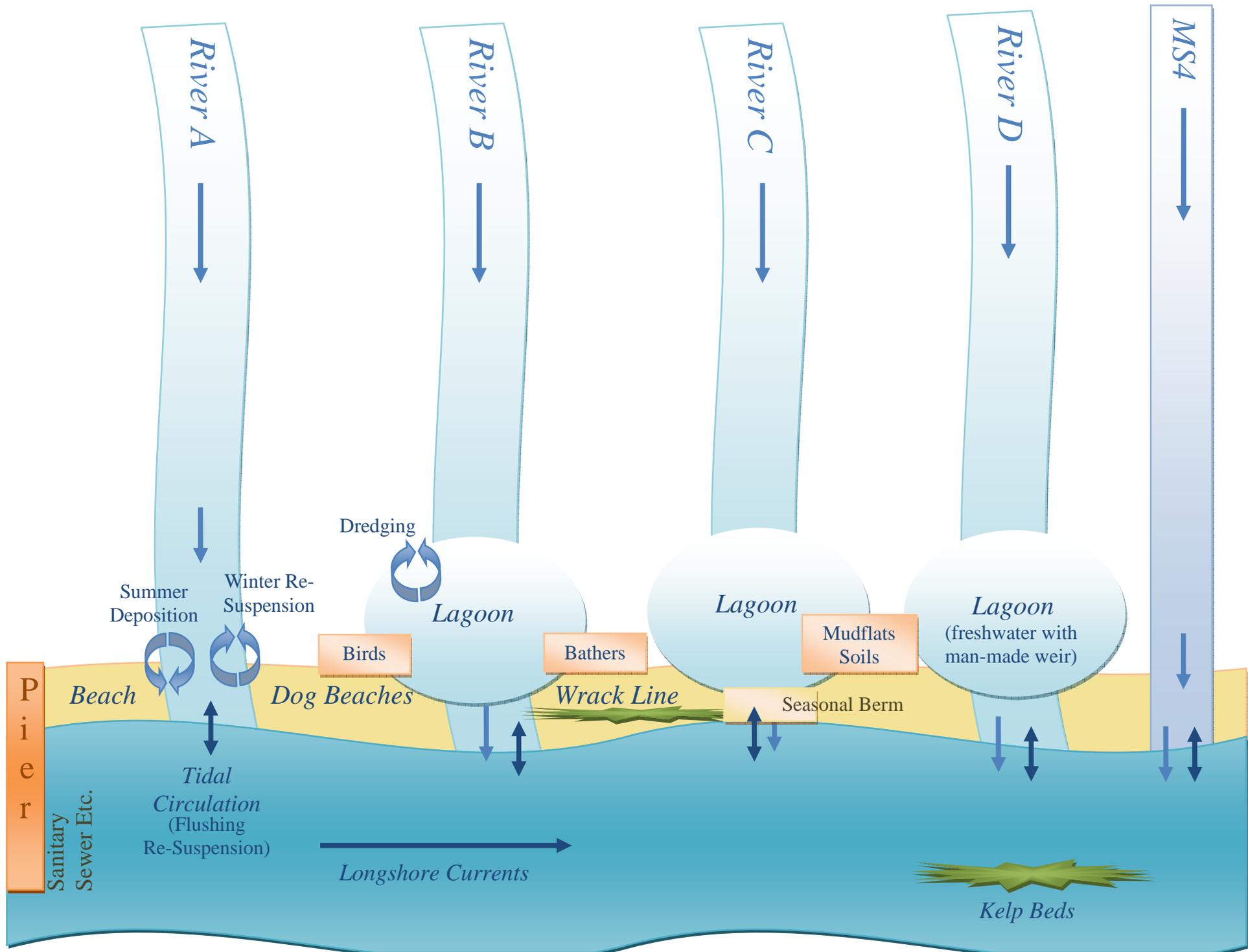


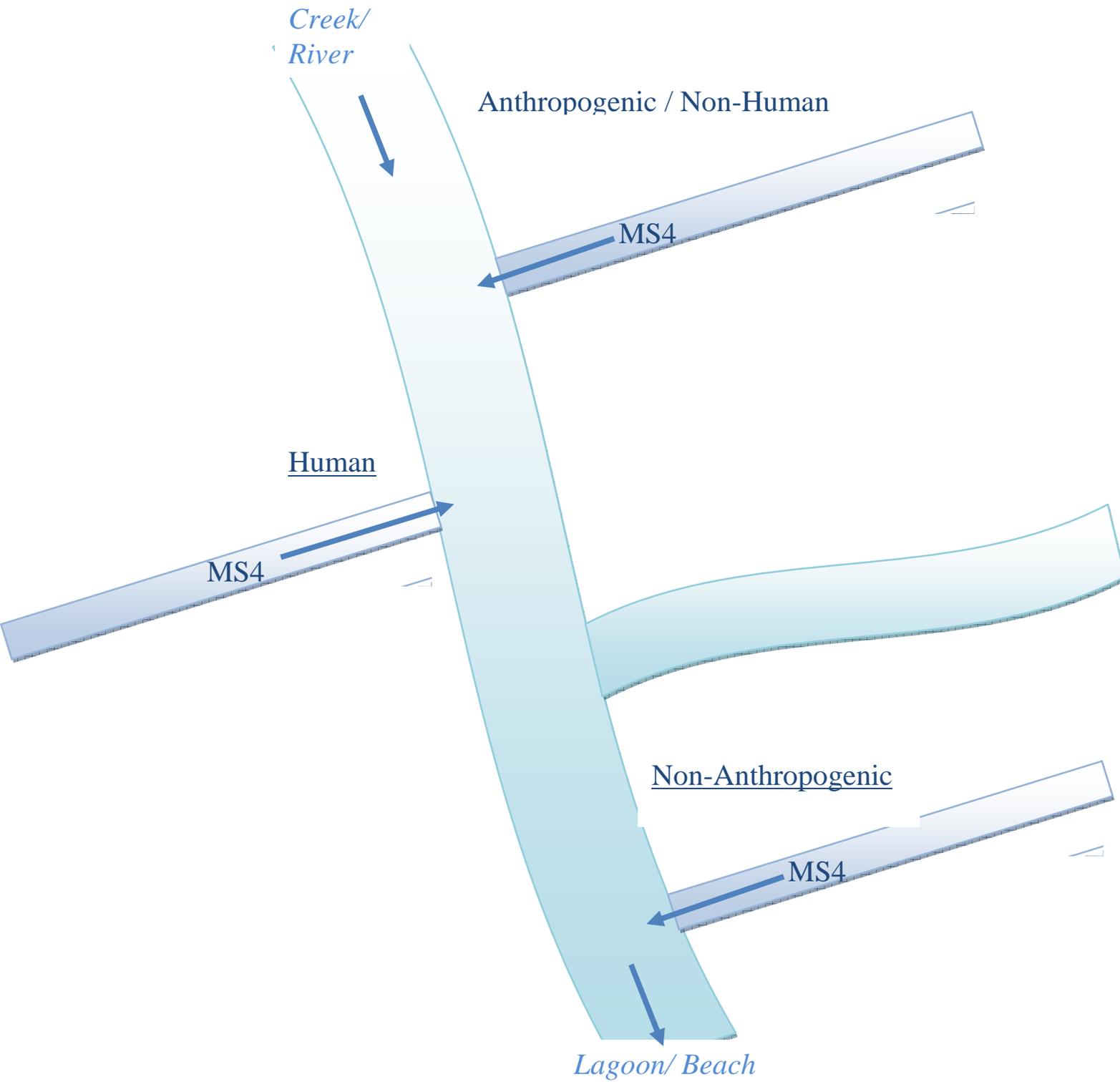
## **APPENDIX G**

### **Bacterial Conceptual Models and Literature Review**

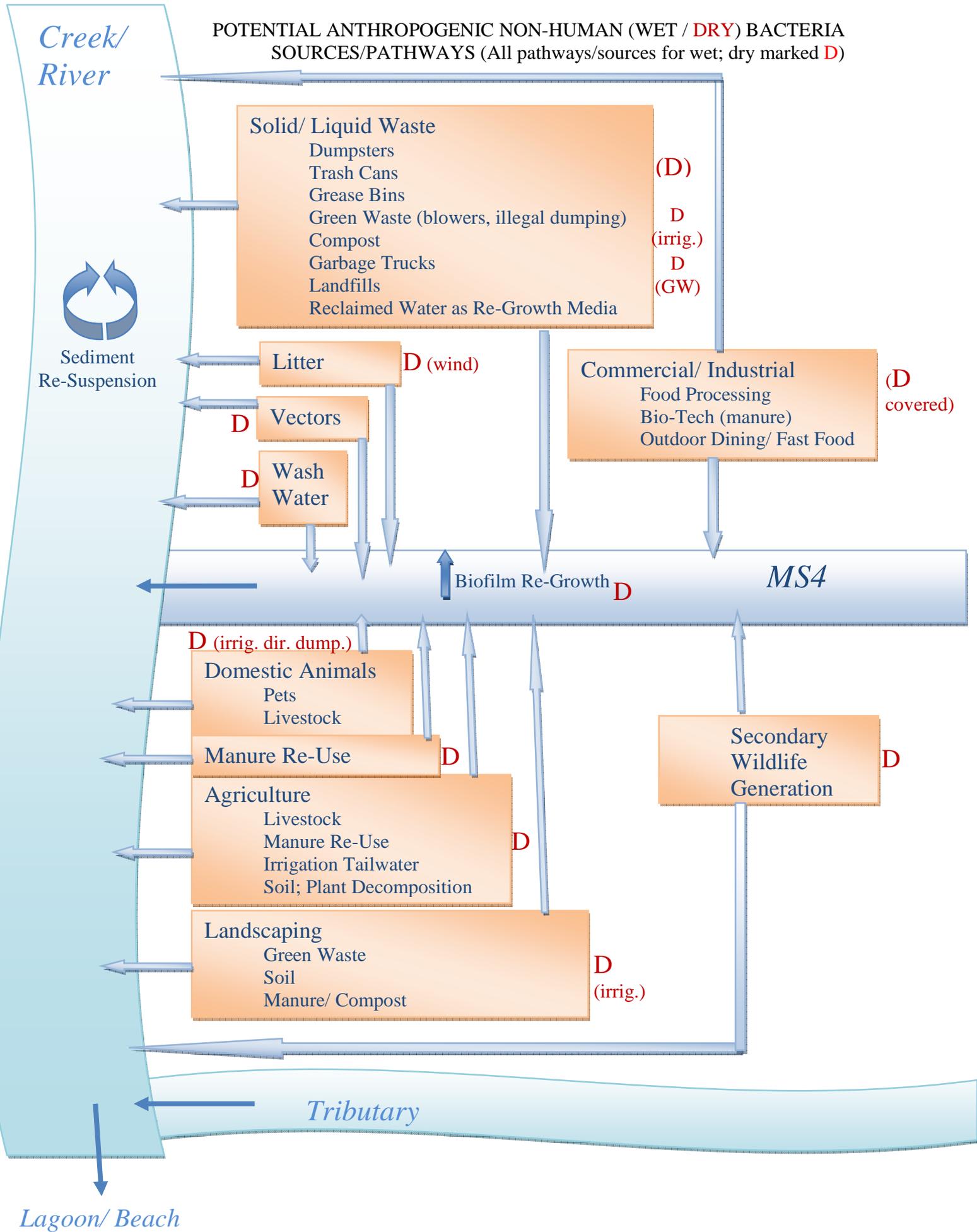
**Intentionally Left Blank**



# Conceptual Overview of Bacteria Sources

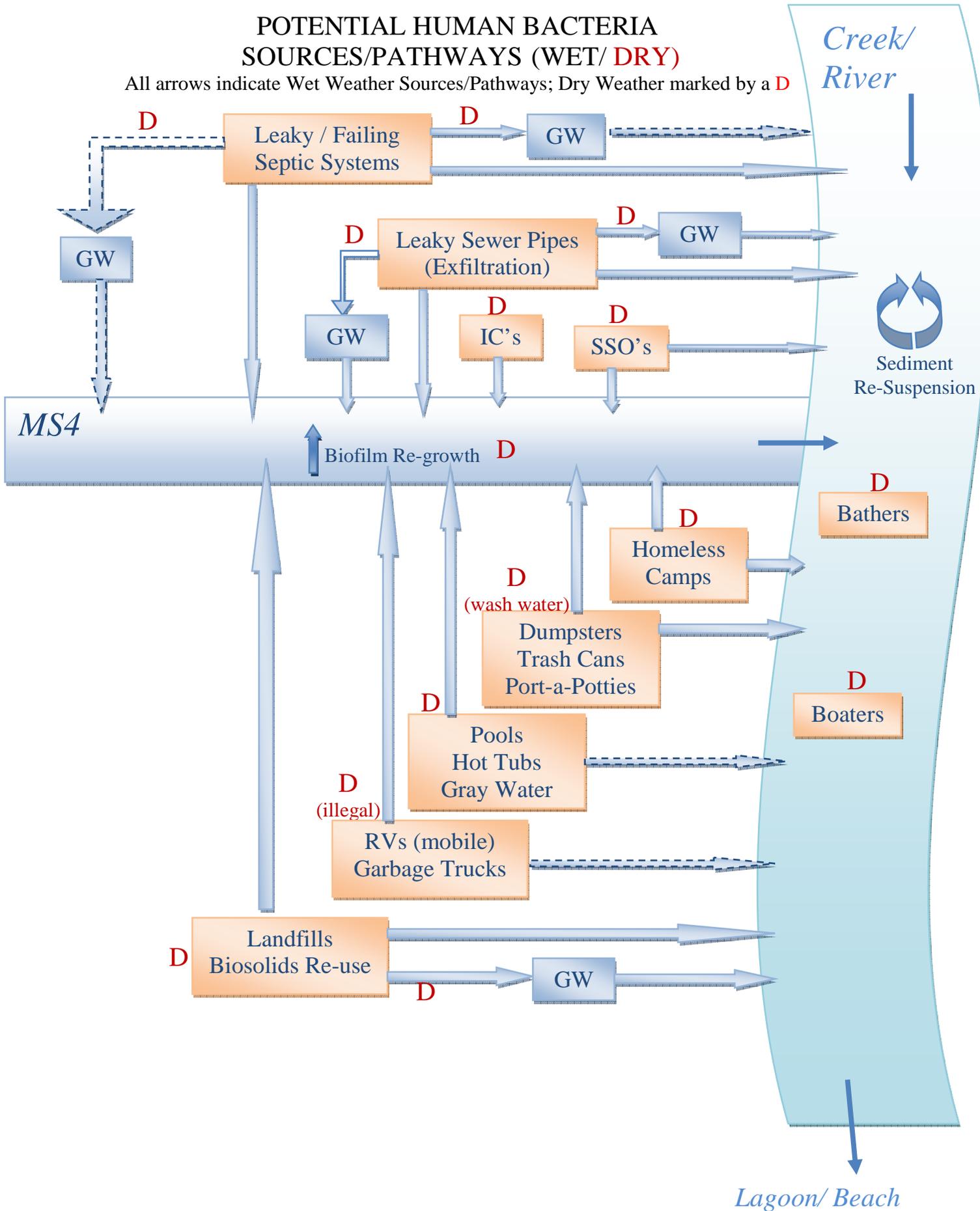


POTENTIAL ANTHROPOGENIC NON-HUMAN (WET / DRY) BACTERIA SOURCES/PATHWAYS (All pathways/sources for wet; dry marked **D**)



# POTENTIAL HUMAN BACTERIA SOURCES/PATHWAYS (WET/ DRY)

All arrows indicate Wet Weather Sources/Pathways; Dry Weather marked by a **D**





**DRAFT TECHNICAL MEMORANDUM**  
**Summary of Literature Review, Bacteria Source Identification**  
**March 12, 2012**

**Prepared by: Armand Ruby Consulting in Association with AMEC**

This Technical Memorandum summarizes work performed under Task 2, Literature Search and Data Review, for the County of San Diego Bacterial Indicators Source Identification Services Project. The work was overseen by a workgroup of San Diego County Stormwater Copermittee representatives, and included communication with scientists who have expertise in bacteria source tracking and identification. The literature review focused on identifying and summarizing studies that quantify sources and sinks for bacterial constituents in urban watersheds, and was international in scope.

