centre (PESC) identified bacteria sources (hosts) by employing a technique that has been developed and adapted from the published articles by Dr. Katharine Field (Oregon State University) (Field et al, 2003). This method is a genetic assay that detects 16-S ribosomal genomic DNA from the host-specific intestinal bacterial group *Bacteroides* and thereby identifies the organisms responsible for fecal contamination in water samples. Currently PESC is able to distinguish between fecal contamination from humans, ruminants, pigs, dogs, and elk; however, the ability to identify dog and elk contamination was added after April 2005, thus was only applied to samples collected after that date.

The B.C. Centre for Disease Control (B.C.CDC) identified *Giardia* cyst and *Cryptosporidium* oocyst concentrations in water and scat samples, using filtration. Methods in 2004 followed the description in EPA (1995). From 2005 to 2007 the USEPA Method 1623 was employed. Scat analysis employed the same filtration method of diluted samples at the lab. The B.C.CDC also established whether strains/genotypes found in the Kiskatinaw were infectious to humans. A similar molecular analysis was planned for the oocysts/cysts isolated from the collected scats. However, an interference of scat material prevented a successful analysis. Scat collection, scat sample analysis, sequencing and sequence analysis were partnership contributions to the project by the Centre.

Parasite cysts/oocysts were derived through the method described in EPA (1995) and by using the USEPA Method 1623. Subspecies and strain identification was achieved by amplifying (using PCR) and sequencing of the  $\beta$ -giardin gene found only in *Giardia* species (Lalle et al., 2005), using Applied Biosystems (ABI) 3100 sequencer in forward and reverse direction and duplicated to confirm results. Sequence analysis was performed using the BLAST tool provided on the National Centre for Biotechnology Information site (NCBI, www.ncbi.nlm.nih.gov) and by Cluster W alignment and phylogenetic tree construction using the MegAlign program in the DNAStar Software Package. BLAST is a simple search alignment tool that compares the sequence to published sequences for all organisms as a tool to identify potential host species.

#### 3.6 Quality Assurance/Quality Control (QA/QC)

The monitoring project included quality assurance and control (QA/QC) procedures to ensure acceptability of the data and precision from the field probes and laboratory analysis. Besides the development of sampling protocols, proper field staff training and calibration of field probes prior to each sample trip, data quality samples were submitted to the analyzing laboratory. Approximately 10% of all samples submitted were field blanks and duplicates. The laboratory analysis followed required standards and provided additional quality assurance measures and samples. Data quality objectives listed in Appendix A were used to evaluate data for inclusion into data analysis.

#### 4 Results and Discussion

#### 4.1 Data Quality

Most bacteria blank results met the data quality objectives (Appendix A); however, fecal *Streptococci* contamination occurred on September 14, 2004 and April 06, 2005 (8 and 17 CFU/100mL, respectively). *E.coli* and fecal coliform contamination was detected on April 23, 2007 (just exceeding the disinfection only guideline of 10 CFU/100mL). Since similar contamination of ambient samples collected during the same sample trip may have occurred, results of these ambient samples for the above parameters cannot be trusted and will be excluded from data analysis and interpretation.

The high frequency of bacteria duplicates exceeding the data quality objectives (in five out of seven samples; Table A.2, Appendix A), may be due to high natural variability. However, with the exception of the fecal *Streptococci* values of April 23, 2007, the difference between duplicates was much less than the more significant differences between sites and dates, thus not influencing data interpretation. For that reason, only fecal *Streptococci* values of April 23, 2007 were removed from data analysis.

#### 4.2 Water Quality

#### 4.2.1 General Results

The sampled streams show a slightly alkaline pH and moderately high specific conductance and hardness, which were highest during the lower flows in the fall (Oct 2004) and winter (Feb 2005), suggesting groundwater influence. No pesticides were detected and most analysed parameters were well below B.C. Water Quality Guidelines; however, 10 parameters exceeded these guidelines at varying frequencies. Results for these parameters are discussed below.

#### 4.2.2 Water Chemistry – Brief Summary (for details see Matscha et al. 2006)

- Hardness generally exceeded 200 mg/L CaCO<sub>3</sub>, which, under the provincial guidelines, classifies
  drinking water quality as "poor", but "tolerable". The fact that the highest values occurred during
  low flows and periods of little overland flow suggests groundwater and natural sources.
- Total and dissolved organic carbon at the pump house was consistently above the recommended 4 mg/L threshold for chlorination treatment. The threshold is based on acceptable levels of potentially toxic chlorination-by-products that may form during the chlorination process in water with high organic carbon levels. Most of the organic carbon in samples from the pump house was dissolved, thus would not be removed by a settling process. Concentrations of total organic carbon were similarly high throughout the watershed, including headwaters upstream of most land use activities. Concentrations were not flow related, but increased in late summer and fall. The results strongly suggest natural sources.
- <u>Total cadmium</u> concentrations typically exceeded Provincial aquatic life guidelines during periods of higher flows (fall 2004, spring 2005). However, drinking water guidelines were always met and risk to human health remains low with highest values at least one order of magnitude below the guidelines. Most of the cadmium was in particulate form with highest values coinciding with suspended solids peaks, suggesting erosion as a main source.
- A similar pattern was observed for <u>total manganese and total iron</u>, which frequently exceeded the Provincial aesthetic drinking water guideline of 0.3 mg/L for iron and 0.05 mg/L for manganese, which are based on colour and taste. Values do not indicate risk to human health, but iron concentrations exceed aquatic life guidelines. Both parameters were largely present in particulate form, which limits their bio-availability and increases reduction through settling. The data suggest erosion as the main contributor.

• Turbidity and total suspended solids (TSS) varied significantly throughout the year, with highest values during freshet and high summer flows. Suspended solids can interfere with the disinfection process during water treatment and provide surface area upon which bacteria can grow. High levels of turbidity and TSS can decrease light penetration which can affect aquatic plant growth, influence visibility and respiration by aquatic life and impact fish reproduction success. Likely sources are erosion and sloughing banks.

#### 4.2.3 Microbiological Issues (for details see below)

- Most bacteria types were detected at the City of Dawson Creek pump house on each sample date, with the exception of May 07, 2007 (Table 2). Since the community water for the City of Dawson Creek undergoes sufficient treatment, no drinking water guidelines apply; however, with fecal coliform levels of up to 140 colony forming units (CFU)/100 mL and Enterococci concentrations of up to 58 CFU/100 mL there is potential for bacterial-related human illness should some water treatment components become ineffective.
- <u>Cryptosporidium and Giardia</u> tests resulted in Giardia cyst detection and counts from 20 to 3914 cysts / 100 L (median of 170.4 cysts / 100 L) at the intake during the open water period, except for May 07, 2008, when no parasites were detected at any sample site in the watershed. Although Dawson Creek's treatment system eliminates these parasite cysts during normal operation, these concentrations pose a potential human health risk in case of a treatment system failure. Cryptosporidium numbers in the water column were substantially lower. Scat sample analysis resulted in the opposite: Cryptosporidium was detected in feces, while Giardia was not.

Details for each microbiological result under this study (2004 to 2007), their importance for drinking water quality, a comparison to historic data and potential sources are discussed in the following paragraphs.

#### 4.2.3.1 Bacterial Contamination

The bacterial data for the City of Dawson Creek raw water intake are summarised in Table 2. Spatial and temporal trends of fecal coliform, *E.coli*, fecal *Streptococci* and *Enterococci* concentrations in the Kiskatinaw Watershed are shown in Figure 3 and 4 and are tabled in Appendix B. Spatial and temporal trends of fecal coliform concentrations in the Brassey Creek Watershed are displayed in Figure 6.

The measured fecal bacteria are used as indicators for fecal contamination and its risk to human health. The treatment system employed by the City of Dawson Creek is capable of eliminating bacteria from the water before distribution to users; however, in case of system component failures water quality guidelines would apply. For example if only disinfection with filtration or settling would be available (="partial treatment"), guidelines of 100 CFU/100 mL (based on 90<sup>th</sup> percentile of 10 samples) for fecal coliforms and *E.coli* as well as 25 CFU/100 mL (based on 90<sup>th</sup> percentile of 10 samples) for *Enterococci* would apply (Table 3). No guidelines exist for fecal Streptococci. Ten times in 30 day sampling would have to be conducted to calculate the 90<sup>th</sup> percentile. Since latter was not done it is not clear if this guideline was exceeded; however, it should be noted that 44% (4) of the *Enterococci* results and 11% (1) of the *E.coli* and fecal coliform values each as listed in Table 2 exceeded the above concentrations.

Although numbers were reduced during late fall and winter sampling, fecal bacteria were detected at the intake for each sampling event. Highest concentrations occurred during summer, early fall and spring freshet. Historic data collected at the City of Dawson Creek raw water intake show similar seasonal patterns (Matscha et al., 2006).

Other sensitive water users exist throughout the watershed, such as irrigation, livestock watering and recreation. Table 3 summarizes Provincial Guidelines to protect these water uses. This study did not include five times in 30 day sampling, which would be required to identify whether the guidelines (based on geometric mean) for primary contact (swimming) and irrigation of crops that are eaten raw (20 CFU/100 mL for *Enterococci* and 77 CFU/100 mL for *E.coli*) were exceeded (Table 3). However, it should be noted that *Enterococci* concentrations in the Kiskatinaw Watershed exceeded the 20 CFU/100 mL at least once at all sample sites, except for Halfmoon Creek (on Sep 2004) and Kiskatinaw River upstream of most agricultural areas (K4) (on Aug 2005). In the lower Brassey Creek

(B1) and in the Kiskatinaw River below Brassey (K2) the value was exceeded, both 33% of the time (three times out of nine). During this study, *E.coli* counts also exceeded the guideline value of 77 CFU/100 mL once (11%) each at the intake (K1), in the Kiskatinaw River downstream of Halfmoon Creek (K3) and downstream of Brassey Creek (K2) and three times (33%) at Brassey Creek mouth (B1) (Figures 3 and 4). These results suggest a potential risk to human health of swimmers and residents, who irrigate crops that are eaten raw (e.g. lettuce, tomatoes) with water from these sections of the river during the summer months.

Table 2: Results of bacterial analysis of the City of Dawson Creek's raw water supply (2004-2007). (The grey marker indicates exceedance of 100 CFU/100 mL for fecal coliforms and E.coli and 25 CFU/100 mL for Enterococci.

Date	Fecal Coliforms (CFU/100mL)	E.coli (CFU/100mL)	Fecal Streptococci (CFU/100mL)	Enterococci (CFU/100mL)
Sep 14, 2004	38	30	76	28
Oct 26, 2004	8	3	3	<1
Feb 21, 2005	3	3	4	3
Apr 06, 2005	20	8	60	58
Apr 19, 2005	30	20	10	10
Aug 15, 2005	140	120	90	40
Sep 04, 2006	3	3	1	3
Apr 23, 2007	14	14	260	50
May 07, 2007	<10	<10	10	<1

The livestock watering guidelines (for farm animals not confined and not on the range) are based on the maximum concentration of 200 CFU/100 mL for Fecal Coliforms and *E.coli* and 50 CFU/100 mL for *Enterococci*. The *Enterococci* guideline was exceeded infrequently in the lower Brassey Creek, Kiskatinaw River, Oetata and Halfmoon Creeks during summer sampling events and once at the intake (K1) during freshet. *E.coli* and Fecal coliform livestock watering guideline was exceeded only at Brassey Creek mouth. The data indicate a potential health risk during summer months to livestock grazing adjacent to these stream sections.

Table 3: Provincial Water Quality Guidelines to protect the indicated Forms of Water Use.

