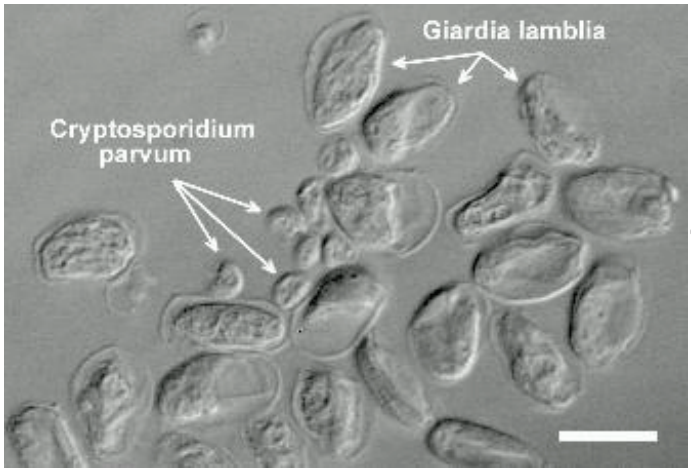
Conceptual Model For
Pathogens and Pathogen Indicators in the Central Valley and Sacramento-San Joaquin Delta

August 24, 2007



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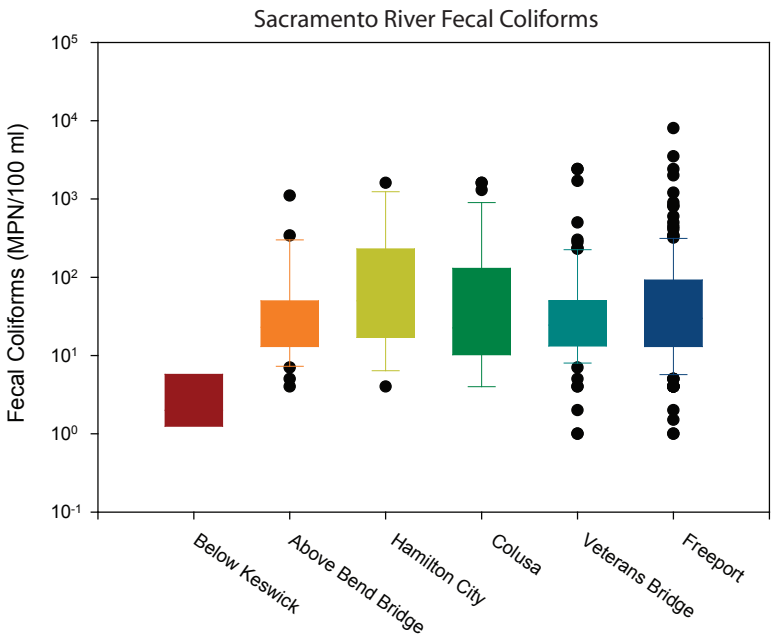

Prepared for:

US Environmental Protection Agency, Region IX

Central Valley Drinking Water Policy Workgroup

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CONCEPTUAL MODEL FOR

PATHOGENS AND PATHOGEN INDICATORS IN THE CENTRAL VALLEY AND SACRAMENTO-SAN JOAQUIN DELTA

FINAL REPORT

Prepared for

US Environmental Protection Agency, Region IX

Central Valley Drinking Water Policy Workgroup

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EXECUTIVE SUMMARY

This report presents a conceptual model of pathogens and indicators for pathogens in the Central Valley and the Sacramento-San Joaquin Delta. The conceptual model was based on previously collected data from a variety of monitoring programs over the last decade and can be used to direct future investigations to improve understanding of pathogen sources, transport, and impacts to drinking water quality. The underlying data used in this work was focused on fecal indicators (total coliforms, fecal coliforms, *Escherichia coli*, and other bacteria) that are widely used in lieu of data on pathogens. Pathogens, because of their typically low abundance in most waters used for drinking water supply, are much less abundant and therefore much harder to detect than indicator bacteria.

Evaluation of the data performed as part of the conceptual model development included mapping and plotting of available data by location and source type across the Central Valley and Delta. Although a large quantity of data was available for this analysis, the size of the Central Valley watershed, and complexity of fecal indicator and pathogen response, especially rapid dieoff, prevented a detailed quantitative analysis of indicator loads in the manner performed in prior work for organic carbon and nutrients (Tetra Tech, 2006a, 2006b). Of the known sources of coliforms into the waters of the Central Valley, it was found that wastewater total coliform concentrations for most plants were fairly low (<1000 MPN/100 ml). Coliform loads from the largest wastewater treatment plant in the Central Valley were substantially lower than from a canal draining a rapidly urbanizing watershed (NEMDC). In general, the highest total coliform concentrations in water (>10,000 MPN/100 ml) were observed near samples influenced by urban areas. Similar total coliform concentration data were not available for the San Joaquin Valley (the highest values were capped at ~2400 MPN/100 ml). However, *E. coli* data were not similarly capped, and for this parameter, comparably high concentrations were observed for waters affected by urban environments and intensive agriculture in the San Joaquin Valley. Finally, wetland sites in the Delta and the San Joaquin Valley had elevated concentrations of coliforms, likely as a result of the contribution of aquatic wildlife.

Fecal indicator data showed minimal relationships with flow rates, although most of the high concentrations were observed during the wet months of the years, possibly indicating the contribution of stormwater runoff.

Data on true pathogens was available primarily for *Cryptosporidium* and *Giardia* along the Sacramento River. Where monitored, these parameters were often not detected, and when detected, the concentrations were generally very low, typically less than one organism per liter. Given the flows of the Sacramento River and estimates of *Cryptosporidium* generation by mammals, typical loads flowing into the Delta from the Sacramento River are of the same order of magnitude as the number of organisms generated by a single calf (one of the most prolific producers of *Cryptosporidium*). This result could be caused by the presence of natural or artificial barriers/processes that limit transport to water, by the significant die off of oocysts that do reach the water, as well as limitations in the analytical detection of *Cryptosporidium* oocysts in natural waters.

Coliform bacteria are recognized to be less than ideal indicators for pathogens, and a wide variety of new indicators are under development although their applicability, generality, and cost remain concerns. For the foreseeable future, it appears that despite all limitations coliform measurements, these will remain the *de facto* standard for identifying the presence of pathogens. It is recommended that the Central Valley Drinking Water Policy Workgroup continue to support collection of data on coliforms for consistency with historical data, but also continually evaluate new analysis techniques for systematic application in the Central Valley.

Unlike chemical constituents analyzed as part of other conceptual models developed for the Central Valley Drinking Water Policy Workgroup, coliform indicators vary by orders of magnitudes over small distances and short time-scales. Accurate quantification of such parameters requires substantial data, which are often not available. A key observation of the source evaluation presented in this report is that fecal indicator levels are most responsive to sources and events in close proximity to the monitoring location, and that large scale modeling, with consideration of transport over many days, may be of limited benefit. While the large watershed modeling approach, i.e., on the scale of the Central Valley, is appropriate for somewhat stable parameters such as total dissolved solids and organic carbon, a fundamentally different approach is recommended for modeling fecal indicator loading, with an emphasis on relatively small watershed and surface water areas. Within these smaller areas of interest, individual sources, for example, wild and domestic animals, aquatic species, urban stormwater runoff, discharge from wastewater treatment plants, and agricultural point and non-point sources such as confined feeding lots and runoff, can be characterized with greater precision. Given the strength of the stormwater source, more detailed evaluation needs to be performed of the linkage between rainfall and coliform loads, with a view to develop management practices for minimizing the loading from stormwater.

Although, computer tools can be used to make more detailed estimates of bacterial loads in surface waters, the additional effort and data collection needed to make such

predictions meaningful has to be weighed against the collection of data on pathogens. In this respect, somewhat greater data collection, particularly in the San Joaquin Valley, is recommended for *Cryptosporidium* and *Giardia*. Sampling of *Cryptosporidium and Giardia* from potential sources such as wastewater, urban stormwater runoff and agricultural drainage will also help characterize the pathogen loads to surface waters. In general, sampling of San Joaquin and Sacramento River source waters for a wide range of potential pathogens including bacteria and viruses of concern, even on a limited scale and frequency, will provide valuable information on the health of this extremely critical water source.

CHAPTER 1.0
INTRODUCTION

Although source waters, particularly surface waters, are subject to treatment and disinfection before supply for municipal use, the presence of pathogens is a major concern, because of the potential of pathogen breakthrough into treated drinking water supplies. Pathogens are a concern also because the degree of treatment for drinking water is based on total coliform levels in source waters. Following implementation of the Long Term 2 Enhanced Surface Water Treatment Rule (LT2ESWTR), additional actions may be required based on *Cryptosporidium* levels detected in source waters. This report presents a conceptual model of pathogens in the waters of the Central Valley, summarizing existing data and identifying potential sources and transformations. The rivers of the Central Valley, particularly as they flow into the Sacramento-San Joaquin Delta (hereafter referred to as the Delta) are a vital source of water to more than 23 million people in the Southern California, Central Coast, and San Francisco Bay regions (CALFED Water Quality Program Plan, 2000). The tributaries of the Sacramento and San Joaquin rivers that originate in the Sierra Nevada Mountains generally have high quality water; however, as the tributaries flow into lower elevations, they are affected by urban, industrial, and agricultural land uses, natural processes, and a highly managed water supply system.

The Central Valley Drinking Water Policy Workgroup (CVDWPWG) is working with the Central Valley Regional Water Quality Control Board (Regional Board) to conduct the technical studies needed to develop a policy that will ensure reasonable protection to drinking water supplies in the Central Valley. The policy is initially focused on five categories of constituents: organic carbon, nutrients, salinity, bromide, and pathogens and indicator organisms. This conceptual model report is focused on pathogens and coliforms routinely monitored as indicators of pathogens. The geographic scope of this conceptual model is the Central Valley, comprising the Sacramento and San Joaquin River basins, and the Delta.

A variety of pathogens and indicators are currently regulated in finished drinking water supply as summarized in Table 1-1. These are legally enforceable standards that apply to public water suppliers. In addition to these standards other regulations

apply to ambient waters for other beneficial uses, specifically recreation and shellfish harvesting. These criteria are summarized in Table 1-2.

Epidemiological data does indicate that in some regions of the developed world (Australia, Canada) there are adverse health impacts from consumption of tap water (Payment et al., 1991, 1997; Hellard et al., 2001). However, these findings are not uniform, likely due to the presence of different pathogens in different areas as well as potential problem in survey techniques. Pathogens in source waters are a concern because of the potential risk of breaking through due to plant failure or operational errors during treatment. The wide variety of land uses in the watershed that can potentially serve as pathogen sources, such as urban land, grazing land, and confined animal feeding operations also indicate the potential presence of pathogens in source waters.

Unlike other constituents of concern evaluated in preceding work (organic carbon, Tetra Tech, 2006a; nutrients, Tetra Tech, 2006b; salinity, Harader et al., 2006), pathogens differ in that there is considerably less available information on their abundance, sources, and transport in the Central Valley. Most data that does exist is on indicator organisms. Furthermore, there is a great variety of potential pathogen species in source waters for which the analysis is not routinely done. Although many of these pathogens are not currently regulated, some are on US EPA's candidate contaminant list, and may be considered for future regulation. Yet others may draw public attention because of widespread outbreaks they cause (FDA, 2006), such as the recent infections due to the pathogenic strains of *E. coli* O157:H7 in California farms. For these reasons, this conceptual model evaluates data on fecal indicators, where quantification is possible, and also includes qualitative descriptions of currently regulated and emerging pathogens of concern to assist in long-term planning and data collection.

The objective of this report is to present a summary of relevant information on fecal indicators and pathogens in the Central Valley and Delta and to identify the importance of different sources, where the data allow. Recommendations are provided for future work, balancing the focus of indicator organisms, which are relatively easy to measure but not always predictive of pathogens, versus measurements of true pathogens.

Table 1-1 National Primary Drinking Water Regulations for Microorganisms and Related Contaminants (Source: USEPA, 2006)

Contaminant	MCLG[1] *(mg/L)2*	MCL or TT[1] *(mg/L)2*	Potential Health Effects from Ingestion of Water	Sources of Contaminant in Drinking Water
Cryptosporidium	zero	TT[2]	Gastrointestinal illness (e.g., diarrhea, vomiting, cramps)	Human and fecal animal waste
Giardia lamblia	zero	TT[2]	Gastrointestinal illness (e.g., diarrhea, vomiting, cramps)	Human and animal fecal waste
Heterotrophic plate count (HPC)	n/a	TT[2]	Heterotrophic plate count (HPC) has no health effects; it is an analytic method used to measure the number of bacteria that are common in water. The lower the concentration of bacteria in drinking water, the better maintained the water system is.	HPC measures a variety of bacteria that are naturally present in the environment
Legionella	zero	TT[2]	Legionnaires' disease, a type of pneumonia	Found naturally in water; multiplies in heating systems
Total Coliforms (including fecal coliform and *Escherichia coli*)	zero	5.0%[3]	Not a health threat in itself; it is used to indicate whether other potentially harmful bacteria may be present.	Coliforms are naturally present in the environment as well as feces. Fecal coliforms and *E. coli* only come from human and animal fecal waste.
Turbidity	n/a	TT[2]	Turbidity is a measure of the cloudiness of water. It is used to indicate water quality and filtration effectiveness (e.g., whether disease-causing organisms could be present). Higher turbidity levels are often associated with higher levels of disease-causing microorganisms such as viruses, parasites and some bacteria.	Soil runoff
Viruses (enteric)	zero	TT[2]	Gastrointestinal illness (e.g., diarrhea, vomiting, cramps)	Human and animal fecal waste

[1] Definitions:
Maximum Contaminant Level (MCL) - The highest level of a contaminant that is allowed in drinking water. MCLs are set as close to MCLGs as feasible using the best available treatment technology and taking cost into consideration. MCLs are enforceable standards.
Maximum Contaminant Level Goal (MCLG) - The level of a contaminant in drinking water below which there is no known or expected risk to health. MCLGs allow for a margin of safety and are non-enforceable public health goals.
Treatment Technique (TT) - A required process intended to reduce the level of a contaminant in drinking water.

[2] EPA's surface water treatment rules require systems using surface water or ground water under the direct influence of surface water to (1) disinfect their water, and (2) filter their water or meet criteria for avoiding filtration so that the following contaminants are controlled at the following levels:
***Cryptosporidium*:** (as of1/1/02 for systems serving >10,000 and 1/14/05 for systems serving <10,000) 99% removal.
***Giardia lamblia*:** 99.9% removal/inactivation
Viruses: 99.99% removal/inactivation
Legionella: No limit, but EPA believes that if *Giardia* and viruses are removed/inactivated, *Legionella* will also be controlled.
Turbidity: At no time can turbidity (cloudiness of water) go above 5 nephelolometric turbidity units (NTU); systems that filter must ensure that the turbidity go no higher than 1 NTU (0.5 NTU for conventional or direct filtration) in at least 95% of the daily samples in any month. As of January 1, 2002, turbidity may never exceed 1 NTU, and must not exceed 0.3 NTU in 95% of daily samples in any month.
HPC: No more than 500 bacterial colonies per milliliter.
Long Term 1 Enhanced Surface Water Treatment (Effective Date: January 14, 2005); Surface water systems or GWUDI (Groundwater under the direct influence of surface water) systems serving fewer than 10,000 people must comply with the applicable Long Term 1 Enhanced Surface Water Treatment Rule provisions (e.g. turbidity standards, individual filter monitoring, *Cryptosporidium* removal requirements, updated watershed control requirements for unfiltered systems).
Filter Backwash Recycling; The Filter Backwash Recycling Rule requires systems that recycle to return specific recycle flows through all processes of the system's existing conventional or direct filtration system or at an alternate location approved by the state.
Long Term 2 Enhanced Surface Water Treatment Rule (Published in January, 2006); applied to all systems. WTPs will be granted credit toward *Cryptosporidium* removal, depending on the filtration technology used: conventional treatment (includes softening), 3 log credit; direct filtration, 2.5 log credit; slow sand or diatomaceous earth filtration, 3.0 log credit; and alternative filtration technologies, determined by state. For systems required to sample *Cryptosporidium*, the average *Cryptosporidium* level determines the additional treatment required: < 0.075 oocysts/L, no additional treatment; 0.075 to <1.0 oocysts/L, 1 log or 1.5 log additional treatment; 1.0 to <3.0 oocysts/L, 2.0 log or 2.5 log additional treatment required, > 3.0 oocysts/L, 2.5 log or 3 log additional treatment required.

[3] More than 5.0% samples total coliform-positive in a month. (For water systems that collect fewer than 40 routine samples per month, no more than one sample can be total coliform-positive per month.) Every sample that has total coliform must be analyzed for either fecal coliforms or *E. coli* if two consecutive TC-positive samples, and one is also positive for *E.coli* fecal coliforms, system has an acute MCL violation.

Table 1-2 Pathogen Indicator Criteria for Beneficial Uses Other than Municipal Water Supply for Surface Waters (Source: USEPA, 2001)

Beneficial Use	Indicator Organism	Criteria[1]
Recreation	*E. coli*	Geometric mean of 126 CFU per 100 mL, based on not less than 5 samples equally spaced over a 30-day period; no sample should exceed a one-sided confidence limit (CL) calculated using the following as guidance: designated bathing beach - 75% CL; moderate use for bathing - 82% CL; light use for bathing - 90% CL; infrequent use for bathing - 95% CL; based on a site-specific log standard deviation, or if site data are insufficient to establish a log standard deviation, then using 0.4 as the log standard deviation.
	Enterococci	Geometric mean of 33 CFU per 100 mL, based on not less than 5 samples equally spaced over a 30-day period; no sample should exceed a one-sided confidence limit (CL) calculated using the following as guidance: designated bathing beach - 75% CL; moderate use for bathing - 82% CL; light use for bathing - 90% CL; infrequent use for bathing - 95% CL; based on a site-specific log standard deviation, or if site data are insufficient to establish a log standard deviation, then using 0.4 as the log standard deviation. Geometric mean of 200 CFU per 100 mL, based on not less than 5 samples equally spaced over a 30-day period and no more than 10 percent of the samples exceeding 400 CFU per 100 mL during any 30-day period. [Note: fecal coliform criteria are used by many states; however, EPA recommends the use of the E. coli and enterococci criteria.]
	Fecal coliform	Geometric mean of 200 CFU per 100 mL, based on not less than 5 samples equally spaced over a 30-day period and no more than 10 percent of the samples exceeding 400 CFU per 100 mL during any 30-day period. [Note: fecal coliform criteria are used by many states; however, EPA recommends the use of the *E. coli* and enterococci criteria.]
Shellfish harvesting	Total coliform	Geometric mean of 70 MPN per 100 mL, with not more than 10 percent of the samples taken during any 30-day period exceeding 230 MPN per 100 mL.
	Fecal coliform	Median concentration should not exceed 14 MPN per 100 mL with not more than 10 percent of the samples taken during any 30-day period exceeding 43 MPN per 100 mL.

[1]Definition
MPN/100 ml = Most probable number per 100 ml
CFU/100 ml = Colony forming units per 100 ml

The contents of the chapters that follow are briefly summarized below:

- Chapter 2 presents an overview of regulated and emerging pathogens in water supplies, their routes of transmission, and the role of indicator species.
- Chapter 3 summarizes the data on pathogens and indicator organisms that have been reported in the Central Valley. This includes information collected by the Central Valley Drinking Water Policy Workgroup as well as other sources.
- Using the data summarized in Chapter 3, Chapter 4 provides an estimate of loads of pathogen indicators from key sources in and near the Delta.
- Chapter 5 identifies recommendations for data collection to better understand the sources of pathogens and highlights the key findings of the analysis presented in this conceptual model.