The work products delivered for this task include this technical memorandum, a separate spreadsheet summary of each study/report reviewed, and a compilation of reviewed studies/reports on the AMEC ftp site:

<ftp://ftp.mactec.com/Incoming/Copermittee%20Bact%20Lit%20Review/>

The entries in this memorandum are ordered alphabetically by last name of primary author. Each entry begins with the study number (for cross-referencing back to the spreadsheet matrix), followed by the study title. Web links are provided when available.

A number of studies were found that contained information on indicator bacteria but did not include specific information related to source identification within urban watersheds. These studies are summarized as NSC (Not Source Characterization) studies, beginning on p. 53.

The “Bacteria Source ID Lit Review Matrix” Excel workbook contains the following worksheets:

- The “Source ID Studies Summary Table” worksheet contains summaries of all studies reviewed and found to have useful information on bacteria sources; for each of these studies, any identified sources are indicated as Probably, Potential, Low or Suspected (see “Legend” worksheet for definitions)
- The “# Citations by Source” worksheet contains a tally of the numbers of studies with identified information on each source type
- The “Sources Summary Table” worksheet contains condensed summaries of the studies that have information on each particular source type
- The “Data Summary Table” worksheet contains brief summaries of study data (this is a work in progress)
- The “NSC Studies” worksheet provides summaries of the NSC (Not Source Characterization) studies

## **56 - Human and bovine adenoviruses for the detection of source-specific fecal pollution in coastal waters in Australia**

Warish Ahmed, A. Goonetilleke, and T. Gardner

[http://eprints.qut.edu.au/37690/1/Human\\_and\\_bovine\\_adenoviruses\\_for\\_the\\_detection\\_of\\_source-specific\\_fecal\\_pollution\\_in\\_coastal\\_waters\\_in\\_Australia.pdf](http://eprints.qut.edu.au/37690/1/Human_and_bovine_adenoviruses_for_the_detection_of_source-specific_fecal_pollution_in_coastal_waters_in_Australia.pdf)

Purpose - To enhance the scientific foundation for preemptive public health warnings, examine the relationship between rainfall and beach indicator bacteria concentrations using five years of fecal coliform data taken daily at 20 sites in southern California.

Results - There was a clear relationship between the incidence of rainfall and reduction in beach bacterial water quality in Los Angeles County. Bacterial concentrations remained elevated for five days following a storm, although they generally returned to levels below state water quality standards within three days. The length of the antecedent dry period had a minimal effect on this relationship, probably reflecting a quickly developing equilibrium between the decay of older fecal material and the introduction of new fecal material to the landscape.