Water Use	Fecal Coliforms (CFU/100mL)	E.coli (CFU/100mL)	Fecal Streptococci (CFU/100mL)	Enterococci (CFU/100mL)
1.Raw Drinking Water*     2.Raw Water for Watering of closely confined Livestock**	0	0	No provincial guideline	0
1.Disinfected Drinking Water*     2.Disinfected Water for Watering of closely confined Livestock*	10	10	No provincial guideline	3
1.Raw Water for Irrigation of Crops eaten raw***     2.Recreation Primary Contact (swimming)***	200	77	No provincial guideline	20
1.Partially treated**** Drinking Water*     2.Partially treated**** Water for     Livestock Watering*	100	100	No provincial guideline	25
1.Raw Water for non-confined livestock, not on the range**	200	200	No provincial guideline	50

<sup>\*</sup> Based on 90<sup>th</sup> percentile of 10 samples in 30 days

<sup>\*\*</sup> Based on Maximum

<sup>\*\*\*</sup> Based on geometric mean of 5 samples in 30 days

<sup>\*\*\*\*</sup> Partial treatment = disinfection after settling or filtration

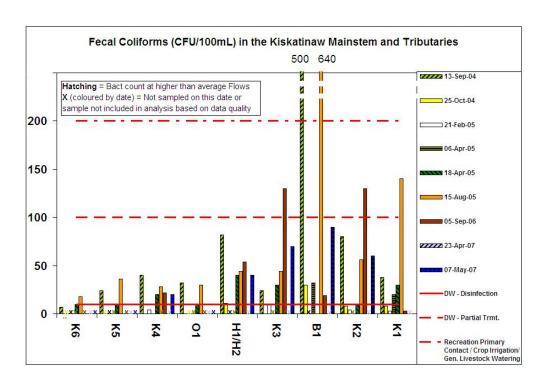


Figure 3a): Fecal coliform concentrations in the Kiskatinaw River main stem and at the mouths of the monitored tributaries by date. Bars with hatching represent samples collected during higher than average flows; bars without hatching represent samples collected during lower flows. Red lines indicate B.C. Water Quality Guideline limits for various levels of drinking water treatment, recreation and livestock watering.

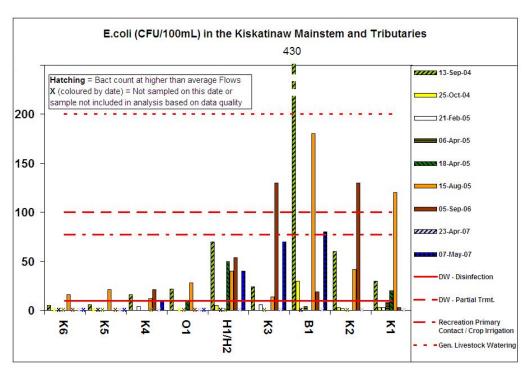


Figure 3b): E.coli concentrations in the Kiskatinaw River main stem and at the mouths of the monitored tributaries by date. Bars with hatching represent samples collected during higher than average flows; bars without hatching represent samples collected during lower flows. Red lines indicate B.C. Water Quality Guideline limits for various levels of drinking water treatment, recreation and livestock watering.

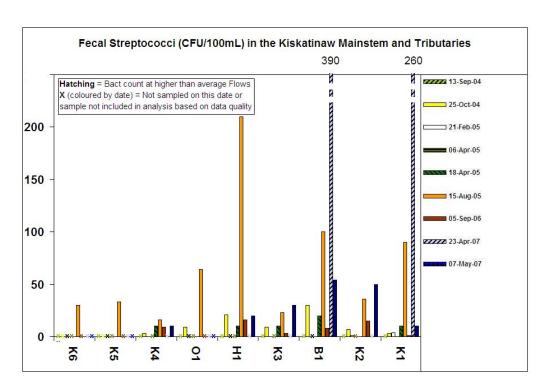


Figure 4a): Fecal Streptococci in the Kiskatinaw River main stem and at the mouths of the monitored tributaries by date. Bars with hatching represent samples collected during higher than average flows; bars without hatching represent samples collected during lower flows. No B.C. Water Quality Guidelines apply for Fecal Streptococci as a group.

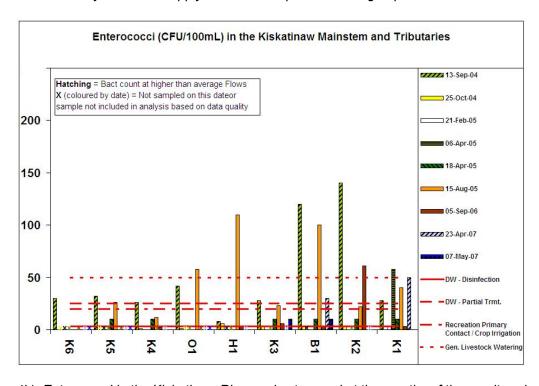


Figure 4b): Enterococci in the Kiskatinaw River main stem and at the mouths of the monitored tributaries by date. Bars with hatching represent samples collected during higher than average flows; bars without hatching represent samples collected during lower flows. Red lines indicate B.C. Water Quality Guideline limits for various levels of drinking water treatment, recreation and livestock watering.

Figures 3 and 4 show strong seasonal trends with highest *E.coli*, fecal coliform, fecal *Streptococci* and *Enterococci* values in late summer and early fall (Sep 2004, Aug 2005), and lowest during the winter months. This finding confirms historical data from Brassey Creek (2002 – 2003; Matscha et al, 2006; n=10), where fecal coliform densities were also highest during late summer months.

In 2007, fecal Streptococci were also abundant during spring freshet (Figure 4a).

Highest concentrations of all four bacteria groups were found in Brassey Creek, Oetata Creek, Halfmoon Creek and the Kiskatinaw River below these tributaries (Figures 3 and 4).

In an effort to segregate sources of high bacterial contamination, a source tracking method using *Bacteroides* (as described under Sample and Analysis Methods) was employed for samples from the Kiskatinaw River (K1-K3), Brassey and Halfmoon Creeks. Results are summarised in Figure 5 and Tables C1 and C2 (Appendix C).

A number of studies (Bernhard & Field, 2000; Bower et al., 2005; Kreader, 1995; Wang et al., 1996) indicate that *Bacteroides* spp. may be one of the most sensitive fecal indicator genetic markers present in fecal pollution at a much higher abundance than fecal coliforms. In spite of the high sensitivity as a fecal contamination indicator, *Bacteroides* were not always detected when fecal coliform or *Streptococci* numbers were significant (Appendix C and Figure 3, 4 and 5). According to the analysing lab, filtering problems were the likely reason for this discrepancy on September 13, 2004, when turbidity was exceptionally high. However, *Bacteroides* were detected on other dates with similarly high suspended solids concentrations and turbidity. For October 25, 2004 and April 18, 2005, the lab theorized that an agent causing the water to turn yellow may have interfered with genetic marker detection. Other factors, such as survival of the strictly anaerobic *Bacteroides* outside the digestive tract compared to the less specialised fecal coliforms may play a role (Bower et al., 2005)

The following limitations of the *Bacteroides* based source tracking method are considered in the data interpretation below:

- Difficulties filtering water samples with high suspended solids concentrations.
- Water colour or chemistry may influence genetic marker detection.
- Potentially different survival of Bacteroides and fecal coliforms.
- Capability to detect presence/absence, but not relative abundance of source specific genotypes.
- Markers have been identified for Bacteroides in general and specifically for those originating from human, ruminant, pig, dog, and elk fecal contamination. Other Bacteroides sources may contribute, but cannot yet be identified through this method.
- The level of confidence in a positive pig result is not as high as any of the other organisms because the pig primers for one of the markers have been noted to cross-prime with ruminant animal (PESC lab reports).
- The dog marker may also indicate contamination from related wild animals, such as coyotes and wolfs (PESC lab reports).

In 2004 and 2005, bacteria source tracking was conducted at key sites in the Kiskatinaw downstream of Oetata and at Brassey mouth. In 2006 and 2007 additional sites were added (B2, B3, BT, B4, K4, and H2) to further understand contaminant sources in areas with high fecal contamination (Appendix C). To use the method most effectively, this analysis was only requested, when fecal bacteria numbers were over 10 CFU/100 mL.

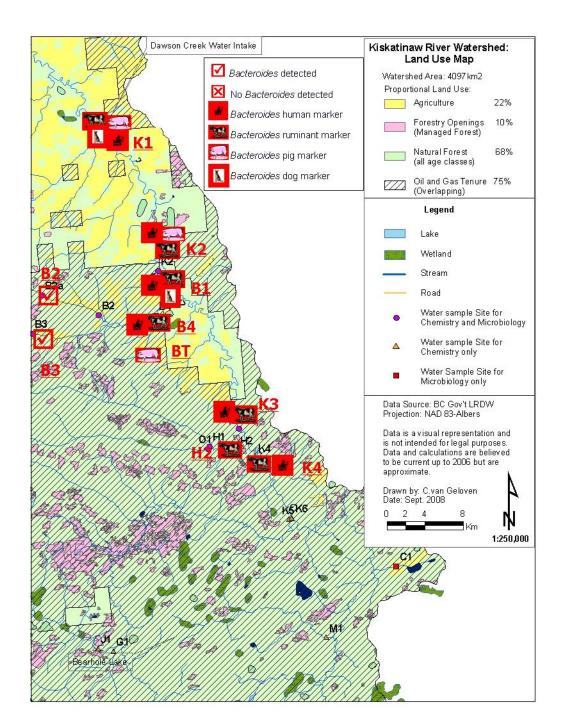


Figure 5: Summary of Bacteroides Source Tracking

The results indicate frequent fecal bacteroidal contamination at almost all sampled sites. Host species of the detected *Bacteroides* were identified for all but the headwater control sites in Brassey Creek, which suggests host species other than the ones that can currently be detected by PESC for these sites. So far, PESC can identify the following host species: human, dog (including wild canine), ruminant (including cattle, horse, moose, deer, elk), elk (specifically), pig (this marker is not very reliable because it cross references with cattle markers). Human and ruminant contamination was detected at all tested sites in the Kiskatinaw mainstem (downstream of the East-West-Arm confluence) and in the lower Brassey Creek (Figure 5). In the lower Halfmoon Creek (H2) ruminant fecal contamination was measured in September, 2006, when livestock grazed in the watershed. In comparison, no *Bacteroides* were found in the spring sample of 2007, when livestock was absent from the area. Since these observations are based on the

total of two samples at this site, additional samples are needed to confirm a relationship between livestock grazing and bacteroides detection in Halfmoon Creek.

With its location upstream of all commercial farms, no relevant upstream range tenure and few upstream residences, K4 (just downstream of the East-West-Arm confluence) was originally selected as a control site. However, cattle and cattle feces were observed between the confluence and K4 during the summer of 2006, when *Bacteroides* with ruminant markers were detected at K4. Source tracking results also indicated sewage contamination upstream of this site, suggesting sources in the East or West arm of the river. With no known potential sewage source to the West Kiskatinaw River, the presence of residences adjacent to One Island Lake and Cutbank Lake, the history of sewage overflow from an oil and gas camp near Cutbank Lake and the existence of provincial parks at One Island and Bear Hole Lake in the East Kiskatinaw Watershed, further source identification efforts are recommended focussing on the East Arm.

Identified ruminant contamination does not exclude wildlife, such as deer, moose and elk. However, it should be noted that no ruminant contamination was detected upstream of agricultural use in Brassey Creek, where moose would be expected to be more abundant than in pasture land. Elk were quite abundant in pasture land, but *Bacteroides* results did not indicate elk specific contamination in these creek sections, suggesting that most ruminant contamination adjacent to pasture lands originated from livestock. Ruminant contamination may not explain all fecal contamination in Brassey Creek below the headwaters. A high frequency of beaver dams, in both the headwaters and adjacent to pasture land, suggest beavers as a potentially important bacteria source. A bacteria source tracking study in the Okanagan Valley (using *E.coli*) identified a significant influence of these rodents on bacteria concentrations in the water column (Meays, C.L, 2005). For that reason future bacteria or parasite source tracking methods should include rodents or at least beaver.

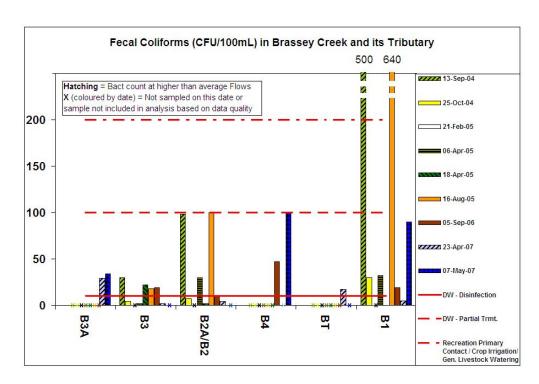


Figure 6: Fecal Coliform counts in the headwaters of Brassey Creek (B2, B3) in comparison to the mouth (B1) in 2004/05. Bars with hatching represent samples collected during higher than average flows; bars without hatching represent samples collected during lower flows. Red lines indicate B.C. Water Quality Guideline limits for various levels of drinking water treatment, recreation and livestock watering.

#### 4.2.3.2 Parasite Contamination

As Figure 7 and Figure 8 show, *Giardia* cysts have been detected with a higher prevalence and in substantially higher numbers in the water column than *Cryptosporidium*. A higher survival rate of *Giardia* in the water column compared to *Cryptosporidium* (Karim et al., 2004, Gibbs et al., 1995) may be one of the reasons for this discrepancy.

