

Prepared by:
Emmons & Olivier Resources, Inc.
for the Minnesota Pollution Control Agency

Literature Summary of Bacteria - Environmental Associations Developed for the Upper Mississippi River Bacteria TMDL Project



December 2009

Document Component Specs

Text: Corporate Express • Signature white, 20 lb. text – 30% post-consumer fibers, Green Seal® Certified

Back Cover: Neenah Paper • Esse • Texture, Sapphire • 100 lb. cover • 30% post-consumer fibers, Green Seal® Certified

Wire Binding: Manufactured using recycled high carbon steel

Literature Summary of Bacteria – Environmental Associations

Developed for the Upper Mississippi River Bacteria TMDL

December 2009

Primary Authors and Contributors

Minnesota Pollution Control Agency

Barb Peichel
Phil Votruba

Minnesota Department of Health

Art Persons

Emmons & Olivier Resources, Inc.

Pat Conrad
Andrea Plevan
Toben Lafrancois

Table of Contents

Executive summary..... 1
Purpose of literature review 2
Background..... 2
Literature Review Methods 3
 Sources..... 3
 Search rubric 4
Factors associated with bacterial contamination 5
Detecting bacterial contamination from fecal material 8
Source partitioning 8
Recent advances in modeling..... 9
Literature..... 10
Appendix A. Citations and background literature relevant to bacterial TMDL analyses. 11

EXECUTIVE SUMMARY

Minnesota’s current water quality standards use *E. coli* as an indicator for bacterial contamination from human and animal fecal material. However, bacterial contaminants are difficult to quantify, despite their direct impact on human and ecosystem health. Sources and supporting conditions are highly variable and monitoring protocol and methods introduce a large amount of uncertainty. This analysis summarizes the most recent scientific literature concerning the factors that predict, measure, or indicate fecal bacterial contamination. Topics include known factors responsible for the introduction, transport, and/or outbreak of fecal bacteria, studies of detection methods, source identification, and models. A concise summary of factors is listed in Table 1 (Page 6). Factors that are themselves associated with water quality directly are listed in Table 2 (Page 6) with representative citations. All relevant studies found in the literature review are listed with a brief summary of findings in Appendix A.

PURPOSE OF LITERATURE REVIEW

This literature review is part of the Upper Mississippi River Bacteria TMDL project. With the aim of improving the ability to develop not only this TMDL, but also other bacteria TMDLs throughout Minnesota, multiple literature reviews are being completed. The goal of this literature review was to identify relationships between *E. coli* in surface waters and other pollutants, contaminants of concern, or water quality parameters. While the TMDL will focus on setting loading limits for *E. coli* in particular, understanding how the indicator relates to other parameters will shed light on sources of bacterial contamination from fecal material and how to address the sources.

The literature search resulted in a compilation of available literature on the factors associated with fecal bacteria outbreaks in streams. Although the papers are not all discussed in detail in this report, the references are included in Appendix A.

BACKGROUND

Bacterial contamination of surface waters from human wastes is one of the primary interfaces between human and ecosystem health (history reviewed in Brown 2005). Development of wastewater treatment was an important step addressing this contamination and led to point source mitigation of human waste impacts. Unfortunately, strains of bacteria from urban sources are now a permanent part of stream ecosystems (Higgins et al. 2005). Bacteria can grow and reproduce in stream sediments and outbreaks can occur in the absence of new waste inputs (Byappanahallie et al. 2003; MPCA 2007; Scherer et al. 1992). Reductions in point source inputs are no longer sufficient to prevent bacterial contamination of surface and ground waters (Meyers et al. 1998). Current problems with bacterial contamination are reviewed in Francy et al. 2000. Wastewater treatment plants can be a source of bacterial contamination, but often outbreaks are introduced by other sources related to both urban and rural landscape use (e.g. impervious surfaces, agriculture) or caused by factors that support an outbreak of bacteria already present in the system from previous wastewater or natural inputs (e.g. high temperatures, nutrients).

Determining the source of bacterial contamination is a primary concern for predicting and mitigating bacterial outbreaks. Difficulties with source partitioning are a problematic element for TMDL assessments (He et al. 2007; MPCA 2006, revised). High natural variation and the interaction of multiple sources with multiple environmental factors strongly influence the incubation, transport, and inactivation of bacterial contaminants. Detection is also an issue. Bacterial contamination from fecal material is notoriously difficult to measure because different pathogenic organisms and forms differentially survive, require costly and time sensitive measurement, and are highly variable in space and time. Current U.S. Environmental Protection Agency (EPA) and Minnesota water quality standards rely on *E. coli* as an indicator of general bacteria contamination.

The state standard for *Escherichia (E.) coli* is as follows:

Not to exceed 126 organisms per 100 milliliters as a geometric mean of not less than five samples representative of conditions within any calendar month, nor shall more than ten percent of all samples taken during any calendar month individually exceed 1,260 organisms per 100 milliliters. The standard applies only between April 1 and October 31.

Bacterial contamination does not always vary with or follow the same spatial/temporal patterns as other contaminants with similar sources. Different bacterial types (e.g. *E. coli* and *Salmonella* sp.) are often found together (responding to similar conditions) but do not necessarily correlate enough to be used as proxies for each other. Lack of knowledge about the environmental conditions that sustain bacterial impacts and lead to outbreaks has been identified as a primary concern for future TMDLs. This literature review collects and summarizes the most recent and pertinent information on the factors related to bacterial outbreaks. Also represented are recent advances in detecting, modeling, predicting, and mitigating bacterial contamination. A summary of this literature is presented in Appendix A.

Two challenges remain for addressing bacterial outbreaks in TMDLs. First, the complexity of non-point sources, incubation, multiple enabling factors, and the failure of some BMPs to address outbreaks confound the TMDL approach (Clary et al. 2008; He et al. 2007). Careful source partitioning and monitoring plans, however, allow accurate distribution of pollutant allocations, and multiple integrated management options can then lead to successful outcomes (e.g. Mississippi Dept. Env. Qual., 1999; Rifai 2006). Secondly, water quality standards are not always flexible enough to handle the non-anthropogenic and anthropogenic variation in bacterial concentrations (Clary et al. 2008). One effective solution is to carefully select reference systems to define exceedences. These measures allow exceedence evaluation and source partitioning to be handled effectively for a TMDL (Clary et al. 2008; He et al. 2007).

LITERATURE REVIEW METHODS

Sources

Several methods were used to search and assess available literature on the factors associated with fecal bacterial outbreaks in streams. The literature review was performed in four stages. First, USGS SIRs (scientific investigations reports) were searched using the online USGS data base. This search method produced several key papers. Some of these reports are not available (the links are dead); in some of these cases, an Internet search located a .pdf version of the report.

Secondly, the EPA website was searched manually, particularly the TMDL section. This produced several good examples of bacterial TMDLs cited below, but far fewer than expected; future reviews may need to search each state's website for relevant TMDL projects.

Third, the scientific literature was searched in several ways. A set of journals was chosen for intensive searching based on the journal content. The following journals were searched from 1972 (year chosen because of the Clean Water Act) to 2009:

- Environmental Microbiology

- Applied and Environmental Microbiology
- Water Science and Technology
- Journal of Environmental Quality
- Environmental Science and Technology
- Environmental Toxicology and Water Quality
- Environmental Pollution
- Water Research

In addition, the biological abstracts search engine was searched. This search did not produce any new articles that passed selection criteria (see below). This confirmed the journal selections for the intensive search.

Finally, the works cited of the most relevant papers were checked for papers of interest. This process was iterated until a ‘closed loop’ was found with regard to papers relevant to the task at hand.

Search rubric

In all cases where search criteria were available, each the following search terms was used:

Where X = {fecal, faecal, bacteria, bacterial},

- Indicator X
- X contamination
- Model* X
- Factor* X
- Factor* X indicator
- Causes X
- Escherichia coli
- {all of the above} with “water quality”
- {all of the above} with “tmdl”
- {all of the above} with “river” or “stream”

Search terms were applied to fields for titles and abstracts only. Full text searches were unwieldy and produced papers with little or no relation to the desired information. These search terms were also used in the USGS database and the EPA website. Web based browsers did not produce reliable results but in some cases led to author’s websites where key papers were available.

Selection criteria

Papers were selected based on professional judgment guided by the following criteria:

- Direct relevance to bacterial TMDL work on rivers
- Direct relevance to determining factors underlying bacterial outbreaks in rivers
- Any work on mechanisms, causal pathways, or methods relevant to the above issues
- Any work on relevant scientific, management, or methodological advances

Over the course of the literature review and discussions with experts, it was noted that quite a bit of literature is devoted to beaches and beach closings. Such work, particularly from the Great Lakes area, was included because many of the models of fecal contamination in beaches depend upon input from stream or river sources. Consequently, models of beach closings in lentic systems are primarily lotic factor models and highly relevant to river systems.

FACTORS ASSOCIATED WITH BACTERIAL CONTAMINATION

Bacterial contamination can be the result of many combinations of factors including non-point sources and landscape use, transport in streams and stream water quality, and other environmental factors. Since the implementation of the Clean Water Act, it has been found that decreases in point source loading do not always lead to less bacterial contamination. Non-point sources are increasingly recognized as major contributors to bacterial loads. It is also becoming clear that the growth and reproduction of bacteria in stream sediments from previous human and animal inputs can be the source of outbreaks if supported by other environmental factors (e.g., increases in nutrients, temperature, and stormflow).

Survival of bacteria and non-point loading underscores the importance of environmental factors that lead to bacterial outbreaks. Some factors act like proxies, correlating with outbreaks. Other factors, alone or in concert, are known causes of outbreaks from pre-existing and/or recently introduced bacteria populations. The most commonly identified factors related to bacterial outbreaks are shown in Table 1. Known factors positively associated with bacterial outbreaks and representative citations listed according to EPA drinking water quality standards and Minnesota Pollution Control Agency (MPCA) water quality standards are shown in Table 2.