Sources:

Probable –Septic (human waste), bovine (domestic animals), animal farms (agriculture),

Potential -

Possible -

## **31 - Evaluation of Multiple Sewage-Associated Bacteroides PCR Markers for Sewage Pollution Tracking**

Warish Ahmed, A. Goonetilleke, D. Powell, and T. Gardner

<http://eprints.qut.edu.au/29217/1/c29217.pdf>

Purpose - The host specificity of the five published sewage-associated Bacteroides markers (i.e., HF183, BacHum, HuBac, BacH and Human-Bac) was evaluated in Southeast Queensland, Australia by testing fecal DNA samples (n = 186) from 11 animal species including human fecal samples collected via influent to a sewage treatment plant (STP).

Results - For the 5 sewage-associated markers tested in this study, the HF183 marker performed better than others. This marker showed 99% specificity to distinguish between the sources of human and animal fecal pollution. The performance of the five markers in terms of specificity was HF183 > BacHum > BacH > Human-Bac > HuBac.

## **78 - Detection and source identification of faecal pollution in non-sewered catchment by means of molecular markers host-specific**

Warish Ahmed, D. Powell, A. Goonetilleke, and T. Gardner

<http://s3.amazonaws.com/publicationslist.org/data/w.ahmed/ref-23/WST%20Article.pdf>

Purpose - To validate the previously published host-specific PCR markers (i.e. HF183, HF134, CF128, BacCan and esp) for the detection of sources of faecal pollution by testing a large number of faecal samples from 13 host groups in Southeast Queensland, Australia.

Results - All 197 faecal samples (100%) from the 13 host groups were positive for general Bacteroides. Of the 42 (i.e. 30 sewage and 12 septic samples) sewage/septic samples tested, all were positive for the human-specific HF183 and HF134 Bacteroides markers. The HF183 marker could not be detected in any faecal samples from animal host groups suggesting that the suitability of this marker to detect human faecal pollution. In contrast, the HF134 marker was detected in 7 (35%) samples from dogs. The presence of this marker in dogs could be due to the transfer of faecal bacteria between human and their companion pets (Dick et al. 2005).

### **79 - Evaluation of Bacteroides markers for the detection of human faecal pollution**

Warish Ahmed, J. Stewart, D. Powell, and T. Gardner

<http://onlinelibrary.wiley.com/doi/10.1111/j.1472-765X.2007.02287.x/pdf>

Purpose - Evaluating the specificity and sensitivity of human-specific HF183 and HF134 Bacteroides markers in various host groups and their utility to detect human faecal pollution in storm water samples collected from non-sewered catchments in Southeast Queensland, Australia.

Results - The specificity and sensitivity of the HF183 and HF134 Bacteroides markers was evaluated by testing 207 faecal samples from 13 host groups, including 52 samples from human sources (via sewage and septic tanks). Polymerase chain reaction analysis of these samples revealed the presence/absence of HF183 and HF134 across these host groups, demonstrating their suitability for distinguishing between human and animal faecal pollution. The HF183 marker was found to be more reliable than that of HF134, which was also found in dogs.

### **35 - Quantitative PCR assay of sewage-associated Bacteroides markers to assess sewage pollution in an urban lake in Dhaka, Bangladesh**

Warish Ahmed, R. Yusuf, I. Hasan, A. Goonetilleke, and T. Gardner

[http://eprints.qut.edu.au/37689/1/Quantitative\\_PCR\\_assay\\_of\\_sewage-associated\\_Bacteroides\\_markers\\_to\\_assess\\_sewage\\_pollution\\_in\\_an\\_urban\\_lake\\_in\\_Dhaka,\\_Bangladesh.pdf](http://eprints.qut.edu.au/37689/1/Quantitative_PCR_assay_of_sewage-associated_Bacteroides_markers_to_assess_sewage_pollution_in_an_urban_lake_in_Dhaka,_Bangladesh.pdf)

Purpose - To assess the magnitude of sewage pollution in an urban lake in Dhaka, Bangladesh 34 by using Quantitative PCR (qPCR) of sewage-associated Bacteroides HF183 markers.

Results – From the 20 water samples tested, 14 (70%) and 7 (35%) were PCR positive for the HF183 and CF128 markers, respectively. The high numbers of enterococci and the HF183 markers indicate sewage pollution.

Sources:

Probable - Slum-like establishments (human waste), MS4 Infrastructure (human waste),

Potential -

Possible – Dogs and cows

### **139 - Coastal water quality impact of storm water runoff from an urban watershed in Southern California**

Jong Ho Ahn, S.B. Grant, C.Q. Surbeck, P.M. DiGiacomo, N.P. Nezlin, and S. Jiang

[ftp://ftp.sccwrp.org/pub/download/DOCUMENTS/TechnicalReports/528\\_B03\\_WQ\\_Appendix\\_I.pdf](ftp://ftp.sccwrp.org/pub/download/DOCUMENTS/TechnicalReports/528_B03_WQ_Appendix_I.pdf)

Purpose - Assess the coastal water quality impact of storm water runoff from the Santa Ana River, which drains a large urban watershed located in southern California. This is the first wet weather study to examine the linkage between water quality in the surf zone -- where routine monitoring samples are collected and most human exposure occurs -- and water quality offshore of the surf zone.

Results - Storm water runoff from the Santa Ana River negatively impacts coastal water quality, both in the surf zone and offshore. However, the extent of this impact, and its human health significance, is influenced by numerous factors, including prevailing ocean currents, within-plume processing of particles and pathogens, and the timing, magnitude and nature of runoff discharged from river outlets over the course of a storm.

Sources:

Probable - Slum-like establishments (human waste), MS4 Infrastructure (human waste),

Potential -

Possible – Dogs and cows

### **17 - Lower San Luis Rey River Bacteria Source Identification Study**

AMEC, UNC, City of Oceanside, SCCWRP, and USC

Purpose - The goal of the Project was to identify hot spots of fecal indicator bacteria; identify potential sources and prioritize those sources and locations for future bacteria reductions through management measures.

Results - There is evidence of the human-related bacterial sources throughout the river system. Sediment in the river mouth is a contributing source of fecal bacteria to the water column when the river mouth is closed to tidal exchange. The resident gull population was a probable source of fecal bacteria in the river mouth. Additional, monitoring is needed to identify human sources.