The highest cyst and oocyst concentrations were found in Brassey Creek and in the Kiskatinaw below the Brassey confluence. However, it should be noted that *Giardia* cysts were frequently detected in the Kiskatinaw mainstem upstream of most agricultural areas at K4, where levels were 25, 83, 150 and 825 cysts/100 L. Potential sources upstream of this site include wildlife, small hobby farms, few residences, camps and Provincial Parks.

The substantial concentration differences between the headwater site and the mouth in Brassey Creek (Appendix B) suggest the presence of significant sources between the two sites, where agricultural land use, residential sewage seepage and wildlife, particularly beavers, need to be considered. In many countries, *Giardia* is typically widely distributed in surface water, but is often found in higher frequencies in areas with livestock operations (Ionas et al, 1998). Heitman et al (2002) showed that highest concentrations for both *Giardia* and *Cryptosporidium* in animal/human waste were found in cattle feces, although the highest frequency of detection occurred in human sewage.

In the Kiskatinaw Watershed, highest concentrations of both parasites were found after rain events (>20 mm within two days) and in turbid waters, indicating land runoff and flushing of slow flowing areas or beaver dams as sources. Literature confirms a strong correlation between *Giardia* cyst or *Cryptosporidium* oocyst concentrations and turbidity (e.g. Hsu et al, 2000). However, not all runoff events resulted in peak *Giardia* concentrations in the Kiskatinaw River. Numbers remained below the relatively high detection levels of 75-100 cysts/100 L at all sites during the headwater snow melt runoff on May 07, 2007. A few weeks earlier, when snow melt occurred in low land areas in the Brassey Creek watershed, but the Kiskatinaw mainstem was still frozen, cyst counts were comparable to those at low flow conditions. It is not clear, why cyst/oocyst numbers were lower during the 2007 freshet compared to other runoff events.

After a substantial rain event on August 15, 2007 (about 70 mm within two days), the *Giardia* cyst concentration reached 3914 cysts/100L at the community intake (K1). No *Cryptosporidium* oocysts were detected during this event. At this point, Health Canada does not provide a guideline threshold, due to the often poor recovery during detection, but recommends that if any *Giardia* cysts or *Cryptosporidium* oocysts are detected in raw water, a watershed protection plan should be pursued (<a href="http://www.hc-sc.gc.ca/ewh-semt/pubs/water-eau/protozoa/index-eng.php">http://www.hc-sc.gc.ca/ewh-semt/pubs/water-eau/protozoa/index-eng.php</a>). Should the treatment system ever become dysfunctional during such an event, the likelihood of a Giardiasis outbreak would be very high if the strains in the water were infectious to humans.

Four water samples collected on September 4 and 5, 2006 and three water samples taken on April 23, 2007 that were positive for *Giardia* cysts, were analysed to identify whether the detected strain was infectious to humans. Of these samples, a total of four (57%) were identified as *Giardia lamblia*, Assemblage B, a strain infectious to humans. On one of the two dates the strain was found at the intake, reinforcing the importance of treatment. *Giardia lamblia* was also detected at Brassey Creek mouth and downstream of Halfmoon Creek, but not upstream of most agriculture in the mainstem (K4) and not in Brassey Creek headwaters (B2, B3) (Table 4). This finding suggests introduction of this species in Brassey Creek, Halfmoon Creek watershed and/or the Kiskatinaw River below Halfmoon. However, since this is based on only two sample events introduction from other sources cannot be ruled out entirely. The comparison of the detected sequences with sequences found in the NBCI bank, show that *Giardia* found in the Kiskatinaw River has a similar genotype than those found in humans in the Netherlands and causing a giardiasis outbreak in Norway (Table 4).

Literature suggests that *Giardia lamblia*, Assemblage B has a wide variety of hosts, including humans, cattle, dogs, coyotes, rabitts, horses, and rodents (Lihua and Fayer, 2008). Since all host groups are present in the Kiskatinaw Watershed, any one of these may have shed the cysts detected at Dawson Creek's water intake and thus need to be considered as a potential source. However, through a literature review, the above authors also found a relatively high prevalence of Assemblage B in beaver and

muskrat, while *Giardia lamblia* infection in cattle were more often caused by Assemblage A than by Assemblage B. The other animal groups listed above host Assemblage B in addition to other assemblages more or less frequently (Sulaiman et al., 2003; Trout et al., 2006a), with a rare occurrence in dog feces (Reade et al, 2004; Traub et al, 2004). Human contamination should also be considered as a potential source in the Kiskatinaw Watershed. Epidemiological evidence supports *Giardia lamblia* transmission from human to human or through their waste (Lihua and Fayer, 2008).

Table 4: Results of Giardia strain identification, using the  $\beta$ -giardin gene sequence analysis and assemblage identification in seven samples that were positive for Giardia.

Sample Date	Sample Location	Detected Strain	Comparison with NBCI data bank
Sep. 04, 2006	K1 (Community intake)	PCR negative*	N/A
Sep. 05, 2006	K2 (Kiskatinaw d/s Brassey)	Assemblage B	99% sequence match w. Giardia in water borne giadiasis outbreak in Norway
Sep. 05, 2006	K3 (Kiskatinaw d/s Halfmoon)	Assemblage B	99% sequence match w. <i>Giardia</i> in human in the Netherlands
Sep. 05, 2006	K4 (Kiskatinaw u/s most agriculture)	PCR negative*	N/A
April 23, 2007	K1 (Community intake)	Assemblage B	No comparison done
April 23, 2007	B1 (Brassey Creek Mouth)	Assemblage B	No comparison done
April 23, 2007	B2 (North Brassey at Hwy)	PCR negative*	No comparison done

<sup>\*</sup> PCR negative may indicate one of the following: 1. Detected cysts are not *Giardia lamblia*; 2. The detected cysts were false positives due to cross reaction of the dye with an algae; 3. Cyst may have lost one or more nuclei, each containing only one copy of the β-giardin gene.

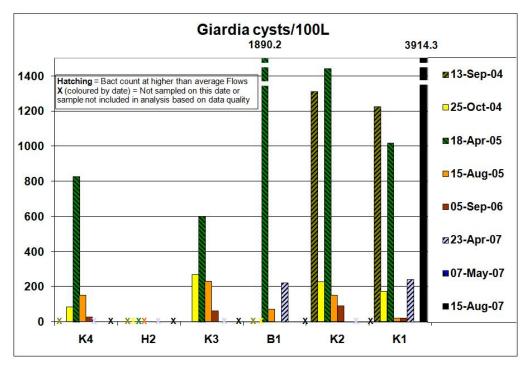


Figure 7: Giardia cyst counts in the Kiskatinaw River main stem and at the mouths of the monitored tributaries by date. Bars with hatching represent samples collected during higher than average flows; bars without hatching represent samples collected during lower flows. Red lines indicate B.C. Water Quality Guideline limits for various levels of drinking water treatment, recreation and livestock watering. (X = not sampled on the day matching the font colour).

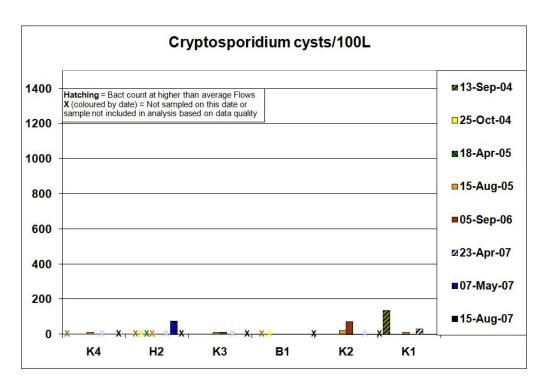


Figure 8: Cryptosporidium oocyst counts in the Kiskatinaw River main stem and at the mouths of the monitored tributaries by date. Bars with hatching represent samples collected during higher than average flows; bars without hatching represent samples collected during lower flows. Red lines indicate B.C. Water Quality Guideline limits for various levels of drinking water treatment, recreation and livestock watering. (X = not sampled on the day matching the font colour).

Wildlife and livestock scat was sampled in September 2006 in partnership with the B.C. Centre for Disease Control to identify parasite hosts in the watershed. A summer rain event sample was not possible that year due to the exceptionally dry summer. For that reason the scat and water collection program was conducted during sub-optimal dry conditions. Scat dried out faster resulting in a large portion of the collected scat being relatively dry (about 50%). Since the cyst/oocyst survival may be influenced by dryness, analysis results of the 2006 samples may not reflect typical distribution.

Scat analysis results are summarized in Appendix E.

31 scat samples were collected from the following animals with the following frequency:

- Moose: 6 samples,
- Elk: 1 sample,
- Deer: 4 samples,
- Cattle: 6 samples.
- Horses: 4 samples,
- · Geese: 3 samples,
- Other birds: 3 samples,
- Small rodents: 1 sample, and
- Not clearly identified host: 3 samples.

Beaver droppings are hard to collect from the environment were not located during the sampling event.

In the watershed, *Cryptosporidium* oocysts were found in 8 of 31 (26%) of samples, exclusively in cattle, deer and horse feces. No *Giardia* cysts were detected in scat samples. Although cyst and oocyst walls protect against desiccation and heat, the very dry and hot summer may have reduced cyst and oocyst survival in scat. Other reasons for the absence of *Giardia* cysts could be seasonal concentration

variations of this parasite in feces. Although results may not reflect all species that carry *Cryptosporidium* and *Giardia*, they indicate that livestock and wildlife are hosts and potential sources for parasites.

Cryptosporidium was detected in feces from the Kiskatinaw mainstem downstream of Halfmoon (K3) and Brassey Creeks (K2), in the lower Halfmoon Creek (H2) and in Brassey Creek headwaters (B3). During the same sample event, the genus was also identified in the water column at K2 and K3.

It is recommended to repeat a scat sampling program during a wet summer and to include beaver feces in the program. Since beaver scat are difficult to collect from the environment, trappers in the watershed should be contacted to request beaver carcases for feces extraction. Since beaver defecate directly into the water, they need to be considered as an important contaminant source.

#### 5 Summary

- Groundwater and geology influence the water hardness in the Kiskatinaw River.
   Based on its naturally hard water, the Kiskatinaw River drinking water is classified as "poor, but tolerable".
- High manganese and iron levels impact taste of drinking water, but do not pose a
  risk to human health. Data suggests cadmium, manganese and iron are being
  introduced through erosion and are typically bound to particulates, which makes
  manganese and iron less bioavailable to aquatic life.
- High turbidity and suspended solid concentrations may result in higher water treatment costs to ensure effective protection.
- Fecal bacteria concentrations at the community intake were found to be highest during summer months with slightly lower numbers during freshet. These seasonal patterns are similar to historical data for this site.
- Identified fecal bacteria concentrations pose no risk to drinking water quality as long as Dawson Creek's water treatment facility is fully functional. However, it should be noted that bacteria counts exceed partial treatment guidelines during summer months. Should the treatment facility ever fail and be reduced to settling or filtration in combination with disinfection, fecal contamination will pose a potential risk to human health.
- The study results indicate that fecal bacteria exceed primary contact, irrigation of crop eaten raw and livestock watering guideline values in Oetata Creek, Brassey Creek and the Kiskatinaw below these two tributaries during summer months. This suggests a periodic risk to swimmers, people who irrigate their crop with stream water and to livestock in or near these stream sections.
- Highest concentrations of all four tested fecal bacteria types were identified in Brassey Creek and in the Kiskatinaw River below the Brassey confluence, suggesting main sources in these sections.
- The bacteria source tracking work identified human and ruminant waste as the most wide spread sources (of human, ruminant, elk, pig and dog) for intestinal bacteria (Bacteroides) in the water column. At Dawson Creek's water intake (K1) human and ruminant fecal contamination was detected in 80% of all samples. At Brassey Creek mouth (B1), both were detected in 38% of all samples and in the Kiskatinaw River below the Brassey confluence (K2), human contamination was

identified in 38% and ruminant waste in 25% of all samples. However, none of the above sources were identified in the headwater of Brassey Creek, which are situated above most agricultural and residential use. Potential sources for human contamination include failing septic systems and lagoons of rural residences.