Table 1. Factors most commonly found to relate to bacterial contamination in surface waters. No single factor explains bacteria outbreaks in all systems. These factors have been used in models and found to be predictive of bacterial contamination from fecal matter. Some factors correlate with each other, independently affect bacteria, or combine synergistically to enhance outbreaks depending on the study system, nature of the input, and environmental conditions. The exact values are dependent upon local conditions, and values reported in these studies should not be directly applied to other systems. Complete citations and summaries are listed in Appendix A.

Most commonly reported factors or strong positive relationship to bacterial contamination	Less commonly reported factors or weaker positive relationship to bacterial contamination
High storm flow (the single most important factor in multiple studies)	High nutrients
% rural or agricultural areas greater than % forested areas in the landscape (entire watershed area)	Loss of riparian wetlands (but constructed wetlands or retention ponds can increase bacteria loading from waterfowl)
% urban areas greater than % forested areas in the landscape (riparian area)	Shallow depth (bacteria decrease with depth)
High water temperature	Amount of sunlight (increased UV-A deactivates bacteria)
High impervious surfaces*	Sediment type (higher organic matter, clay content and moisture; finer-grained)
Livestock (riparian area) present	Soil characteristics (higher temperature, nutrients, organic matter content, humidity, moisture and biota; lower pH)
Suspended solids	Stream ditching (present or when increased)
	Epilithic periphyton present
	Presence of waterfowl or other wildlife
	Conductivity

*"High impervious surfaces" is the measurement that has been found in models or statistical analyses to be predictive of fecal contamination. Several associated or underlying mechanisms linked to landscape development, such as housing density, population density, and pet density, correlate with fecal contamination (Young 1999) but were not the measurements actually used in the models.

Table 2. Parameters with water quality standards that are positively associated with bacterial outbreaks, organized by EPA drinking water standards and MPCA water quality standards. Other water quality standards exist, but the associated parameters were not found in the literature review. A complete list of recent work is presented in Appendix A. No single factor is 100% explanatory in every system, and many factors interact or are correlated with one another.

Existing standards	Representative citations
National (EPA) primary drinking water standards: Class 1B	
<i>Cryptosporidium</i>	Bushon et al. 2007; Francy et al. 2000
Enteric viruses	Bushon et al. 2007; Francy et al. 2000
<i>Giardia lamblia</i>	Bushon et al. 2007; Francy et al. 2000
Total coliforms	Bushon et al. 2007; Francy et al. 2000
Nitrate and nitrite (measured as nitrogen)	Schumacher, 2003
Turbidity	Brady 2007
State (MPCA) water quality standards: Classes 2A-C	
Chl-a	Nevers et al. 2007 (lentic)
<i>E. coli</i>	Byappanahallie et al. 2003; Francy et al. 2000; Olyphant 2005
Temperature	MPCA 2007; Olyphant 2005; Rhodes et al. 1988
Total phosphorus	Byers et al. 2005
Turbidity	Brady et al. 2007; Nevers et al. 2007

Factors related to non-point sources and landscape use can be very complicated but are not surprising. *E. coli* concentrations increase with stream ditching, agricultural tiling and ditching, increased drainage from rural or urban landscapes, and wetland loss. There is a very strong link between agriculture, particularly animal husbandry, and high concentrations of fecal indicator bacteria (Crowther et al. 2002). Livestock in streams or riparian areas has a direct impact that can last long after livestock are removed (Byers et al. 2005; Kay et al. 2007). In the absence of bacterial contamination from fecal material, soil can contain high indicator bacteria concentrations (such as *E. coli*) that are not necessarily pathogenic, producing false positive readings for bacterial contamination (Harding et al. 1991). Changes in runoff can introduce this background source into streams in high quantities. In other watersheds, soil and/or sediment acts as an incubator for anthropogenic and/or wildlife sources of fecal bacteria (Byappanahallie et al. 2003). Housing density, population density, house pet density, impervious surfaces, and other factors relating to landscape development are also strongly related to fecal bacteria concentrations (Young 1999).

Transport of fecal bacteria is difficult to model because of bacterial life cycles, highly stochastic population distributions, movement downstream, and incubation in sediments. Nonetheless, several in-stream factors are commonly related to high bacterial counts. Stormwater inputs are the single most important factor leading to bacterial contamination. A single day of storm loading can introduce the equivalent bacterial counts of years of dry loading and the settle-able component of bacterial input is highest at the beginning of storm events (Krometis et al. 2007). Resuspension of sediments at high flow re-introduces incubated *E. coli* (MPCA 2007).

Turbidity is associated with bacterial outbreaks (Bushon et al. 2006; Nevers et al. 2007). Likewise total suspended solids, total phosphorus, and other nutrients correlate with outbreaks in some systems (Byer et al. 2005; Ellis et al. 1995). This is not always the case, however (Surbeck et al. 2006). Nutrients may correlate directly with fecal inputs, especially during storms, but they also can directly increase the growth of bacteria in the system. Consequently, fecal bacteria from past inputs can be the source of an outbreak in the absence of new nutrient loading. This can be true of fecal bacteria and/or their indicators. This indicates the possibility of false positives from monitoring indicators but also serious outbreaks in the absence of actual fecal matter introduced in the system. This relationship between nutrients and bacteria is not always clear. Bacterial concentrations can vary independently from nutrients even below waste water treatment facilities (Rasmussen et al. 2005). In addition to nutrients, stream temperature increases have a similar effect on new and relic bacterial inputs (MPCA 2007).

Fecal bacteria are known to grow very well in epilithic algae and noxious algae like *Cladophora* (Ksoll et al. 2007; Englebert et al. 2008). Increases in algae can lead to increases in fecal bacteria counts, but not in all cases (Englebert et al. 2008). Waterfowl are a known biological source of fecal coliform, and confound source studies tracking anthropogenic bacterial contamination from fecal material. Waterfowl are increasingly concentrated in urban and suburban areas, suggesting that some water quality best management practices (BMPs) actually attract waterfowl in high densities and increase bacterial contamination from fecal material (Clary et al. 2008).

Some environmental factors are known to reduce bacterial contamination. Sunlight (UV-A but not UV-B) directly inactivates fecal bacteria (Crowther et al. 2001; Davies-Colley et al. 1994). However, Kleinheinz et al. (2006) found that bacteria concentrations decrease with water depth between 1 and 4 feet. Direct application of these factors is most easily employed at point sources and difficult to address for BMPs for non-point sources.

DETECTING BACTERIAL CONTAMINATION FROM FECAL MATERIAL

Laboratory methods for detecting bacterial contamination from fecal material (for example, beta-D-glucuronidase activity, which is an enzyme specific to *E. coli*, predicts outbreaks and is a good rapid assessment – Servais et al. 2005) are reviewed in Maul et al. 1983 and Lifshitz 1998. For comparison purposes, a list of EPA and MPCA approved laboratory methods is available in Appendix D of MPCA's *Volunteer Surface Water Monitoring Guide* at <http://www.pca.state.mn.us/water/monitoring-guide.html>.

The use of *E. coli* as a useful indicator has recently come into question. It is important not to misunderstand criticism of *E. coli* as an indicator because under most known conditions, higher concentrations of *E. coli* do correlate with higher concentrations of other pathogenic bacteria. The criticism of *E. coli* standards centers on the fact that despite this positive relationship, other pathogens can be found in high concentrations when *E. coli* is not, leading to false negative reports (see Bushon 2004 for a very useful comparison of indicators and detection methods). Compared with using fecal coliform as an indicator, *E. coli* is considered a better indicator of gastroenteritis (i.e. inflammation of the stomach and the intestines that can cause nausea and vomiting and/or diarrhea).

A second issue with *E. coli* as an indicator for bacterial contamination is the large amount of error introduced by monitoring protocols (Lifshitz 1998). Recently this uncertainty has been addressed by updating laboratory and analytical methods (McCarthy et al. 2008). Most monitoring protocols lead to false positive reports (Stoeckel et al. 2004). Taken together, *E. coli* as an indicator of bacterial contamination from fecal material is thus subject to both high type I and II errors (false positive and false negative reports).

Errors due to spatial and temporal variability in bacterial concentrations can be somewhat mitigated by increasing the number of samples and sampling sites, which relies on cheaper methods of rapid detection (Servais et al. 2005; Love et al. 2007). Fifteen-minute sampling regimes show significant diurnal variation in *E. coli* concentrations (Maeyns et al. 2006). A significant amount of variation is caused by the biology of microorganisms. Oocysts have been found to remain when the indicator species has died off (Medema et al. 1997). Other factors impacting incubation and transport are addressed below. Issues with the detection of bacterial contamination, field and laboratory protocol, and data analysis need to be carefully weighed to address these issues (McCarthy et al. 2008).

SOURCE PARTITIONING

A major component of detection is source partitioning, which is particularly relevant to TMDL work. The importance of sewage improvements to human and ecosystem health cannot be underestimated. However, in many cases sewage improvements can have no impact on the

number and frequency of water quality standard exceedances in some systems (Crowther et al. 2007). This fact underscores the importance of identifying and quantifying non-point sources of bacterial contamination.

There is no single agreed upon method of source partitioning (reviewed in Blanch et al. 2006)¹. Techniques for source partitioning are reviewed in Stoeckel et al. (2007). Antibody techniques for source partitioning are reviewed in Love et al. (2007). Multiple lines of evidence are often required to identify and quantify bacterial sources (Edge et al. 2007). Ahmed et al. identifies advantages and disadvantages to library-dependent and library-independent microbial source tracking methods; for library-independent methods, host specificity of potential marker genes needs to be identified in order to determine the gene's utility in source partitioning (Ahmed et al. 2008). The complicated array of sources and factors impacting bacterial outbreaks from non-point sources make TMDL studies extremely difficult (He et al. 2007). Nonetheless, sources can be identified with a great deal of accuracy by combining methods, and some methods are very cheap (for example, simply using spatial analysis of a large number of monitoring points). Recent advances suggest that bacteriophage and genetic fingerprinting methods are becoming cheaper as well.