Sources:

Probable - Non-specific source (human waste),

Potential–Gulls (secondary wildlife), soil, sediment and sand (seasonal),

Possible - Sewage infrastructure, mobile sources (human waste), domestic animals

### **43 - Monitoring and Mitigation to Address Fecal Pathogen Pollution along California Coast**

Applied Marine Sciences, Inc., University of California Davis, California Department of Fish and Game, and Marine Wildlife Veterinary Care and Research Center

Purpose - The goals of this research program were to use both laboratory and field approaches to investigate issues related to water quality monitoring and mitigation of fecal pathogen pollution along the central California coast.

Results - The universal Bacteroidales marker was detected in all water samples (100%). The human Bacteroidales marker was detected in 37% of samples, while the cow (8%) and dog (6%) bacteroidales markers were detected in less than 10% of samples. Overall, Bacteroidales concentrations ranged from 87-1.3 million gc/mL for universal markers, 45-17,268 gc/mL for human markers, 3-92 gc/mL for cow markers, and 12-575 gc/mL for dog markers.

Sources:

Probable – Non-specific source (human waste),

Potential - Dogs and livestock,

Possible –

### **68 - Little Sac River Watershed Bacterial Source Tracking Analysis**

Dr. Claire Baffaut, Dr. C.A. Carson, and W. Rogers

<https://mospace.umsystem.edu/xmlui/bitstream/handle/10355/3029/LittleSacBacterial.pdf?sequence=1>

Purpose - To identify the sources of bacteria found in the Little Sac River using rep-PCR analyses of fecal material.

Results - The data show that the highest fecal coliform loads come from unknown sources, geese, and human. Data show that sources differ by season but the magnitude of the contamination is not significantly affected by season.

Sources:

Probable – Wastewater treatment plant, Geese (non-specific source)

Potential – Cattle and horses

Possible – Septic (sewage infrastructure)

### **117 - SOURCES OF POLLUTANTS IN WISCONSIN STORMWATER**

R.T. Bannerman, D.W. Owens, R.B. Dodds, and N.J. Hornewer

<http://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.176.2404&rep=rep1&type=pdf>

Purpose - Identification of critical source areas (streets, roads, parking lots, etc.) could reduce the amount of area needing best-management practices in two areas of Madison, WI. Targeting best-management practices to 14% of the residential area and 40% of the industrial area could significantly reduce contaminant loads by up to 75%.

Results - Streets will probably be a critical source area in every land use. The majority of the runoff loads for many contaminants may be from streets in residential and commercial land uses. Parking lots are probably another critical source for commercial and industrial land uses. About 77% of the area in the commercial land use would have to be managed to control at least 75% of the loads for all contaminants except fecal coliform bacteria.

Sources:

Probable – Sewer outfall, Street runoff (residential, commercial and industrial)

Potential – Cattle and horses  
Possible – Septic (sewage infrastructure)

## **82 - Tiered Approach for Identification of a Human Fecal Pollution Source at a Recreational Beach: Case Study at Avalon Bay, Catalina Island, California**

Alexandria B. Boehm, J.A. Fuhrman, R.D. Morse, and S.B. Grant

<http://dornsife.usc.edu/labs/fuhrman/Documents/Publications/Tiered%20Approach.pdf>

Purpose - In this study, a three-tiered approach is used to identify human and nonhuman sources of FIB in Avalon Bay, a popular resort community on Catalina Island in southern California.

Results - Most of the FIB contamination along the shoreline of the City of Avalon is due to sources inside the bay and, in particular, from the land side of the beach. During the 24-h survey, the most contaminated shoreline sites exhibited a semi-diurnal FIB pattern in which the concentrations increased during ebbing tides. The multiple instances of positive HF and HV assay results at shoreline stations indicate that human fecal contamination exists in Avalon Bay. The nuisance runoff and bird feces had the highest levels of FIB with TC, EC, and ENT consistently near or above the upper limit of detection for water samples 24 192 MPN/100 mL. With the exception of sample R101, pipe discharges from underneath the pier and wharf and the cooling water boat discharge had relatively low levels of FIB. Sample R101 was taken from a broken pipe carrying gray water underneath the wharf and had TC and EC levels above our detection limit of 24 192 MPN/100 mL and ENT levels of 10 462 MPN/100 mL, which is 100 times higher than the CDHS single-sample standard. City officials repaired this pipe in early October. Subsurface water collected from within the five trenches had sporadically high levels of FIB.

Sources:

Probable – Non-specific source (urban land use; human waste), MS4 Infrastructure (dry weather runoff; human waste), birds (secondary wildlife), reclaimed water (leaking graywater pipe)

Potential –

Possible – Commercial/Industrial (boat cooling water, pier, and wharf discharges from pipes)

## **153 - Cross-Shelf Transport at Huntington Beach Implications for the Fate of Sewage Discharged through an Offshore Ocean Outfall**

Alexandria B. Boehm, B.F. Sanders, and C.D. Winant

<http://www-ccs.ucsd.edu/~cdw/mypubs/109.pdf>

Purpose - Evaluate the potential for internal tides to transport wastewater effluent from the Orange County Sanitation District (OCSD) ocean outfall toward Huntington Beach.

Results - On the basis of these analyses, it remains unclear whether OCSD effluent impairs surf-zone water quality. However, OCSD plume cannot be ruled out as a contributor to poor bathing-water quality at Huntington Beach.

### **131 - Source Tracking in Lake Darling Watershed**

Janice Boekhoff

<http://www.igsb.uiowa.edu/wqm/Publications/Reports/LakeDarlingFinalReport.pdf>

Purpose - Determine the source of fecal contamination in Lake Darling and the surrounding watershed.

Results - E. coli bacteria from most of the water samples at Lake Darling have been identified by DNA ribotyping as coming from unknown sources of fecal contamination (75% of the water samples had bacteria from unknown sources using the WHU library). More unknown source classifications than known sources suggested the E. coli isolate library was either not large enough or was not representative of all of the sources in the watershed.