- Ruminant fecal contamination may be caused by livestock, such as cattle, bison and horse or wildlife, including deer, moose and elk. However, low moose densities on pastures and no detection of elk markers in the stream downstream of fields frequented by elk suggest livestock as one of the main contributors to the ruminant fecal contamination from farm land.
- An indicator for human waste that was detected at K4, just downstream of the East-West-Arm, proposes a sewage source in one of the two Kiskatinaw headwater arms. No potential sources are known to be located in the West Arm, while numerous possible sources, such as residences around One Island and Cutbank Lakes, oil and gas camps and provincial parks are situated in the East Arm.
- Parasite filtration of water samples revealed a Giardia cyst detection rate of 69% (24 of 35), while Cryptosporidium oocysts were discovered in only 29% (10 of 35) of all samples. In addition, Giardia concentrations ranged from 20 to 3914.3 cysts/100 L with a median of 221.1 cysts/100 L, while Cryptosporidium concentrations ranged from 10-241 oocysts/100 L with a median of 20 oocysts/100 L.
- In comparison, scat sampling results showed a reversed relationship. Cryptosporidium oocysts were discovered in 26% (8 of 31 samples) of all analysed scat samples, while no Giardia cysts were recovered from any of these scat. Different survival rates between these groups in water and dry scat under the influence of prolonged summer heat before and during the sampling event in 2006 may have contributed to this discrepancy. Of the feces collected from nine species/animal groups, Cryptosporidium oocysts were detected in scat of only three species: moose, deer and cattle.
- The discrepancy between detection frequencies of Giardia cysts and Cryptosporidium oocysts in water versus feces reduces the potential for conclusions about the sources for waterborne parasites. In addition, scat of one potential host, the beaver, have not been analysed for parasites. Atwill et al (2002) found that rodents can significantly contribute to the Cryptosporidium parvum loading within a watershed. A repeat of the scat sampling program during a wet, cool summer with the inclusion of beaver scat retrieval directly from trapped animals, may provide additional useful information.
- Highest Giardia values occurred at the Brassey Creek mouth (B1) and in the Kiskatinaw below the Brassey confluence (K1-K2). Results of this study show that 57% (4) of all Giardia samples that were analysed for strain identification, were classified as Giardia lamblia, Assemblage B, a strain that is infectious to humans. This outcome reinforces the importance of drinking water treatment and the need for management of parasite sources, where possible to ensure a multi-barrier protection.

- Highest Cryptosporidium oocyst counts of this study occurred near Brassey Creek mouth (221 cysts/100 L), in Halfmoon Creek (75 cysts/100 L) and in the Kiskatinaw River at the community intake (136 cysts/100 L). These sites are downstream of the sites where scat with detected Cryptosporidium were collected. A repeat of the feces and accompanying water sampling program may provide further information on sources for waterborne Cryptosporidium and Giardia.
- A genotype analysis of Giarida cysts from the Kisakatinaw identified the cysts as Giardia lamblia Assemblage B, a strain that is infecuous to humans. Comparison with an existing parasite database found that the genotypes were similar to those that caused a giardasis outbreak in Norway. Potential hosts for Giardia lamblia, Assemblage B include humans, horses, cattle, rabbits, coyotes, beaver, muskrat and dog (latter less likely).

#### 6 Recommendations

Based on the above conclusions, the following measures are recommended to reduce risk of drinking water related disease outbreaks using a multi barrier approach:

- In order to identify whether water quality guidelines for partial treatment, recreation (swimming), irrigation of crops and livestock watering are exceeded, five/ten times in thirty day water sampling should be conducted during the summer at critical sites, such as the community intake, Brassey Creek mouth, and stream sections that are highly frequented by livestock or are accessible and used for recreation and crop irrigation.
- The bacteria source tracking identified human and ruminant waste as sources for fecal bacteria in the stream. Failing septic systems / lagoons have been discovered in the area (Sheila Withrow, Northern Health, pers. com. (2004); residences in Brassey Creek watershed pers. com. during March 2007 meeting). Also livestock enter the river and tributaries from adjacent pasture land for water. In order to manage these sources, support rural residents to pursue funding options for septic system / lagoon upgrades and for the development of watering holes away from the river and its tributaries. Studies have shown that off-stream watering significantly reduce the time spent by livestock in riparian areas (Miner et al. 1992, Godwin and Miner 1996, Sheffield et al. 1997).
- In an effort to identify human waste contamination upstream of K4, a <u>sampling program should focus around potential sources in the East Kiskatinaw River</u>, such as residences around One Island Lake and Cutbank Lake, oil and gas camps and provincial parks.
- The detection of human infectious Giardia strains and high Giardia concentrations in the river and at the community intake underline the importance of a multi-barrier protection approach in the watershed. A parasite source tracking program is recommended to be continued and should focus on the identification of host species in the watershed through scat and concurrent water sampling. Specific attention should be given to host species for Giardia lamblia, Assemblage B (humans (sewage), beaver, muskrat, cattle, coyotes and rabbits), a human infectious strain detected in the river. In addition, a repeat of

the scat sampling program during wet and/or cool conditions. Lastly, the collection of <u>beaver scat</u> should be added to the program (using trapped beavers) to identify its role in parasite contamination of the Kiskatinaw River. This program can focus on areas with high wildlife and livestock densities.

Health Canada Drinking Water Guidelines for Giardia and Cryptosporidium are: "If the presence of viable, human-infectious cysts or oocysts is known or suspected in source waters, or if Giardia or Cryptosporidium has been responsible for past waterborne outbreaks in a community, a treatment and distribution regime and a watershed or wellhead protection plan (where feasible) or other measures known to reduce the risk of illness should be implemented" (http://www.hc-sc.gc.ca/ewh-semt/pubs/water-eau/protozoa/index-eng.php). Based on this direction, we advise to consider this study's results and recommendations regarding parasite monitoring, parasite source identification and management for the Kiskatinaw Watershed Management Plan review and formulation of next steps. Management activities should focus on septic system upgrades and development off-stream watering options in the Kiskatinaw River mainstem, Halfmoon and Oetata Creeks (just watering holes), Brassey Creek, and the East Kiskatinaw Arm (latter for sewage sources, once these have been identified). If beaver is confirmed as one of the main hosts for Giardia in the watershed, additional options for Giardia management may need to be contemplated. It may be most effective to pursue funding opportunities for these activities as a group or centrally by the watershed management committee.

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# **APPENDIX**

## **Appendix A**

Table A1: Data Quality Objectives for bacteria and parasite samples.

Sample Type	Parameter	Data Quality Acceptance Limit
Blank	Bacteria (CFU/100 mL)	< Five times the method detection limit (MDL)
	Parasites (cysts or oocysts/100 L)	< Five times the MDL
	Bacteria source tracking	No blank samples collected.
Duplicate	Bacteria (CFU/100 mL)	< ("+" or "-" 25% relative percent difference (applies for values > five times the MDL)
	Parasites (cysts or oocysts/100 L)	< ("+" or "-" 25% relative percent difference (applies for values > five times the MDL)
	Bacteria source tracking	Data not acceptable if one sample results in "absent", the other in "present".

Table A2: Field Blank Results for Bacteria and Bacteria Source Tracking: 2004-2007 (No blanks were collected for parasites and only a few for bacteria source tracking due to the high analysis cost.)

Parameter	Unit	MDL	Sample Date								
			Sep. 14, 2004	Oct. 25, 2004	Feb. 21, 2005	Apr. 18, 2005	Apr. 19, 2005	Aug. 16, 2005	Sep 6, 2006	Apr 23, 2007	May 7, 2007
Lab Data						11000		- 111	141	101	
Biological											
E.coli	CFU/100mL	1	<1	<1	N/S	<1	<1	<1	<1	10	<1
Enterococci	CFU/100mL	1	<1	<1	N/S	<1	<1	<1	<1	<1	<1
Fecal Coliforms	CFU/100mL	1	<1	<1	N/S	<1	<1	<1	<1	11	<1
Fecal Streptococci	CFU/100mL	1	8	<1	N/S	17	<1	<1	<1	<1	<1
Bacteria Source Tracking 1,2,3	.4										
Bacteroides			No	No	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Human fecal contamination			absent	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Ruminant fecal contamination			absent	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Pig fecal contamination			N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Horse fecal contamination			N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Dog fecal contamination			N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Elk fecal contamination			N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
1 = "present" = positive result for	or both markers										
2 = "absent" = no fecal contam		species det	ected								
3 = "potential" = positive result	for one marker o	nly (old mate	erial or caused by one	animal							
4 = "Yes" under bacteroides = I					not.						
MDL = Method Detection Limit											
N/S = Not sampled											
RPD = Relative percent differen	ce between dupl	icates									
N/A = RPD not applicable beca	use values < 5 x	the MDL									
grey shaded value = exceedance			Guideline for livestock	watering, the chronic	value for primary conta	act or for irrigation of	crops eaten raw				
bold italic = blank for this sam				•							
bold underlined = field duplica				sampling event and	> 5 x DL						

Table A3: Field Duplicate Results for Bacteria and Bacteria Source Tracking: 2004-2007 (No duplicates were collected for parasites).

Date		Samp	le Date and L	ocations		1											
Parameter	Unit	MDL	Sep. 14, 2	004		Apr. 19, 20	05		Aug. 16, 2	005		Sep. 05, 2	006		Apr. 23, 20	07	
			K1	K1	RPD	K1	K1	RPD	B1	B1	RPD	B2	B2	RPD	B1	B1	RPD
Lab Data										100		100		101			
Biological																	
E.coli	CFU/100mL	1	30	38	-23.53	20	40	-66.67	180	170	5.71	10	7	35.29	5	2	N/A
Enterococci	CFU/100mL	1	28	22	24.00	10	10	0.00	100	80	22.22	7	14	-66.67	30	30	0.00
Fecal Coliforms	CFU/100mL	1	38	36	5.41	30	40	-28.57	640	690	-7.52	10	7	35.29	5	2	N/A
Fecal Streptococci	CFU/100mL	1	76	82	-7.59	10	<10	N/A	100	110	-9.52	22	49	-76.06	280	30	161.29
Bacteria Source Tracking 1.2.3	3,4					30									.0, .00	725 - 814 - 3	
Bacteroides			faint	faint		Yes	N/S		Yes	Yes		Yes	Yes		Yes	Yes	
Human fecal contamination			absent	potential		absent	N/S	40	present	present	\	Absent	Absent		Absent	Absent	
Ruminant fecal contamination			absent	absent		absent	N/S		present	present		Absent	Absent		Absent	Absent	
Pig fecal contamination			N/S	N/S		absent	N/S		absent	absent	7	Absent	Absent		Absent	Absent	
Horse fecal contamination	30		N/S	N/S		N/S	N/S		absent	absent	ė.	Absent	Absent		Absent	Absent	
Dog fecal contamination			N/S	N/S		N/S	N/S		present	present		Absent	Absent		Absent	Absent	
Elk fecal contamination			N/S	N/S		N/S	N/S		absent	absent		Absent	Absent		Absent	Absent	
1 = "present" = positive result for	or both markers																
2 = "absent" = no fecal contam	ination from this	species de	tected														
3 = "potential" = positive result	for one marker of	only (old ma	terial or caused	by one animal		1											
4 = "Yes" under bacteroides =	bacteroides use	d to source	track are in gen	eral present. "I	No" = they ar	e not.											
MDL = Method Detection Limit			-			1											
N/S = Not sampled						10											
RPD = Relative percent differen	ce between dup	licates				II											
N/A = RPD not applicable beca	use values < 5	x the MDL															
grey shaded value = Exceedand	ce of the B.C. W	ater Quality	Guideline for li	vestock waterir	ng, the chroni	ic value for prima	ary contact or	for irrigation of	of crops eaten r	aw							
bold italic = blank for this sam	ple event shows	contamina	tion >5 x DL					1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1									
bold underlined = field duplication	ate Relative Per	cent Differer	nce (RPD) > 259	% for this samp	ling event an	d > 5 x DL											

## **Appendix B**

Table B1: Kiskatinaw River Bacteria, Bacteria Source Tracking and Parasite Data: 2004-2005