CHAPTER 2.0
PATHOGENS OF CONCERN IN AQUATIC SYSTEMS AND DRINKING WATER SUPPLIES

Although the majority of pathogen-caused disease outbreaks in the United States occur as a result of ingestion during recreation or through consumption of contaminated food, the presence of pathogens in surface waters, albeit at low levels, is a subject of continuing interest for water suppliers because of the possibility of pathogens not being fully removed during treatment. In the widely studied *Cryptosporidium* contamination episode in Milwaukee in 1993 (MacKenzie et al., 1994; Eisenberg et al., 2005), the drinking water treatment plant in question had been meeting operational targets with respect to indicator coliforms, and yet managed to result in the infection of nearly 400,000 people, about 25% of the population supplied by the utility. Because of the potential failure of treatment and disinfection to remove and/or inactivate pathogens, there is a great deal of interest in minimizing, and at the very least, characterizing the abundance of pathogens in ambient waters used for municipal supply.

This chapter provides an overview of pathogens in aquatic systems, including a description of routes of transmission, a summary of known pathogens, and the role of indicators widely used in lieu of actual data on pathogens.

2.1 MECHANISMS OF WATERBORNE PATHOGEN TRANSMISSION

Many pathogens of concern in source waters for drinking water supply are spread by the fecal-to-oral route. In recent years there has been greater focus on pathogens that can infect both humans and animals, and for which the pathogens may originate from natural sources other than sewage. Figure 2-1 is a schematic of the processes by which pathogens may cause human infection. This schematic shows that pathogens may originate in six potential sources: domestic animals during grazing or in confined animal facilities, wild animals in natural lands, aquatic avian and mammalian species that inhabit surface waters, human water-contact recreational activity, urban stormwater runoff, and wastewater discharge. Pathogens that have animal hosts

(zoonoses) can be transported from the watershed to source waters from natural lands, from grazed lands, and from confined animal facilities. Some animal hosts can be aquatic species (such as geese) and contribute pathogens and other bacterial loads directly to water bodies. Stormwater runoff from urban/rural areas that contains organisms shed by domestic pets, birds, rodents and sewage spills that enter storm drain systems can also contaminate source waters. Municipal wastewater can also be a source because of the presence of pathogens in the feces of infected humans. The *Cryptosporidium* episode in Milwaukee cited above, the source of the pathogens was found to have been wastewater (Eisenberg et al., 2005). Once in the ambient environment, pathogens often dieoff at varying rates (depending on the organism), although in some instances they can survive and even reproduce in sediments. In most instances, the pathogens in source waters are removed by filtration or membranes or destroyed by disinfection techniques. Infections in humans may arise from pathogens that break through into treated drinking water or from external sources such as food ingestion and ingestion of untreated water during recreation.

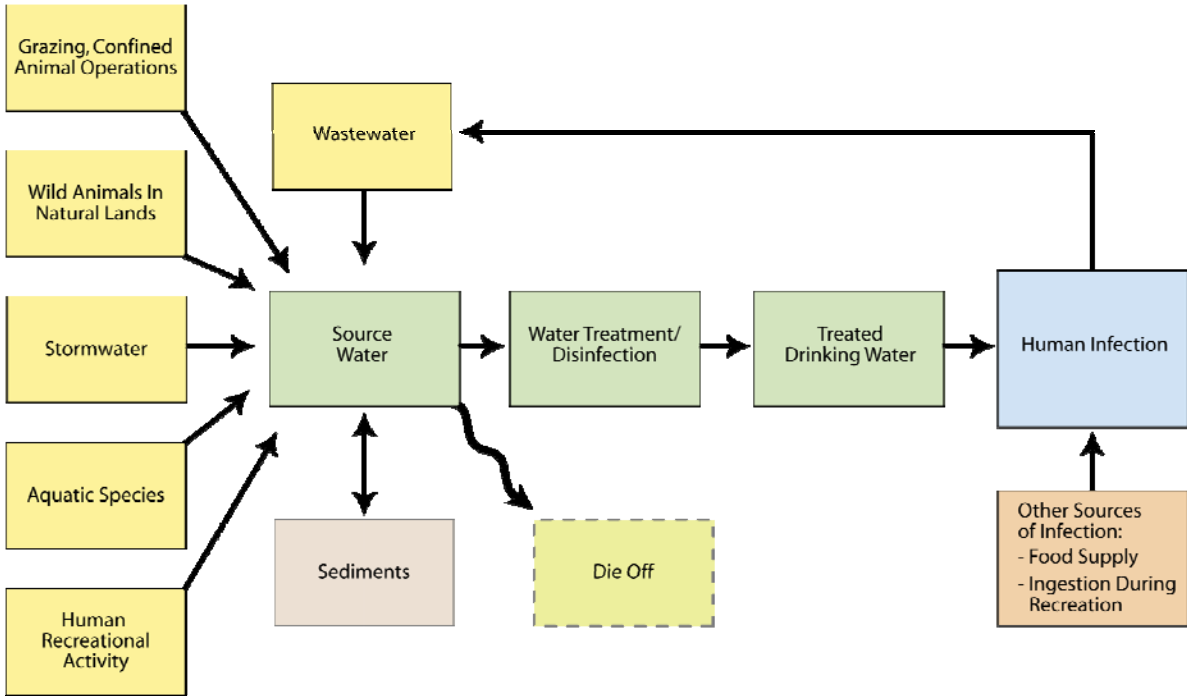

Figure 2-1 Schematic of pathogen contamination of drinking waters.

Several pathogens have emerged as concerns to drinking water in recent years because of their newly recognized pathogenesis (e.g. *Helicobacter pylori*) or because of their involvement in outbreaks of waterborne diseases (Crittenden et al. 2005). Many of these organisms are opportunistic pathogens that can grow in natural water and soil environment and are transmitted through water and therefore are of concern to drinking water. Some of them are now considered by EPA as candidate contaminants for as part of the second update of the candidate contaminant list (CCL2) (US EPA, 2005). Table 2-1 lists these emerging microbial contaminants. Of

these candidate contaminants, cyanobacteria and the toxins they release have been discussed in the conceptual model for nutrients (Tetra Tech, 2006b).

Table 2-1. Emerging Microbial Contaminants Identified in USEPA's Candidate Contaminant List 2 (Source: USEPA, 2005).

Microbial Contaminants	
Adenoviruses	Microsporidia (*Enterocytozoon* & *Septata*)
Aeromonas hydrophila	*Helicobacter pylori*
Caliciviruses	Echoviruses
Coxsackieviruses	*Mycobacterium avium intracellulare* (MAC)
Cyanobacteria (blue-green algae), other freshwater algae, and their toxins	

2.2 FATE OF PATHOGENS IN THE AMBIENT ENVIRONMENT

Organisms in general require energy and carbon sources for metabolism. Different organisms generally have their preferred temperature range, pH range and oxygen level for survival. For many pathogenic organisms that have reservoirs in human and warm blooded-animal intestines, warm temperatures are preferred. These parasites also rely on their hosts for energy and carbon sources and prefer anaerobic conditions. Although they may die off rapidly once excreted by their host, they may survive under warm, wet conditions. Many organisms of interest can also exist in an environmentally resistant stage. For example, viruses can exist as virons, bacteria can exist as spores, cystlike forms that are resistant to extreme environmental conditions, and protozoa can exist in the environmentally resistant stages as cysts and oocysts outside their hosts.

2.3 BACTERIA THAT CAUSE DISEASE

Bacteria are single celled organisms ranging in size from 0.1-1 µm. There are two groups of bacteria in surface waters: the autochthonous group and allochthonous group. Most bacteria of concern to public health are allochthonous. Allochthonous bacteria prefer the warm environment of intestines of warm-blood animals, and spend only a limited portion of their life span in natural waters. As shown schematically in Figure 2-1, they are carried to natural waters through contamination, rainfall and runoff. Outside the intestinal environment, these bacteria tend to die off. The presence of allochthonous bacteria is generally an indicator of stormwater, wastewater or fecal contamination.

There are a variety of bacterial pathogens that cause waterborne disease in humans. Some are classical pathogens that have been known to affect human health for a long time including *Vibrio cholerae*, *Salmonella spp.*, and *Shigella spp*. Some pathogens have become concerns to human health in recent years, including pathogenic *Escherichia coli* (*E. coli)*, *Yersinia enterocolitica*, and *Campylobacter jejuni*. Many of these organisms live inside humans or animals and can be transmitted through human

or animal wastes. Most of these organisms have been related to recent waterborne disease outbreaks (summarized in Table 2-2). Key characteristics of these organisms are summarized below. Some emerging bacterial pathogens, including *Helicobacter pylori* and *Mycobacterium avium intracellulare* listed under US EPA CCL2, are gaining increasing interest from a human health standpoint and are also discussed below (Table 2-3, sections 2.3.4 - 2.3.8).

Table 2-2. Summary of bacteria recently associated with waterborne disease (After Crittenden et al. 2005)

Organism or Bacteria	Size, µm	Motile	Health effects in healthy persons	Evidence of waterborne pathway
Enteropathogenic *E. coli* (EPEC)	0.3-0.5 × 1-2	No	Traveler's diarrhea	Numerous waterborne outbreaks
Enteroaggregative *E. coli.* (EaggEC)	0.3-0.5 × 1-2	No	Childhood diarrhea and diarrhea among immunocompromised	Numerous waterborne outbreaks
Enteroinvasive *E. coli* (EIEC)	0.3-0.5 × 1-2	No	Childhood diarrhea	Numerous waterborne outbreaks
Enterohemorrhagic *E. coli* (EHEC)	0.3-0.5 × 1-2	No	Bloody diarrhea, occasionally hemolytic uremic syndrome	Six waterborne outbreaks, notably Cabool, MI and Walkerton, Ontario
Enterotoxigenic *E. coli.* (ETEC)	0.3-0.5 × 1-2	No	Traveler's diarrhea	Numerous waterborne outbreaks
Yersinia enterocolitica	0.3-0.5 × 1-2	No	Fever, abdominal pain, gastroenteritis with diarrhea and vomiting	Outbreaks associated with contaminated spring water
Campylobacter jejuni	0.3 × 1-5	Yes	Diarrhea, abdominal pain, nausea, fever, malaise	Numerous outbreaks

Table 2-3. Summary of bacteria of emerging concern in drinking water (After Crittenden et al. 2005)

Organism	Size, µm	Motile	Normal Habitat	Health effects in healthy persons	Modes of transmission	Evidence of waterborne pathway
Legionella pneumophila	0.3-0.9 × 2-20	Yes	Warm water	Legionnaire's disease, Pontiac fever	Aerosols	Outbreaks associated with warm-water aerosols
Aeromonas hydrophila	0.3-1.0 × 1.0-3.5	Yes	All fresh waters	Gastroenteritis (controversial)	Water exposure	Drinking contaminated water; water in open wounds
Helicobacter pylori	0.3-1.0 × 1.0-3.5	Yes	Human stomach and upper intestinal tract	Dominant cause of peptic and duodenal ulcers; associated with gastric carcinoma	Fecal-oral	Some indirect evidence
Mycobacterium avium intercellulare	0.2-0.6 ×1-10	No	Soil, dust, water, and animals	Lung infection, fatigue	Inhalation or ingestion	Increasing incidence of gastrointestinal illness in AIDS patients
Pseudomonas aeruginosa	0.5-0.8 × 1.5-3	Polar flagellum	Inhabitant of soil and water; opportunistic human pathogen	Infections of urinary tract, respiratory system, and soft tissue; dermatitis, bacteremia, and systemic infections	Contact with compromised tissue	Only for immunocompromised patients

2.3.1 PATHOGENIC *ESCHERICHIA COLI*

Escherichia coli is a facultative, anaerobic, gram-negative rod shaped bacteria that lives in the gastrointestinal tract of warm blooded animals. The presence of *E. coli* normally is beneficial to the host through the suppression of harmful bacteria and synthesis of vitamins. However, some strains of *E.coli* are pathogenic. There are several groups of *E.coli* that have been identified to be pathogenic including: the enterotoxigenic *E. coli* (ETEC), enteroinvasive *E. coli* (EIEC), enterohemorrhagic *E.coli* (EHEC), enteropathogenic *E. coli* (EPEC), and enteroaggregative *E.coli* (EaggEC).

ETEC impacts human through generating toxins that result in diarrhea without invading the epithelial wall. EPEC also impacts human through the production of a toxin but by invading the epithelial wall, which can result in inflammation and fever. EIEC does not produce toxins, but can penetrate and grow in the epithelial cells of the intestine, which causes severe inflammation, fever and bacillary dysentery. EaggEC is less studied but is generally thought to adhere to intestine without inflammation or fever. EHEC, which includes the well known *E. coli* O157:H7 implicated in recent *E. coli* outbreaks from California produce (FDA, 2006), produces a Shiga-like toxin. *E. coli* O157:H7 is unique in that some patients, particularly children, can develop hemolytic uremic syndrome, leading to destruction of red blood cells and occasional kidney failure.

The presence of *E. coli* is generally an indicator of fecal contamination, either by human waste water or animal wastes. A recent case of waterborne outbreak occurred in Walkerton, Ontario during May to June 2000, was attributed to the contamination of Enterohemorrhagic *E.coli* in a drinking well by farm manure. Among the 1,346 cases reported, about half were infected with *E.coli* O157:H7.

2.3.2 *CAMPYLOBACTER*

Campylobacter is a gram-negative, motile, rod shaped bacteria. *Campylobacter* can be found in natural waters throughout the year. The presence of *Campylobacter* is not directly related to indicators of fecal contamination. *Campylobacter jejuni* is commonly present in the gastrointestinal tract of healthy cattle, pig and poultry. The organism survives better in cold temperatures. When stressed, it can enter a state that can still be transmitted to animals. *Campylobacter* is a leading cause of bacterial gastroenteritis in U.S., followed by salmonellosis, shigellosis, and *E. coli* O157:H7 infection. Virtually all human illness associated with *Campylobacter* is caused by one species, *Campylobacter jejuni*, but 1% are caused by other species. *Campylobacter* infection in some rare cases may be followed by Guillain-Barre Syndrome (GBS), a form of neuromuscular paralysis. Strains of *Campylobacter* have developed resistance to antibiotics, resulting in clinical treatment difficulty.

2.3.3 *YERSINIA ENTEROCOLITICA*

Yersinia enterocolitica is a small rod-shaped, gram-negative bacterium and is not a normal flora in the human gastrointestinal tract. *Yersinia enterocolitica* is able to grow in cold temperature but dies off under normal room temperature. It also prefers neutral to alkaline pH. *Yersinia enterocolitica* is an invasive pathogen that penetrates

the intestinal lining and enters lymph nodes, causing systemic infection. *Yersinia enterocolitica* releases enterotoxins that cause yersiniosis, a disease exhibiting pain and intestine inflammation. *Yersinia enterocolitica* can live in different animals including pigs, rodents, rabbits, sheep, cattle, horses, dogs, and cats. *Yersinia enterocolitica* has been detected widely in environmental and food sources such as lakes, ponds, meats, and milk.

2.3.4 *LEGIONELLA PNEUMOPHILA*

Legionella pneumophila is a motile, rod-shaped, gram-negative, aerobic bacterium. *Legionella* grows in warm aquatic environments with rust, algae, and organic particles. The organism can survive in tap water at room temperature for over a year. Among the many species and serogroups, the strain responsible for Legionnaires' disease is the *Legionella pneumophila* serogroup. *Legionella pneumophila* is transmitted to humans via inhalation of aerosols, particularly under high relative humidity since it allows the organism to survive longer. *Legionella pneumophila* can move into a host cell, reproduce and eventually lyse the cell. Keeping *Legionella pneumophila* out of the water distribution system is an effective way to prevent spread of the disease. Incidences of *Legionella pneumophila* infections are generally associated with air conditioning equipment and hot-water supplies.

2.3.5 *AEROMONAS HYDROPHILA*

Aeromonas hydrophila occur as gram-negative, motile, non-spore forming, facultatively anaerobic rods or coccobacilli. These organisms are heat sensitive, destroyed easily by pasteurization. *Aeromonas hydrophila* inhabits fresh or sea water and is found widely in different sources of water. *Aeromonas hydrophila* is of particular concern to immunocompromised hosts. *Aeromonas* causes diarrheal illness through production of heat-sensitive enterotoxins. *Aeromonas hydrophila* is opportunistic pathogen that is ubiquitous in the environment that can potentially be transmitted through contaminated drinking water but also can be transmitted through foods that come in contact with contaminated water.

2.3.6 *HELICOBACTER PYLORI*

Helicobacter pylori is a spiral-shaped, gram-negative rod that is motile. *Helicobacter pylori* lives in the stomach and duodenum of human and animals. It is thought to be the most common cause of gastritis in humans (Crittenden et al., 2005). *Helicobacter pylori* adheres to the plasma membranes of surface epithelial cells, which protects it from the immune system. It is found that *Helicobacter pylori* infection increases the risk of gastric cancer. *Helicobacter pylori* is transmitted through fecal-oral route and is considered a potential waterborne pathogen.

2.3.7 *MYCOBACTERIUM AVIUM COMPLEX*

Mycobacterium avium complex (*M. avium* and *M. intracellulare*) are an aerobic, non-spore-forming, non-motile family of bacilli. *Mycobacterium avium* complexes (MAC) are abundant in soil, food and water. Members of MAC are able to grow in water samples without any additional substrate and are resistant to chlorination. They can grow over a wide range of temperature and salinities. The cell walls of these organisms contain high level of lipid and can colonize the wet surfaces in water

systems. MAC organisms attack healthy individuals and result in serious tuberculosis-like infections for immuno-compromised individuals. MAC organisms have been found in water, food and soil samples from patient care sites.

2.3.8 *PSEUDOMONAS AERUGINOSA*

Pseudomonas aeruginosa is a gram-negative, aerobic motile rod of the Pseudomonadaceae family. *Pseudomonas aeruginosa* is one of the most vigorous, fast-swimming bacteria seem in pond water samples. *Pseudomonas aeruginosa* are usually found in soil and water. The organism has a wide array of virulence factors. Most *Pseudomonas* infections are both invasive and toxinogenic. *Pseudomonas* adhere to the epithelial cells of upper respiratory tract and other epithelial cells as well (e.g., the gastrointestinal tract). *Pseudomonas aeruginosa* is resistant to antibiotics and can be waterborne. However, it is uncertain whether drinking water is an important means for transmitting of the organism.

2.4 VIRUSES OF CONCERN

Viruses have simpler structure than other organisms. A basic virus consists of a core of nucleic acid (either DNA or RNA) surrounded by a protein coat. Viruses are parasites that depend on the host for resources and reproduction. Viruses can survive outside the host for a longer time than bacteria since it has no metabolic needs. Viruses are small in size and are more host-specific. Enteric viruses shed by animals and humans are abundant in untreated surface waters. Water treatment plants are typically effective in removing viruses, however inadequate treatment can results in viruses passing through to drinking water. Some viruses that have been associated with waterborne disease are those that affect the gastrointestinal tract system such as polio, coxsackie, echo-virus, and more recently identified viruses such as rota-, calici-, and adeno-viruses (Crittenden et al. 2005). Most of these viruses are known to be present in wastewater effluent and are transmitted through the fecal-oral route. Among these, adenoviruses, caliciviruses, coxsackie viruses, and echoviruses are candidate contaminants in CCL2 identified in Table 2-1.