RECENT ADVANCES IN MODELING

Pitt (2007) provides an excellent overview of problems associated with modeling, detection, and prediction of bacterial outbreaks. While many criteria for assessing bacterial outbreaks are based on previous day counts, new predictive models for beaches are more accurate (Nevers et al. 2007). Model construction and components for predicting bacterial outbreaks at beaches are reviewed by Olyphant (2005) and Dyble et al. (2008). Beach models are included insofar as they relate to river or stream input. These models included factors found to relate to the introduction and transport of fecal bacteria in streams even though the ultimate purpose is to predict beach outbreaks. Most models of outbreaks rely on some combination of streamflow, rainfall, and turbidity or other environmental measures of material input to streams (Brady 2007).

Jobson et al. (2001) used a Branched Lagrangian Transport Model (BLTM) to predict the transport of bacteria through single-dimensional channels. This type of model requires discharge, cross sectional area, geometric information on the number of branches, and coefficients of bacterial decay. Bacterial decay rates are affected by several of the factors in Table 1, particularly UV radiation and temperature. The model was successfully applied to predicting outbreaks on the Cuyahoga River, Ohio (USA). Rasmussen et al. (2005) used a similar but two dimensional model, finding that decay rates had little seasonal variation but that bacteria and nutrients did not vary together over time. Nonetheless, the model was able to predict bacterial concentrations (at low flow). Models can be calibrated by dye tracer studies, genetic analysis, decay rates, and further source partitioning (Schumacher 2003).

¹ The two methods in Blanch et al. 2006 that were shown to be useful indicators: the ratio of the densities of somatic coliphages and phages infecting *Bacteroides thetaiotaomicron* to the density of somatic coliphages and the ratio of the densities of fecal coliform bacteria and phages infecting *Bacteroides thetaiotaomicron* to the density of fecal coliform bacteria.

LITERATURE

All relevant studies found in the literature review are summarized in a table in Appendix A. The studies can be generally categorized based on content: factors analysis or model, assessment of methodology, review of literature or methods, source partitioning, explicit application to a TMDL or BMP. Each of these categories have been assigned a code, and each citation is paired with all relevant codes for targeted reference and review.

APPENDIX A. CITATIONS AND BACKGROUND LITERATURE RELEVANT TO BACTERIAL TMDL ANALYSES.

Citations are given one or more codes indicating the content:

F indicates a factors analysis or model

M indicates an assessment of methodology

R indicates a review of literature or methods

S indicates work on source partitioning

T indicates explicit application to a TMDL or BMP

Citation		Summary
Ahmed, W., J. Stewart, T. Gardner, D. Powell. 2008. A real-time polymerase chain reaction assay for quantitative detection of the human-specific enterococci surface protein marker in sewage and environmental waters. <i>Env. Microbiol.</i> 10(12):3255-3264.	M S	<ul style="list-style-type: none"> • PCR technique that identifies and quantifies human sources of bacterial contamination. • Markers were particularly present in surface water after storm events.
Ahmed, W., J. Stewart, D. Powell, T. Gardner. 2008. Evaluation of the host-specificity and prevalence of Enterococci surface protein (<i>esp</i>) marker in sewage and its application for sourcing human fecal pollution. <i>J. Environ. Qual.</i> 37: 1583-1588.	M S	<ul style="list-style-type: none"> • The <i>esp</i> marker is a highly reliable indicator of human sewage pollution and distinguishes it from animal wastes.
Armon, R., Y. Kott. 1995. Distribution comparison between coliphages and phages of anaerobic bacteria (<i>Bacteroides fragilis</i>) in water sources, and their reliability as fecal pollution indicators in drinking water. <i>Wat. Sci. Tech.</i> 31(5-6): 215-222.	M	<ul style="list-style-type: none"> • Bacteriophages correlate with fecal contamination. • Authors recommend bacteriophages as indicators of pollution.
Bell, A. A.C. Layton, L. McKay, D. Williams, R. Gentry, G.S. Saylor. 2009. Factors influencing the persistence of fecal <i>Bacteroides</i> in stream water. <i>J. Environ. Qual.</i> 38(3): 1224-1232.	F M	<ul style="list-style-type: none"> • Assessed factors impacting <i>Bacteroides</i> gene detection as a monitoring tool. • Higher temperatures and presence of background bacterial community were most significantly correlated to indicator presence.
Bennear, L.S., K.K. Jessoe, S.M. Olmstead. 2009. Sampling out: regulatory avoidance and the total coliform rule. <i>Environ. Sci. and Tech.</i> 43(14): 5176-5182.	M	<ul style="list-style-type: none"> • A significant number of total coliform violations were missed due to (intentional) over-sampling that depressed the monthly geometric mean.
Blanch, AR; Belanche-Munoz, L; Bonjoch, X; Ebdon, J; Gantzer, C; Lucena, F; Ottoson, J; Kourtis, C; Iversen, A; Kuhn, I; Moce, L; Muniesa, M; Schwartzbrod, J; Skraber, S; Papageorgiou, GT; Taylor, H; Wallis, J; Jofre, J. 2006. Integrated analysis of established and novel microbial and chemical methods for microbial source tracking. <i>App. and Environ. Microbiology</i> 72(9): 5915-5926.	F S	<ul style="list-style-type: none"> • Tested 26+ parameters to distinguish human and non-human fecal sources. • Several indicators and combinations of indicators; however none were 100% predictive by themselves. • At a minimum, 2 variables are needed for 100% distinction; the variables are two ratios made up of the densities of somatic coliphages, phages infecting <i>Bacteroides thetaiotaomicron</i>, and fecal coliform.
Bolster, C.H., S.L. Walker, K.L. Cook. 2006. Comparison of <i>Escherichia coli</i> and <i>Campylobacter jejuni</i> transport in saturated porous media. <i>J. Environ. Qual.</i> 35: 1018-1025.	M	<ul style="list-style-type: none"> • Compared transport of indicator and target organisms to test suitability of indicators. • Differences in cell structure led to differential transport of indicator and target, particularly in conditions of low attachment rates. • Implies indicators are under-representing actual contamination.
Brooks, J.P., A. Adeli, J.J. Read, M.R. McLaughlin. 2009. Rainfall simulation in greenhouse microcosms to assess bacterial associated runoff from land-applied poultry litter. <i>J. Environ. Qual.</i> 38:218-229.	F	<ul style="list-style-type: none"> • Rainfall on poultry litter produced increased microbial run-off, including several key bacterial pathogens but not necessarily all indicator organisms.
Bradford, S.A., E. Segal. 2009. Fate of indicator microorganisms under nutrient management plan conditions. <i>J. Environ. Qual.</i> 38: 1728-1738.	M	<ul style="list-style-type: none"> • Biotic factors in soil control die-off of fecal bacteria. • NMPs dramatically reduce bacterial input to groundwater.

Citation		Summary
Brady, A.M.G., 2007, Rapid method for <i>Escherichia coli</i> in the Cuyahoga River: U.S. Geological Survey Open-File Report 2007–1210, 5 p.	M	<ul style="list-style-type: none"> • Compared 1hr vs. 24 hr techniques for measuring <i>E. coli</i>. • Tested a previous model based on turbidity, rainfall, and streamflow. • Conclude models work if site specific and constantly refined.
Brion, G.M., H.H. Mao, S. Lingireddy. 2000. New approach to use of total coliform test for watershed management. <i>Wat. Sci. and Tech.</i> 42(1): 65-69.	F M	<ul style="list-style-type: none"> • Combined several indicator tests to determine most important ones for models.
Burton, G.A., D. Gunnison, and G.R. Lanza. 1987. Survival of pathogenic bacteria in various freshwater sediments. <i>App. and Env. Microbiolo.</i> 53(4):633-638.	F	<ul style="list-style-type: none"> • Survival of four human associated bacteria was tested; linear die-off rates were calculated for each.
Bushon, E., G.F. Koltun. 2004. Microbiological water quality in relation to water-contact recreation, Cuyahoga River, Cuyahoga Valley National Park, Ohio, 2000 and 2002. USGS WRIR 03-04333.	F M	<ul style="list-style-type: none"> • Examined relationship between <i>E. coli</i> as an indicator and other microorganisms/viral pathogens. • Used coliphage bacteria as indicator. • Includes useful table comparing methods for detecting various microorganisms. • In cases where analysis was available, other pathogenic organisms were larger in samples violating <i>E. coli</i> standards than in samples that did not (single sample exceedances, not geometric mean exceedances). • Conclude: Other harmful pathogens can be present when <i>E. coli</i> is not (or below standard), but when <i>E. coli</i> is present, other harmful pathogens are more likely to be present and in greater abundance.
Bushon, R., A. Brady. 2006. Testing of a rapid method for monitoring bacteria in the Cuyahoga River. Cuyahoga Watershed Symposium, 18 October 2006. USGS.	M	<ul style="list-style-type: none"> • Showed site specific models for relation of <i>E. coli</i> with turbidity. • Compared lab methods.
Bushon, R.N., G.F. Kultun. 2003. Microbiological water quality in relation to water-contact recreation, Cuyahoga River, Cuyahoga Valley National Park, Ohio, 2000 and 2002. USGS WRIR 03-4333.	F M	<ul style="list-style-type: none"> • See above. (NOTE: this is the same document as Bushon et al. 2004; this citation is included because some citations list this paper as 2003. The official USGS citation is for 2004.)
Byappanahalli, M. and others. 2003. Ubiquity and persistence of <i>Escherichia coli</i> in a Midwestern coastal stream. <i>App. and Env. Microbiol.</i> 69(8): 4549-4555.	F M	<ul style="list-style-type: none"> • Direct fecal input does not explain abundance or distribution of <i>E. coli</i>. • <i>E. coli</i> in water, sediment, bank sediment, and margin sediment all correlate. • Higher sediment moisture correlates with <i>E. coli</i>. • <i>E. coli</i> persistence and distribution enhanced by ditching, higher drainage, and wetland loss.
Byappanahalli, M.N., R.L. Whitman, D.A. Shively, M.J. Sadowsky, S. Ishii. 2006. Population structure, persistence, and seasonality of autochthonous <i>Escherichia coli</i> in temperate, coastal forest soil from a Great Lakes watershed. <i>Environmental Microbiology.</i> 8(3):504–513.	F	<ul style="list-style-type: none"> • Report the variety of factors influencing <i>E. coli</i> populations in soil. • Soil strains are genetically distinct from human and animal strains.
Byers, H.L., M.L. Caberera, and others. 2005. Phosphorus, sediment, and <i>Escherichia coli</i> loads in unfenced streams of the Georgia Piedmont, USA. <i>J. Environ. Qual.</i> 34:2293-2300.	F T	<ul style="list-style-type: none"> • Cattle directly in stream have high impact. • TSS and TP (DRP) correlate with outbreaks of <i>E. coli</i>. • BMPs are alternate water sources for livestock, reduce runoff and act as buffers.
Campos, C., G. Oron. M. Salgot, L. Gillerman. 2000. Behavior of the fecal pollution indicators in a soil irrigated with treated wastewater under onsurface and subsurface drip irrigation. <i>Wat. Sci. and Tech.</i> 42 (1-2): 75-79.	M	<ul style="list-style-type: none"> • Factors that impact incubation or deactivation of fecal bacteria in soils are temperature, pH, rainfall, sunlight, soil composition (various aspects), and antagonism by soil microbiota.