Date Darameter	He!4	MDL	Sep. 13-14							Oct. 25-26,	2004		_		-
arameter	Unit	MUL	Sample Loc K6	K5	K4	КЗ	K2	K1	K1 (Dup)	K6	К5	K4	КЗ	K2	K1
ield Data															
pecific Conductance	μS/cm		233	283	257	261	257	260	N/S	308	374	335	344	342	356
emp in Stream	°C NTU		8.1/8.0/9.0	7.5/8.1/8.1	6.5/7.0	7.2/7.0/7.4	7.2	7.9	N/S	-0.1/-0.2	-0.1/-0.3	0.0/-0.2	0.0/-0.3	0.6/0.1	0.1/0.
urbidity H	NIU		96.4/97.7 7.2	510/530 7.2	260/254 8.1	314/309 8.3	>1000	819/814 8.2	N/S N/S	11.4/9.61	59.2/61.4 7.3	33.6/34.8 8.5	40.3/36.9 8.5	69/67 8.6	73.3/76 N/S
Diss. Oxygen	mg/L		11.1	11.3	12.1	11.7	11.4	10.9	N/S	13.1	13.1	13.1	13.2	11.9	11.7
_ab Data	, i														
Biological															
coli	CFU/100mL	1	5	6	16	24	60	30	38	N/S	N/S	<1	<1	3	3
nterococci ecal Coliforms	CFU/100mL CFU/100mL	1	30 7	32 24	26 40	28 24	140 80	28 38	22 36	N/S N/S	N/S N/S	<1	3 <1	8	<1 8
ecal Streptococci	CFU/100mL	1	34	72	32	128	220	76	82	N/S	N/S	3	9	7	3
Bacteria Source Tracking 1.2.3.	4														
Bacteroides			N/S	N/S	N/S	N/S	No	faint	faint	N/S	N/S	N/S	N/S	Yes	N/S
Human fecal contamination Ruminant fecal contamination			N/S N/S	N/S N/S	N/S N/S	N/S N/S	absent absent	absent absent	potential absent	N/S N/S	N/S N/S	N/S N/S	N/S N/S	absent absent	N/S
ig fecal contamination			N/S	N/S	N/S	N/S	absent	N/S	N/S	N/S	N/S	N/S	N/S	potential	
forse fecal contamination			N/S	N/S	N/S	N/S	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
og fecal contamination			N/S	N/S	N/S	N/S	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Elk fecal contamination Parasites			N/S	N/S	N/S	N/S	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Cryptosporidium oocysts	oocysts/100L	K1:136,K2:131	N/S	N/S	N/S	<286.8	<131	136	N/S	N/S	N/S	<82.6	<89	<112.5	<85
Giardia cysts	cysts/100L	286.8	N/S	N/S	N/S	<286.8	1311.1	1224.3	N/S	N/S	N/S	82.6	267	225.1	170.
				781	1111				100		111				
Date			Feb. 21, 20	005						Apr. 06, 200	05			-	
Parameter	Unit	MDL	Sample Loc												
2043000000			K6	K5	K5 (dup)	K4	КЗ	K2	K1	K6	K5	K4	КЗ	K2	K1
ield Data															
Specific Conductance	μS/cm		N/S	381	N/S	515	230	523	N/S	N/S	N/S	N/S	N/S	N/S	295
emp in Stream urbidity	°C NTU		N/S N/S	0.0/0.5	N/S N/S	0.1/-0.5 21.9/20.8	0.0/-0.6 18.5/20.0	0.0/-0.6 19.1/25.4	N/S N/S	N/S N/S	N/S N/S	N/S N/S	N/S N/S	N/S N/S	0.3/1
H	MIO		N/S	7.5	N/S	7.5	7.5	7.4	N/S	N/S	N/S	N/S	N/S	N/S	7.98
Diss. Oxygen	mg/L		N/S	13.7	N/S	N/S	14	12.7	N/S	N/S	N/S	N/S	N/S	N/S	12
_ab Data															
Biological		10.00													
.coli Interococci	CFU/100mL CFU/100mL	1	N/S N/S	N/S N/S	N/S N/S	4 <1	6 <1	2 <1	3	N/S N/S	N/S N/S	N/S N/S	N/S N/S	N/S N/S	8 58
ecal Coliform	CFU/100mL	1	N/S	N/S	N/S	4	10	4	3	N/S	N/S	N/S	N/S	N/S	20
ecal Streptococci	CFU/100mL	1	N/S	N/S	N/S	<1	<1	1	4	N/S	N/S	N/S	N/S	N/S	60
Bacteria Source Tracking <sup>1,2,3,</sup>	4														
Bacteroides			N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Human fecal contamination Ruminant fecal contamination			N/S N/S	N/S N/S	N/S N/S	N/S N/S	N/S N/S	N/S N/S	N/S N/S	N/S N/S	N/S N/S	N/S N/S	N/S N/S	N/S N/S	N/S N/S
ig fecal contamination			N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
forse fecal contamination			N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
log fecal contamination			N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Elk fecal contamination Parasites			N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Cryptosporidium oocysts	oocysts/100L	K1:136,K2:131	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Giardia cysts	cysts/100L	286.8	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Date			Apr. 19, 20	005						Aug. 15-16,	2005		_		_
Parameter	Unit	MDL	Sample Loc							Aug. 10-10,	2000				
			K6	K5	K4	K3	K2	K1	K1 (Dup)	K6	K5	K4	K3	K2	K1
ield Data															
Specific Conductance	μS/cm		235	315	273	282	278	269	N/S	375					
emp in Stream urbidity	°C NTU		0.9/1.5 103/103	0.1/0.8 671/677	1.1/1.5 352/347	1.8/2.3 479/470	3.3/2.8	3.2/4.3 >1000/>1000	N/S N/S	10.4/11.3					
urbiaity H	INIU		8.2	8.3	8.2	4/9/4/0 N/A	×1000/×1000 8.2	\$1000/\$1000 8.2	N/S	14.1/13.8					
Diss. Oxygen	mg/L		12.8	12.8	12.9	12.9		11.5	N/S	10.4					
_ab Data															
Biological	oruu														
Ecoli Enterococci	CFU/100mL CFU/100mL	1	<10 <10	<10 10	<10 10	<10 10	<10 10	20 10	10	16 <1	21	12	14 23	42 22	120 40
ecal Coliforms	CFU/100mL	1	10	10	20	30	10	30	40	18	36	28	44	56	140
ecal Streptrococci	CFU/100mL	1	<10	<10	10	10	<10	10	<10	30	33	16	23	36	90
Bacteria Source Tracking 1,2,3,	4														
Bacteroides			N/S	N/S	N/S	N/S	Yes	Yes	N/S	N/S	N/S	N/S	Yes	Yes	Yes
Human fecal contamination Ruminant fecal contamination			N/S N/S	N/S N/S	N/S N/S	N/S N/S	potential absent	absent absent	N/S N/S	N/S N/S	N/S N/S	N/S N/S	absent absent		
rig fecal contamination			N/S	N/S	N/S	N/S	absent	absent	N/S	N/S	N/S	N/S	absent		absent
forse fecal contamination	- 1		N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	absent	absent	absent
og fecal contamination			N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	absent	absent	presen
Elk fecal contamination Parasites			N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	absent	absent	absent
Cryptosporidium oocysts	oocysts/100L	75-145	N/S	N/S	<75	<75	<120	<145	N/S	N/S	N/S	10	10	20	_
Giardia cysts	cysts/100L	75-145	N/S	N/S	825				N/S	N/S	N/S	150			
Giardia cysts = "present" = positive result fo	cysts/100L r both markers nation from this	s species dete	ected			600	1440	1015	N/S	N/S	N/S	150	230	150	
= postive result of != "absent" = no fecal contamin != "potential" = positive result fi != "Yes" under bacteroides = b #DL = Method Detection Limit						e not.									
= "absent" = no fecal contamir = "potential" = positive result fi = "Yes" under bacteroides = b IDL = Method Detection Limit						e not.									
= "absent" = no fecal contamir = "potential" = positive result fi = "Yes" under bacteroides = b						e not.									

Table B2: Kiskatinaw River Bacteria, Bacteria Source Tracking and Parasite Data: 2006-2007

Date			Sep. 04-06	6, 2006						Apr. 23, 20	07				
Parameter	Unit	MDL	mple Locati	ons						-					1
			K6	K5	K4	К3	K2	K1		K6	K5	K4	К3	K2	K1
Field Data				1 237		1075				100000					
Specific Conductance	μS/cm		N/S	N/S	421	420	388	379		N/S	N/S	N/S	N/S	N/S	281
Temp in Stream	°C		N/S	N/S	14.1	14 1	14 4	16.3: 16.4: 16.9		N/S	N/S	N/S	N/S	N/S	2.8. 2.8. 2
Turbidity	NTU		N/S	N/S	10; 12	N/S	32.9: 33.2	8.59: 8.19		N/S	N/S	N/S	N/S	N/S	>1000, >10
pH	NIU		N/S	N/S	8.2	6.89	8.12	7.4		N/S	N/S	N/S	N/S	N/S	8.17
			N/S	N/S	9.94	10.46	10.41	9.85		N/S	N/S	N/S	N/S	N/S	12.52
Diss. Oxygen	mg/L		11/1/5	14/5	9.94	10.46	10.41	3.00		IV/S	IV/S	11/15	11/15	11/5	12.52
Lab Data															
Biological															
E.coli	CFU/100mL	1	N/S	N/S	21	130	130	3		N/S	N/S	N/S	N/S	N/S	14
Enterococci	CFU/100mL	1	N/S	N/S	2	<u>6</u>	<u>61</u>	3		N/S	N/S	N/S	N/S	N/S	50
Fecal Coliforms	CFU/100mL	1	N/S	N/S	22	<u>130</u>	130	3		N/S	N/S	N/S	N/S	N/S	14
Fecal Streptococci	CFU/100mL	1	N/S	N/S	9	3	<u>15</u>	1		N/S	N/S	N/S	N/S	N/S	260
Bacteria Source Tracking 1,2,3	4				1000										
Bacteroides			N/S	N/S	Yes	Yes	Y	'es		N/S	N/S	N/S	N/S	N/S	Yes
Human fecal contamination			N/S	N/S	Potential	Potential	Pot	ential		N/S	N/S	N/S	N/S	N/S	absent
Ruminant fecal contamination			N/S	N/S	Yes	Yes	Yes or	Potential		N/S	N/S	N/S	N/S	N/S	potentia
Pig fecal contamination			N/S	N/S	Absent	Absent		r Potential		N/S	N/S	N/S	N/S	N/S	absent
Horse fecal contamination			N/S	N/S	Absent	Absent		sent		N/S	N/S	N/S	N/S	N/S	absent
Dog fecal contamination	1		N/S	N/S	Absent	Absent		sent		N/S	N/S	N/S	N/S	N/S	absent
Elk fecal contamination			N/S	N/S	Absent	Absent		sent		N/S	N/S	N/S	N/S	N/S	absent
Parasites				1,,,,	7.000.11	, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	700	T			1.00	1.00	100	1.0	aboont
Cryptosporidium oocysts	oocysts/100L	K1-136 K2-131	N/S	N/S	<10	10	70	<10		N/S	N/S	N/S	N/S	N/S	30.1
Giardia cysts	cysts/100L	286.8	N/S	N/S	25	60	90	20		N/S	N/S	N/S	N/S	N/S	241
Giardia Cysts	CyatariooL	200.0	TEG	100	23	00	30	20		1470	140	14/0	160	14/0	241
	1				-										
D-4-			MA 07 0	007						A 45 O	207				_
Date			May. 07, 2				12			Aug. 15, 20	JU1				4
Parameter	Unit	MDL	mple Locati		200		242			100					
	1 1		K6	K5	K4	K3	K2	K2 (Dup)	K1	K6	K5	K4	K3	K2	K1
Field Data															
Specific Conductance	µS/cm		N/S	N/S	173.1	177	178.5	N/S	178.6	N/A	N/S	N/S	N/S	N/S	N/A
Temp in Stream	°C		N/S	N/S	5.8, 5.7, 5.8	5.8, 5.8, 5.8	5.6, 5.6, 5.6	N/S	6.0, 6.0, 5.9	N/A	N/S	N/S	N/S	N/S	N/A
Turbidity	NTU		N/S	N/S	896, 912	>1000, >1000	E3, E3	N/S	N/S	N/A	N/S	N/S	N/S	N/S	N/A
pH	1		N/S	N/S	8.06	7.9	7.9	N/S	7.92	N/A	N/S	N/S	N/S	N/S	N/A
Diss. Oxygen	mg/L		N/S	N/S	13.48	11.31	11.4	N/S	13.65	N/A	N/S	N/S	N/S	N/S	N/A
Lab Data					150.00		1.57.5						10.0		
													-		
Biological	0511/400 1	1	N/S	N/S	10	70	<10	60	< 10	N/A	N/S	N/O	NVO	NUO	NI/A
E.coli	CFU/100mL											N/S	N/S	N/S	N/A
Enterococci	CFU/100mL	1	N/S	N/S	<10	10	<10	10	< 10	N/A	N/S	N/S	N/S	N/S	N/A
Fecal Coliform	CFU/100mL	1	N/S	N/S	20	70	<10	60	< 10	N/A	N/S	N/S	N/S	N/S	N/A
Fecal Streptococci	CFU/100mL	1	N/S	N/S	10	30	50	40	10	N/A	N/S	N/S	N/S	N/S	N/A
Bacteria Source Tracking 1,2,3	. 9	_													
Bacteroides			N/S	N/S	N/S	Yes	Yes	Yes	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Human fecal contamination			N/S	N/S	N/S	absent	absent	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Ruminant fecal contamination			N/S	N/S	N/S	absent	absent	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Pig fecal contamination			N/S	N/S	N/S	absent	present	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Horse fecal contamination			N/S	N/S	N/S	absent	absent	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Dog fecal contamination			N/S	N/S	N/S	absent	absent	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Elk fecal contamination			N/S	N/S	N/S	absent	absent	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S
Parasites					-	22011									1.00
Cryptosporidium oocysts	oocysts/100L	K1:136 K2:131	N/S	N/S	<10	<100	<75	N/S	<100	N/S	N/S	N/S	N/S	N/S	<28.6
Giardia cysts	cvsts/100L	286.8	N/S	N/S	<10	<100	<75	N/S	<100	N/S	N/S	N/S	N/S	N/S	3914.3
Oldraid Cyoto	Cyatar TOOL	200.0	140	14/0	~10	~100	713	14/0	~100	140	140	14/0	140	14/3	0014.0
1 = "present" = positive result for	or both markers							-			1		-		
2 = "absent" = no fecal contami			eted												1
				by one oni											
3 = "potential" = positive result						net		-							
4 = "Yes" under bacteroides = I	pacteroides use	a to source tr	ack are in ger	eral present.	No = they are	not.		-			-				-
MDL = Method Detection Limit															
N/S = Not sampled															
Dup = Duplicate Sample															4
grey shaded value = exceedance	e of the B.C. W	/ater Quality (	Guideline for In	estock wateri	ng or the chron	ic values for pr	imary contact	or for irrigation	of crops eat	en raw					
<b>bold italic</b> = blank for this sam					-	-	_	the state of the s	-						