2.4.1 POLIOVIRUS

Poliovirus is the virus that causes poliomyelitis which was a common disease fifty years ago in U.S. Poliovirus is an enterovirus that is highly contagious. It is transmitted through the fecal-oral route. The virus has three serotypes. Type I is the most common cause of disease in human. Today the use of vaccines has greatly reduced the incidence of the disease.

2.4.2 HEPATITIS

Hepatitis is a virus that causes liver inflammation and sometimes leads to jaundice. The virus is classified into Types A, B, C, D, E and G. All these viruses can cause acute viral hepatitis. The hepatitis B, C, D, and G viruses can also cause chronic hepatitis. Type A and E are infectious hepatitis that are transmitted through the fecal-oral route. Type C, D, and G are serum hepatitis that are transmitted through direct exposure of the blood serum. Hepatitis A is a well documented waterborne disease and it is widespread worldwide. To date no outbreaks of Hepatitis E have been reported in the U.S. due to effective water treatment.

2.4.3 ROTAVIRUS

Rotaviruses are the most important viruses causing diarrhea worldwide. Rotavirus was estimated to contribute to 30 to 50 percent of severe diarrhea disease in humans. Rotavirus group A, B, and C are particularly of interest for human gastroenteritis. Among these, the group A subtypes 1, 2, 3 and 4 are the leading cause of severe diarrhea in infants and children. The rotaviruses are round particles about 80nm in diameter. Persons with gastroenteritis caused by rotavirus can excrete large numbers of viruses (10^8 to 10^{10} infective units per ml of stool) and the infective dose is on the order of 10 to 100 infectious units. The virus can be transmitted through fecal-oral route and via contaminated food and water.

2.4.4 ADENOVIRUSES

Adenoviruses are large, non-enveloped viral particles. Adenoviruses are the only human enteric viruses with double-stranded DNA. Adenoviruses 40 and 41 are thought to infect human intestines. Adenoviruses are more commonly found in patients with gastroenteritis. Person to person transmission is presumably the principal mechanism for infection. Neither food nor water has been demonstrated as a means of transmission, although adenoviruses have been reported as possible agents in waterborne outbreaks and have been found in raw and finished drinking water.

2.4.5 HUMAN CALICIVIRUSES

The Norwalk and Norwalk-like viruses (*Norovirus*) are groups of single stranded RNA nonenveloped viruses in *Caliciviridae* family that cause acute gastroenteritis. *Noroviruses* have been associated with many waterborne and foodborne outbreaks. The infectious doses are low, with perhaps 10 to 100 particles constituting a 50% infectious dose. Some instances associated with contaminated food have also been shown to be related to contaminate drinking water as well.

2.5 PROTOZOANS OF CONCERN

The protozoans are a group of unicellular, non-photosynthetic organisms. Protozoans are usually motile. Several protozoans are transmitted by the fecal-oral route. Protozoans associated with waterborne disease mainly include *Entamoeba histolytica, Entamoeba dispar, Giardia lamblia,* and *Cryptosporidium parvum* (Crittenden et al. 2005). Parasitic protozoa can live in resting and living stages. In resting stages, cysts, oocysts and spores can survive outside the host. Inside the host, in living stages, trophozoites (*Giardia*) and sporozoites (*Cryptosporidium*) are released and grow.

2.5.1 *ENTAMOEBA*

Entamoebas are single-celled parasitic amoeboid protozoa. *Entamoebas* can exist in two forms: trophozoites measuring 20 to 40 µm in diameter and sporozoites measuring 10 to 16 µm in diameter. In recent years, it was found that *Entamoebas histolytica* and *Entamoebas dispar* are the two species that cause invasive and noninvasive infections in humans. Infection mostly occurs in the digestive tract. *Entamoebas* infect mostly human and other animals such cats and dogs. The *Entamoeba* are transferred through fecal contamination of drinking water, but also through direct contact with contaminated hands or objects.

2.5.2 *GIARDIA*

Giardia is a single-celled, microscopic parasite that can be found in intestinal linings of a wide range of animals (in trophozoite form) and in feces of infected individuals and in contaminated water (in cyst form). *Giardia* can exist in the environment in sporozoite form (a cyst) or a trophozoite. As cysts, *Giardia* is about 11 to 14 µm long and 7 to 10 µm wide. *Giardia* can survive a wide range of temperature from ambient temperature of fresh water to internal temperature of animals. Among the many species of *Giardia*, *Giardia lamblia* (also known as *Giardia intestinalis*) infects humans. Infection by *Giardia lamblia* causes diarrhea and abdominal pain. *Giardia lamblia* has been found in wastewater and have also been related to several outbreaks

of waterborne disease. *Giardia* infection is transmitted by the fecal-oral route. The infectious dose is low: ingestion of 10 cysts has been reported to cause infection. In the U.S., nearly 20,000 or more cases of giardiasis were reported each year during 1998 to 2002 (Hlavsa et al. 2005) as shown in Figure 2-3. The number of reported cases peaked in June to October, suggesting a relationship to recreational activities.

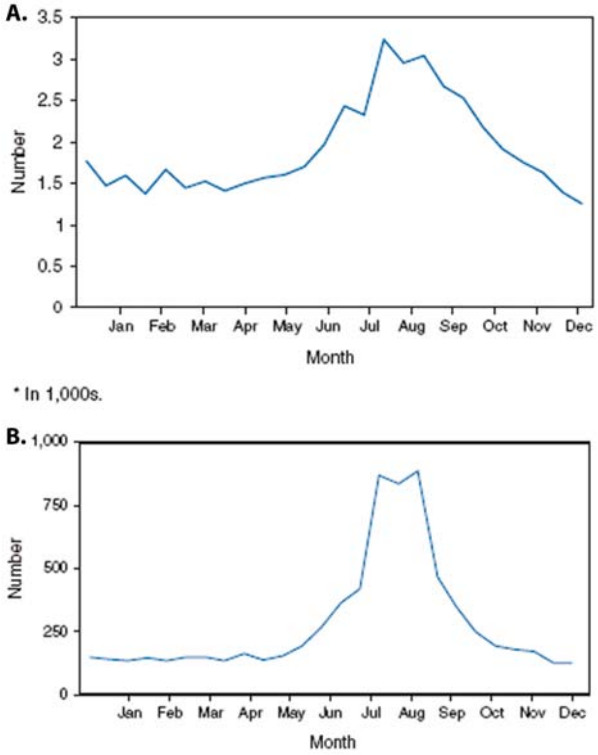

Figure 2-3 Incidence of Giardiasis (upper panel) and Cryptosporidiosis (lower panel) in the U.S, by month between 1998 and 2002 (Source Hlavasa et al., 2005). Giardiasis numbers are reported in thousands.

2.5.3 *CRYPTOSPORIDIUM*

Cryptosporidium spp. are single-celled, intestinal parasites that infect human and a variety of animals. *Cryptosporidium* can infect epithelial cells of the intestine wall and be excreted in feces as oocysts. An oocyst is approximately 3 to 7 μm in diameter.

Cryptosporidium is primarily transmitted through fecal-oral route with infection occurring as a result of the ingestion of oocysts in contaminated food or water. Two species of *Cryptosporidium*, *Cryptosporidium hominis* and *Cryptosporidium parvum*, are most relevant to humans. *Cryptosporidium hominis* only infects humans while *Cryptosporidium parvum* can infect a wide range of animals including humans. Symptoms of cryptosporidiosis, a disease caused by ingestion of *Cryptosporidium*, include diarrhea, stomach cramps, upset stomach, and slight fever. The infectious dose of *Cryptosporidium* is relatively low. The range of the dose-to-cause infection in 50 percent of the subjects (ID50) is reported to range from 9 to 1,042 oocysts (Okhuysen et al., 1999). *Cryptosporidiosis* is a major cause of gastrointestinal illness

around the world. Outbreaks of cryptosporidiosis have been reported in several countries, most notably the waterborne outbreak in Milwaukee in 1993 with more than 400,000 people infected (MacKenzie et al., 1994; Edwards, 1993). In the U.S., there were usually two-to-three thousand cases reported annually between 1998 and 2002 (Figure 2-3 from Hlavsa et al., 2005). For 2002, cryptosporidiosis incidence ranged from 0.2 cases to 9.5 cases per 100,000 people. Numbers of cryptosporidiosis cases reported by illness onset are five-fold to six-fold higher during June-October than other months (Hlavsa et al., 2005).

Cryptosporidium has a wide range of hosts including cows, goats, sheep, pigs, horses, dogs, cats and wild animals. When infected, these animals can shed large numbers of oocysts in the environment. In watersheds with grazed lands in proximity to water bodies, infected cattle may be a source of oocysts in surface waters.

Cryptosporidium oocysts once shed by the animals can be retained by soil particles and vegetation or retained in soil matrix during infiltration, with only a portion of the oocysts being transported to surface waters through runoff. In the aquatic environment, *Cryptosporidium* oocysts can be aggregated to larger particles and are subject to settling, grazing, and inactivation due to temperature and solar radiation (Brooks et al. 2004). Oocysts are subject to grazing by rotifers, cilitates and other predators that can ingest these organisms. Temperature is one of the most important factors regulating the fate of *Cryptosporidium* oocysts in the environment (King and Monis, 2006). *Cryptosporidium* oocysts can persist in the environment for longer than a year at temperatures below 15°C (Jenkins et al. 2002). However, a slight increase of temperature to 20 or 25 °C significantly increases oocysts inactivation rates. Very low temperature (below freezing) also affects oocyst survival. Ocysts are also susceptible to inactivation via solar radiation, and when present on soil surfaces or near the surface of waters, can be inactivated quickly due to solar exposure. Moisture is another factor that influences the survival of *Cryptosporidium* oocysts in the environment. Desiccation of soil in arid environments increases rates of oocysts inactivation.

2.6 MEDIAN DOSE TO CAUSE INFECTION

Median infectious dose, N50, is usually used as a measure of the "typical" dose required to infect humans. N50 varies significantly among different microorganisms. The infection dose for some pathogenic *E. coli* is relatively high ($> 10^6$) , however low infection dose of generally ranging from 10-100 has been observed for *E. coli* O157:H7 in various studies (Mead and Griffin, 1998; Hancock et al. 1997; U.S.FDA 2002). Some other microorganisms also require substantially low doses to cause infection. For example, the median dose of *Campylobacter jejuni* is around 1,000. *Giardia lamblia* only requires a median dose of 10 and median dose of *Cryptosporidium parvum* range from 10 to 100. Adenovirus 4 has the lowest dose of less than 10. *Rotavirus* also has a median dose less than 10. Figure 2-4 shows the median dose of organisms required in drinking water to cause infection. The median doses highlight the highly infectious nature of some organisms, the detection of which is very challenging at these low levels.

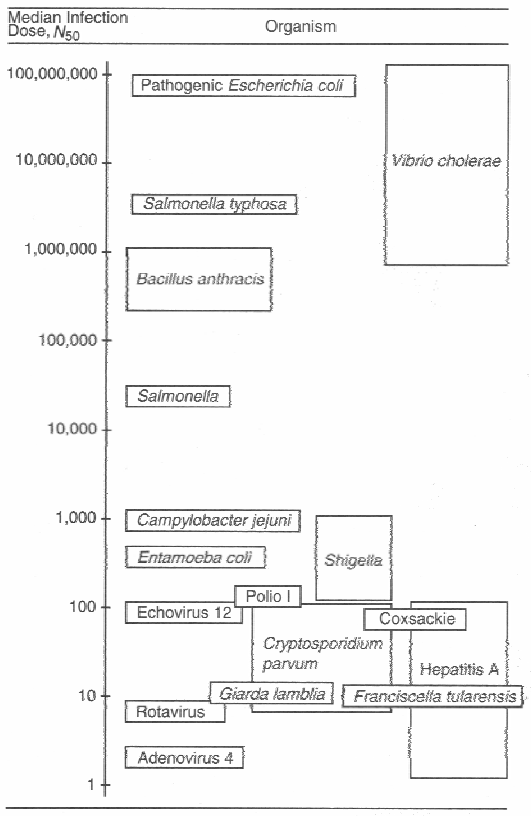

Figure 2-4 Median dose of organisms required in drinking water to cause infection (Source: Crittenden et al., 2005).

2.7 TREATMENT EFFICIENCY

Water treatment processes that are focused on the removal of particulates, such as coagulation/ filtration and membranes are generally effective at removing pathogens. Coliform removal rates of 97 to 99.5% can be expected in a properly operated treatment plants (Viessman and Hammer, 1993) with prior chemical pretreatment. Organisms that are motile, such as protozoa, may be more resistant to removal by these mechanisms.

Disinfection of bacteria pathogens can be achieved effectively through either chemical oxidation using chlorine or ozone, or through exposure to ultraviolet light (Table 2-4). Viruses can also be removed effectively through chlorine or ozone oxidation. The treatment of protozoans is more challenging, as cysts and oocysts of protozoans cannot be fully removed by sand filtration and are resistant to chemical disinfection. *Giardia*, was found to be resistant to chlorine disinfection. *Cryptosporidium* is even more resistant to chlorine than *Giardia*. However, disinfection using ultraviolet light was found to be effective in inactivating *Giardia* (Stolarik et al. 2001) and *Cryptosporidium* (Craik et al., 2001).

Table 2-4. Effectiveness in disinfection by five most common disinfectants

Pathogen	Free chlorine	Combined chlorine	Chlorine dioxide	Ozone	Ultraviolet light
Bacteria	Excellent	Good	Excellent	Excellent	Good
Viruses	Excellent	Fair	Excellent	Excellent	Fair
Protozoa	Fair to Poor	Poor	Good	Good	Excellent

2.8 ROLE OF INDICATOR SPECIES

Some bacterial indicator species have been used for over a century for detecting of pathogens because they are easier to detect using traditional culture methods and their presence in the environment often correlates with the presence of pathogens. Some of the most commonly used indicators are total coliforms, fecal coliforms, and fecal streptococci/enterococci. These organisms are abundant in the gastrointestinal tract of humans and other animals and are commonly used as indicators of fecal contamination. Most historical data on pathogens in surface waters and treated waters are derived from data on indicators species.

Although in recent years there is agreement that the indicator organisms do not fully capture the likely presence of pathogens, there is no agreement on alternative indicators that may be used instead. In a recent study by the National Academy of Sciences (NAS, 2004), it was found that no single indicator was suitable for all purposes. Rather a flexible indicator or indicator system was recommended for use for each circumstance. For example, the suitability of the coliform group as indicator of pathogens is complicated by the environmental behavior of viruses and protozoa. Viruses are known to be able to survive longer than members of coliform group in the environment due to their lack of metabolic activity. Protozoa such as *Giardia* and *Cryptosporidium* are known to exist in environment as cysts or oocysts, which can survive longer in the environment and are resistant to chemical disinfection. Therefore, the absence of coliforms in water does not necessary guarantee the absence of pathogenic viruses and protozoa. For warm waters, indicators such as *Clostridium perfringens* and other sulfite-reducing clostridia may also be used. *Clostridium perfringens* is an anaerobic, Gram-positive, spore-forming, rod shaped bacterium. The spores of *Clostridium perfringens* can survive for decades. The persistence of *Clostridium perfringens* spores in environment suggests that they could be good indicators for protozoa. Other indicators such as coliphages can also be useful components in a system of indicators.

A review of the literature suggests that the search for an ideal pathogen indicator, one that is accurate, as well as relatively easy to measure, will continue into the foreseeable future. For the time being, it appears that fecal indicators will remain a common source of information on the potential occurrence of microbial contamination in surface waters.

2.9 SUMMARY

A wide variety of pathogens may be present in surface waters. The fact that they often occur at low numbers and are living organisms with different degrees of survivability

in the ambient environment, makes it challenging to measure them either directly or indirectly through the use of indicator organisms. Despite advances in water treatment and pathogen monitoring across the U.S., outbreaks of waterborne disease nonetheless continue to occur. Municipal water suppliers need to be vigilant particularly because of the episodic, rather than continuous, nature of pathogen contamination and the potential for drinking water pathogens to impact sensitive populations such as the young, the elderly, as well as immunocompromised individuals.

CHAPTER 3.0
OVERVIEW OF DATA USED FOR ANALYSIS

The conceptual model for pathogens is based on a database compiled by the Drinking Water Policy Workgroup in 2004-2005. Data in the database originate from a variety of agricultural, urban, point source, and surface water monitoring programs and intake locations throughout the watersheds of the Sacramento and San Joaquin Rivers. The database was supplemented with data from the Natomas East Main Drainage Canal (NEMDC) Studies (MWQI, 2005; Zanoli, personal communication), North Bay Aqueduct Sampling, and the United States Geological Survey's (USGS) National Water Information System (NWIS) database. This report includes an appendix that contains a listing of all stations with pathogen and related data, including the number of data points for each parameter and the period over which sampling was conducted. This listing can be used as a reference to identify the quantity of relevant data associated with specific stations in the database, particularly for future work to identify patterns at greater spatial detail than presented in this report.

This chapter provides an overview of the data contained in the database, notably the forms measured, the quantity and spatial distribution of the data, and the concentrations observed at various stations. The plots in this chapter present an informative snapshot of the available data, and set the stage for semi-quantitative analyses in the next chapter. The geographic scope of the conceptual model, including key watersheds, stream reaches, important sampling locations, and current and future water supply intakes, has been presented in previous reports (Tetra Tech, 2006b) and is not repeated here.

As noted in the introduction, the vast majority of data on pathogens are not true measurements of pathogens, but indicator species that are likely to be present whenever fecal contamination is present. This feature is common to all pathogen monitoring programs nationally. The indicator species data that are contained in the database include total coliforms, fecal coliforms, and *E. coli*. Much of the evaluation that follows is limited to these constituents, although where possible, data on pathogens, notably, *Cryptosporidium* and *Giardia*, are presented.

3.1 OVERVIEW OF CONCENTRATION DATA OF INDICATOR SPECIES

Maps of median concentration data for total coliforms, fecal coliforms, and *E. coli* are presented in Figures 3-1 through 3-3[1]. The maps show the spatial intensity of data collection as well as the actual levels observed in the Central Valley and in the Delta. In general, there are significantly more total coliform data available than fecal coliform or *E. coli* data. The total coliform data show low concentrations in the Sacramento River basin, especially upstream of the Sacramento urban area. Concentrations are generally higher near Sacramento as well as in the San Joaquin basin, indicating the potential sources of coliforms from urban areas and the San Joaquin watershed. Concentrations shown for the San Joaquin River and its tributaries may be biased low because the sampling reported data only up to ~2400 MPN/100 ml, and a large number of stations exceeded this limit. Fecal coliform measurements are very limited and some high concentrations are observed above Sacramento and in the San Joaquin Valley. *E. coli* values show some similarities with total coliforms, except that some of the highest values are found in the middle portion of the San Joaquin River. *E. coli* concentrations decline with proximity to the Delta. *E.Coli* concentrations in the Delta are somewhat higher than in the San Joaquin River and the Sacramento River, again indicating the importance of in-Delta sources.