Sources:

Probable – Secondary wildlife (cattle and swine), Wildlife (unknown)

Potential –

Possible – Commercial/Industrial (boat cooling water, pier, and wharf discharges from pipes)

### **83 - Detection of Genetic Markers of Fecal Indicator Bacteria in Lake Michigan and Determination of Their Relationship to Escherichia coli Densities Using Standard Microbiological Methods**

Patricia A. Bower, C.O. Scopel, E.T. Jensen, M.M. Depas, and S.L. McLellan

<http://aem.asm.org/content/71/12/8305.full.pdf+html>

Purpose - Lake Michigan surface waters impacted by fecal pollution were assessed to determine the occurrence of genetic markers for Bacteroides and Escherichia coli.

Results - Human-specific Bacteroides spp. were found at three of the nine beach sites tested. Human-specific Bacteroides genetic marker is a sensitive measure of sewage contamination. Sanitary sewage overflow samples taken in the suburban part of the watershed showed the presence of cow-specific genetic marker, since the cow-specific primers do not differentiate between types of ruminants, i.e., elk, deer, and cows.

Sources:

Probable – CSO and SSO (Sewage infrastructure; human waste)

Potential – Sanitary sewer infiltration into the storm drain (Sewage infrastructure; human waste), Ruminant (wildlife; non-anthropogenic)

Possible – Sanitary sewer infiltration into the storm drain (Sewage infrastructure; human waste)

### **27 – Antibiotic Resistance Analysis of Fecal Coliforms to Determine Fecal Pollution Sources in a Mixed-Use Watershed**

Brian S. Burnes

<http://www.springerlink.com/content/q3213338g1578x88/fulltext.pdf>

Purpose - Antibiotic resistance analysis was performed on fecal coliform (FC) bacteria from a mixed-use watershed to determine the source, human or nonhuman, of fecal coliform contamination.

Results - Human sources contribute a majority (>50%) of the baseflow FC isolates found in the watershed in urbanized areas. Chicken and livestock sources are responsible for the majority of the baseflow FC isolates found in the rural reaches of the watershed. Stormwater introduces FC isolates from domestic (~16%) and wild (~21%) sources throughout the watershed and varying amounts (up to 60%) from chicken and livestock sources. These results suggest that antibiotic resistance patterns of FC may be used to determine sources of fecal contamination and aid in the direction of water quality improvement.

Sources:

Probable – Urbanized watershed (human waste), cows and chickens (rural watershed)

Potential – Stormwater runoff,

Possible –

### **13 - Results from a Microbial Source-Tracking Study at Villa Angela Beach, Cleveland, Ohio 2007**

Rebecca N. Bushon, E.A. Stelzer, and D.M. Stoeckel

Purpose - The overall goal of the study was to provide NEORSD with source-tracking information to aid in their understanding of elevated bacterial concentrations at Villa Angela Beach in Cleveland Ohio. To understand these elevation concentrations, 13 source samples (influent/effluent to sewage treatment plant, waterfowl feces from beach area, combined sewer overflow, stormwater outfall) and 33 beach-area water and sand samples were analyzed for E coli and 3 Bacteroides DNA markers

Results - Therefore, Btheta does not appear to be a useful human-associated marker for this beach area. In the Lake, human source is not a likely contributor of fecal bacteria, however, the gulls are a probable source. In Euclid Creek, there were strong signals of human sources on two occasions and gulls were not present. The sand did not have human sources present and gull sources were present in low concentrations.

Sources:

Probable -

Potential - Combined sewer overflow, influent/effluent to sewage treatment plant, waterfowl feces from beach area,

Possible -

### **85 - Population structure, persistence, and seasonality of autochthonous Escherichia coli in temperate, coastal forest soil from a Great Lakes watershed**

Muruleedhara N. Byappanahalli, R.L. Whitman, D.A. Shively, M.J. Sadowsky, and S. Ishii

<http://www.glsc.usgs.gov/files/publications/population.pdf>

Purpose - In this study, undisturbed, forest soils within six randomly selected 0.5 m enclosure plots (covered by netting of 2.3 mm mesh size) were monitored from March to October 2003 for *E. coli* in order to describe its numerical and population characteristics.

Results - In this study, soil was found as a potential habitat for the persistent, perhaps resident, *E. coli* populations in temperate conditions. While our studies showed that *E. coli* can occur in temperate forest soils, albeit at low densities, it also had the ability to persist for extended periods in these habitats, suggesting that it is not a transient organism in soil but perhaps part of the natural microflora. Even if this is not the case, its population resiliency suggests that soil-borne *E. coli* should be treated as background concentration in source and impact evaluation investigations.

Sources:

Probable – Soil/Sediment/Sand (non-anthropogenic)

Potential –

Possible – Gull, deer, geese, terns (wrackline; non-anthropogenic)

#### **84 - Ubiquity and Persistence of Escherichia coli in a Midwestern Coastal Stream**

Muruleedhara Byappanahalli, M. Fowler, D. Shively, and R. Whitman.

<http://aem.asm.org/content/69/8/4549.full.pdf+html>

Purpose - Dunes Creek, a small Lake Michigan coastal stream that drains sandy aquifers and wetlands of Indiana Dunes, has chronically elevated *Escherichia coli* levels along the bathing beach near its outfall. This study sought to understand the sources of chronically elevated *Escherichia coli* levels along the bathing beach near its outfall in Dunes Creek's central branch.

Results - Water samples analyzed during the 1999 and 2000 monitoring seasons clearly demonstrated that *E. coli* concentrations in Dunes Creek were significantly correlated with the park's beach water. Dunes Creek empties directly onto the state park's only swimming beach, indicating that the creek directly impacts bathing water quality. *E. coli* is common within the stream basin, especially in submerged, margin, and wetted bank sediments, with numbers rapidly decreasing landward beyond the banks. The relationship between *E. coli* concentration and stream order suggests that excessive ditching and, consequently, non-point source input via sediment transport are responsible for elevated *E. coli* density in the watershed.

Sources:

Probable – Soil/Sediment/Sand (non-anthropogenic)

Potential –

Possible – Non-specific source (groundwater; non-anthropogenic)

#### **3 - Pismo Beach Fecal Contamination Source Identification Study; Final Report. Aug. 12, 2010**

CAL POLY and City of Pismo Beach

[http://www.coastalrcd.org/images/cms/files/PismoFinalReport-v1\\_4%5B1%5D.pdf](http://www.coastalrcd.org/images/cms/files/PismoFinalReport-v1_4%5B1%5D.pdf)

Purpose - To identify biological sources of fecal contamination. Primary sources found were bird fecal contamination.