Table B3: Brassey Creek Bacteria, Bacteria Source Tracking and Parasite Data: 2004-2007

Date			Sep. 13, 2			Oct. 25, 20	004		Feb. 21, 2	005		Apr. 06, 20	05		Apr. 18, 20	005		Aug. 26, 2	005		
Parameter	Unit	MDL	Sample Loc					-						4.700	1 10 10			7 3		-	
7			B3	B2	B1	B3	B2	B1	B3	B2	B1	B3	B2	B1	B3	B2	B1	B3	B2	B1	B1 (Dup)
Field Data																					
Specific Conductance	µS/cm		131	65	153	240	109	277	N/S	N/S	N/S	276	143	227	145	80	193	312	153	381	N/S
Temp in Stream	°C		5.3/5.9/5.9	5.4/5.5/5.0	6.0/5.6/6.2	0.2/0.1/-0.1	0.0/0.1/-0.2	0.0/0.1/-0.2	N/S	N/S	N/S	0.2/0.8	0.3/0.7	1.8/0.2	3.9/3.2	1.0/2.5	2.7/3.5	11.0/11.1	10.5/10.3	12.3/12.3	N/S
Turbidity	NTU		45.9/36.3	78.7/75.4	>1000	5.94/8.29	17.8/14.1	106/99.4	N/S	N/S	N/S	33.7/34.5	138/142	332/329	38.6/41.5	N/S	>1000/>1000	23.9/24.7	59.4/63.8	408/398	N/S
pH			6.8	6.6	8.2	7.7	8.6	8.4	N/S	N/S	N/S	8	7.9	8	7.9	7.5	8.1	7.9	7.7	8.3	N/S
Diss. Oxygen	mg/L		11.9	12	12.3	12.7	12.6	12.9	N/S	N/S	N/S	12.6	12.8	12.6	12.1	12.5	12.8	9.9	10.1	9.9	N/S
Lab Data																					
Biological	CFU/100mL		0.4	20	430			20	NUO	11/0	11/0	_			40		.40	44	00	400	470
E.coli Enterococci	CFU/100mL	1	24 14	32 42	120	<1	9 <1	30 4	N/S N/S	N/S N/S	N/S N/S	2 <2	16	4 <1	<u>16</u> <2	<u>4</u> <2	<10 10	14 48	98 120	180 100	170 80
Fecal Coliforms	CFU/100mL	1	30	98	500	4	7	30	N/S	N/S	N/S	2	30	32	22	2	<10	18	100	640	690
Fecal Streptococci	CFU/100mL	1	46	180	390	4	134	30	N/S	N/S	N/S	16	18	14	<2	8	20	58	120	100	110
Bacteria Source Tracking <sup>1,2,3</sup>			40	100	330		154	- 50	11/0	100	14.0	10	10	1.7		·	20	30	120	100	110
Bacteroides			N/S	N/S	No	N/S	N/S	No	N/S	N/S	N/S	N/S	N/S	Yes	N/S	N/S	No	N/S	N/S	Yes	Yes
Human fecal contamination			N/S	N/S	absent	N/S	N/S	absent	N/S	N/S	N/S	N/S	N/S	present	N/S	N/S	absent	N/S	N/S	present	present
Ruminant fecal contamination			N/S	N/S	absent	N/S	N/S	absent	N/S	N/S	N/S	N/S	N/S	present	N/S	N/S	absent	N/S	N/S	present	present
Pig fecal contamination			N/S	N/S	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	absent	N/S	N/S	absent	absent
Horse fecal contamination			N/S	N/S	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	absent	absent
Dog fecal contamination			N/S	N/S	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	absent	N/S	N/S	present	present
Elk fecal contamination			N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	absent	absent
Parasites	1 (400)		11/0	11/0	N/O	NIO	11/0	11/0	NVO	NIO	11/0	N/O	N/O	N/O	N/O	11/0	-00	N/O	NIG	-40	NVO
Cryptosporidium oocysts	oocysts/100L		N/S	N/S N/S	N/S	N/S	N/S N/S	N/S	N/S N/S	N/S N/S	N/S N/S	N/S	N/S	N/S N/S	N/S	N/S	<90	N/S	N/S	<10	N/S
Giardia cysts	cysts/100L	286.8	N/S	IV/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	1890.2	N/S	N/S	70	N/S
Date			Sep. 5-6, 2						Apr. 23, 20	007				1	May. 07, 2	007					
Parameter	Unit	MDL	Sample Loc																		
			B3	B2	B2 (dup)	B d/s	B 1km u/s	B1	B3A	B3 at Hwy	B2 N-Arm at	Trib into	B1	B1 (Dup)	B3A	1km u/s	B1				
						confluence	cutbank Rd.			crossing	Hwy	Brassey				cutbank Rd.					
Field Date			<u> </u>			of N&S-Arm					crossing										
Field Data	0/		100	200	1110	707	000	540	047	000	470	475.4	040		00.4	410.7	440.0				
Specific Conductance	μS/cm		408 13.2	306 12.2	N/S	535 10.5	620	540	217	293	176	175.1	240		80.4	146.7	148.9				
Temp in Stream Turbidity	°C NTU		23: 19.5	25: 26.7	N/S N/S	14.1: 14.2	11.3 21.8; 22.2	11.6 59.9: 58.7	35, 32	95, 95	0.6, 0.6, 0.6 749, 723	2.6, 2.6, 2.6 308, 302	2.2, 2.3, 2.3 >1000,>1000		59.5. 62.7	3.8, 3.8, 3.8	4.2, 4.2, 4.3 E3, E3				
pH	NIU		7.44	7.53	N/S	7.78	8.21	7.69	7.75	7.98	7.83	7.87	\$1000,\$1000 8.06		7.51	>1000,>1000 8.07	8.1				
Diss. Oxygen	mg/L		5.58	9.21	N/S	8.91	8.65	7.03	13.2	13.07	13.3	12.55	13		12.3	11.89	11.87		-		
Lab Data	nigre												10		12.0						
Riological																					
Biological E coli	CELI/100ml	1	19	10	7	7			25	2	4	15	5	2	32	90					
E.coli	CFU/100mL	1 1	<u>19</u> 10	10 7	7 14	7 4	<u>47</u>	19 4	25	2		15 30	5	2 30	32 <10	90	80				
	CFU/100mL CFU/100mL CFU/100mL		10	10 7 10	7 14 7	<u>7</u>	47 32	<u>19</u>	25 < 1 29	2 10 2	4 10 4	15 30 17	5 30 5	2 30 2	32 <10 34	90 <10 100					
E.coli Enterococci Fecal Coliform Fecal Streptococci	CFU/100mL CFU/100mL CFU/100mL	1		7	7 14 7 49	<u>7</u>	<u>47</u>	19 4	< 1	10	10	30	30	30	<10	<10	80 10				
E.coli Enterococci Fecal Coliform Fecal Streptococci Bacteria Source Tracking <sup>1,2,3,4</sup>	CFU/100mL CFU/100mL CFU/100mL	1	10 19 29	7 10 22	7 49	7 4 7 6	47 32 47 33	19 4 19 8	< 1 29 40	10 2 20	10 4 100	30 17 240	30 5 280	30 2 30	<10 34 70	<10 100 70	80 10 90 54				
E.coli Enterococci Fecal Coliform Fecal Streptococci Bacteria Source Tracking <sup>1,2,3</sup> Bacteroides	CFU/100mL CFU/100mL CFU/100mL	1	10 19 29 Yes	7 10 22 Yes	7 49 Yes	7 4 7 6 N/S	47 32 47 33 Yes	19 4 19 8 Yes	< 1 29 40 Yes	10 2 20 N/S	10 4 100 N/S	30 17 240 Yes	30 5 280 Yes	30 2 30 Yes	<10 34 70 Absent	<10 100 70 Yes	80 10 90 54 Potential				
E.coli Enterococci Fecal Coliform Fecal Streptococci Bacteria Source Tracking <sup>1,2,3</sup> . Bacteroides Human fecal contamination	CFU/100mL CFU/100mL CFU/100mL	1	10 19 29 Yes Absent	7 10 22 Yes Absent	7 49 Yes Absent	7 4 7 6 N/S N/S	47 32 47 33 Yes Potential	19 4 19 8 Yes	< 1 29 40 Yes Absent	10 2 20 N/S N/S	10 4 100 N/S N/S	30 17 240 Yes Absent	30 5 280 Yes Absent	30 2 30 Yes Absent	<10 34 70 Absent Absent	<10 100 70 Yes Absent	80 10 90 54 Potential Absent				
E.coli Entercocci Fecal Coliform Fecal Streptococci Bacteria Source Tracking 12.3 Bacteroides Human fecal contamination Ruminant fecal contamination	CFU/100mL CFU/100mL CFU/100mL	1	10 19 29 Yes Absent Absent	7 10 22 Yes Absent Absent	Yes Absent Absent	7 4 7 6 N/S N/S N/S	47 32 47 33 Yes Potential Yes	19 4 19 8 Yes Potential Yes	< 1 29 40 Yes Absent Absent	10 2 20 N/S N/S N/S	10 4 100 N/S N/S N/S	30 17 240 Yes Absent Absent	30 5 280 Yes Absent Absent	30 2 30 Yes Absent Absent	<10 34 70 Absent Absent Absent	<10 100 70 Yes Absent Absent	80 10 90 54 Potential Absent Absent				
E coli Enterococi Fecal Coliform Fecal Streptococi Bacteria Source Tracking 12.3 Bacteroides Human fecal contamination Ruminant fecal contamination Pig fecal contamination	CFU/100mL CFU/100mL CFU/100mL	1	10 19 29 Yes Absent Absent Absent	7 10 22 Yes Absent Absent Absent	Yes Absent Absent Absent	7 4 7 6 N/S N/S N/S	47 32 47 33 Yes Potential Yes Absent	19 4 19 8 Yes Potential Yes Absent	< 1 29 40  Yes Absent Absent Absent	10 2 20 N/S N/S N/S N/S	10 4 100 N/S N/S N/S N/S	30 17 240 Yes Absent Absent Yes	30 5 280 Yes Absent Absent Absent	30 2 30 Yes Absent Absent Absent	<10 34 70 Absent Absent Absent Absent	<10 100 70 Yes Absent Absent Absent	80 10 90 54 Potential Absent Absent				
E.coli Enterococi Fecal Coliform Fecal Streptococci Bacteria Source Tracking 1,2,3 Bacteria Source Tracking 1,2,3 Bacterides Human fecal contamination Ruminant fecal contamination Pig fecal contamination Horse fecal contamination	CFU/100mL CFU/100mL CFU/100mL	1	10 19 29 Yes Absent Absent Absent Absent	7 10 22 Yes Absent Absent Absent Absent	Yes Absent Absent Absent Absent Absent	7 4 7 6 N/S N/S N/S N/S N/S	47 32 47 33 Yes Potential Yes Absent	19 4 19 8 Yes Potential Yes Absent	Yes Absent Absent Absent Absent	10 2 20 N/S N/S N/S N/S N/S N/S	10 4 100 N/S N/S N/S N/S N/S	30 17 240 Yes Absent Absent Yes Absent	30 5 280 Yes Absent Absent Absent Absent	30 2 30 Yes Absent Absent Absent Absent	<10 34 70  Absent Absent Absent Absent Absent Absent	<10 100 70 Yes Absent Absent Absent Absent	80 10 90 54 Potential Absent Absent Absent Absent				
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E coli Enterococi Fecal Coliform Fecal Streptococci Bacteria Source Tracking¹ 2.3. Bacterioles Human fecal contamination Ruminant fecal contamination Pig fecal contamination Dog fecal contamination Dog fecal contamination	CFU/100mL CFU/100mL CFU/100mL	1	10 19 29 Yes Absent Absent Absent Absent	7 10 22 Yes Absent Absent Absent Absent	Yes Absent Absent Absent Absent Absent	7 4 7 6 N/S N/S N/S N/S N/S	47 32 47 33 Yes Potential Yes Absent	19 4 19 8 Yes Potential Yes Absent	Yes Absent Absent Absent Absent	10 2 20 N/S N/S N/S N/S N/S N/S	10 4 100 N/S N/S N/S N/S N/S	30 17 240 Yes Absent Absent Yes Absent	30 5 280 Yes Absent Absent Absent Absent	30 2 30 Yes Absent Absent Absent Absent	<10 34 70  Absent Absent Absent Absent Absent Absent	<10 100 70 Yes Absent Absent Absent Absent	80 10 90 54 Potential Absent Absent Absent Absent				
E-coli Enterococci Fecal Coliform Fecal Streptococci Bacteria Source Tracking <sup>1,2,3</sup> Bacterio Source Tracking <sup>1,2,3</sup> Bacterioides Human fecal contamination Pig fecal contamination Horse fecal contamination Dog fecal contamination Elk fecal contamination Plarasites	CFU/100mL CFU/100mL CFU/100mL	1 1 1	10 19 29 Yes Absent Absent Absent Absent Absent Absent	T 10 22 Yes Absent Absent Absent Absent Absent Absent	Yes Absent Absent Absent Absent Absent Absent Absent Absent	7 4 7 6 N/S N/S N/S N/S N/S N/S N/S N/S N/S	47 32 47 33 Yes Potential Yes Absent Absent Absent Absent	19 4 19 8 Yes Potential Yes Absent Absent Absent	Yes Absent Absent Absent Absent Absent Absent Absent	10 2 20 N/S N/S N/S N/S N/S N/S N/S N/S N/S	10 4 100 N/S N/S N/S N/S N/S N/S N/S N/S	30 17 240 Yes Absent Absent Yes Absent Absent Absent	30 5 280 Yes Absent Absent Absent Absent Absent Absent	30 2 30 Yes Absent Absent Absent Absent Absent Absent Absent	<10 34 70  Absent Absent Absent Absent Absent Absent Absent Absent	<10 100 70 Yes Absent Absent Absent Absent Absent Absent Absent Absent	80 10 90 54  Potential Absent Absent Absent Absent Absent Absent Absent				
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E coli Enterococi Fecal Coliform Fecal Streptococci Bacteria Source Tracking <sup>1,2,3</sup> Bacterioles Human fecal contamination Ruminant fecal contamination Pig fecal contamination Horse fecal contamination Elk fecal contamination Elk fecal contamination Parasites Cryptospondium oocysts Giardia cysts  1 = "present" = positive result fo 2 = "absent" = no fecal contamination 3 = "potential" = positive result fo	CFU/100mL CFU/100mL CFU/100mL GFU/100mL	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 286.8 3 3 5 5 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	Yes Absent Absent Absent Absent Absent Absent Control Absent Absent Absent Absent Absent Absent Absent	Yes Absent	Yes Absent	I	47 32 47 33 Yes Potential Yes Absent Absent Absent Absent	19 4 19 8 Yes Potential Yes Absent Absent Absent	< 1 29 40 Yes Absent Absent Absent Absent Absent Absent Absent Absent Acceptable Absent Absent	10 2 20 N/S	10 4 100 N/S N/S N/S N/S N/S N/S N/S N/S N/S	30 17 240 Yes Absent Absent Yes Absent Absent Absent Absent Absent Absent	30 5 280 Yes Absent Absent Absent Absent Absent Absent Absent Assent Assent Assent	30 2 30 Yes Absent Absent Absent Absent Absent Absent Absent Absent	<10 34 70  Absent	<10 100 70 Yes Absent	80 10 90 54  Potential Absent Absent Absent Absent Absent Absent Absent Absent				
E-coli Enterococi Fecal Coliform Fecal Streptococci Bacteria Source Tracking 1,2,3 Bacterioldes Human fecal contamination Ruminant fecal contamination Rig fecal contamination Dog fecal contamination Elk fecal contamination Parasites Cryptosporidium oocysts Giardia cysts  1 = "present" = positive result for 2 = "absent" = no fecal contamin 3 = "potential" = positive result for 4 = "Yes" under bacterioides = b	CFU/100mL CFU/100mL CFU/100mL GFU/100mL	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 286.8 3 3 5 5 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	Yes Absent Absent Absent Absent Absent Absent Control Absent Absent Absent Absent Absent Absent Absent	Yes Absent	Yes Absent	I	47 32 47 33 Yes Potential Yes Absent Absent Absent Absent	19 4 19 8 Yes Potential Yes Absent Absent Absent	< 1 29 40 Yes Absent Absent Absent Absent Absent Absent Absent Absent Acceptable Absent Absent	10 2 20 N/S	10 4 100 N/S N/S N/S N/S N/S N/S N/S N/S N/S	30 17 240 Yes Absent Absent Yes Absent Absent Absent Absent Absent Absent	30 5 280 Yes Absent Absent Absent Absent Absent Absent Absent Assent Assent Assent	30 2 30 Yes Absent Absent Absent Absent Absent Absent Absent Absent	<10 34 70  Absent	<10 100 70 Yes Absent	80 10 90 54  Potential Absent Absent Absent Absent Absent Absent Absent Absent				
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E-coli Enterococci Fecal Coliform Fecal Streptococci Bacteria Source Tracking 1,2,3, Bacterio Source Tracking 1,2,3, Bacterioles Human fecal contamination Pig fecal contamination Dog fecal contamination Dog fecal contamination Dog fecal contamination Elk fecal contamination Cryptosporidium occysts Giardia cysts  1 "present" = positive result fo 2 = "absent" = no fecal contamin 3 = "potential" = positive result fo 4 = "Yes" under bacteroides = b MDL = Method Detection Limit N/S = Not sampleb Upp = Duplicate Sample	CFU/100mL CFU/100mL CFU/100mL  oocysts/100L cysts/100L r both markers acteroides use	K1:136.K2:131 286.8 as species detectionly (old materal do source training to source training	10 19 29 Yes Absent Absent Absent Absent Absent Absent Absent absent control c	T 10 22 Yes Absent	Yes Absent Absent Absent Absent Absent Absent Absent N/S N/S	I	47 32 47 47 33 Yes Potential Yes Absent Absent Absent NVS NVS	19 4 19 9 Yes Potential Yes Absent Absent Absent Absent	< 1 29 40  Yes Absent Absent Absent Absent Absent <a href="#">4</a> 10	10 2 20 WS N/S N/S N/S N/S N/S N/S N/S N/S N/S N/	10 4 100 N/S N/S N/S N/S N/S N/S N/S N/S N/S	30 17 240 Yes Absent Absent Yes Absent Absent Absent Absent Absent	30 5 280 Yes Absent Absent Absent Absent Absent Absent Absent Assent Assent Assent	30 2 30 Yes Absent Absent Absent Absent Absent Absent Absent Absent	<10 34 70  Absent	<10 100 70 Yes Absent	80 10 90 54  Potential Absent Absent Absent Absent Absent Absent Absent Absent				
E coli Enterococci Facal Coliform Facal Streptococci Bacteria Source Tracking 1,2,3, Bacteria Source Tracking 1,2,3, Bacterides Human fecal contamination Ruminant fecal contamination Pig fecal contamination Dog fecal contamination Des fecal contamination Parasites Cryptosponidium occysts Giardia crysts  1 = "present" = positive result fo 2 = "absent" = no fecal contamin 3 = "potential" = positive result f 4 = "Yes" under bacteroides = b MDL = Method Detection Limit NS = Not sampled	CFU/100mL CFU/100mL CFU/100mL CFU/100mL  oocysts/100L cysts/100L r both markers action from thin or one marker acteroides use	K1:136,K2:131  K1:136,K2:131  286.8  s species detectionly (old material do source training to source training the source training training the source training trai	10 19 29 Yes Absent Absent Absent Absent Absent Absent ident Absent	T 10 22 Yes Absent	Yes Absent Absent Absent Absent Absent Absent Absent N/S N/S	I	47 32 47 47 33 Yes Potential Yes Absent Absent Absent NVS NVS	19 4 19 9 Yes Potential Yes Absent Absent Absent Absent	< 1 29 40  Yes Absent Absent Absent Absent Absent <a href="#">4</a> 10	10 2 20 WS N/S N/S N/S N/S N/S N/S N/S N/S N/S N/	10 4 100 N/S N/S N/S N/S N/S N/S N/S N/S N/S	30 17 240 Yes Absent Absent Yes Absent Absent Absent Absent Absent	30 5 280 Yes Absent Absent Absent Absent Absent Absent Absent Assent Assent Assent	30 2 30 Yes Absent Absent Absent Absent Absent Absent Absent Absent	<10 34 70  Absent	<10 100 70 Yes Absent	80 10 90 54  Potential Absent Absent Absent Absent Absent Absent Absent Absent				