[1] Coliform concentration data are reported as most probable number per 100 ml (MPN/100 ml) or as colony forming units per 100 ml (CFU/100 ml). The differences in units relate to differences in the analytical methods used. However, the numerical values are generally correlated, and for the purpose of this chapter, data with either unit will be used interchangeably for maps and plots. For the Natomas East Main Drainage Canal, where measurements of total coliforms using both methods exist, the data show a good correlation ($r^2 = 0.65$).

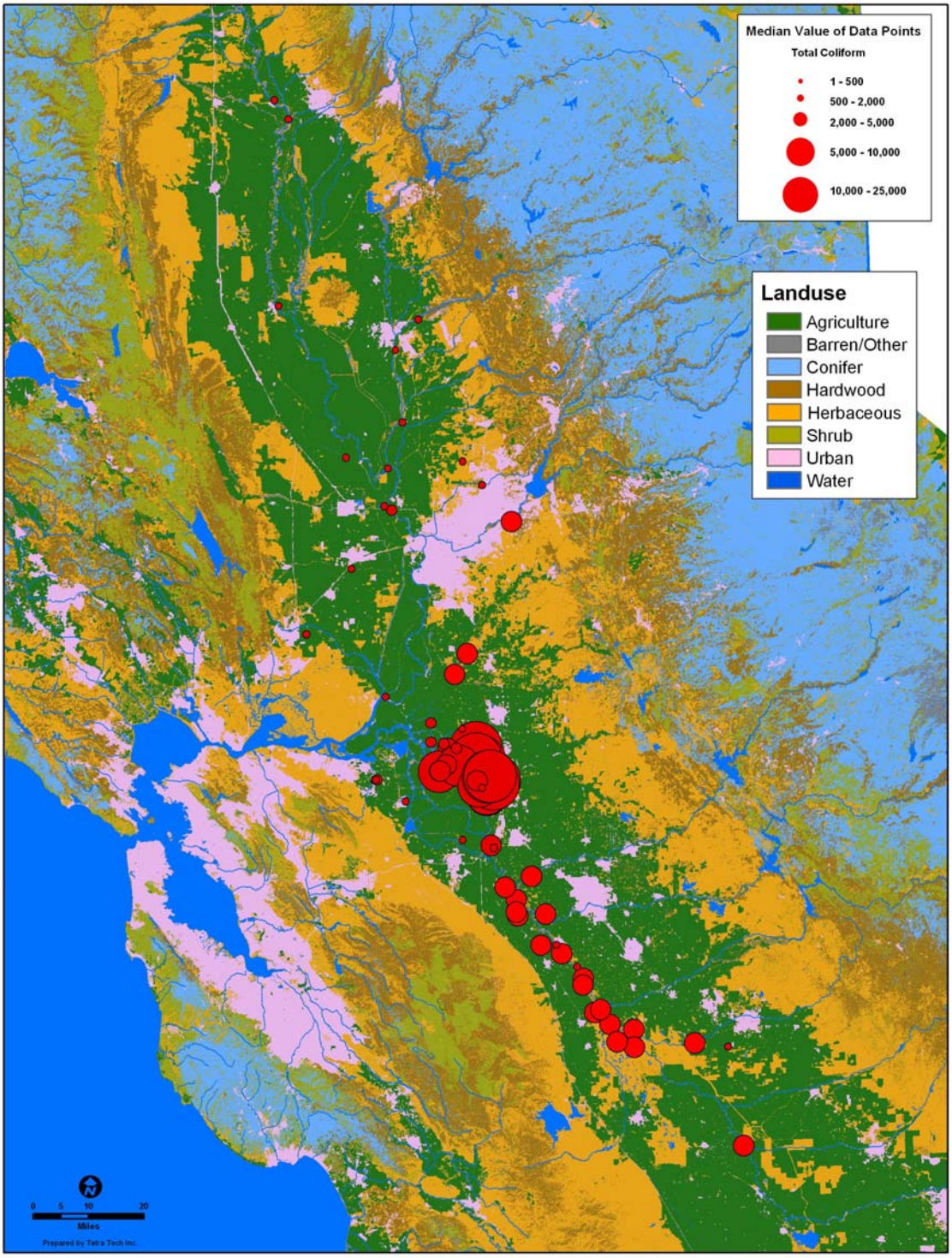

Figure 3-1. Total coliform concentrations in the Central Valley and Delta.

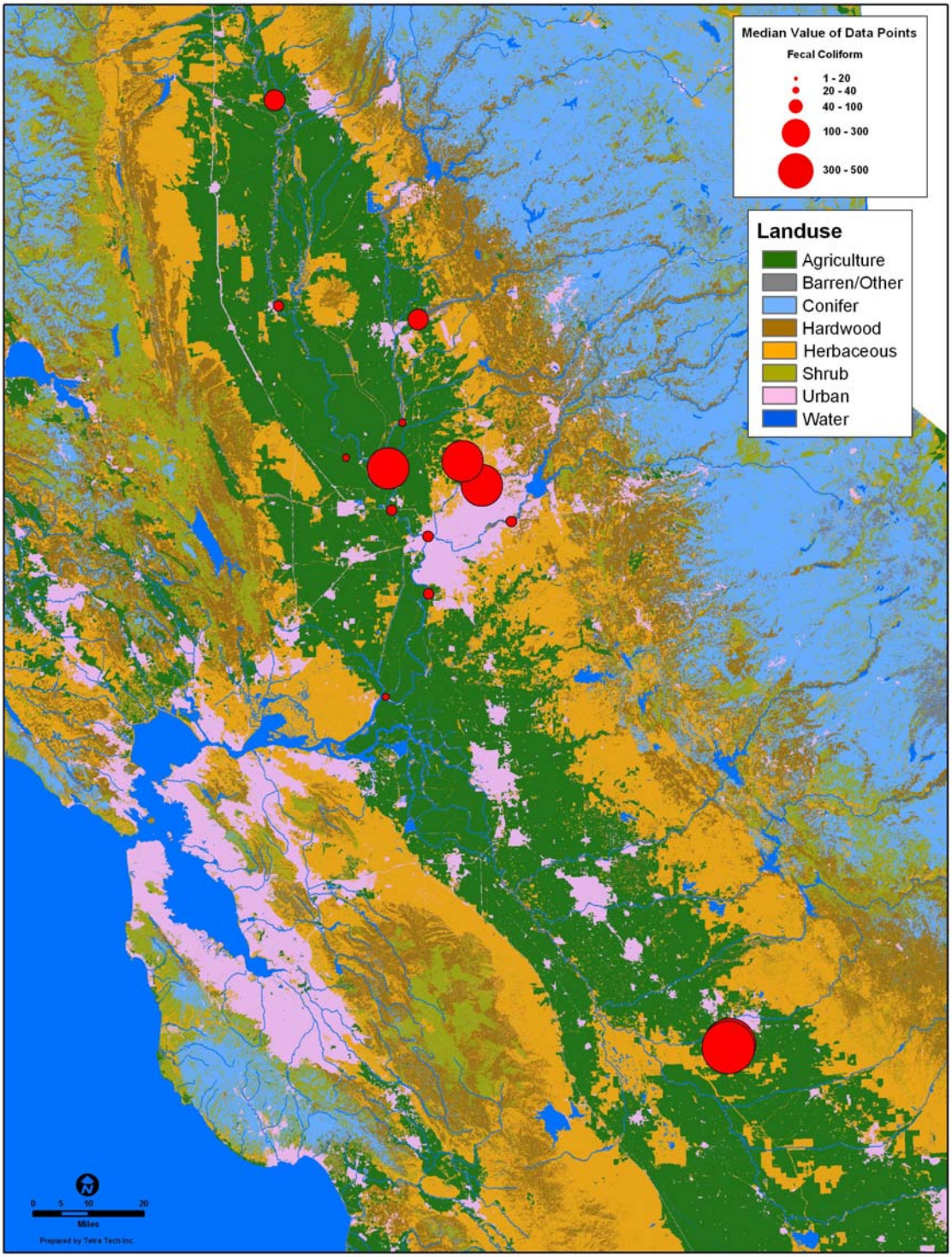

Figure 3-2. Fecal coliform concentrations in the Central Valley and Delta.

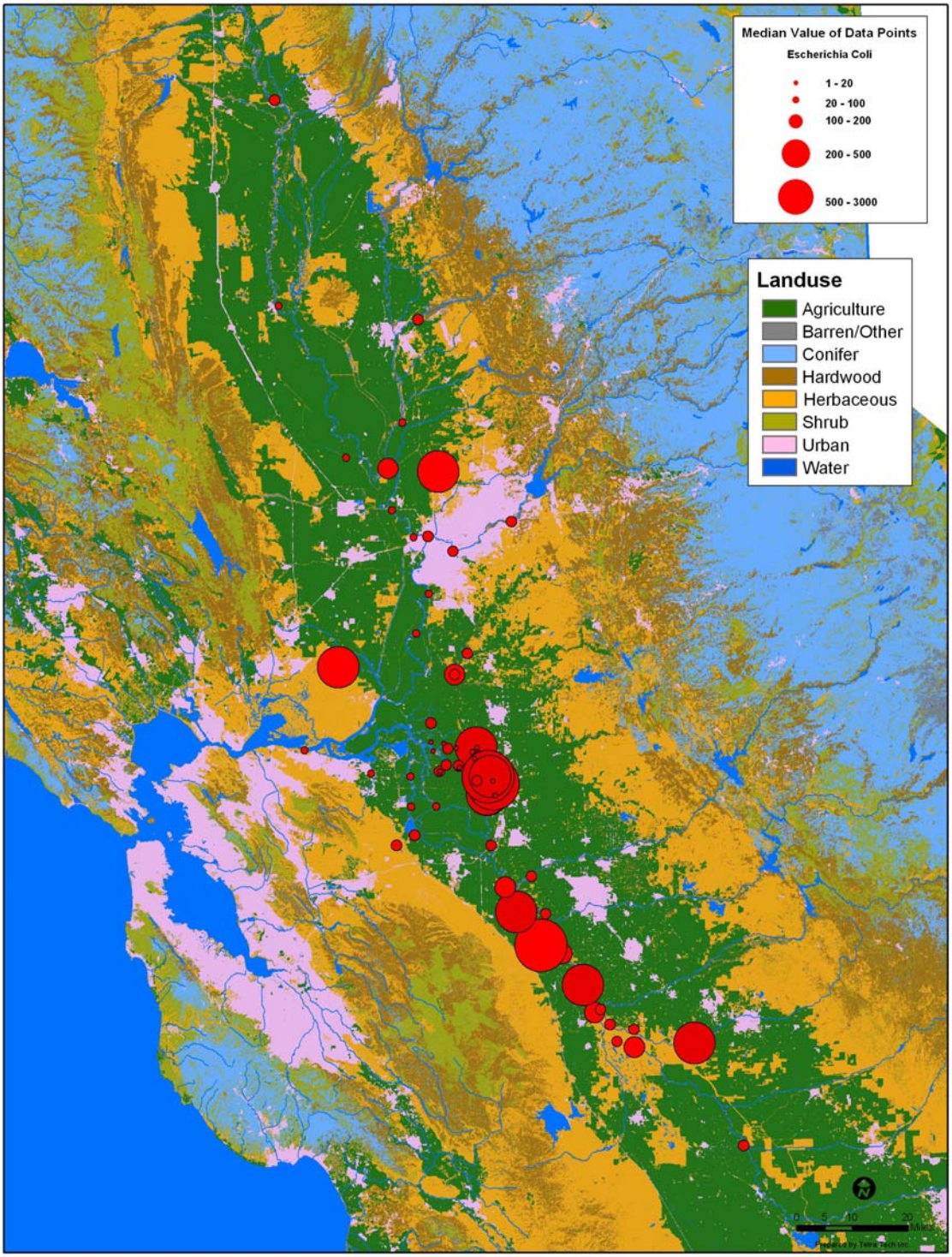

Figure 3-3. *E. coli* concentrations in the Central Valley and Delta.

3.2 PATHOGEN DATA IN SACRAMENTO RIVER BASIN

A significant quantity of data on regulated drinking water pathogens (i.e., *Cryptosporidium* and *Giardia*) was collected as part of the Coordinated Monitoring Program in the Sacramento River between 2001 and 2004. These data are plotted in Figure 3-4. In general, the samples are overwhelmed by the number of non-detects of either of the two pathogens, although *Giardia* was detected considerably more often than *Cryptosporidium*. Where detected, concentrations were very low (< 1 count per liter), although counts were marginally higher for *Giardia*. The locations with the highest concentrations observed for *Giardia* (at American River near Discovery Park and Sacramento River at Mile 44) also show higher concentrations for total coliforms and *E coli*. Although the quantity of data is too limited to draw strong conclusions, these data do show the benefit of collecting coliform data, and suggest perhaps that there might be common sources.

The pathogen data collection shown in Figure 3-4 is unique in its scope and has not been replicated elsewhere in the Central Valley at this scale. However, this sampling was discontinued in 2004 because results could not be clearly interpreted compared to numeric objectives.

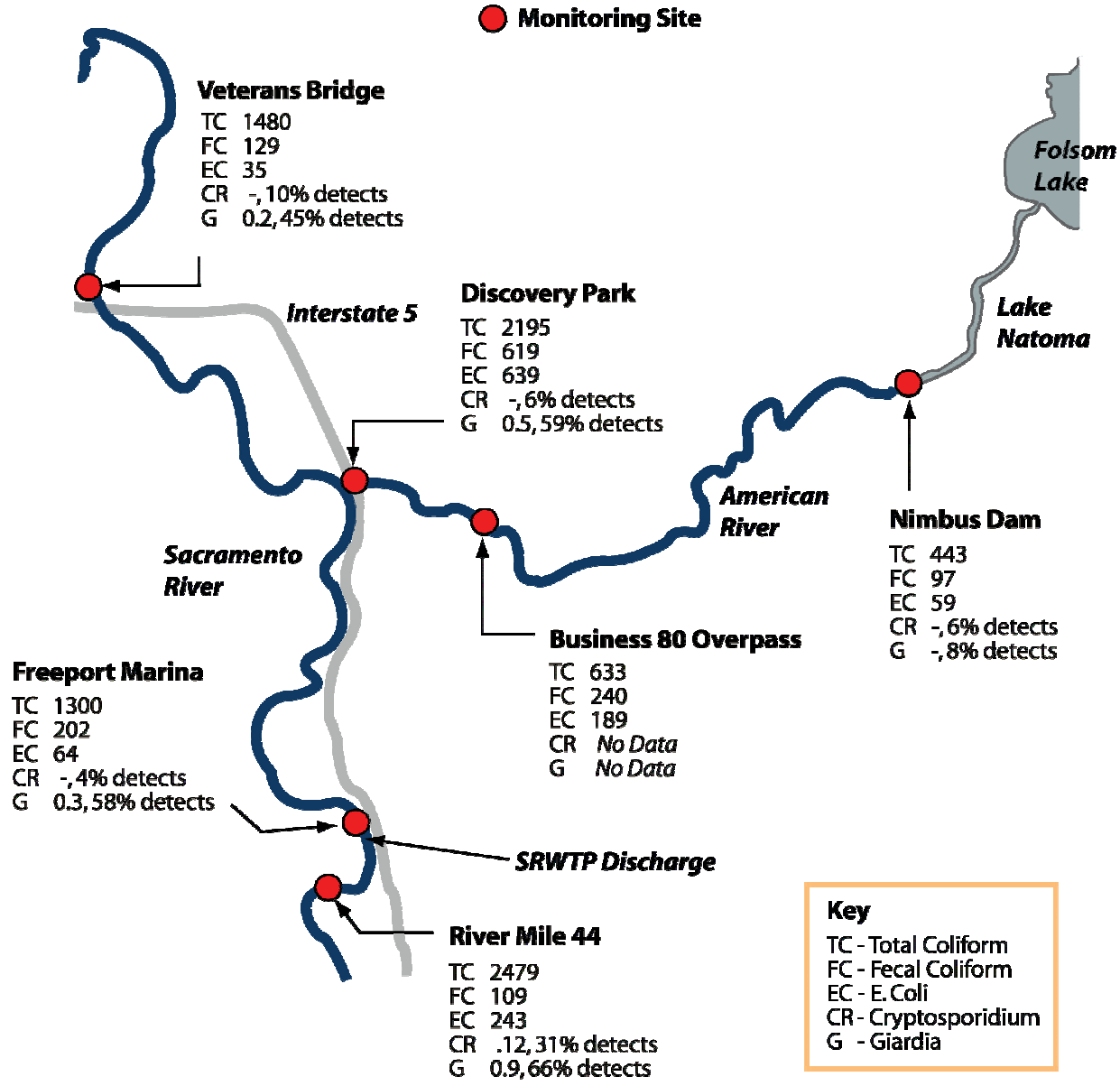

Figure 3-4. A variety of bacterial and pathogen indicators sampled as part of the Coordinated Monitoring Program on Sacramento River (CMP). Data averages are shown for total coliforms, fecal coliforms, *E. coli*, *Cryptosporidium*, and *Giardia*. A "-" indicates no average was determined.

3.3 DATA RANGES FOR SURFACE WATER

To provide further background and more detail on the ranges of concentrations observed for different coliform parameters across the Central Valley, a series of box plots has been prepared for all available data. All stations are shown in alphabetic order. Data from wastewater effluent and from urban runoff were excluded from these plots and are presented separately. Figures 3-5 to 3-7 show the total coliform, fecal coliform and *E. coli* concentrations across a variety of surface water locations throughout the Central Valley. Data are shown in both linear and logarithmic scales in

these plots to allow comparison of numerical values across several orders of magnitude. The plots show that the highest concentrations were observed in the discharge from Natomas East Main drainage Canal as well as several stations that were near sloughs. The former indicates the role of urban stormwater in these measurements, whereas the latter indicate the contribution of wildlife. The same pattern is seen for both total coliform and *E. coli* concentrations (there were fewer slough stations that reported fecal coliform data).

Figure 3-5. The range of total coliform concentrations observed at different surface water locations in the Central Valley and Delta.