Results - The data collected in this study clearly shows the main source of fecal contamination on the beach is bird droppings near the pier. Nearly 40% of the E. coli strains collected in this study matched bird fecal sources, and E coli strains with a pigeon-specific fingerprint were collected. In addition, measuring the time since a tide last washed the part of the beach being sampled was an excellent predictor of FIB count, indicating that deposition of fecal matter on the beach itself was a predominate contamination mode.

Sources:

Probable - Bathers, dogs, pigeons (secondary wildlife)

Potential - Cows

Possible -

### **86 - Sourcing faecal pollution from onsite wastewater treatment systems in surface waters using antibiotic resistance analysis**

S. Carroll, M. Hargreaves, and A. Goonetilleke

<http://eprints.qut.edu.au/4018/1/4018.pdf>

Purpose - To identify the sources of faecal contamination in investigated surface waters and to determine the significance of onsite wastewater treatment systems (OWTS) as a major contributor to faecal contamination.

Results - Antibiotic resistance patterns (ARP) were established for a library of 717 known Escherichia coli source isolates obtained from human, domesticated animals, livestock and wild sources. The resulting ARP DA indicated that a majority of the faecal contamination in more rural areas was nonhuman; however, the percentage of human isolates increased significantly in urbanized areas using OWTS for wastewater treatment.

Sources:

Probable – Sewage infrastructure (onsite wastewater treatment systems; human waste)

Potential –

Possible –

### **28 - Faecal pollution source identification in an urbanising catchment using antibiotic resistance profiling, discriminant analysis and partial least squares regression**

Steven P. Carroll, L. Dawes, L., M. Hargreaves, and A. Goonetilleke

<http://eprints.qut.edu.au/19108/1/c19108.pdf>

Purpose - Antibiotic Resistance Patterns (ARP) were established for a library of 1005 known E. coli source isolates obtained from human and non-human (domesticated animals, livestock and wild) sources in an urbanising catchment in Queensland State, Australia. Discriminant Analysis (DA) was used to differentiate between the ARP of source isolates and to identify the sources of faecal contamination.

Results - The resulting ARP (Antibiotic Resistance Patterns) DA (Discriminant Analysis) indicated that a majority of the faecal contamination in the rural areas was non-human. However, the percentage of human isolates increased significantly in urbanised areas using onsite systems for wastewater treatment. The PLS regression was able to develop predictive models which indicated a high correlation of human source isolates from the urban area.

Sources:

Probable - Urbanized watershed (human waste), agriculture, other (land use)

Potential –

Possible -

#### **47 - Middle Santa Ana River Bacterial Indicator TMDL Data Analysis Report**

CDM and Risk Sciences

Purpose - The primary goal of this study was "to develop an investigative strategy at the highest priority sites, including site-specific or subwatershed-specific activities."

Results – Analysis showed significant differences in the frequency with which molecular markers for humans, dogs, and cattle were detected at the various source evaluation sites. The sites with highest frequency of detection of host-specific markers included the Human marker at Box Springs Channel and Chris Basin; Bovine marker at Anza Drain, Cypress Channel and San Antonio Channel; and Domestic canine marker at Chris Basin, County Line Channel and Day Creek. Where the universal marker was measured, it was quantified at levels much higher than the other measured markers, indicating the presence of many other sources of bacteria, e.g. birds, rodents, small mammals and reptiles. Preliminary review of land use data indicates that bacterial concentrations are positively correlated with degree of urban development and negatively correlated with the proportion of agricultural acreage and open space in the area.

Sources:

Probable – Non-specific source (human waste; 1 of 13 sites), dogs(1 of 13 sites) and cows(3 of 13 sites), commercial/industrial (anthropogenic non-human source), residential, commercial, and industrial (land use)

Potential -

Possible – Agriculture (anthropogenic non-human source), natural land use (non-anthropogenic) natural and agricultural (land use)

#### **127 - Densities of fecal indicator bacteria in tidal waters of the Ballona Wetlands, Los Angeles County, California**

John. H. Dorsey

<http://www.freepatentsonline.com/article/Bulletin-Southern-California-Academy-Sciences/151712972.html>

Purpose - Densities of fecal indicator bacteria (FIB) represented by total coliforms, E. coli and enterococci were measured within tidal channels of the Ballona Wetlands (Los Angeles County) to see if the wetlands act as a sink or source for these bacteria and to measure increases in FIB densities during wet weather.

Results - Results suggest that the wetlands may act as a sink in that FIB densities tended to be greater during flood flows into the wetlands, but less in water draining out of the system during ebb flows. However, this condition was not consistently met, especially at stations farthest from the tide gates. These sites could be reflecting increased FIB densities through regrowth within sediments and other unidentified sources.

Sources:

Probable –Storm drains

Potential –

Possible -

### **181 - Reduction of fecal indicator bacteria (FIB) in the Ballona Wetlands saltwater marsh (Los Angeles County, California, USA) with implications for restoration actions**

John H. Dorsey, P.M. Carter, S. Bergquist and R. Sagarin

<http://www.sciencedirect.com/science/article/pii/S004313541000388X/>

Purpose - Determine FIB tidal dynamics within the wetland

Results - The wetlands act as both a source and sink for FIB depending on tidal conditions and exposure to sunlight. Future restoration actions would result in a tradeoff – increased tidal channels offer a greater surface area for FIB inactivation, but also would result in a greater volume of FIB-contaminated re-suspended sediments carried out of the wetlands on stronger ebb flows. As levels of FIB in Ballona Creek and Estuary diminish through recently established regulatory actions, the wetlands could shift into a greater sink for FIB.

### **119 - FECAL COLIFORM AND STREPTOCOCCUS CONCENTRATIONS IN RUNOFF FROM GRAZED PASTURES IN NORTHWEST ARKANSAS**

D. R. Edwards, M.S. Coyne, P.F. Vendrell, T.C. Daniel, P.A. Moore, Jr., and J.F. Murdoch

<http://www.pcpw.tamu.edu/docs/lshs/end->

[notes/Fecal%20Coliform%20and%20Streptococcus%20Concen-0982758667/Fecal%20Coliform%20and%20Streptococcus%20Concentrations%20in%20Runoff%20from%20Grazed%20Pastures%20and%20Northwest%20Arkansas.pdf](http://www.pcpw.tamu.edu/docs/lshs/end-notes/Fecal%20Coliform%20and%20Streptococcus%20Concen-0982758667/Fecal%20Coliform%20and%20Streptococcus%20Concentrations%20in%20Runoff%20from%20Grazed%20Pastures%20and%20Northwest%20Arkansas.pdf)

Purpose - Assess the effects of grazing, time of year, and runoff amounts on FC and FS concentrations and to evaluate whether FC/FS concentration ratios are consistent with earlier values reported as characteristic of animal sources.