Table B4: Oetata Creek, Halfmoon Creek, and Cutbank Lake Tributary Bacteria, Bacteria Source Tracking and Parasite Data: 2004-2007

Date			Sep. 13, 2	004	Oct. 25, 20	004	Feb. 21, 2	005	Apr. 18, 20	05	Aug. 16, 2	005	Sep 5, 2006	Apr 23, 2007	May 7, 2007	
Parameter	Unit	MDL	Sample Loc	ations					# 10 W - 1		V		220 0	1 -00-		
			H1	01	H1	01	H1	01	H1	01	H1	01	H2	H2	H2	C1
Field Data				- ALLES				100000				1111			22.22	
Specific Conductance	μS/cm		280	276	394	411	N/S	N/S	311	315	481	470	515	N/S	230	193.6
Temp in Stream	°C		6.8/7.1	6.3/5.6/6.2	0.8/0.1	0.0/0.5/-0.2	N/S	N/S	3.1/3.2	0.8/0.2	11.1/11.8	10.5/11.1	13.2	N/S	4.4	5.21, 5.6, 5.5, 5.
Turbidity	NTU		482/485	684/687	30.5/29.6	42/37	N/S	N/S	614/605	743/714	169/173	69.3/67.4	121; 119	N/S	>1000, >1000	5.21, 4.98
pH			7.4	7	8.6	8.5	N/S	N/S	8.2	8.2	8.3	8.3	7.67	N/S	8.06	7.4
Diss. Oxygen	mg/L		11.7	10.8	12.9	13	N/S	N/S	12.4	12.7	10.2	10.4	6.89	N/S	11.28	10.5
Lab Data																
Biological																
E.coli	CFU/100mL	1	70	22	5	<1	N/S	N/S	50	10	40	28	54	N/S	40	1
Enterococci	CFU/100mL	1	8	42	6	1	N/S	N/S	<10	<10	110	58	4	N/S	<1	<1
Fecal Coliforms	CFU/100mL	1	82	32	11	<1	N/S	N/S	40	10	44	30	54	N/S	40	1
Fecal Streptococci	CFU/100mL	1	82	46	21	9	N/S	N/S	10	<10	210	64	16	N/S	20	42
Bacteria Source Tracking 1.2.	3,4												-			
Bacteroides			N/S	N/S	No	N/S	N/S	No	N/S	N/S	N/S	N/S	Yes	N/S	Absent	N/S
Human fecal contamination			N/S	N/S	absent	N/S	N/S	absent	N/S	N/S	N/S	N/S	Absent	N/S	Absent	N/S
Ruminant fecal contamination			N/S	N/S	absent	N/S	N/S	absent	N/S	N/S	N/S	N/S	Yes	N/S	Absent	N/S
Pig fecal contamination	- 8		N/S	N/S	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S	Absent	N/S	Absent	N/S
Horse fecal contamination			N/S	N/S	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S	Absent	N/S	Absent	N/S
Dog fecal contamination			N/S	N/S	absent	N/S	N/S	N/S	N/S	N/S	N/S	N/S	Absent	N/S	Absent	N/S
Elk fecal contamination			N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	Absent	N/S	Absent	N/S
Parasites								-				2100000			101,000,000,000	
Cryptosporidium oocysts	oocysts/100L	K1:136,K2:131	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	<10	N/S	75	N/S
Giardia cysts	cysts/100L	286.8	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	N/S	<10	N/S	<75.0	N/S
1 = "present" = positive result f	or both markers															
2 = "absent" = no fecal contam	ination from this	species dete	ected													
3 = "potential" = positive result	for one marker of	only (old mate	erial or caused	by one anima				1								
4 = "Yes" under bacteroides =	bacteroides use	d to source to	ack are in ger	neral present. "	No" = they are	not.										
MDL = Method Detection Limit																
N/S = Not sampled																
Dup = Duplicate Sample																
grey shaded value = exceedan	e of the B.C. W	ater Quality	Guideline for li	vestock wateri	ng or the chron	nic values for p	rimary contact	or for irrigation	n of crops eate	n raw	1					
bold italic = blank for this san					100											
hold underlined = field duplic	ata Palativa Par	cont Difference	o (DDD) > 25	% for this came	oling event and	I S E V DI										