Citation		Summary
Chaer, G.M., M.F. Fernandes, D.D. Myrold, P.J. Bottomley. 2009. Shifts in microbial community composition and physiological profiles across a gradient of induced soil degradation. <i>Soil Sci. Soc. Am.</i> 73: 1327-1334.	M	<ul style="list-style-type: none"> Microbiological assay techniques differentially detect community changes from disturbance.
Clary, J., J.E. Jones, B.R. Urbonas, M.M. Quigley, E. Strecker, T. Wagner. 2008. Can stormwater BMPs remove bacteria? <i>Stormwater</i> . Online http://www.stormh2o.com/may-2008/bacterial-research-bmps.aspx	M T	<ul style="list-style-type: none"> No single BMP removes all bacteria in all conditions. Some BMPs can export bacteria (those that attract waterfowl like swales and detention ponds). Upper quantitation limits for bacteria are determined by sample dilution. This makes comparing studies (or even sites within a study) extremely difficult.
Collado, L. I.Inza, J. guarro, M.J. Figueras. 2008. Presence of <i>Arcobacter</i> spp. in environmental waters correlates with high levels of fecal pollution. <i>Env. Microbiol.</i> 10(6): 1635-1640.	M	<ul style="list-style-type: none"> Introduced an emerging family of bacterial pathogens that correlate with fecal contaminants.
Collins, R. 2004. Fecal contamination of pastoral wetlands. <i>J. Environ. Qual.</i> 33:1912-1918.	F	<ul style="list-style-type: none"> Cattle were found to prefer shallow wetlands, greatly increasing fecal output to streams during storm events. Some analysis of remediation practices.
Coulliette, A.D., E.S. Money, M.L. Serre, R.T. Noble. Forthcoming 2009. Space / time analysis of fecal pollution and rainfall in an Eastern North Carolina estuary. <i>Environ. Sci. Technol.</i>	F	<ul style="list-style-type: none"> Used a Bayesian Maximum Entropy model to develop maps predicting <i>E. coli</i> as a proxy for fecal coliforms. Primary factors related to fecal coliform concentrations were rainfall and temperature.
Crane, S.R., P.W. Westerman, M.R. Overcash. 1980. Die-off of fecal indicator organisms following land application of poultry manure. <i>J. Environ. Qual.</i> 9:531-537.	F M	<ul style="list-style-type: none"> An empirical model of die-off to estimate non-point source bacterial contamination from agricultural lands.
CREST, City of Los Angeles. 2007. Conceptual approach report for the Los Angeles River bacteria source identification study. http://www.crestmdl.org/studies/FINAL_LAR_BSISudy_Conceptual_A.pdf	R S	<ul style="list-style-type: none"> Outline of bacterial source tracking proposal for the Los Angeles River. Review of methods, issues, and solutions; Particular focus on shifting from mass-balance monitoring of indicators towards microbial source tracking (library dependent and independent). Recommend tiered approach starting with traditional indicators, then focused on microbial source tracking.
Crowther, J., D. Kay, M.D. Wyer. 2001. Relationships between microbial water quality and environmental conditions in coastal recreational waters. The Fylde Coast, UK. <i>Wat. Res.</i> 35(17): 4029-4038.	F	<ul style="list-style-type: none"> After sewage improvements, still found same or greater exceedances. Attributed to rainwater, lack of sunshine, and tidal factors. Combination of incubation in soils and high runoff.
Crowther, J., D. Key, M.D. Wyer. 2002. Fecal indicator concentrations in waters draining lowland pastoral catchments in the UK: Relationship with land use and farming practices. <i>Water Res.</i> 36(7): 1725-1734.	F	<ul style="list-style-type: none"> Highly significant relationship between fecal indicator bacteria (FIB) and livestock intensity land use practice.
Davies, C.M., S.C. Apte. 1998. Field evaluation of a rapid portable test for monitoring fecal colliforms in coastal waters. <i>Env. Tox. and Water Qual.</i> 14(3): 355-359.	M	<ul style="list-style-type: none"> Rapid field assessment for fecal bacterial enzymes was successful. Focus was on coastal waters and human access.
Davies-Colley, R.J., R.G. Bell and A.M. Donnison. 1994. Sunlight inactivation of enterococci and fecal coliforms in sewage effluent diluted in seawater. <i>Applied and Environmental Microbiology</i> 60(6):2049-2058.	F	<ul style="list-style-type: none"> Enterococci need 2.3 times more exposure to sunlight before inactivation as compared to fecal coliforms. Depth-dependence of inactivation correlates with light attenuation (UV-A; UV-B does not appear as important).
Davis, E.M., M.T. Garrett, T.D. Skinner. 1995. Significance of indicator bacteria changes in an urban stream. <i>Wat. Sci. Tech.</i> 31(5-6): 243-246.	M T	<ul style="list-style-type: none"> Point source study showing improvements after wastewater treatment improvements.

Citation		Summary
Dentel, S.K., Y. Qi, D.S. Heron. 2008. Improving the assessment of risk from pathogens in biosolids: fecal coliform regrowth, survival, enumeration, and assessment. <i>Wat. Sci. Tech.</i> 57(2):189-193.	M	<ul style="list-style-type: none"> Identifies re-growth as a source of increased fecal contamination after treatment of solids. Possible source of re-entry into aquatic systems.
Dolgonosov, B.M., K.A. Korchagin, E.M. Messineva. 2006. Model of fluctuations in bacteriological indices of water quality. <i>Wat. Res.</i> 33(6):637-650.	F	<ul style="list-style-type: none"> Developed a stochastic differential equation to model bacterial outbreaks and predict exceedences.
Dyble, J. and others. 2008. Environmental controls, oceanography, and population dynamics of pathogens and harmful algal blooms: connecting sources to human exposure. <i>Env. Health</i> 7(Suppl 2):S5	F R	<ul style="list-style-type: none"> Discuss model construction to combine physical and biological parameters for predicting outbreaks. Looks like good source material for starting a model. No real data used however.
Edge, T.A., S. Hill. 2007. Multiple lines of evidence to identify the sources of fecal pollution at a freshwater beach in Hamilton Harbour, Lake Ontario. <i>Water Res.</i> 41:3585-3594.	F M	<ul style="list-style-type: none"> Coastal study, <i>E. coli</i> correlates with depth (increases in shallow water and wet sands) and bird droppings. Key point is they needed multiple lines of evidence to evaluate sources of <i>E. coli</i>.
Ellis, J. B. and Y. Wang. "Bacteriology of urban runoff: the combined sewer as a bacterial reactor and generator." <i>Water Science and Technology.</i> 31: 7, 303-310. 1995.	F	<ul style="list-style-type: none"> Human fecal bacteria show extended in-stream survival. Bacterial generation occurs when nutrient inputs are increased, even in absence of new bacterial inputs.
Englebert, E.T., C. McDermott, G.T. Kleinheinz. 2008. Effects of the nuisance algae, <i>Cladophora</i> , on <i>Escherichia coli</i> at recreational beaches in Wisconsin. <i>Sci. of the Tot. Env.</i> 404:10-17.	F	<ul style="list-style-type: none"> <i>E. coli</i> found at higher concentrations in <i>Cladophora</i> mats than without. But no correlation between <i>Cladophora</i> density and <i>E. coli</i> exceedences. Authors conclude that more study is needed to determine the impact of <i>Cladophora</i> mats on beach water quality and likely sources of <i>E. coli</i> in the mats.
Faust, M.A. 1982. Relationship between land-use practices and fecal bacteria in soils. <i>J. Environ. Qual.</i> 11:141-146.	F	<ul style="list-style-type: none"> <i>E. coli</i> effectively correlates with patterns of fecal contamination in soils for cornfield, cow pasture, and forest plots.
Francy, D. S.; Hart, T. L.; Virosteck, C. M., 1996, Effects of receiving-water quality and wastewater treatment on injury, survival, and regrowth of fecal-indicator bacteria and implications for assessment of recreational water quality, WRIR 96-4199	F M	<ul style="list-style-type: none"> <i>In situ</i> flow-through incubation chambers used to measure decay, survival, growth. Models based on unchlorinated effluent were most accurate. Chlorinated or dechlorinated treatments were not accurate. (I.e., the method of measurement impacts decay models if measuring at point sources to predict concentrations downstream).
Francy, D.S., D.N. Myers, D.R. Helsel. 2000. Microbiological monitoring for the USGS national water-quality assessment program. USGS WRIR 00-4018.	M R	<ul style="list-style-type: none"> General protocol and guidance document and literature review. Point out inconsistent use of indicator organisms and document attempts to standardize monitoring. Recommends specific data collection and protocol, most relevantly a list of other environmental factors (WQ parameters and land-use).
Fujioka, R.S., B.S. Yoneyama. 2002. Sunlight inactivation of human enteric viruses and fecal bacteria. <i>Wat. Sci. Tech.</i> 46(11-12): 291-295.	F	<ul style="list-style-type: none"> Recommend using coliphages rather than coliform bacteria as indicator of fecal contamination.
Gargiulo, G., A. Bradford, J. Simunek, P. Ustohal, H. Vereecken, E. Klumpp. 2008. Bacteria transport and deposition under unsaturated flow conditions: the role of water content and bacterial surface hydrophobicity. <i>Vadose Zone J.</i> 7:406-419.	F	<ul style="list-style-type: none"> Bacteria retained in sand decrease with increasing water saturation. Good discussion of sub-surface transport.
Gino, E., J. Starosvetsky, R. Armon. 2007. Bacteriophage ecology in a small community sewer system related to their indicative role in sewage pollution of drinking water. <i>Env. Microbial.</i> 9(10): 2407-2416.	F R	<ul style="list-style-type: none"> A study of coliphage ecology in sewer systems to determine the impact of coliphage activity on indicator bacteria. No immediately applicable model but good review.