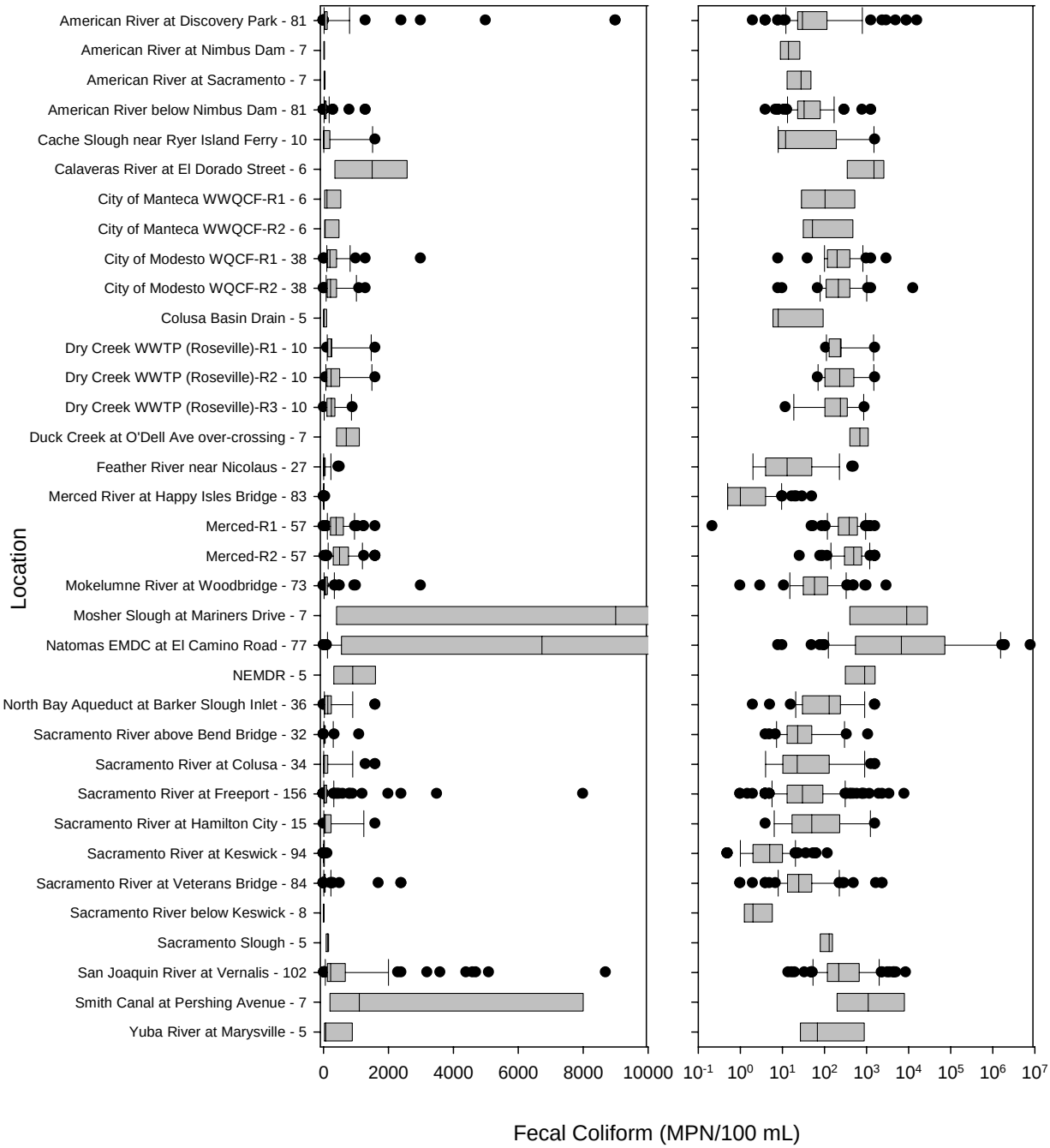

Figure 3-6. The range of fecal coliform concentrations observed at different surface water locations in the Central Valley and Delta.

Figure 3-7. The range of *E. coli* concentrations observed at different surface water locations in the Central Valley and Delta.

3.4 SPATIAL AND TEMPORAL TRENDS IN THE SACRAMENTO AND SAN JOAQUIN RIVER BASINS

A closer look at the fecal indicator data is provided in Figures 3-8 through 3-12, where concentrations are explored along the main stems of the Sacramento and San Joaquin Rivers.

For total coliforms, there is a clear increasing trend with distance downstream in the Sacramento River. For fecal coliforms, concentrations increased below Keswick and remain relatively constant downstream. Trends in *E. coli* concentration are not apparent because data are only available for the urban-impacted portion of the Sacramento River, and no data were available for upstream reaches. The spatial trends for total coliforms in the San Joaquin River are obscured by the fact that the higher level concentrations are capped at ~2400 MPN/100 ml. However, *E. coli* data in the San Joaquin River do show spatial variation over the distance of travel, with the highest concentrations not at the most downstream location but at an intermediate location near Hills Ferry. This trend is also visible in the map of the data shown in Figure 3-3.

In general, temporal trends are not very strong, however, the highest concentrations in the Sacramento River were observed during the wet months, with the generally lower values found in the July and August.

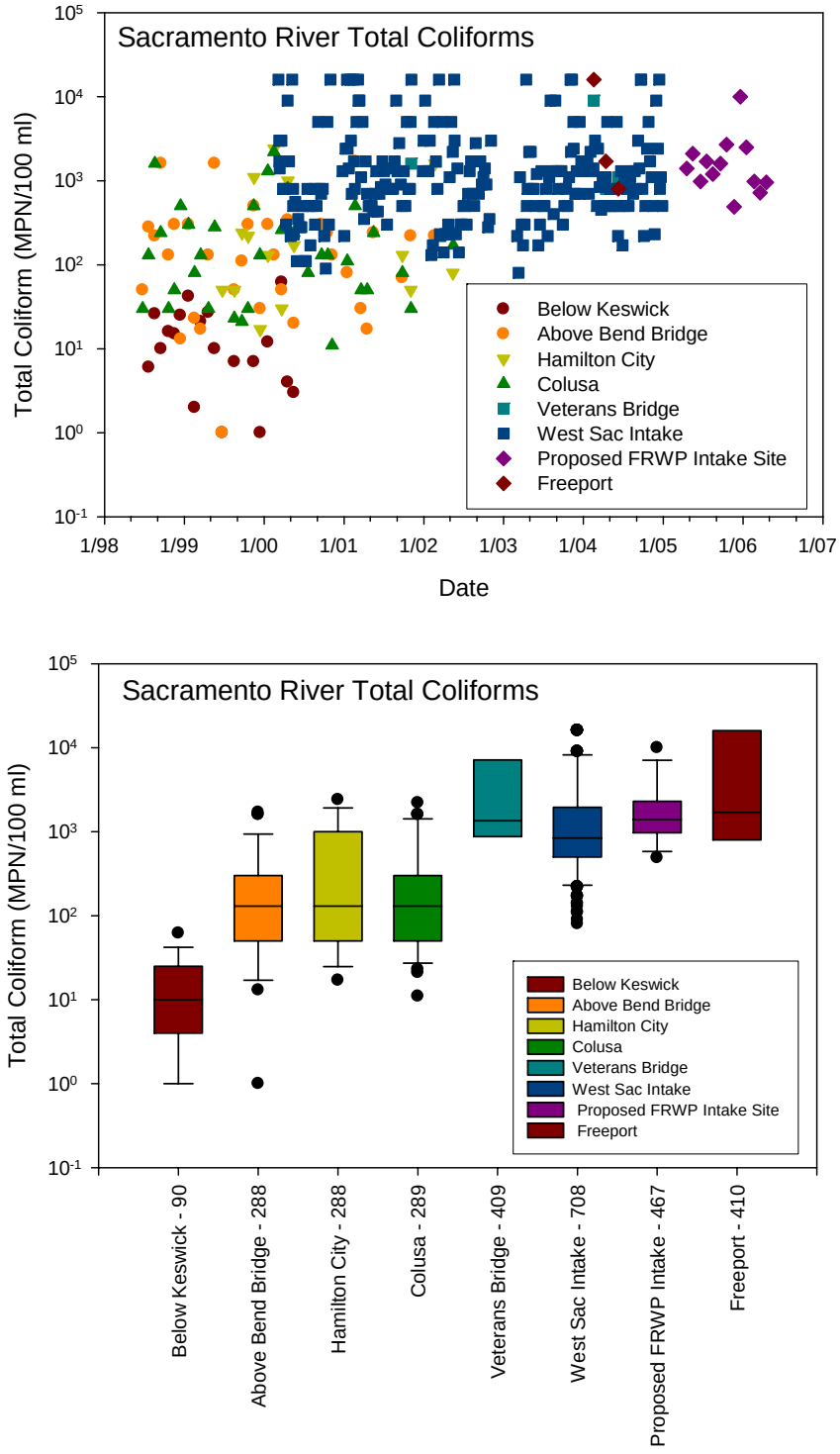

Figure 3-8. Total coliforms in the Sacramento River, as a function of time and location.

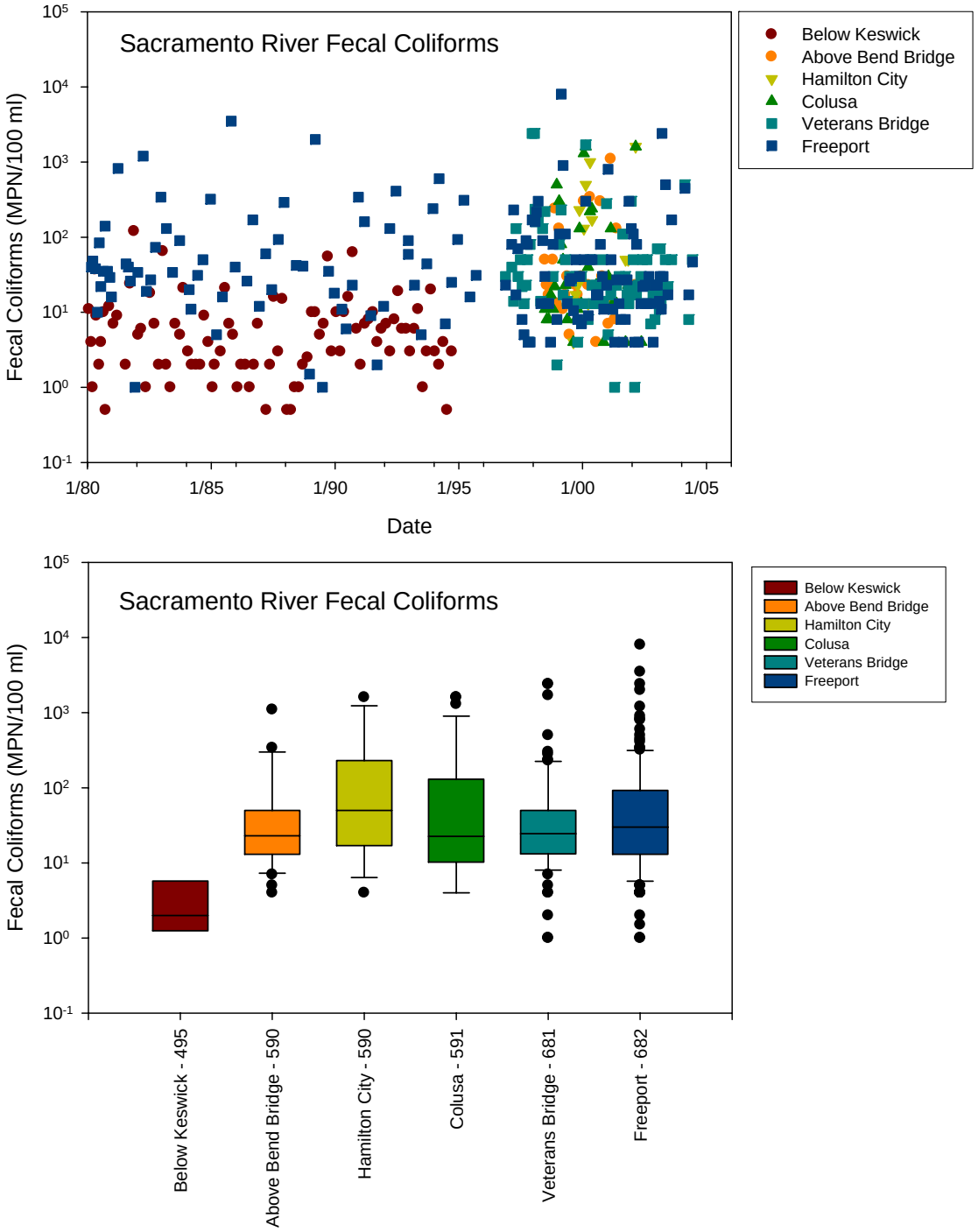

Figure 3-9. Fecal coliforms in the Sacramento River, as a function of time and location.

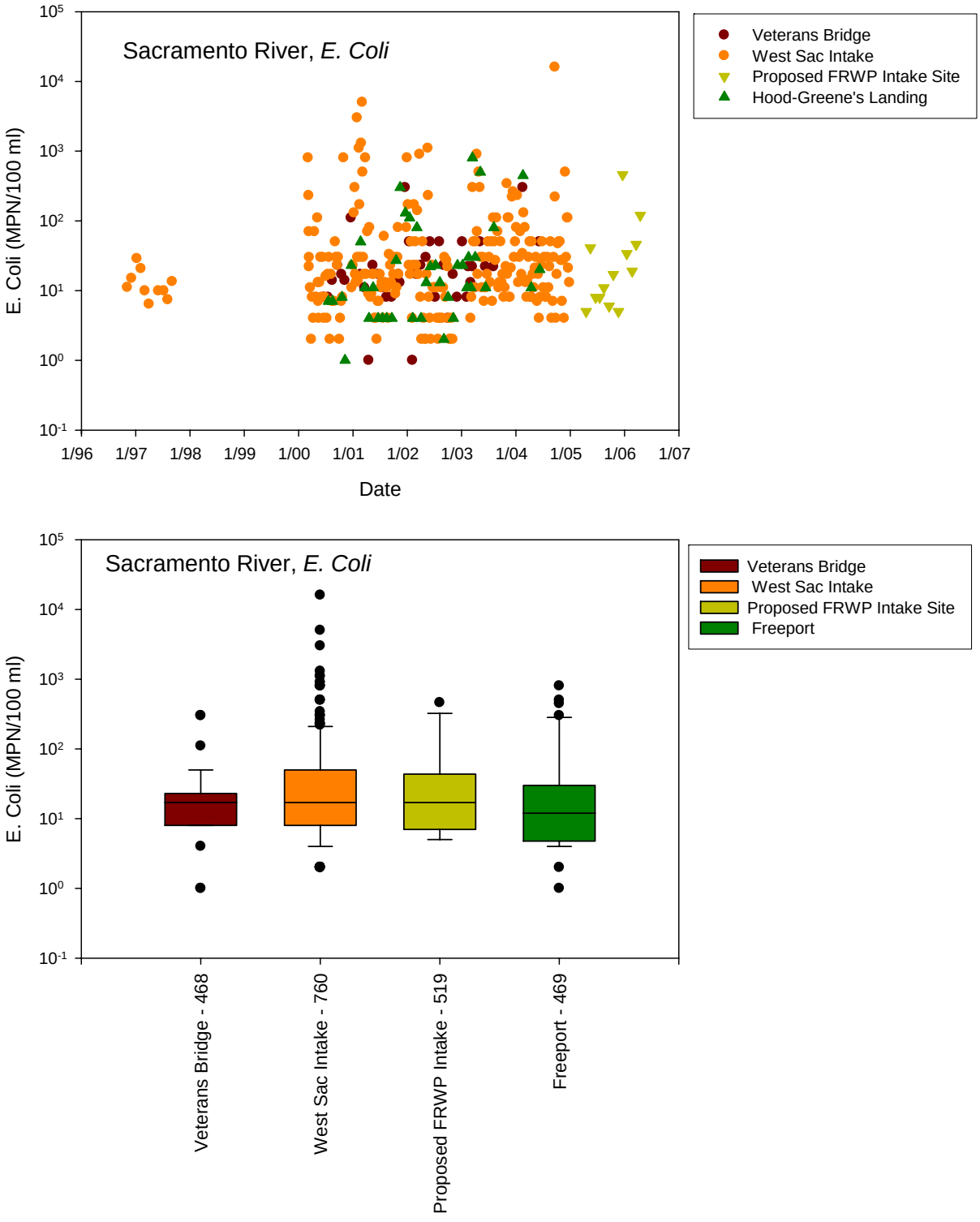

Figure 3-10. *E. coli* in the Sacramento River, as a function of time and location.

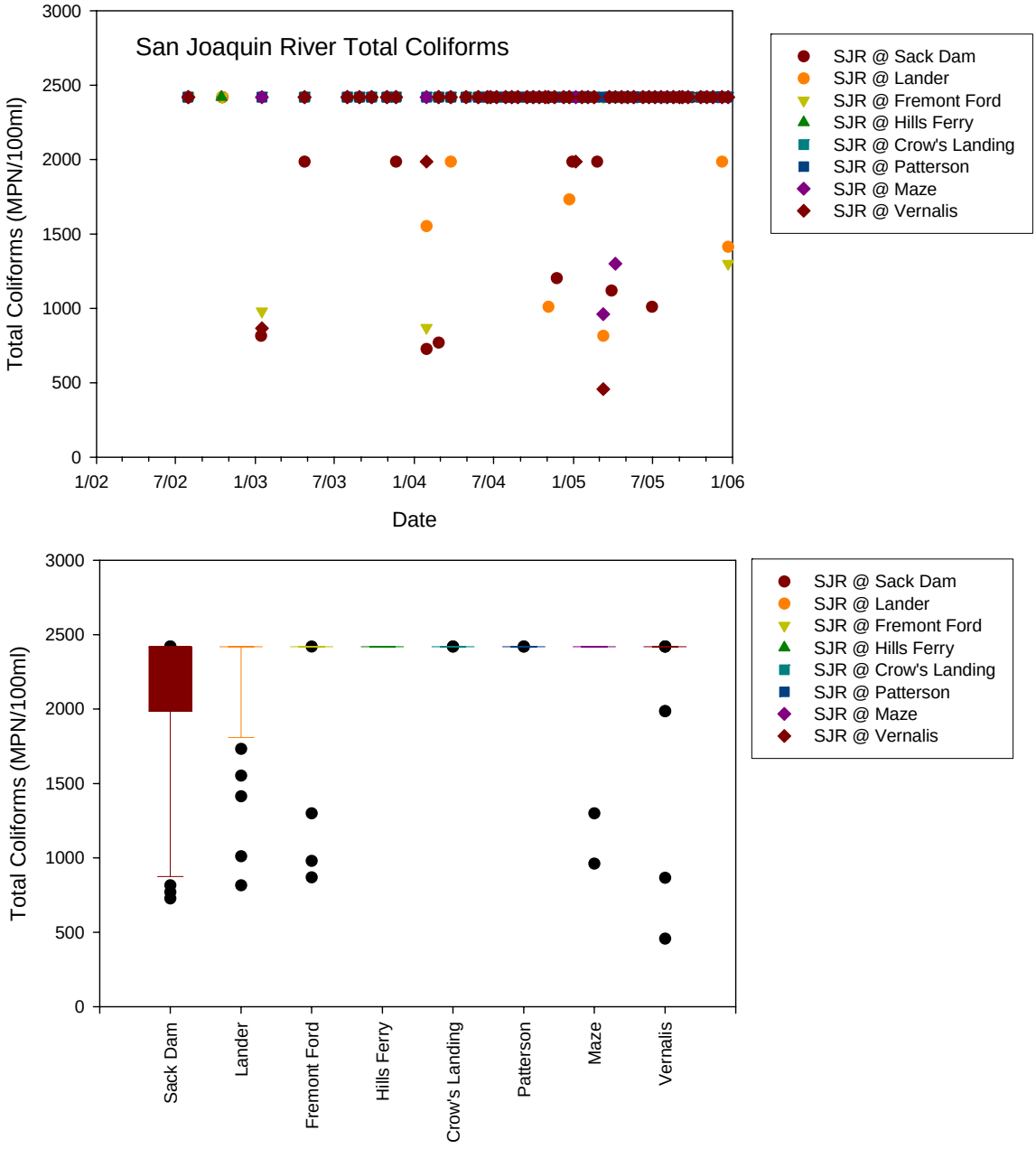

Figure 3-11. Total coliforms in the San Joaquin River, as a function of time and location.