### **Appendix C**

Table C1: Results of bacteria source tracking analysis at the City of Dawson Creek raw water intake and at upstream sample sites in the Kiskatinaw mainstem and at the mouth of its tributaries

Sample Date	Kiskatinaw u/s of Halfmoon d/s of E-and W-Arm Confluence (K4)		Halfmoon d/s of Oetata		Kiskatinaw u/s of Brassey, d/s of Oetata and Halfmoon (K3)		Brassey Creek at the Mouth (B1)		Kiskatinaw down- stream (d/s) of Brassey (K2)		Dawson Creek Raw Water Intake (K1)		
	Bacteroi- des detected	Animal source marker(s) detected	Bacteroi- des detected	Animal source marker(s) detected	Bacteroi- des detected	Animal source marker(s) detected	Bacteroi- des detected	Animal source marker(s) detected	Bacteroi- des detected	Animal source marker(s) detected	Bacteroi- des detected	Animal source marker(s) detected	
September 13, 2004	Not sampled		Not sampled		Not sampled		No <sup>4</sup>	No	No <sup>4</sup>	No	Yes <sup>3</sup>	Human	
October 25, 2004	Not sampled		Not sampled		Not sampled		No <sup>6</sup>	No	Yes	Pig <sup>5</sup>	Not s	ampled	
April 06, 2005	Not sampled		Not sampled		Not sampled		Yes	Human, Ruminant	Not sampled		Not s	Not sampled	
April 18, 2005	Not sampled		Not sampled		Not sampled		No	No	Yes	Human	Yes	No	
August 15/16, 2005 2	Not sampled		Not sampled		Yes	No	Yes	Human, Ruminant Dog	Yes	Human, Ruminant	Yes	Dog Human Ruminant	
September 04-06, 2006	Yes	Ruminant Human <sup>3</sup>	Yes	Ruminant	Yes	Ruminant Human <sup>3</sup>	Yes	Ruminant Human <sup>3</sup>	Yes	Ruminant <sup>7</sup> Human <sup>3</sup> Pig <sup>7</sup>	Yes	Ruminant <sup>7</sup> Human <sup>3</sup> Pig <sup>7</sup>	
April 23, 2007	Not sampled		Not sampled		Not sampled		Yes	No	Not sampled		Yes	Ruminant <sup>3</sup>	
May 07, 2007	Not sampled		No No		Yes No		Yes <sup>3</sup>	No	Yes Pig <sup>5</sup>		Not sampled		

1=Analysed for human, ruminant and pig only. 2=Analysed for Human, ruminant, pig, dog, elk.3= Faint result. A faint result may be due to the following potential reasons: a) The method is at the edge of detection for this sample with respect to the amount of fecal matter for a particular species. b) Not every single organism may carry both markers in a herd and the detected fecal pollution was caused by one to two organisms. c) The fecal material inoculation is old and so the bacteria and DNA are degrading (bands can become smeared). 4=Samples were extremely silty and filtering difficult. Numerous pre-filtering necessary. 5=The level of confidence in a positive pig result is not as high as any of the other organisms because the pig primers for one of the markers have been noted to cross-prime with ruminant animal. 6=Water had yellow colour. Lab theorized that some component inhibited marker detection. 7=Samples from K1 and K2 could not be distinguished due to lost bottle marking. Human and ruminant were detected for both, ruminant once both markers, once faint. Pig marker was detected once, faint.

Table C2: Results of bacteria source tracking analysis in the Brassey Creek Waterdhed

Sample Date	Brassey Creek South Arm u/s most Agriculture (B3 + B3A)		Brassey Creek North Arm u/s most Agriculture (B2 + B2A)		Mouth of Tributary into Brassey Creek		Brassey Creek 1km u/s Cutbank Road		Brassey Creek at the Mouth (B1)	
	Bacteroi- des detected	Animal source marker(s) detected	Bacteroi- des detected	Animal source marker(s) detected	Bacteroi- des detected	Animal source marker(s) detected	Bacteroi- des detected	Animal source marker(s) detected	Bacteroi- des detected	Animal source marker(s) detected
September 13, 2004	Not sampled		Not sampled		Not sampled		Not sampled		No <sup>4</sup>	No
October 25, 2004	Not sampled		Not sampled		Not sampled		Not sampled		No <sup>6</sup>	No
April 06, 2005	Not sampled		Not sampled		Not sampled		Not sampled		Yes	Human, Ruminant
April 18, 2005 1	Not sampled		Not sampled		Not sampled		Not sampled		No	No
August 15/16, 2005 2	Not sampled		Not sampled		Not sampled		Not sampled		Yes	Human Ruminant Dog
September 04-06, 2006	Yes	No	Yes	No	Not sampled		Yes	Ruminant Human <sup>3</sup>	Yes	Ruminant Human <sup>3</sup>
April 23, 2007	Yes	No	Not sa	ampled	Yes Pig <sup>7,5</sup>		Not sampled		Yes	No
May 07, 2007	No	No	Not sa	ampled	Not sa	ampled	Yes No		Yes <sup>3</sup>	No

1=Analysed for human, ruminant and pig only. 2=Analysed for Human, ruminant, pig, dog, elk.3= Faint result. A faint result may be due to the following potential reasons: a) The method is at the edge of detection for this sample with respect to the amount of fecal matter for a particular species. b) Not every single organism may carry both markers in a herd and the detected fecal pollution was caused by one to two organisms. c) The fecal material inoculation is old and so the bacteria and DNA are degrading (bands can become smeared).
4=Samples were extremely silty and filtering difficult. Numerous pre-filtering necessary. 5=The level of confidence in a positive pig result is not as high as any of the other organisms because the pig primers for one of the markers have been noted to cross-prime with ruminant animal.

### Appendix D

#### Giardia (Cysts/100L) at Brassey Creek Mouth and in Headwaters

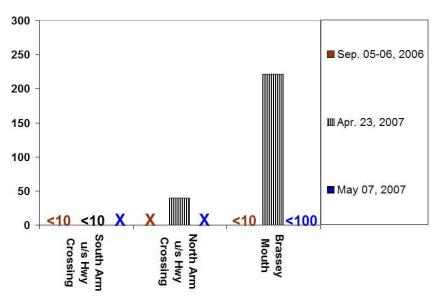


Figure D1: Giardia cyst counts in the headwaters of Brassey Creek (North Arm at Hwy, South Arm at Hwy) in comparison to the mouth in 2004/05. Bars with hatching represent samples collected during higher than average flows, bars without hatching represent samples collected during lower flows. (X= not sampled on the day matching the font colour; <# = less than indicated detection level)

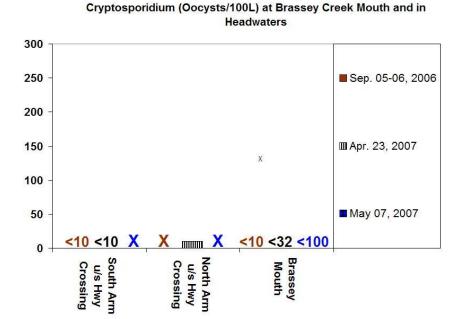


Figure D2: Cryptosporidium oocyst counts in the headwaters of Brassey Creek (North Arm at Hwy, South Arm at Hwy) in comparison to the mouth in 2004/05. Bars with hatching represent samples collected during higher than average flows, bars without hatching represent samples collected during lower flows. (X= not sampled on the day matching the font colour; <# = less than indicated detection level)

**Appendix E** 

Date of Collection	Animal Source	Scat Condition F=fresh; O=old; D=dusty	Parasite (G=giardia; C=cryptosporidiu m; NEIP=no evidence of intestinal	Scat collection within 30m wide, 1km long transect upstream of the following water sample sites:	Microsite	Distance to Water	
Sep 6/06	Elk	O-dry	NEIP	Kiskatinaw d/s Halfmoon	Forest	20 M	
Sep 6/06	Moose	O-D	NEIP	Kiskatinaw d/s Brassey	Grassy hill	18 M	
Sep 6/06	Bird	0	NEIP	Community Intake	100 M upstream from pump house	2.5 M	
Sep 5/06	Cow pattie	0	NEIP	Kiskatinaw u/s Halfmoon	Forested area		
Sep 6/06	Deer	0	NEIP	Kiskatinaw u/s Halfmoon	Forested area 3 M above stream	3 M	
Sep 6/06	Moose	0	NEIP	Halfmoon d/s Oetata	Forest	20 M	
Sep 6/06	Moose	0	NEIP	Kiskatinaw d/s Halfmoon	Forest	30 M	
Sep 6/06	Moose	0	NEIP	South Brassey u/s Hwy	Grass upstream	9 M	
Sep 6/06	Goose	F-dry	NEIP	Community Intake	100 M upstream from pump house on bank	2 M	
Sep 6/06	Deer?	F, O	С	Halfmoon d/s Oetata	Forest	15 M	
Sep 6/06	Deer	F but dry	С	Kiskatinaw d/s Brassey	Grassy hill	13 M	
Sep 6/06	Deer	F	С	Kiskatinaw d/s Brassey	Grassy hill	13 M	
Sep 6/06	Horse	F	С	South Brassey u/s Hwy	Uphill in grass/forested area	11 M	
Sep 5/06	Cow	F	С	Brassey Mouth	Grassy mound		
Sep 5/06	Cow	F	С	Kiskatinaw u/s Halfmoon	Forest	18 M	
Sep 6/06	Cow pattie	F	NEIP	Kiskatinaw d/s Halfmoon	Forest	8 M	
Sep 6/06	Deer	F	NEIP	Halfmoon d/s Oetata	Upstream up hill	12 M	
Sep 6/06	Goose	F	NEIP	Kiskatinaw d/s Brassey	Grass bank	13 M	
Sep 6/06	Goose	F	NEIP	Kiskatinaw d/s Halfmoon	Sand bar	15M	
Sep 6/06	Goose or swan	F	NEIP	Kiskatinaw d/s Brassey	Gravl/rock bank	1.5 M	
Sep 5/06	Horse	F	С	Brassey Mouth	Grassy mound	8	
Sep 5/06	Horse	F	NEIP	Brassey Mouth			
Sep 6/06	Horse	F	NEIP	Kiskatinaw d/s Halfmoon	Forest	10 M	
Sep 6/06	Moose	F	NEIP	Halfmoon d/s Oetata	Forest	20 M	
Sep 6/06	small rodent	F	NEIP	Halfmoon d/s Oetata	Riverbank	15 M	
		Dry exterior	1.00				
Sep 6/06	Cow pattie	Moist interior	С	Kiskatinaw d/s Brassey	Grassy area	11 M	
Sep 5/06	Cow	D (top), F	NEIP	Kiskatinaw u/s Halfmoon	East Side	3 M	
Sep 6/06	Elk?	D	NEIP	Kiskatinaw d/s Halfmoon	Sandy bank	11 M	
Sep 6/06	Moose	D	NEIP	South Brassey u/s Hwy	Across stream from site	5 M	
Sep 6/06	Beaver?		NEIP	South Brassey u/s Hwy	In water	0 M	
Sep 6/06	Bird		NEIP	Community Intake	100 M upstream from pump house on bank	2.5 M	