Citation		Summary
Graves, A.K., C. Hagedorn, A. Teetor, M. Mahal, A.M. Booth, R.B. Reneau, Jr. 2002. Antibiotic resistance profiles to determine sources of fecal contamination in a rural Virginia watershed. <i>J. Environ. Qual.</i> 31:1300-1308.	M S	<ul style="list-style-type: none"> • Antibiotic resistance profiles successfully yielded correct classification of human, wildlife, and livestock sources of bacterial contamination.
Guber, A.K. A.M. Yakirevich, A.M. Sadeghi, Y.A. Pachepsky, D.R. Shelton. 2009. Uncertainty evaluation of coliform bacteria removal from vegetated filter strip under overland flow condition. <i>J. Environ. Qual.</i> 38:1636-1644.	M	<ul style="list-style-type: none"> • Kinematic wave overland flow model was used to assess ability of vegetated filter strips to reduce bacteria in run-off. • High variation caused significant uncertainty in the model. • High rainfall swamped the vegetated filter strips ability to filter bacteria.
Haack, S.K., J.W. Duris, L.R. Fogarty, D.W. Kolpin, M.J. Focazio, E.T. Furlong, M.T. Meyer. 2009. Comparing wastewater chemicals, indicator bacteria concentrations, and bacterial pathogen genes as fecal pollution indicators. <i>J. Environ. Qual.</i> 38:248-258.	M	<ul style="list-style-type: none"> • Found that fecal indicator bacteria underestimate actual contamination when compared to chemical and genetic indicators. • Recommend multiple indicators with know pathways and persistence to increase confidence in fecal contamination assessments. • Very good discussion of QA/QC as well as other methodological aspects.
Hadas, O., B. Shteinman, R. Pinkas. 2000. Distribution if fecal coliforms in the Jordan River mouth originating from anthropogenic activities in the watershed. <i>Wat. Sci. Tech.</i> 42(1-2): 129-133.	M	<ul style="list-style-type: none"> • Used fecal indicators and fluorescent tracers to determine sources and mixing of bacterial contamination. • Flow velocity and attenuation were driving factors.
Hagedorn, C. D.T. Hansen, G.H. Simonson. 1978. Survival and movement of fecal indicator bacteria in soil under conditions of saturated flow. <i>J. Environ. Qual.</i> 7:55-59.	M	<ul style="list-style-type: none"> • Early example using antibiotic resistance to distinguish human from non-human sources of bacteria.
Hagedorn, C., S.B. Weisberg. 2009. Chemical-based fecal source tracking methods: current status and guidelines for evaluation. <i>Rev. Environ. Sci. Biotechnol.</i> Currently online only, Springer Science Media 10.1007/s11157-009-9162-2.	M	<ul style="list-style-type: none"> • Review of 35 chemicals associated with human waste. • Chemical analysis has several advantages, particularly it avoids issues of incubation in the environment. It is also generally faster (but often more expensive). • One major problem is dilution of these chemicals below detection levels. • Review concludes that optical brighteners (from detergents) show the most promise.
Hardina, CM; Fujioka, RS. 1991. Soil: The environmental source of <i>Escherichia coli</i> and enterococci in Hawaii's streams. <i>Environmental Toxicology and Water Quality.</i> 6: 185-195.	F	<ul style="list-style-type: none"> • Soil was main source of indicator bacteria in their stream (however, the article did not study sources of bacteria in the soil). • Bacteria were found at high concentrations in the surface of soil and up to 0.36 m deep. • Bacteria were also laterally distributed, indicating it was found near the stream and up to 10 m away.
He, L., J. Lu, W. Shi. 2007. Variability of fecal indicator bacteria in flowing and ponded waters in southern California: Implications for bacterial TMDL development and implementation. <i>Water Res.</i> 41(14): 3132-3140.	F T	<ul style="list-style-type: none"> • Unknown sources of FIB (fecal indicator bacteria) make TMDLs difficult. • High variation in FIB in both still and flowing water. • High FIB in sediment; higher concentration in still waters. • FIB increase with temperature. • FIB decrease with salinity/conductivity. • Recommend a holistic approach, esp. the use of reference systems to account for natural background.
Hernandez-Delgado, E.A., M.L. Sierra, G.A. Toranzos. 2006. Coliphages as alternate indicators of fecal contamination in tropical waters. <i>Environ. Tox. And Wat. Qual.</i> 6(2):131-143.	M	<ul style="list-style-type: none"> • Phages were more reliable indicators of human waste contamination of tropical waters while fecal coliforms were shown to be unreliable in these systems.

Citation		Summary
Higgins, J.A. and others. 2005. <i>tir</i> - and <i>stx</i> - positive <i>Escherichia coli</i> in stream waters in a metropolitan area. <i>App. and Env. Microbiol.</i> 71(5): 2511-2519.	M	<ul style="list-style-type: none"> • Genetic monitoring protocol for <i>E. coli</i>. • Conclude that strains from urban sources now a permanent part of stream ecosystems. (Supports inference that the conditions of outbreaks are as important to track as the sources.)
Holly, R. J. Walkty, G. Blank, M. Tenuta, K. Ominski, D. Krause. 2008. Examination of <i>Salmonella</i> and <i>Escherichia coli</i> translocation from hog manure to forage, soil, and cattle grazed on hog manure-treated pasture. <i>J. Environ. Qual.</i> 37:2083-2092.	S	<ul style="list-style-type: none"> • Bacterial concentrations can be amplified through mixed agricultural systems. • No evidence found that bacteria are passed directly from hog manure to pastured cattle.
Hong, P.Y., J.H. Wu, W.T. Liu. 2009. A high-throughput and quantitative hierarchical oligonucleotide primer extension (HOPE)-based approach to identify sources of faecal contamination in water bodies. <i>Environ. Microbiol.</i> 11(7): 1672-1681.	M S	<ul style="list-style-type: none"> • Method of differentiating human, cow, pig, and dog sources of bacterial contamination.
Howell, J.M., M.S. Coyne, P. Cornelius. 1995. Fecal bacteria in agricultural waters of the Bluegrass Region of Kentucky. <i>J. Environ. Qual.</i> 24:411-419.	M	<ul style="list-style-type: none"> • Used fecal coliform to fecal streptococci ratio to assess sources of fecal contamination (bovine vs. human).
Howell, J.M., M.S. Coyne, P. Cornelius. 1996. Effect of sediment particle size and temperature on fecal bacteria mortality rates and the fecal coliform / fecal streptococci ratio. <i>J. Environ. Qual.</i> 25:1216-1220.	F	<ul style="list-style-type: none"> • Fecal coliform mortality rates exceed fecal streptococci mortality rates. • This effect declines as size of particles decreases. • This effect declines with lower temperatures. • Warm temperatures can lead to false indications of human bacterial input.
Hunter, C., J. Perkins, J. Tranter, P. Hardwick. 2000. Fecal bacteria in the waters of an upland area in Derbyshire, England: the influence of agricultural land use. <i>J. Environ. Qual.</i> 29:1253-1261.	M	<ul style="list-style-type: none"> • Used spatial/temporal patterns of fecal coliform sampling with strong statistics to pinpoint sources. • Also found a strong correlation to support causal inference that smaller agricultural streams led to outbreaks downstream.
Jobson, H.E., 2001, Modeling water quality in rivers using the Branched Lagrangian Transport Model (BLTM): U.S. Geological Survey Fact Sheet FS-147-00, 6 p.	F	<ul style="list-style-type: none"> • Use BLTM to model transport of contaminants through interconnected one-dimensional channels. • Requires following data: A) discharge, cross sectional area, top-width, and tributary flow; B) geometric information (e.g. # branches), rate coefficients (e.g. first order decay). • This method successful to evaluate point source reductions in Cuyahoga R. (Meyers et al 1998).
Kay, D; Aitken, M; Crowther, J; Dickson, I; Edwards, AC; Francis, C; Hopkins, M; Jeffrey, W; Kay, C; McDonald, AT; McDonald, D; Stapleton, CM; Watkins, J; Wilkinson, J; Wyer, M. 2007. Reducing fluxes of faecal indicator compliance parameters to bathing waters from diffuse agricultural sources, the Brighthouse Bay study. <i>Scotland. Environmental Pollution</i> 147: 139-149.	F T	<ul style="list-style-type: none"> • Strong relationship between land use (feedlots) and fecal indicators. • BMPs used (stream fencing) decreased fecal indicators but not below water quality standards.
Khatiwada, N.R., C. Polprasert. 1999. Kinetics of fecal coliform removal in constructed wetlands. <i>Wat. Sci. Tech.</i> 40(3):109-116.	F	<ul style="list-style-type: none"> • Temperature, solar radiation, sedimentation rates are key factors in deactivation of fecal coliforms. • Created models for each removal mechanism.
Kleinheinz, G.T., C.M. McDermott, M.C. Leewis. E. Englebert. 2006. Influence of sampling depth on <i>Escherichia coli</i> concentrations in beach monitoring. <i>Water Res.</i> 3831-3837.	F	<ul style="list-style-type: none"> • <i>E. coli</i> dramatically lower with water depth (beach samples in Great Lakes lake systems).
Krometis, L-AH; Characklis, GW; Simmons, ODI; Dilts, MJ; Likirdopoulos, CA; Sobsey, MD. 2007. Intra-storm variability in microbial partitioning and microbial loading rates. <i>Water Research</i> 41(2): 506-516.	F	<ul style="list-style-type: none"> • Settle-able component of bacterial input is highest at beginning of storm events (this has design implications). • 1 day of storm loading is equivalent to months to years of dry loading.