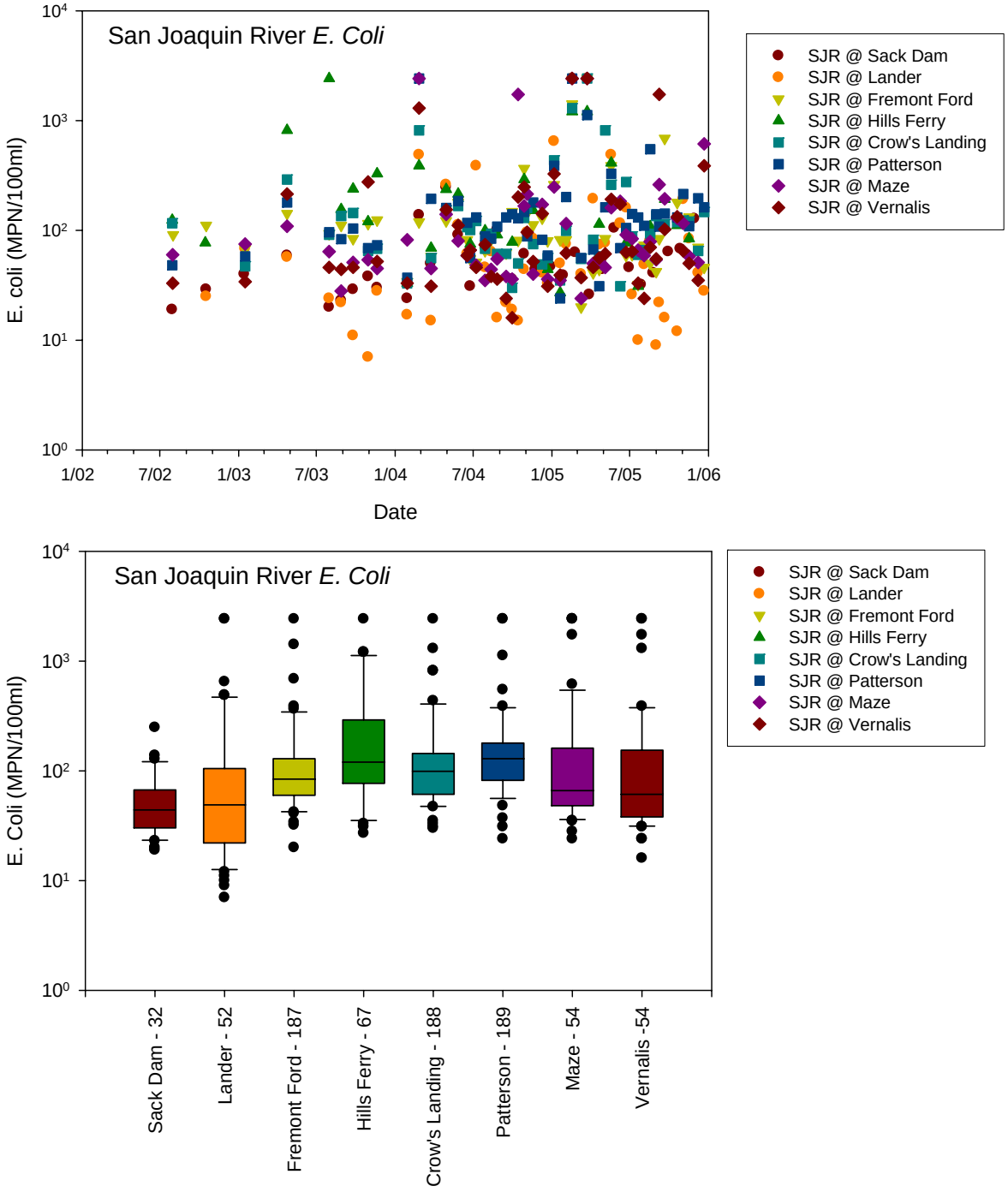

Figure 3-12. *E. coli* in the San Joaquin River, as a function of time and location.

3.5 COLIFORMS AND PATHOGENS IN TREATED WASTEWATER

Although raw sewage has very high concentrations of coliforms (potentially in excess of 10^6 MPN/100 ml), wastewater treatment is effective at removing and inactivating these bacteria through a variety of processes including solids separation and disinfection. Data from wastewater dischargers, shown in Figure 3-13 show relatively low concentrations of total coliforms, generally lower than what would be found in most surface waters. Median concentrations are generally 10 MPN/100 ml or lower for the wastewater plants for which data were available. Data on other coliform groups (fecal coliforms, *E. coli*) were not reported for wastewater samples in the database.

Although some wastewater treatment processes such as solids separation and disinfection using chlorine can be effective in removing the coliforms, low coliform concentrations in wastewater treatment effluents do not guarantee absence of pathogens. As a matter of fact, *Cryptosporidium* oocysts and *Giardia* cysts are resistant to chlorine disinfection and relatively high concentrations of *Cryptosporidium* and *Giardia* concentrations can be observed in wastewater treatment plant effluents. Available data from the Sacramento Regional Wastewater Treatment Plant (SRWTP) effluent for the period of January 1997 through August 2002 indicated relatively high concentrations of *Cryptosporidium* (in a range of 2-192 oocysts/ L) and *Giardia* (in a range of 0.08- 84 cysts/ L). Median and mean concentrations observed at the SRWTP effluent are 1.9 and 7.3 cysts/ L for *Cryptosporidium* and 39 and 44.7 oocysts/L for *Giardia*, respectively.

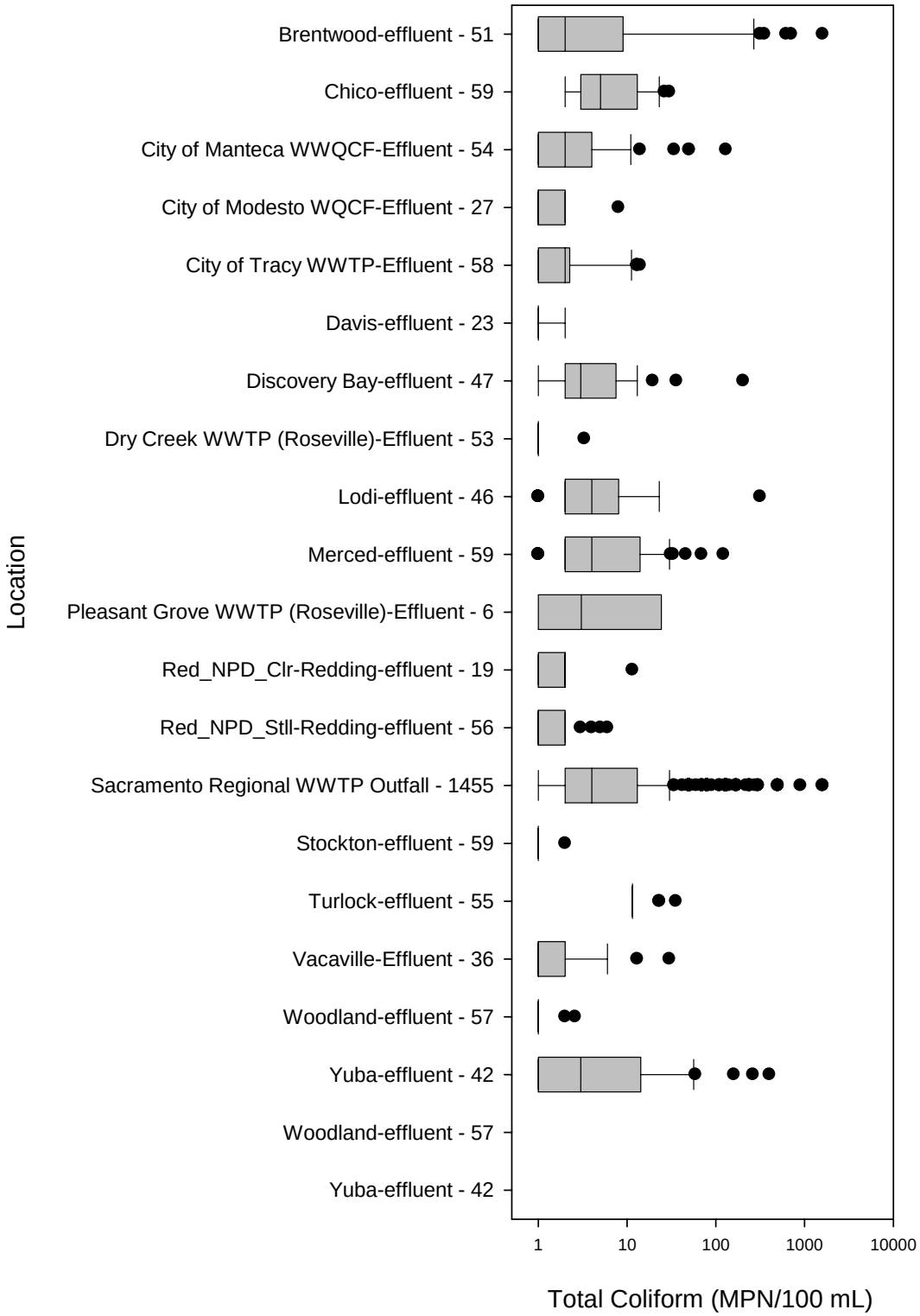

Figure 3-13. Total coliform concentrations in wastewater effluent samples from dischargers in the Central Valley and Delta.

3.6 COLIFORMS IN URBAN RUNOFF

Data on urban runoff concentrations were available for several locations from Sacramento and Stockton for total coliforms, fecal coliforms, and *E. coli*. Measurements were made separately for wet and dry conditions, although flow data were not available. Box plots summarizing these data are shown in Figures 3-14 through 3-16.

Urban runoff concentrations were found to be uniformly high, and higher than concentrations in surface water previously described in this chapter. For example, total coliform concentrations exhibit median concentrations in the vicinity of 10^5 MPN/100 ml during both wet and dry seasons. There was no consistent seasonal difference in concentration between the wet and dry seasons. Concentrations were about an order of magnitude lower for fecal coliforms and for *E. coli*, and with no systematic seasonal differences.

3.7 SUMMARY

The pathogen and indicator data in the database, compiled by the Central Valley Drinking Water Policy Workgroup, consisted primarily of measurements of total and fecal coliforms and *E. coli*. There was limited data on other species of coliforms, and even more limited data on pathogens such as *Cryptosporidium* and *Giardia*. Fecal indicator concentrations are highly variable both temporally spatially, and can vary by orders of magnitude. Despite this variability, the maps and plots of available data do provide a snapshot of the nature and dynamics of indicator concentrations across the Central Valley and Delta.

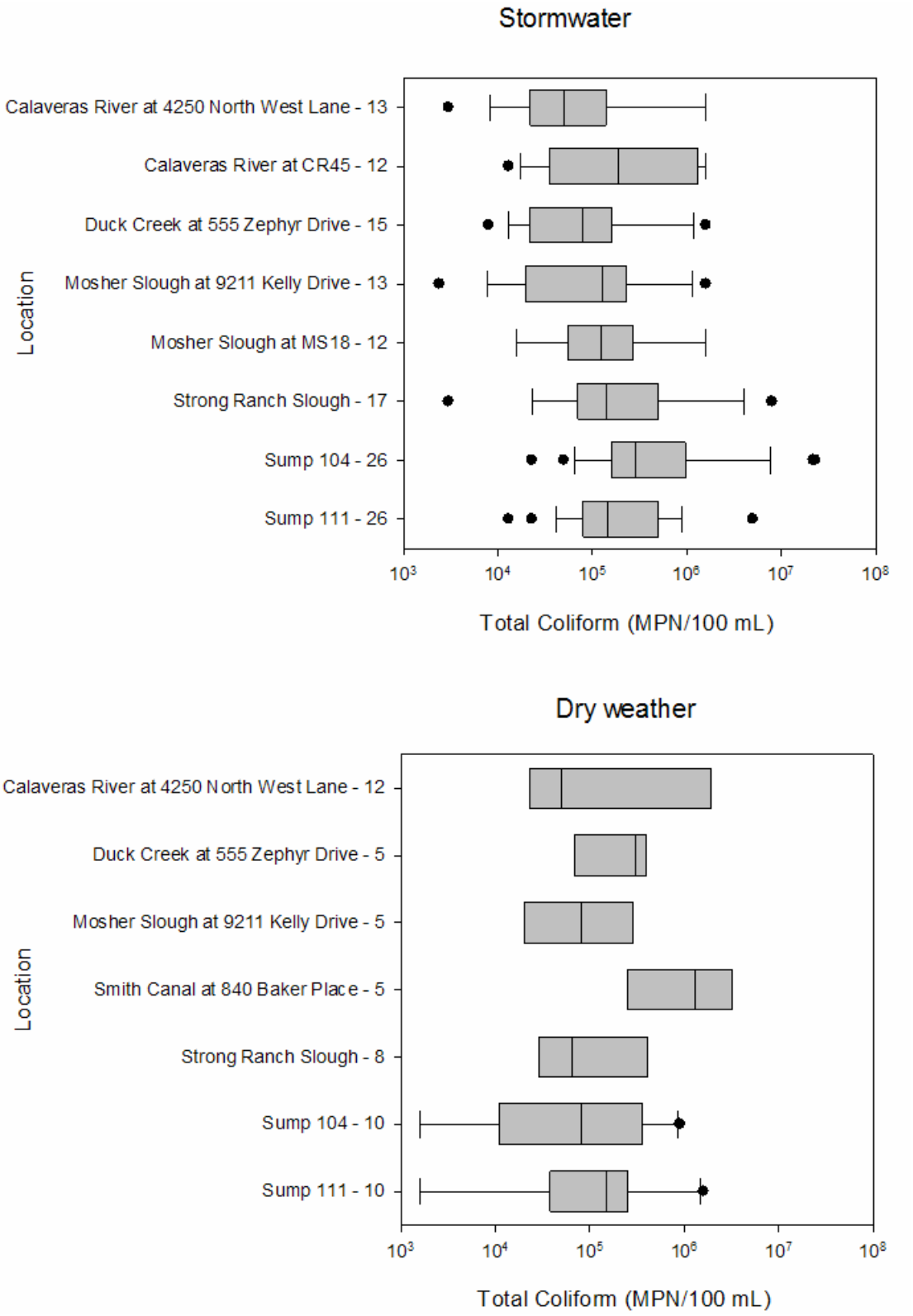

Figure 3-14. Total coliforms in stormwater at selected locations in the Central Valley and Delta, during wet weather and dry weather conditions.

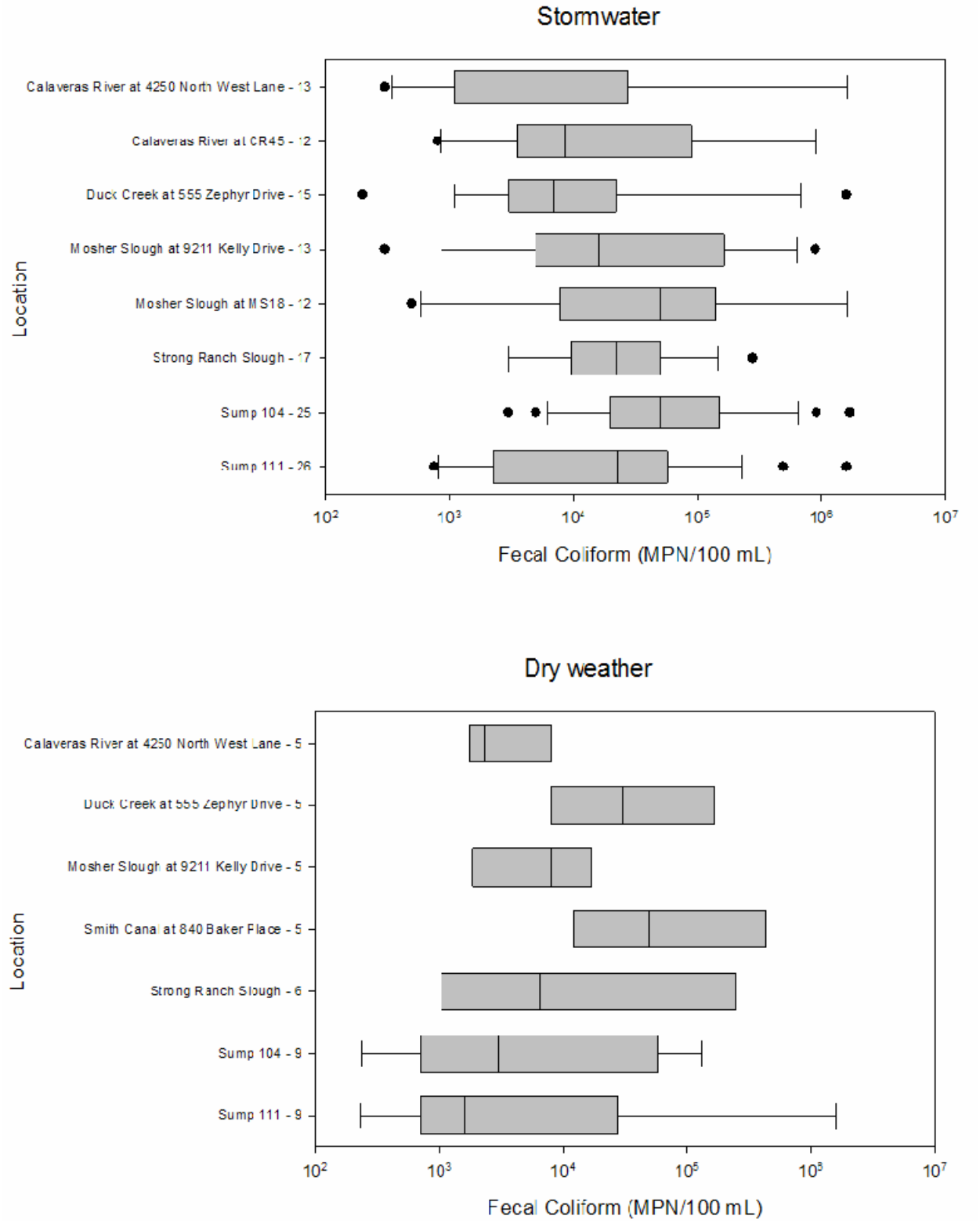

Figure 3-15. Fecal coliforms in stormwater at selected locations in the Central Valley and Delta, during wet weather and dry weather conditions.

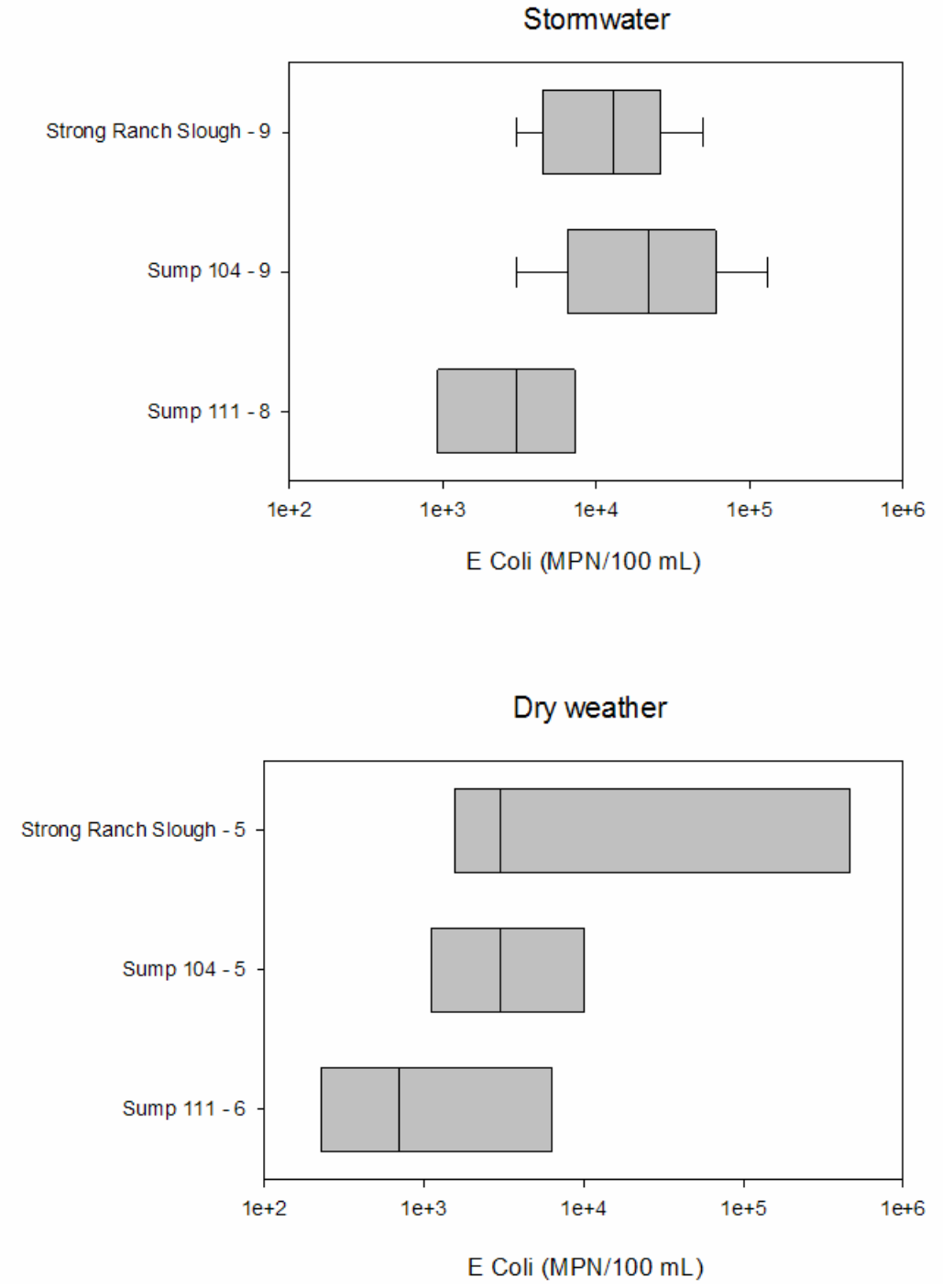

Figure 3-16. *E. Coli* in stormwater at selected locations in the Central Valley and Delta.

CHAPTER 4.0
EVALUATION OF FECAL INDICATOR AND PATHOGEN LOADS

The goal in this chapter is to quantify loads of fecal indicators such as total coliforms from various sources in the Central Valley where such estimates can be made. In general, such quantification is only possible for the coliform indicator organisms because the data are mostly available for such indicators and the pathogen data are very sparse or show a high frequency of non-detects. Furthermore the orders-of-magnitude changes that occur in indicator concentrations in time and space, and the limited frequency of data collection, suggests that only approximate quantification is possible. This chapter presents an overview of microorganism die off in the ambient environment, a key process controlling observed concentrations, and identifies the relative importance of different sources in the Central Valley where adequate flow and concentration data exist.

4.1 DIE OFF OF FECAL INDICATORS AND PATHOGENS

Because pathogens and indicators are living organisms, and typically have human or animal hosts, they exhibit die off in the ambient environment at varying rates depending on the water temperature, exposure to sunlight, and the nature of the organism. Organisms may survive in sediments, and under warmer temperatures, may actually be able to colonize and grow in sediments. It is not known whether conditions appropriate for coliform regrowth exist in some locations in the Central Valley. However, as an illustration, the range of die off rates reported in the literature is shown in Table 4-1. The effect of die off on select fecal indicator and pathogen concentrations is shown for illustration in Figure 4-1. When transport time frames of more than a few days are involved, die off makes linkage of sources and concentrations very difficult. Alternatively, microorganism concentrations, more specifically fecal indicator concentrations, are more closely related to what happens in the proximity of a sampling station, rather than what happens in a large watershed where significant travel time and concomitant pathogen die off can occur.

Table 4-1 Ranges of die-off rate constants (Source: USEPA, 2001)

Organism	First Order Die-Off Rate Constant (1/day)	Medium
Total Coliform	1-5.5	Freshwater, 20 °C
	0.7-3.0	Seawater, 20 °C
	0.42	River water, temperature not specified
Fecal Coliform	37-110	Seawater, in sunlight
	0.51	River water, temperature not specified
	0.043-0.146	Sand, 4 to 35 °C
	0.043-0.156	Loam, 4-35 °C
	0.025-0.083	Clay, 4-35 °C
E. Coli	0.53	River water, 37 °C
	0.102	Surface water, 5 °C
Cryptosporidium	0.01	Surface water, 5 °C
	0.025	Surface water, 15 °C

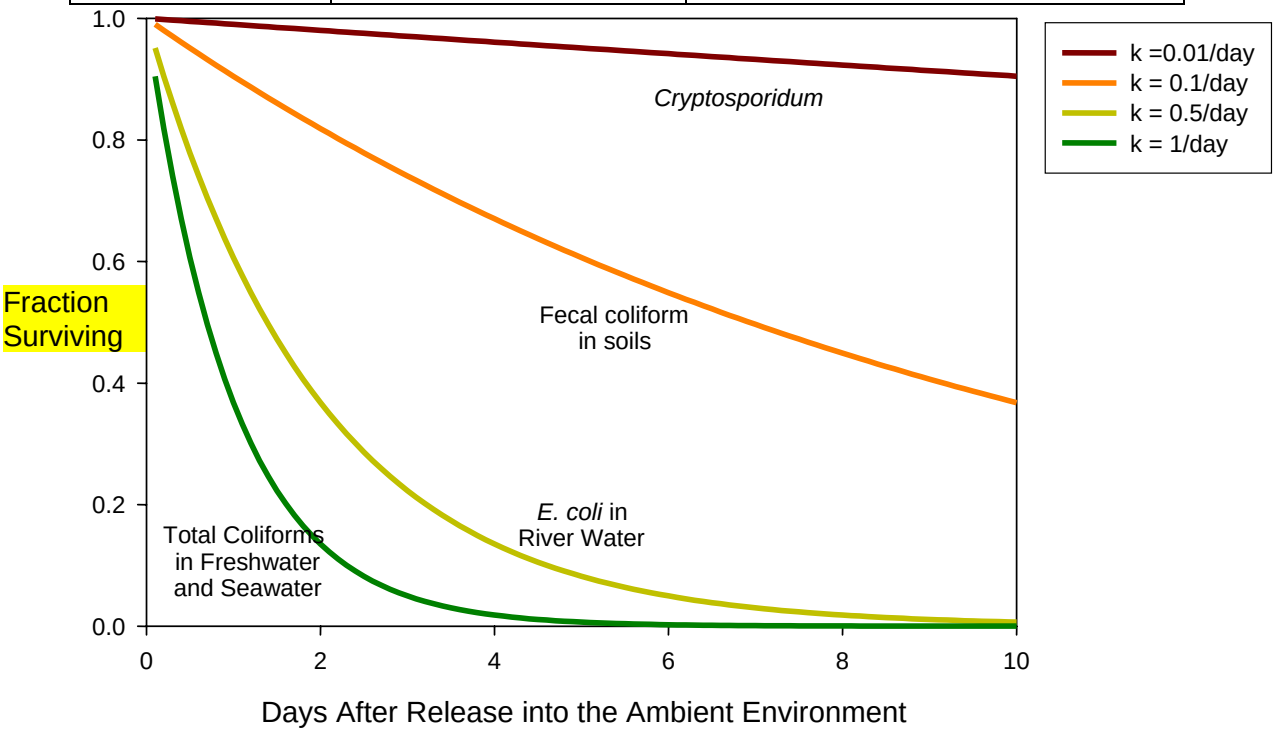

Figure 4-1. Die off of selected bacteria and pathogens in the ambient environment using ranges of rate constants shown in Table 4-1.

4.2 SACRAMENTO RIVER LOADS

Loads were computed at locations sampled by the Sacramento Water Treatment Plant at a point on Sacramento River downstream of the confluence with the American River. Flow data on the Sacramento River at Freeport was used for these calculations. Total coliform counts ranged from 80 to 16,000 MPN/100 ml, and data reporting was capped at the higher number. Daily coliform loads were computed using flow and

concentration data for the same day. Note that flow and coliform concentrations were not correlated (Figure 4-2), although a closer review of the data show that the highest concentrations correspond to the wet months of the year. The concentrations, flows, and estimated daily loads are shown in Figure 4-3. The calculated loads range from less than 10^{12} organisms per day to approximately 10^{15} organisms per day. It is recognized that the higher end values may be underestimated because of the concentration data reporting. This number is a useful basis for comparison against loads that originate from various point and nonpoint sources in the Central Valley and Delta as discussed below. The number is also useful to compare against the excretion rates of coliforms by individual organisms as shown in Table 4-2.

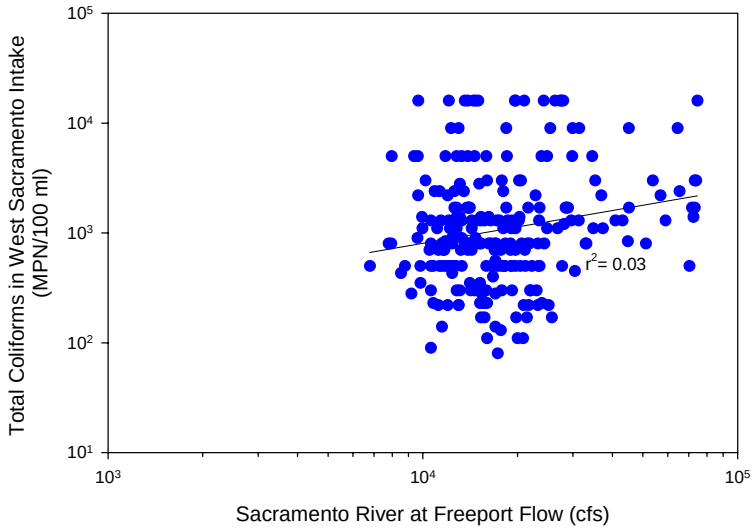

Figure 4-2. Flow and total coliform concentrations in the Sacramento River downstream of American River.

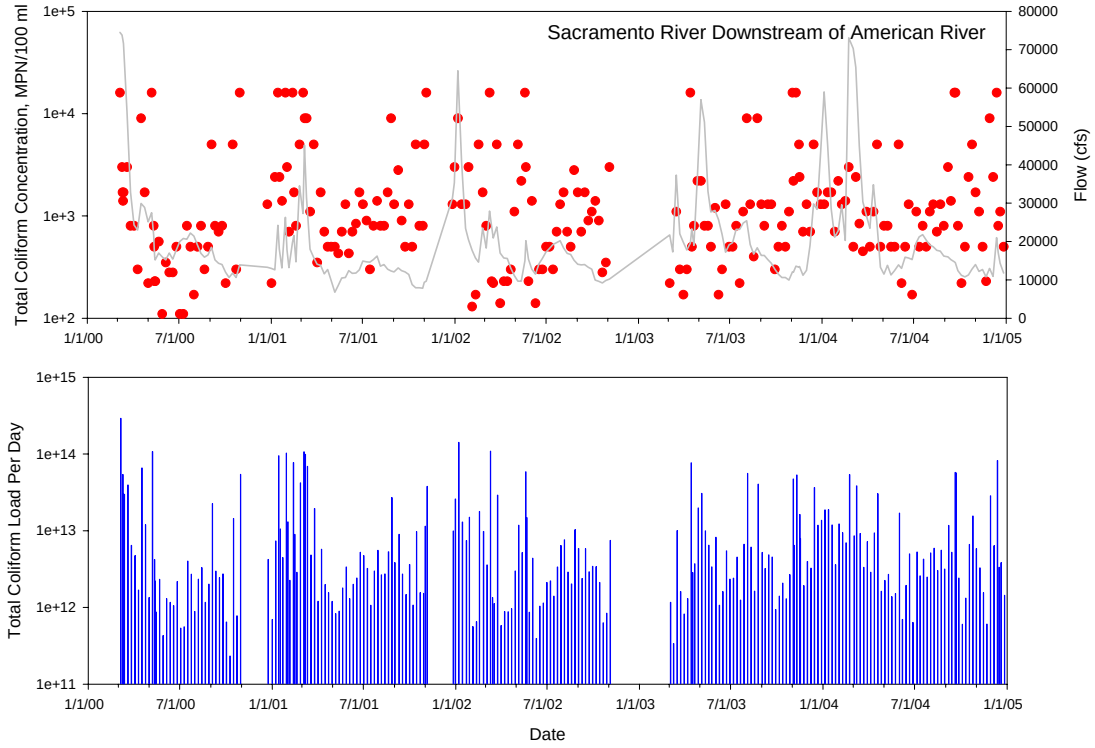

Figure 4-3. Flow (line), total coliform concentration (circles) and total coliform load (lower plot) in the Sacramento River downstream of American River.

Table 4-2. Fecal coliform excretion by different animals (USEPA, 2000).

Animal	Fecal Coliform (count/animal/day)
Dairy cow	1.01E+11
Beef cow	1.04E+11
Hog	1.08E+10
Sheep	1.20E+10
Horse	4.20E+08
Chicken	1.36E+08
Turkey	9.30E+07
Duck	2.43E+09
Goose	4.90E+10
Deer	5.00E+08
Beaver	2.50E+08
Raccoon	1.25E+08
Dog	4.09E+09

4.3 EVALUATION OF URBAN LOADS

Robust data to evaluate coliform loads exist for the Natomas East Main Drainage Canal (NEMDC) (MWQI, 2005; Zanoli, personal communication) with frequent measurement of flow and pathogen counts. Although the watershed of the NEMDC is not fully urban land, the watershed is rapidly urbanizing and remains the best available dataset in the region for estimating the impact of urban land on pathogen runoff. The estimated loads of total coliforms at the NEMDC are shown in Figure 4-4. These data show the extremely variable nature of the coliform source, with concentrations sometimes exceeding values of 500,000 MPN/100 ml. The variability is greater than seen for the Sacramento River in Figure 4-3. Using the flow at this sampling location, it was found that actual coliform loads can range from a little over 10^9 coliforms/day to higher than 10^{15} coliforms/day. At the high end, these numbers are comparable to some of the highest loading rates estimated for the Sacramento River. Although the limited data at the high end in the Sacramento River represent an uncertainty in this calculation, for some days of the year, it is possible for nearly the entire coliform load of the Sacramento River to be of the same magnitude as the load from NEMDC. This calculation highlights the importance of urban runoff as a source of coliforms to the Sacramento River. A further observation from the NEMDC data is that the fecal coliform concentrations are almost equal to the total coliform load, i.e., in this urbanized region, most of the coliform load is fecal in origin, as opposed to originating from other environmental sources (Figure 4-5).

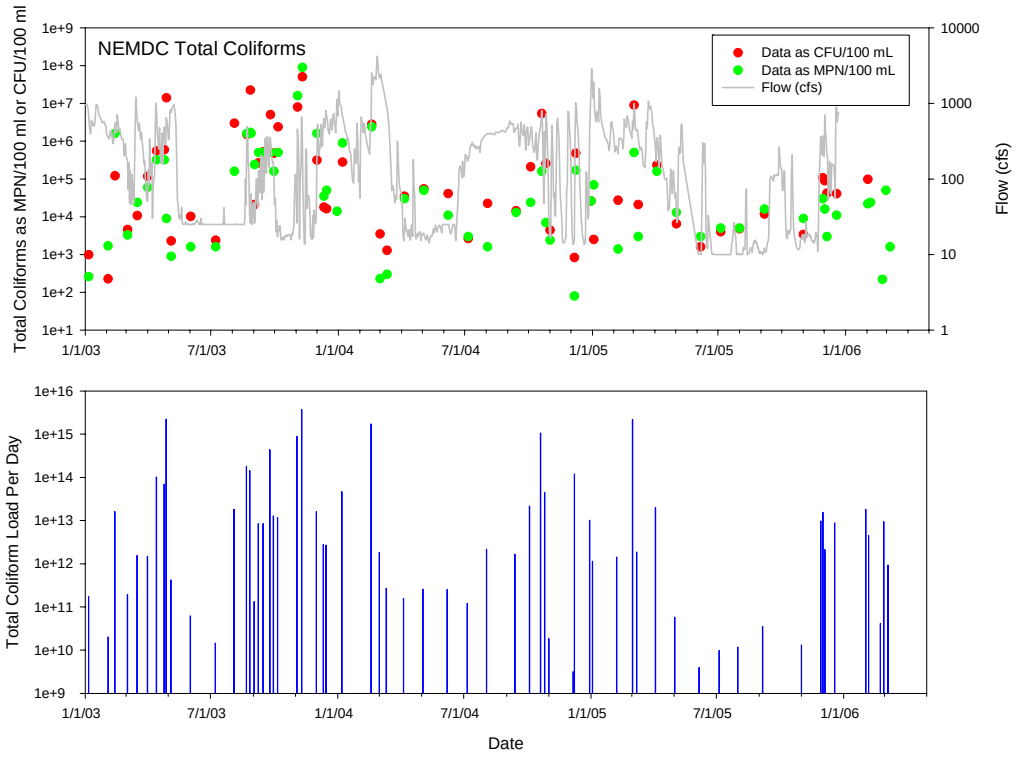

Figure 4-4. Flow, total coliform concentration and load in the Natomas East Main Drainage Canal (NEMDC).

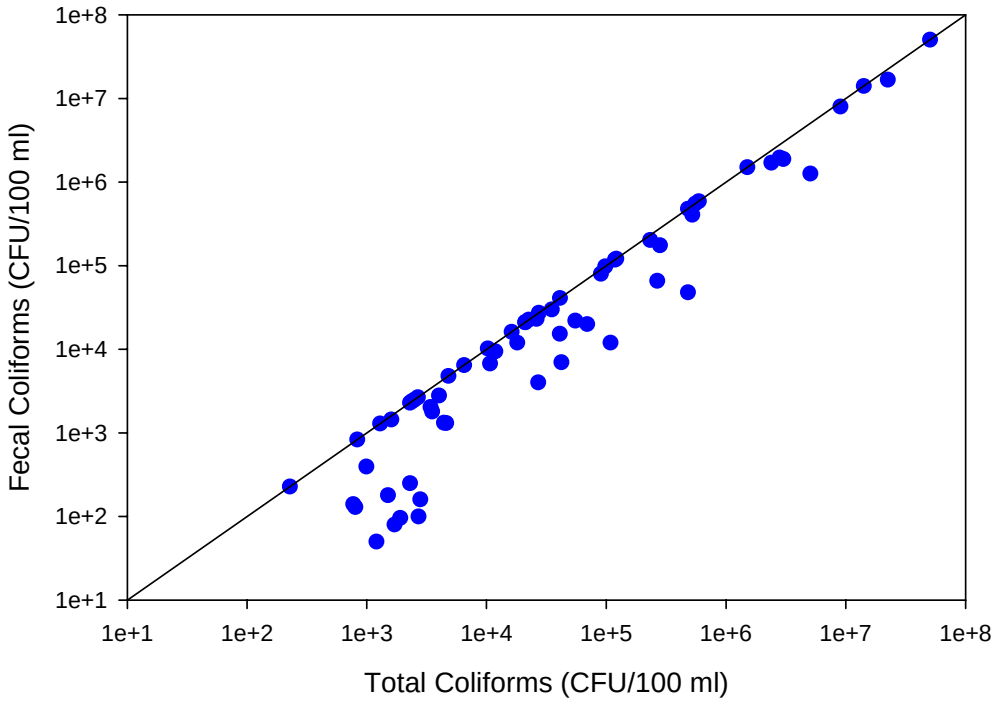

Figure 4-5. Paired samples of total coliform and fecal coliform concentration from the Natomas East Main Drainage Canal (NEMDC).