Citation		Summary
Ksoll, W.B., S. Ishii, M.J. Sadowsky, R.E. Hicks. 2007. Presence and sources of fecal coliform bacteria in epilithic periphyton communities of Lake Superior. <i>App. and Env. Microbiol.</i> 73(12): 3771-3778.	F S	<ul style="list-style-type: none"> • <i>E. coli</i> cultures very well in periphyton (epilithic). • Periphyton sources confound the use of <i>E. coli</i> as an indicator of sewage problems. • Waterfowl, periphyton, and sewage were identified as three main sources (co-equal on average).
Lifshitz, R., R. Joshi. 1998. Comparison of a Novel ColiPlate Kit and the standard membrane filter technique for enumerating total coliforms and <i>Escherichia coli</i> bacteria in water. <i>Environ. Tox. Wat. Qual.</i> 13(2): 156-164.	M	<ul style="list-style-type: none"> • Laboratory methods comparison.
Liu, L; Phanikumar, MS; Molloy, SL; Whitman, RL; Shively, DA; Nevers, MB; Schwab, DJ; Rose, JB. 2006. Modeling the transport and inactivation of <i>E. coli</i> and enterococci in the nearshore region of Lake Michigan. <i>Environmental Science and Technology</i> 40(16): 5022-5028.	F	<ul style="list-style-type: none"> • Enterococci survived longer than <i>E. coli</i>. • Fecal indicator variation explained by inputs from tributaries. • Sunlight was key to inactivation in Lake Michigan.
Love, D.C, Sobsey, M.D. 2007. Simple and rapid F+ coliphage culture, latex agglutination, and typing (CLAT) assay to detect and source track fecal contamination. <i>Applied and Environmental Microbiology: In press.</i>	M S	<ul style="list-style-type: none"> • Cheaper, reliable antibody technique traces sources of specific pathogens.
Maeyns, C.L. and others. 2006. Diurnal variability in concentrations and sources of <i>Escherichia coli</i> in three streams. <i>Can. J. Microbiol.</i> 52: 1130-1135.	M R	<ul style="list-style-type: none"> • Most monitoring protocols for <i>E. coli</i> introduce huge margins of error and are inadequate. • 15-minute sampling shows very significant diurnal variation of <i>E. coli</i>.
Malard, F., J. Reygrobellet, M. Soulie. 1994. Transport and retention of fecal bacteria at sewage-polluted fractured rock sites. <i>J. Environ. Qual.</i> 23:1352-1363.	F	<ul style="list-style-type: none"> • Infiltration mechanisms drastically affect bacterial concentrations and transport, resulting in very patchy distribution. • Focus was on well contamination.
Maul, A., J.C. Block. 1983. Microplate fecal coliform method to monitor stream water pollution. <i>App. and Env. Microbiol.</i> 46(5): 1032-1037.	M R	<ul style="list-style-type: none"> • Lab methods comparison and discussion.
McCarthy, D. T., Deletic, A., Fletcher, T.D. and C. Diaper. 2008. Uncertainties in Stormwater <i>E. coli</i> levels, <i>Water Research</i> 42 (6-7): 1812-1824.	M	<ul style="list-style-type: none"> • Methods for handling uncertainty in field data.
McCorquodale, J.A., I. Georgiou, S. Carnelos, A.J. Englande. 2004. Modeling coliforms in storm water plumes. <i>J. Environ. Eng. Sci.</i> 3:419-431.	F M	<ul style="list-style-type: none"> • Bacterial transport and deactivation models combined with hydrodynamic forecasting to predict fecal coliform outbreaks.
McDonald, J.L., P.G. Hartel, L.C. Gentit, C.N. Belchar, K.W. Gates, K. Rodgers, J.A. Fisher, K.A. Smith, K.A. Payne. 2006. Identifying sources of fecal contamination inexpensively with targeted sampling and bacterial source tracking. <i>J. Environ. Qual.</i> 35:889-897.	M S	<ul style="list-style-type: none"> • Excellent review and test of methods for source identification. A 'must read' for any future work.
McLellan, S.L., A.K. Salmore. 2003. Evidence for localized bacterial loading as the cause of chronic beach closings in a freshwater marina. <i>Water Res.</i> 37: 2700-2708.	F	<ul style="list-style-type: none"> • Most <i>E. coli</i> in beaches is on shoreline. • Found persistent, highly local contamination that confounds monitoring and detection of regional patterns.
McMurry, S.W., M.S. Coyne, E. Perfect. 1998. Fecal coliform transport through intact soil blocks amended with poultry manure. <i>J. Environ. Qual.</i> 27:86-92.	F	<ul style="list-style-type: none"> • Spatial and temporal distribution not uniform through a constructed environment. • Conclude that rainfall on well-structured soil causes preferential movement of fecal bacteria, so soil structure is a major factor in bacterial transport.
Medema, G.J., M. Bahar and F.M. Schets. 1997. Survival of <i>Cryptosporidium parvum</i> , <i>Escherichia coli</i> , faecal enterococci and <i>Clostridium perfringens</i> in river water: influence of temperature and autochthonous microorganisms. <i>Water Science Technology</i> 35(11- 12):249-252.	F M	<ul style="list-style-type: none"> • High persistence of oocysts limits the value of fecal indicator bacteria. • Fecal indicators die off rapidly in test situations where oocysts remain.

Citation		Summary
Meyers, D.N., G.F. Koltun, D.S. Francy. 1998. Effects of hydrologic, biological, and environmental processes on sources and concentrations of fecal bacteria in the Cuyahoga River and implications for management of recreational waters in Summit and Cuyahoga Counties, Ohio. USGS WRIR 98-4089, Columbus, Ohio.	F	<ul style="list-style-type: none"> • Reports results of numerical streamflow and transport simulation models. • Decay rates are reported. This aspect would be very important to include in a TMDL and is site specific. • Models were able to show that point reductions were not enough for resultant <i>E. coli</i> to meet standards. • <i>E. coli</i> in the main stem were greater than the sum of <i>E. coli</i> in tributaries.
Mississippi Department of Environmental Quality, Office of Pollution Control, TMDL / WLA Section/Water Quality Assessment Branch. 1999. Fecal coliform TMDL for Pearl River, Pearl River Basin, Leake and Neshoba Counties, Mississippi.	T	<ul style="list-style-type: none"> • This TMDL has been posted as an example by the EPA. • The watershed was mixed agricultural and urban. Source identification was performed using landscape mapping. Loads were calculated by taking rough values from the literature and multiplying those by farm animal numbers, wildlife population estimates, and so on. • The BASINS model platform was used to integrate this information into WLAs and to assess likelihood of benefits from reductions and BMPs.
Moore, B.C., E. Martinez, J.M. Gay, D.H. Rice. 2003. Survival of Salmonella enterica in freshwater sediments and transmission by the aquatic midge Chironomus tentans (Chironomidae: Diptera). App. and Env. Microbiol. 69(8):4556-4560.	F	<ul style="list-style-type: none"> • Chironomids exposed to salmonella become carriers (even after emergence as terrestrial adults). • No evidence they re-infect sediments.
MPCA. 2006. Revised regional total maximum daily load evaluation of fecal coliform bacteria impairments in the Lower Mississippi River Basin in Minnesota. Final Report, January 2006. wq-iw9-02b.	M R T	<ul style="list-style-type: none"> • Review of water quality standards and how to apply wasteload allocations. • Non-point source identification method was to consider each individual tributary rather than sum a WLA for the entire basin at once.
MPCA. 2007. Fecal coliform TMDL assessment for 21 impaired streams in the Blue Earth River Basin. June 2007. wq-iw7-05b.	F T	<ul style="list-style-type: none"> • Resuspension of sediments at high flow re-introduces incubated <i>E. coli</i>. • <i>E. coli</i> concentrations significantly increase with temperature. • Transport is enhanced by the field tile systems. • Extremely good source and example for upper Mississippi River TMDL.
MPCA 2008. Minnesota Stormwater Manual, version 2. http://www.pca.state.mn.us/publications/wq-strm9-01.pdf	T	<ul style="list-style-type: none"> • Reviews regulations, monitoring and BMPs related to bacterial contamination of stormwater. Table 7.5 (p. 177) reviews some BMPs relevant to bacteria in river systems.
Nevercherya, I.K., V.M. Shestakov, V.T. Mazaev, T.G. Shlepnina. 2005. Survival rate of pathogenic bacteria and viruses in groundwater. Water Resources. 32(2): 209-214).	F M R	<ul style="list-style-type: none"> • Review of mechanisms of inactivation of pathogenic bacteria. • Mathematical model of inactivation described. • Report recommendations for determining inactivation rate factor using temperature for groundwater. • Caution that many inactivation factor studies are done at groundwater temperatures and for short periods of time, while actual inactivation is time and temperature dependent.
Nevers, M.B., R.L. Whitman, W.E. Frick, Z. Ge. 2007. Interaction and influence of two creeks on Escherichia coli concentrations of nearby beaches: exploration of predictability and mechanisms. J. Environ. Qual. 36:1338–1345.	F	<ul style="list-style-type: none"> • Argues that predictive modeling is more accurate than traditional models in assessing monitored <i>E. coli</i> for beaches. • Predicts outbreaks with a model composed of lake turbidity, river turbidity, wave height, and lake chlorophyll. • Models failed to predict actual outbreaks on 5/11 occasions.

Citation		Summary
Nevers, M.B., R.L. Whitman. 2005. Nowcast modeling of <i>Escherichia coli</i> concentrations at multiple urban beaches of southern Lake Michigan. <i>Wat. Res.</i> 39:5250-5260.	F	<ul style="list-style-type: none"> Nowcast modeling dramatically complicated by multiple inputs from several creeks.
Niemela, S.I., R.M. Niemi. 2006. Species distribution and temperature relations of coliform populations from uninhabited watershed areas. <i>Tox. Assess.</i> 4(3): 271-280.	F	<ul style="list-style-type: none"> Natural background of non-fecal coliforms dominated in uninhabited watersheds (such that in some cases no fecal coliforms were found at all, and when found they were not dominant components of the community). Fecal coliforms present were determined to be of recent animal origin. In these natural systems, total coliform is not a good indicator of fecal contamination, while standard fecal coliform estimated actual fecal contamination fairly well.
Niemi, R.M., J.S. Niemi. 2006. Annual variation and reliability of fecal indicators in a polluted river. <i>Tox. Assess.</i> 3(5): 657-677.	M	<ul style="list-style-type: none"> High spatial and temporal variation in fecal coliforms. High numbers under winter ice, highest during spring discharge. Correlated fecal indicators with each other and chemical water quality variables. Correlation coefficients vary with season.
Olyphant, G.A. Developing a prototypical predictive model for beach closings in Indiana. Indiana Geol. Survey project report. http://igs.indiana.gov/survey/projects/BeachClosings/index.cfm	F	<ul style="list-style-type: none"> A general guide to creating a predictive model, reported in Olyphant 2005 as well.
Olyphant, G.A. 2005. Statistical basis for predicting the need for bacterially induced beach closures: Emergence of a paradigm? <i>Water Res.</i> 39:4953-4960.	F	<ul style="list-style-type: none"> Found that waves, outfalls of bacteria from an adjacent stream, sunshine, temperature, and time of day were the most useful predictive factors related to bacterial outbreaks. Regression models were much more reliable and robust than models based on previous day's concentrations.
Oshiro, R., R. Fujioka. 1995. Sand, soil, and pigeon droppings: sources of indicator bacteria in the waters of Hanauma Bay, Oahu, Hawaii. <i>Wat. Sci. Tech.</i> 31(5-6): 251-254.	S	<ul style="list-style-type: none"> Study conducted in a bay with no stream inputs. Fecal indicator bacteria found in sand, entering the water from run-off. Primary source determined to be animal by direct sampling of bacterial fauna of animal feces compared to overland runoff.
Palmateer, G.A., D.E. McLean, M.J. Walsh, W.L. Kutas, E.M. Janzen, D.E. Hocking. 2006. A study of contamination of suspended stream sediments with <i>Escherichia coli</i> . <i>Tox. Assess.</i> 4(3): 377-397.	F	<ul style="list-style-type: none"> Bacterial sorption to sediment results in spread of contamination via suspended sediments. Specific sediment size fractions are mentioned but will be reported in further work.
Pang, L., M. McLeod, J. Aislabie, J. Simunek, M. Close, R. Hector. 2008. Modeling transport of microbes in ten undisturbed soils under effluent irrigation. <i>Vadose Zone J.</i> 7(1): 97-111.	M	<ul style="list-style-type: none"> HYDRUS-1D model (mobile-immobile water model). Soil structure: macroporosity plays the most important role in transport of microbes. Soil composition: lithology has greatest role in attenuation.
Pang, L. 2009. Microbial removal rates in subsurface media estimated from published studies of field experiments and large intact soil cores. <i>J. Environ. Qual.</i>	R	<ul style="list-style-type: none"> Creates large database of microbial removal factors and rates in soils. Review of field methods and models. Reviews relevant literature.

Citation		Summary
<p>Pitt, R. 2007. Microorganisms in Urban Surface Waters. Univ. Alabama. http://unix.eng.ua.edu/~rpitt/Class/ExperimentalDesignFieldSampling/MainEDFS.html</p>	S R	<ul style="list-style-type: none"> • Comprehensive review of bacterial problems in urban settings. • Summary of main microorganism sources. • Offers good comparison of indicators (too detailed to summarize here). • Includes information on types of pathogens found in urban stormwater, bacterial parasites from animals that can be transmitted to humans through contaminated water, and which types of bacteria are associated with humans and different animals.
<p>Qi, Y.N., S. Gillow, D.S. Henderson, S.K. Dentel. 2004. Reactivation and/or growth of fecal coliform bacteria during centrifugal dewatering of anaerobically digested biosolids. <i>Wat. Sci. Tech.</i> 50(9): 115-120.</p>	F R	<ul style="list-style-type: none"> • Fecal coliform numbers after digestion are assumed to be representative of final waste impact. This review shows that dewatering can significantly increase fecal coliform counts. • Consequently, dewatering of biosolids does have an impact on fecal coliform numbers.
<p>Rasmussen, P.P., V.G. Christensen, 2005, Hydrologic and Water-Quality Conditions in the Kansas River, Northeast Kansas, November 2001-August 2002, and Simulation of Ammonia Assimilative Capacity and Bacteria Transport During Low Flow, SIR 2005-5188.</p>	F	<ul style="list-style-type: none"> • <i>E. coli</i> and other microorganisms are much more variable than nutrients below WWTFs and varied in a different pattern over time. • Decay had little seasonal variation. • CE-QUAL-W2 used to model transport (2 dimensional).
<p>Reischer, G.H., J.M. Haider, R. Sommer, H. Stadler, Keiblinger, K.M., R. Hornek, W. Zerobin, R.L. Mach, A.H. Farnleitner. 2008. Quantitative microbial faecal source tracking with sampling guided by hydrological catchment dynamics. <i>Environ. Microbiol.</i> 10(10):2598-2608.</p>	S	<ul style="list-style-type: none"> • Successful source tracking (human vs. bovine) with PCR techniques. • Hydrological catchment dynamics are a prerequisite for successful source tracking studies.
<p>Rhode Island Department of Environmental Management, Office of Water Resources. 2001. Fecal coliform TMDL development for Hunt River, Rhode Island. Final report.</p>	T	<ul style="list-style-type: none"> • This TMDL has been posted as an example by the EPA. • Geometric means for wet and dry periods were averaged to calculate adjusted loads. Wet weather days were adjusted by decay times to estimate the time until bacterial concentrations would drop to pre-storm levels. After these corrections, WLAs were calculated. • Source identification was largely an observational narrative including landscape patterns mapped on to spatial patterns of impairments.
<p>Rhodes, M.A., H. Kator. 1988. Survival of <i>Escherichia coli</i> and <i>Salmonella</i> spp. in estuarine environments. <i>App. and Env. Microbiol.</i> 54(12):2902-2907.</p>	F	<ul style="list-style-type: none"> • Survival of enteric bacteria in estuarine environment is a function of interacting biological and physical factors (specifically: presence of autochthonous microorganisms and temperature).
<p>Rifai, H. 2006. Study on the effectiveness of BMPs to control bacterial loads. Final Quarterly Report: Texas Commission on Environmental Quality. http://www.tceq.state.tx.us/assets/public/implementation/water/tmdl/22buffalobayou/22-bmp-q1mar06.pdf</p>	T	<ul style="list-style-type: none"> • Studied both structural and non-structural practices. • Included wide array from stenciling, street sweeping, wetland systems, ponds. • The most effective BMPs in this system were wet and dry basins, flood control/water quality basins, wetland systems, grass swales, and vegetative filter strips. • Likely mechanisms of bacterial reduction are settling/sedimentation, temperature, increased exposure to sunlight, and physical filtration.
<p>Rodriguez, R.A., I.L. Pepper, C.P. Gerba. 2009. Application of PCR-based methods to assess the infectivity of enteric viruses in environmental samples. <i>App. and Env. Microbiol.</i> 75(2): 297-307.</p>	M R	<ul style="list-style-type: none"> • PCR techniques are very useful and available. • The advantages and limitations of PCR techniques are reviewed.