4.4 EVALUATION OF WASTEWATER LOADS

Substantial data on a wastewater source (including daily flow data) was available for the Sacramento Regional Wastewater Treatment Plant. Using total coliform concentrations and reported effluent discharge volumes from the plant, the estimated coliform loads range from 10^8 to nearly 10^{11} organisms per day (Figure 4-6). Even at the highest level, these loads are orders of magnitude lower than the high values for urban runoff from the Natomas East Main Drainage Canal. This is true even though this wastewater plant serves a population of more than 1 million people and is the largest in the Central Valley.

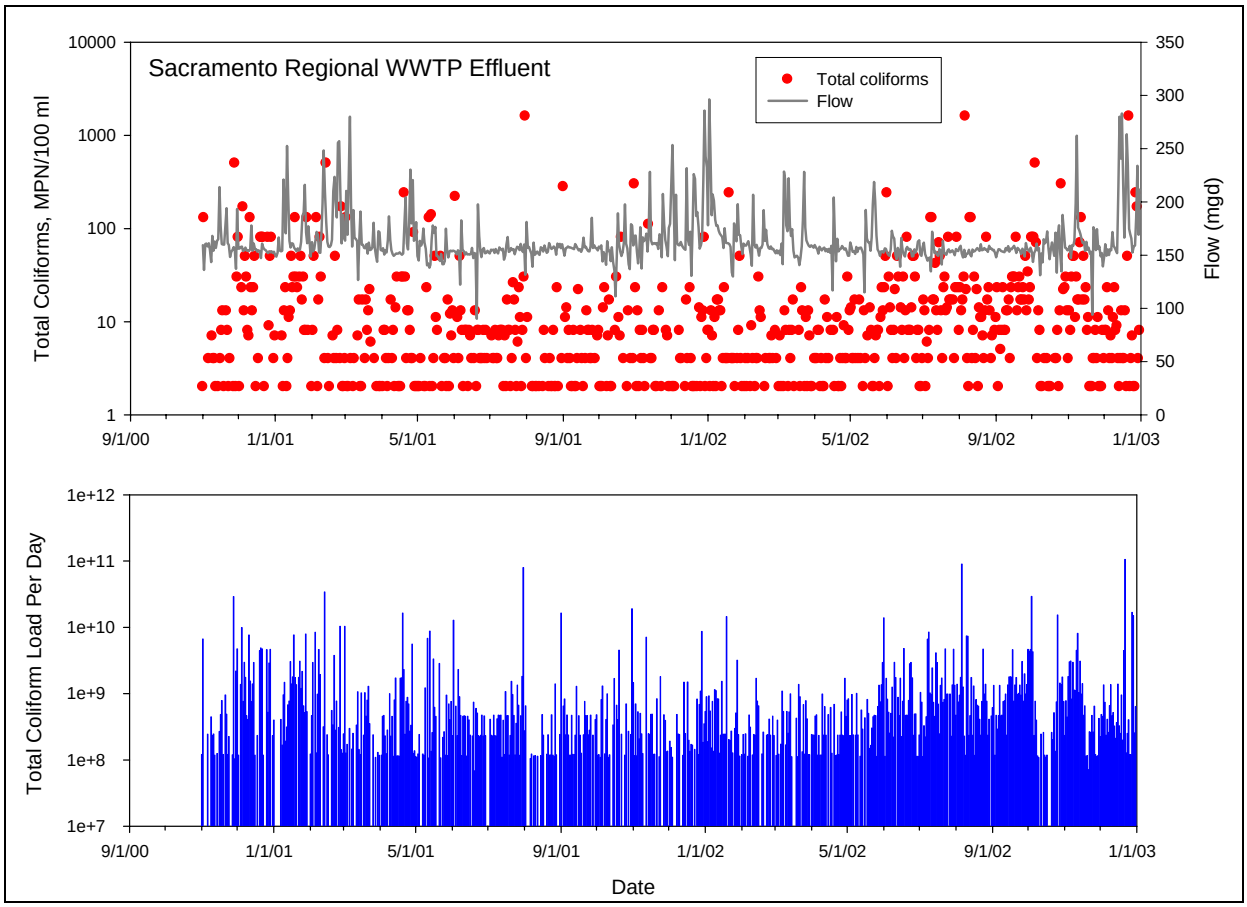

Figure 4-6. Flow and total coliform concentration in Sacramento Regional WWTP effluent.

4.5 LAND-BASED EVALUATION OF COLIFORM LOADS USING LOADING RATES

A simplified approach for estimating the loads from different land uses is to estimate coliform areal loading rates as developed by Horner (1992), and summarized in Table 4-3. Although these rates are gross approximations, and have not been estimated for the climate and conditions of the Central Valley, a rough calculation was performed for lands in the Sacramento River watershed as described below.

The incremental watershed area draining into the Sacramento River between Colusa and Freeport corresponds to an area of 1,590 square miles (1.02 million acres). Assuming that the contribution of upstream watersheds is minimal because of runoff, and assuming a midpoint fecal loading rate of ~5×10^9 fecal coliforms per acre per year from Table 4-2, an estimated load of 1.3×10^{13} fecal coliforms per day is calculated. This load is higher than what is actually seen in the Sacramento River (Figure 4-2) and is likely explained by die off during transport that was not considered.

A similar calculation can be performed for the NEMDC watershed, an area covering approximately 180 square miles. Using the same loading rates as above, a daily estimated load of 1.6×10^{12} fecal coliforms/day is computed. This falls in the middle

range of values shown for the NEMDC in Figure 4-4. The agreement appears to be better than for the Sacramento River because die off is less of a confounding effect for a smaller watershed with shorter travel times.

Table 4-3 Land based loading of fecal coliforms (Source: Horner, 1992)

Land Use	Fecal Coliform Loading (number/acre/year)
Road	7.3E+07
Commercial	2.3E+09
Single Family Residential, Low Density	3.8E+09
Single Family Residential, High Density	6.1E+09
Multifamily Residential	8.5E+09
Forest	1.6E+09
Grass	6.5E+09
Pasture	6.5E+09

4.6 EVALUATION OF *CRYPTOSPORIDIUM* LOADS

There are direct measurements of *Cryptosporidium* loads from various mammals in California, as shown in Table 4-4, based on the work of Atwill et al. (2003). These data show the tremendous contribution of calves to Cryptosporidium production, and the likely importance of grazing and confined animal facilities.

Assuming an average effluent flow rate of 165 mgd (averaged over 1998-2002) at the SRWTP (Chapter 3), and median *Cryptosporidium* concentrations of 1.9 oocysts/liter, results in a median daily load of $1.2x10^9$ oocysts/day.

Data on *Cryptosporidium* exists at different location on Sacramento River and the American River as previously shown in Figure 3-6. The highest average *Cryptosporidium* oocyst counts of 0.12/liter were observed at Sacramento River at Mile 44. This can be translated to an estimated average load of $6x10^9$ cysts per day at this location (using an average flow in the Sacramento River of 20,400 cfs, based on data shown in Figure 4-3).

Both the wastewater and Sacramento River *Cryptosporidium* loads may be compared with the numbers of oocyts shed by a single calf ($3x10^9$ oocysts per day) as shown in Table 4-4. In other words, the *Cryptosporidium* loads flowing through Sacramento River or discharged from SRWTP are of the same order of magnitude as the excretion of a single infected animal. Although wastewater loads are significant, this comparison highlights the importance of animals in the landscape as sources of pathogens. The relatively low concentrations that are observed in the Sacramento Rivers could be caused by the presence of natural or artificial barriers/processes that limit pathogen transport to water, by the significant die off of oocysts that do reach the water, as well as limitations in the analytical detection of *Cryptosporidium* oocysts in natural waters.

Table 4-4 Mean Daily *Cryptosporidium parvum* excretion rates in certain domestic and wildlife species in California (Source: Atwill et al., 2003)

Animal	Species	Daily oocyst excretion rates *(oocysts/day/animal)*	Mean oocyst concentration in feces *(oocysts/kg)*	Total daily fecal production *(kg)*
San Joaquin dairy cattle	Cows	4,000	67	60
	Calves	3,000,000,000	3,000,000,000	1
California beef cattle	Cows	6,000	150	40
	Calves	600,000	150,000	4
California horses	Adults	*Similar to adult beef and dairy cattle*		
	Foals and weanlings	*Not done adequately*		
Striped skunk	Adults	140,000	2,800,000	0.05
	Juveniles	88,000	4,400,000	0.02
California ground squirrels	Adults	78,000	6,500,000	0.012
	Juveniles	412,000	10,300,000	0.004
Coyotes	Adults	41,000	205,000	0.2
	Juveniles	35,000	505,000	0.07
Yellow-bellied marmot	Adults	208,000	10,400,000	0.02
	Juveniles	*Not done*		

4.7 SUMMARY

The variable nature of pathogen and indicator concentrations in surface waters, and the rapid die off of many of these organisms in the ambient environment, makes it very difficult to quantify the importance of different sources on a scale as large as the Central Valley, especially for coliforms that are widely present in water. A single source in close proximity to the sampling location can dominate the coliform concentrations observed at a location downstream of several thousand square miles of watershed. In the Sacramento River, loads of pathogens, especially an animal-derived pathogen such as *Cryptosporidium*, are transported at levels at that are orders of magnitude lower that their excretion in the watershed. Similar data were not available for the San Joaquin River.

CHAPTER 5.0
SUMMARY AND RECOMMENDATIONS FOR FUTURE WORK

The development of the pathogen conceptual model involved the synthesis of a large amount of previously collected data and information from published reports. The information presented in this document can be used to direct future investigations to improve understanding of sources, impacts, and management of fecal indicators and pathogens in the Central Valley and Delta.

5.1 SUMMARY

Evaluation included mapping and plotting of available data by location and source type across the Central Valley and Delta. Unlike other constituents prioritized for evaluation as part of ongoing work toward development of the Central Valley Drinking Water Policy, such as organic carbon and nutrients, that do not have formal numeric criteria, specific numeric criteria do apply to pathogens and fecal indicators as they relate to recreational use and municipal water supply. Levels of fecal indicators and pathogens in source waters directly affect the degree of treatment required for drinking water treatment plants. In the Central Valley and Delta, the recreational standards are routinely exceeded in the San Joaquin River Basin, although they are generally within limits in the Sacramento River Basin.

Although a large quantity of data was available for this analysis, the size of the Central Valley watershed, and complexity of many pathogens and fecal indicator response, especially rapid dieoff, prevented a detailed quantitative analysis of pathogen or indicator loads in the manner performed in prior work for organic carbon and nutrients (Tetra Tech, 2006a, 2006b). Sources considered in this evaluation include wastewater, storm runoff from urban land, and terrestrial wildlife. Aquatic wildlife, although known to a significant contributor of coliforms and possibly pathogens, were not quantified as a source in this analysis.

Substantially more data were available to evaluate fecal indicator organisms, such as coliform bacteria, than true pathogens, such as *Cryptosporidium* and *Giardia*. Of the known sources of coliforms into the waters of the Central Valley, it was found that wastewater total coliform concentrations for most plants were fairly low (<1000 MPN/100 ml). Coliform loads from the largest wastewater treatment plant in the Central Valley were substantially lower than from a canal draining a rapidly urbanizing watershed (NEMDC). In general, along the Sacramento River, the highest total coliform concentrations in water (>10,000 MPN/100 ml) were observed near sample locations influenced by urban areas. Similar total coliform concentration data were not available for the San Joaquin Valley (the highest values were capped at ~2400 MPN/100 ml). However, *E. coli* data were not similarly capped, and for this parameter, comparably high concentrations were observed for waters affected by urban environments and intensive agriculture in the San Joaquin Valley. Finally, sites in the vicinity of the Delta that were close to urban stormwater discharges, had elevated concentrations of coliforms.

Coliform data showed minimal relationships with flow rates, although most of the high concentrations were observed during the wet months of the years, possibly indicating the contribution of stormwater runoff.

Data on pathogens was available primarily for *Cryptosporidium* and *Giardia* along the Sacramento River. Where monitored, these pathogens were often not detected, and when detected, the concentrations were generally very low, typically less than one organism per liter. Given the flows of the Sacramento River and estimates of *Cryptosporidium* oocyst excretion by mammals, typical loads flowing into the Delta from the Sacramento River are of the same order of magnitude as the number of organisms excreted by a single calf (one of the most prolific sources of *Cryptosporidium*). This result could be caused by the presence of natural or artificial barriers/processes that limit transport to water, by the significant die off of oocysts that do reach the water, as well as limitations in the analytical detection of *Cryptosporidium* oocysts in natural waters.

There were limited data on pathogens from one wastewater plant in the Central Valley (Sacramento Regional Wastewater Treatment Plant). These data showed average and median effluent concentrations of both *Cryptosporidium* and *Giardia* well in excess of concentrations in the Sacramento River (*Giardia* >100 times Sacramento River levels; *Cryptosporidium* >50 times Sacramento River levels). Also, the fraction of samples where either of these pathogens was detected in the effluent was high: 100% for *Giardia* and 80% for *Cryptosporidium*. However, the viability of these organisms at the point of discharge is not known.

5.2 RECOMMENDATIONS FOR FUTURE WORK

Coliforms are recognized to not be ideal indicators for pathogens because of their lower survivability compared to some pathogens. A wide variety of new indicators are under development although their applicability, generality, and cost remain concerns (NAS, 2004). For the foreseeable future, it appears that despite all of the limitations of coliform measurements, these will remain the *de facto* standard for identifying the presence of pathogens. It is recommended that the CVDWPWG

continue to support collection of data on coliforms for consistency with historical data, but also continually evaluate new analysis techniques recommended by NAS (2004), described below, for application across the entire Central Valley.

Recent advancement in microbiology, molecular biology and analytical chemistry provides opportunities for more accurate, timely and direct detection and measurements of pathogens (NAS, 2004). Traditional methods for bacterial indicators often are based on measuring organisms by culture or infectivity and often require a prolonged incubation period. Some newer molecular-based or immuno-based techniques are based on measuring cell constituents or components that are unique to the target organisms such as nucleic acids, surface proteins, carbohydrates, some specific enzyme activities, ATP levels or some specific toxins. A combination of the traditional and newer methods has also been used in measuring waterborne pathogens, particularly for the detection of protozoa in water.

Generally there are three groups of newer methods other than the traditional culture methods:

1) Molecular based method of nucleic acids analysis. Nucleic acids analysis generally involves measuring DNA or RNA that are unique to a particular microorganism. DNA from a sample is typically amplified through PCR (polymerase chain reaction) and then analyzed through sequencing or by hybridization to a gene probe or array containing the complementary genetic sequence (microarray method). Detection of PCR products can be performed using electrophoresis or fluorescence technologies. Pulsed-field gel electrophoresis (PFGE), ribotyping and other technologies used to label and measure DNA fragments.

2) Immunological methods for detecting surface proteins of bacteria, protozoa and viruses unique to the microbes. Immno-based methods are based on detection of specific antigens such as soluble proteins and whole microorganisms through antibodies. The most common immunological method is the enzyme-linked immunosorbent assay (ELISA), in which two antibodies are used to bind the antibody of the microorganisms.

3) Measuring of other cell components such as ATP levels or specific toxins of the organisms.

For example, a variety of methods have been used in detection of infectious *Cryptosporidium* oocysts in water samples. Cell culture methods are now being used in measuring *Cryptosporidium* infectivity. Molecular based methods using PCR or RT-PCR techniques that target the nucleic acid components as well as methods combine PCR and cell culture or real-time PCR are now being used. Immuno-based assays using antibodies specific to *Cryptosporidium* parvum and a second antibody conjugated to a fluorescent dye have been also been used.

Compared to traditional culture methods, the molecular and immunological methods generally offer higher precision and higher specificity to the desired target organisms, require less time and smaller sampling volume (NAS, 2004). Traditional culture

methods offer moderate quantification capability compared to low to moderate quantifying capabilities by nucleic acid analysis.

Unlike chemical constituents analyzed as part of other conceptual models developed for the CVDWPWG, coliform indicators vary by orders of magnitudes over small distances and short time-scales. Accurate quantification of such parameters requires substantial data, which are often not available. A key observation of the source evaluation presented in this report is that coliform indicator levels are most responsive to sources and events in close proximity to the monitoring location, and that large scale modeling, with consideration of transport over many days, may be of limited benefit. While the large-watershed modeling approach, i.e., on the scale of the Central Valley, is appropriate for somewhat stable constituents such as total dissolved solids and organic carbon, a fundamentally different approach is recommended for modeling fecal indicator loading, with an emphasis on relatively small watershed and surface water areas. Within these smaller areas of interest, individual sources, specifically wild and domestic animals, and aquatic species, can be characterized with greater precision. US EPA's FecalTool model (US EPA, 2000) is a useful approach for computing coliform loads for such situations.

Given the strength of the stormwater source, more detailed evaluation needs to be performed of the linkage between rainfall and coliform loads, with a view to develop management practices for minimizing the loading from stormwater.

Computer tools can be used to make more detailed estimates of bacterial loads in surface waters, and have the benefit of being developed for use in a predictive mode such that the public or water supply agencies can get advance notice of elevated bacterial levels under specific weather conditions or other forcing events. However, the additional effort and data collection needed to make such predictions meaningful has to be weighed against the collection of data on true pathogens.

Substantially greater data collection, particularly in the San Joaquin Valley, is recommended for *Cryptosporidium* and *Giardia* given their longer survival times in water relative to indicator organisms, and given the numbers of domesticated animals in the watershed. In general, sampling of San Joaquin and Sacramento River source waters as well as potential sources such as urban stormwater drainage/runoff for a wide range of potential pathogens including bacteria and viruses identified in Chapter 2, even on a limited scale and frequency, will provide valuable information on the health of this extremely vital resource. Sampling of pathogens and indicators at delta pump locations is also recommended for direct evaluation of source water quality for export to other parts of the state.

Besides sampling surface water, sampling of other discharges such as wastewater and urban stormwater for pathogens is also strongly desired. The limited pathogen data on wastewater effluent that is currently available indicates that pathogen levels may be much higher than in surface waters, and reflects the survival of these organisms following chlorination. There is no similar data on pathogens for stormwater discharges, although coliform data in stormwater indicate a highly significant microbial source. Given the general proximity of major wastewater and urban stormwater discharges to the Delta, and its significance as a drinking water source,

better understanding of the loads, fate, and transport of pathogens in and around the Delta is of vital importance.

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