Citation		Summary
Rychert, R.C., G.R. Stephenson. 1981. Atypical <i>Escherichia coli</i> in streams. <i>App. and Env. Microbiol.</i> 41(6): 1276-1278.	M	<ul style="list-style-type: none"> Atypical <i>E. coli</i> strains or serotypes can dramatically increase error margins in monitoring.
Santoro, A.E., A.B. Boehm. 2007. Frequent occurrence of the human-specific <i>Bacteroides</i> fecal marker at an open coast marine beach: relationship to waves, tides, and traditional indicators. <i>Environ. Microbiol.</i> 9(8): 2038-2049.	F S	<ul style="list-style-type: none"> Marine system, but reviews use of human specific source determination. Multiple physical factors interact and sampling must be done over multiple states to accurately determine impairments to the system.
Savichtcheva, O., S. Okabe. 2009. Qualitative and quantitative estimation of host-specific fecal pollution using <i>Bacteroides-Prevotella</i> 16s rRNA genetic markers by T-RFLP and real-time PCR analyses. <i>Wat. Sci. Tech.</i> 59(9): 1831-1840.	M S	<ul style="list-style-type: none"> RT-PCR and T-RFLP techniques were combined to produce reliable host-specific bacterial assessments (quantitative) in complex environments.
Scherer, B.M., R. Miner, J.A. Moore, and J.C. Buckhouse. 1992. Indicator bacteria survival in stream sediments. <i>J. of Env. Qual.</i> 21:591- 595.	F M	<ul style="list-style-type: none"> Article not readily available. Abstract: paper documents that survival of indicator bacteria is independent of new inputs.
Schijven, J.F., S.A. Bradford, S. Yang. 2004. Release of <i>Cryptosporidium</i> and <i>Giardia</i> from dairy cattle manure: physical factors. <i>J. Environ. Qual.</i> 33:1499-1508.	F	<ul style="list-style-type: none"> Reports release efficiency factors for oocysts rinsed from manure by sprinkled water. Found no temperature impact on release rates, but flow and mist vs. droplet irrigation has significant, complicated effects on release rates.
Schumacher, J.G., 2003, Survival, transport, and sources of fecal bacteria in streams and survival in land-applied poultry litter in the upper Shoal Creek basin, southwestern Missouri, 2001-2002, WRIR 2003-4243	M S	<ul style="list-style-type: none"> Used a combination of dye-trace studies and PCRs to locate sources and transport of <i>E. coli</i>. Calculated bacterial survival and decay in different environments (e.g. soils and water column) and over different parameters. Fluctuations in <i>E. coli</i> were not all a function of advection and dispersion. (This implies other environmental factors). Possible interaction with nutrients.
Servais, P., T. Garcia-Armisen, A.S. LePeuple, P. LeBaron. 2005. An early warning method to detect faecal contamination of river waters. <i>Annals Micrbiol.</i> 55(2):151-156.	M	<ul style="list-style-type: none"> Beta-D-glucuronidase activity (enzyme specific to <i>E. coli</i>) predicts outbreaks and is a good rapid assessment (detection method).
Seurinck, S., W. Verstraete, S.D. Siciliano. 2005. Microbial source tracking for identification of fecal pollution. <i>Rev. Environ. Sci. and Biotechnol.</i> 4:19-37.	M	<ul style="list-style-type: none"> Argues that chemical based tracers of bacterial sources have no direct relationship with bacterial biology. The usefulness of chemical tracers is limited to treated sewage. Chemical tracers also do not work to distinguish between several non-human sources. Microbial source tracking allows specific identification of fecal sources even in complex multiple source areas and when fecal sources are not of human origin. Microbial source tracking requires a phenotypic-genotypic library, which can be labor intensive and is region-specific.
Shuman, R. and J. Strand. King County water quality assessment: CSO discharges, biological impacts being assessed. <i>Wet Weather. Water Environment Research Foundation.</i> Fairfax, VA. 1(3): 10–14. Fall 1996.	M	<ul style="list-style-type: none"> Used caffeine chemical breakdown products to monitor human waste contribution to bacterial outbreak. This article is cited by several major USGS papers and ongoing efforts by the EPA, but is not readily available. See Hagedorn et al. 2009 and Seurinck et al. 2005 for more recent and comprehensive work on chemical based source tracking).

Citation		Summary
Spangler, L.E., D.D. Susong. 2006. Use of dye tracing to determine ground-water movement to Mammoth Crystal Springs, Sylvan Pass Area, Yellowstone National Park, Wyoming. USGS SIR 2006-5126.	M S	<ul style="list-style-type: none"> • Successfully used dye tracing to determine surface water/ground water interactions. • No direct discussion of bacteria; but informative for situations where <i>E. coli</i> is in the water that moves between surface and groundwater.
Stoddard, C.S., M.S. Coyne, J.H. Grove. 1998. Fecal bacteria survival and infiltration through a shallow agricultural soil: timing and tillage effects. J. Environ. Qual. 27:1516-1523.	F	<ul style="list-style-type: none"> • Manure significantly increases fecal bacterial concentrations of leachate. • Timing and tillage method did not have a significant effect. • Contamination depended most on soil structure and water flow more than survival at the soil surface.
Stoeckel, DM; Mathes, MV; Hyer, KE; Hagedorn, C; Kator, H; Lukasik, J; O'Brien, TL; Fenger, TW; Samadpour, M; Strickler, KM; Wiggins, BA. 2004. Comparison of seven protocols to identify fecal contamination sources using <i>Escherichia coli</i> . Environmental Science and Technology 38: 6109-6117.	M	<ul style="list-style-type: none"> • Most protocols are heavily disposed towards false positive readings. • Better assessment requires more extensive and site-specific libraries and increased classification accuracy.
Stoeckel, DM; Harwood, VJ. 2007. Performance, design and analysis in microbial source tracking studies. App. and Env. Microbiol. 73(8): 2405-2415.	M R	<ul style="list-style-type: none"> • Review of Microbial Source Tracking (MST) studies. • Most MST protocols difficult to apply in field conditions; recommend care.
Surbeck, C.Q., Jiang, S.C., Ahn, J.H. and Grant, S.B. (2006) Flow fingerprinting fecal pollution and suspended solids in stormwater runoff from an urban coastal watershed. Env. Sci. Tech. 40(14), 4435-4441.	F	<ul style="list-style-type: none"> • <i>E. coli</i> and F+ coliphages showed no relationship to flow over several storm events. • Total suspended solids (TSS) showed high correlation to flow. • Differences between TSS and bacteria are attributed to different transport pathways. • Bacterial indicators ubiquitous on urban landscape. • Using flow fingerprinting, authors conclude that bacterial indicators in this case do not indicate a human source.
Texier, S., C. Prigent-Combaret, M.H. Gourdon, M.A. Poirier, P. Faivre, J.M. Dorioz, J. Poulenard, L. Jocteur-Monrozier, Y. Moenne-Loccoz, D. Trevisan. 2008. Persistence of culturable <i>Escherichia coli</i> fecal contaminants in dairy alpine soils. J. Environ. Qual. 37:2299-2310.	S	<ul style="list-style-type: none"> • Sub-populations of <i>E. coli</i> from manure patties survive in soils for long periods, creating an environmental reservoir. • Soil type plays a large role in reservoir function.
Thelin, R., G.F. Gifford. 1983. Fecal coliform release patterns from fecal material of cattle. J. Environ. Qual. 12:57-63.	F	<ul style="list-style-type: none"> • Duration of rainfall and age of cow patties significantly impact bacterial release rate. • Equilibrium in fecal coliform release from the fecal deposit was reached within 10 min.
USEPA (2005) Microbial source tracking guide document. US Environmental Protection Agency, Office of Research and Development, Cincinnati EPA/600-R-05-064	M	<ul style="list-style-type: none"> • Methods and QA/QC for MST.
USEPA (2007) Experts Scientific workshop on critical research needs for the development of new or revised recreational water quality criteria. EPA 823-R-07-006, June 2007, online http://www.epa.gov/waterscience/criteria/recreation/experts/index.html	M	<ul style="list-style-type: none"> • Important review of methods, indicators, and issues for identifying sources (pp. 35-52). • Rationale behind searching for new WQ standards is helpful to make sure current information will be useful in the future.
Viau, E., J. Peccia. 2009. Survey of wastewater indicators and human pathogen genomes in biosolids produced by class A and class B stabilization treatments. Appl. Environ. Microbiol. 75(1): 154-174.	M	<ul style="list-style-type: none"> • This study reports on the dangers of aerosol, not waterborne bacterial pathogens, but the genetic methods are pertinent. • Also reviews inactivation factors.

Citation		Summary
Vogel, J.R., D.M. Stoeckel, R. Lamendella, R.B. Zelt, J.W. Santo Domingo, S.R. Walker, D.B. Oerther. 2007. Identifying fecal sources in a selected catchment reach using multiple source-track tools. J. Environ. Qual. 36:718-729.	M S	<ul style="list-style-type: none"> • Coliphages not detected at all sites, so were not considered in this analysis of source tracking methods. • Different methods worked better depending on whether contamination was in the water column or sediment. • Recommend a multiple tool approach. • Excellent review of methods.
Walters, S.P., K.G. Field. 2009. Survival and persistence of human and ruminant-specific faecal Bacteroidales in freshwater microcosms. Environ. Microbiol. 11(6): 1410-1421.	M S	<ul style="list-style-type: none"> • Human and ruminant markers persist differently in the environment. Quantified results should consequently be adjusted for this. • Host-specific markers are otherwise successful.
Washington State Dept. of Ecology. 2000. Lower Nooksack River Basin total maximum daily load evaluation. Publication number 00-03-006.	T	<ul style="list-style-type: none"> • This TMDL has been posted as an example by the EPA. • Set far more stringent goals than the Class A standard (monthly geometric mean of 39 cfu/100 mL rather than 100 cfu/100 mL). • Non-point sources were the primary contributors to impairment. A statistical rollback method was used to calculate target indicator bacteria concentrations.
Wheeler, A.L., P.G. Hartel, D.G. Godfrey, J.L. Hill, W.I. Segars. 2002. Potential of <i>Enterococcus faecalis</i> as a human fecal indicator for microbial source tracking. J. Environ. Qual. 31:1286-1293.	M S	<ul style="list-style-type: none"> • <i>Enterococcus faecalis</i> is specific to humans, dogs, and chickens. • Bacteria from dogs can be distinguished with simple methodological techniques using special media. • Ribotyping further differentiates humans and chickens. • Good methods review.
Whitman, R.L. and others. 2008. Sunlight, season, snowmelt, storm and source affect <i>E. coli</i> populations in an artificially ponded stream. J. Sci. Total. Env. 448-455.	F T	<ul style="list-style-type: none"> • Experimental retention pond was effective at reducing or eliminating <i>E. coli</i>. • The primary mechanism of the reduction was increased exposure to sunlight (the pond slowed water down, increasing retention and exposure to light). • This effect predominant in summer, weaker or absent in winter. <i>E. coli</i> increased during snowmelt and storm events.
Willey, R.A. 2006. Stormwater management measures and fecal indicator bacteria. M.S. Thesis, U. New Hampshire.	F	<ul style="list-style-type: none"> • Swale and both wetland and gravel drainfields increase the concentrations of indicator bacteria. • Some stormwater management practices are leading to higher indicator concentrations in run-off, producing false positive results for indication of fecal contamination.
Young, K.D. and E.L. Thackston. 1999. Housing density and bacterial loading in urban streams. J. Environ. Engineering 125(12):1177-1180.	F	<ul style="list-style-type: none"> • Fecal counts higher in sewered than un-sewered residential areas. • Fecal counts correlate with: housing density, population (human), population (pet animal), impervious surfaces, development.