Results - In general, FC and FS concentrations were not directly related to either treatment with animal manure or presence of grazing cattle. Ratios of FC to FS concentrations varied widely ranging from almost zero to more than 100. These data confirm earlier findings that FC/FS ratios are not a reliable indicator of the source of FC and FS in the runoff.

### **147 - FECAL-INDICATOR BACTERIA IN STREAMS ALONG A GRADIENT OF RESIDENTIAL DEVELOPMENT**

Steven A. Frenzel and C.S. Couvillion

<http://lshs.tamu.edu/docs/lshs/end->

[notes/fecal%20indicator%20bacteria%20in%20streams%20along%20a%20gradient%20of%20re](http://lshs.tamu.edu/docs/lshs/end-)

[sid-3692103194/fecal%20indicator%20bacteria%20in%20streams%20along%20a%20gradient%20of%20residential%20development.pdf](http://lshs.tamu.edu/docs/lshs/end-)

Purpose - In order to adopt EPA water-quality standards for concentrations of Escherichia coli (E. coli) or enterococci, and study to determine the effects of urbanization on water quality.

Results - Areas served by sewer systems had significantly higher fecal-indicator bacteria concentrations than did areas served by septic systems. The areas served by sewer systems also had storm drains that discharged directly to the streams, whereas storm sewers were not present in the areas served by septic systems. Fecal-indicator bacteria concentrations were highly variable over a two-day period of stable streamflow, which may have implications for testing of compliance to water-quality standards.

### **120 - Soil: the environmental source of Escherichia coli and Enterococci in Guam's streams**

R. Fujioka, C. Sian-Denton, M. Borja, J. Castro, and K. Morpew

<http://onlinelibrary.wiley.com/doi/10.1111/j.1365-2672.1998.tb05286.x/pdf>

Purpose - Test the hypothesis that faecal bacteria are able to establish themselves in the soil environments of tropical islands by conducting a study in Guam, a tropical pacific island with warmer temperatures and higher humidity than Hawaii (covered in a previous study).

Results - Results obtained in Guam were similar to the results obtained in Hawaii and provided convincing evidence that the faecal bacterial indicators selected by USEPA to establish recreational water quality standards are able to colonize the soil environments of warm, humid tropical islands, current hygienic water quality standards which are based on concentrations of faecal indicator bacteria may not be applicable in tropical islands and perhaps other subtropical and tropical countries in the world. In these countries, stream waters can be expected to contain elevated levels of faecal bacteria.

Sources:

Probable - Rainfall

Potential –

Possible -

### **91 - Use of composite data sets for source-tracking enterococci in the water column and shoreline interstitial waters on Pensacola Beach, Florida**

Fred J. Genthner, J.B. James, D.F. Yates, and S.D. Friedman

<http://64.9.200.77/lists/beachnet/2005-07/pdf00002.pdf>

Purpose - Source identification was performed to better understand risk associated with higher densities of enterococci found in swash zone interstitial water (SZIW) as compared to adjacent bathing water on Pensacola Beach, FL.

Results - This study documents higher densities of enterococci in SZIW than in adjacent bathing waters on Pensacola Beach. Entrapment may partially account for increased bacteria densities, however, biological factors (nutrients, protection from predation) and physical factors (particulate matter, periodic wetting and drying, protection from solar irradiation) may not only allow the enhanced survival of bacteria but may actually provide a growth- promoting environmental niche on the beach.

Sources:

Probable – Seagull (secondary wildlife)

Potential –

Possible – **Non-specific source (human waste)**

#### **46 - Laguna Watershed Study and Water Quality Improvement Feasibility Analysis**

Geosyntec and UCSB

Purpose - To evaluate dry weather hydrology, microbiological indicators, bacterial sources and loads, and feasible water quality improvements for the Laguna Channel in Santa Barbara, CA.

Results – Based on the analysis of human-specific *Bacteroides* DNA, it appears that there is significant input of human fecal waste into some Laguna storm drains and into Laguna Channel. An obvious spatial correlation between measured FIB and Human specific *Bacteroides* Marker (HBM) concentrations could not be identified; similar trends between indicator species and HBM concentrations were also not observed.

Sources:

Probable – Non-specific source (human waste),

Potential -

Possible -

#### **148 - Quantitative Detection of Hepatitis A Virus and Enteroviruses Near the United States-Mexico Border and Correlation with Levels of Fecal Indicator Bacteria**

Richard M. Gersberg, M.A. Rose, R. Robles-Sikisaka, and A.K. Dhar

<http://publichealth.sdsu.edu/publications/gersberg684.pdf>

Purpose - To measure the levels of Hepatitis A virus (HAV) and enteroviruses in coastal waters, and compare to *E. coli* and enterococci.

Results - HAV and enterovirus were found in 93% of wet weather samples. Inadequate sewage infrastructure in Tijuana, Mexico, also contributes to the high levels found at some sites.

## **60 - Evaluation of Two Library-Independent Microbial Source Tracking Methods to Identify Sources of Fecal Contamination in French Estuaries**

Michele Gourmelon, M.P. Caprais, R. Segura, C. Le Mennec, S. Lozach, J.Y. Piriou, and A. Rince

<http://aem.asm.org/content/73/15/4857.full.pdf+html>

Purpose - The aim of this study was to optimize and validate the two MST techniques (host-specific 16S rRNA gene markers from Bacteroidales and genotyping of F-specific RNA bacteriophages) on human and animal feces, sewage treatment plant (STP) sludge, wastewater samples, and pig liquid manure (PLM; pig slurry) collected in France. Both techniques were then applied to water samples collected at different times from three estuaries

Results - Humans and animals sources are detected as sources of *E. coli* and Enterococci contamination in the estuaries based on host-specific Bacteroidales and F-specific bacteriophages

Sources:

Probable – Septic (human waste), livestock (domestic animals), livestock (agriculture), birds (wildlife), birds (secondary wildlife)

Potential -

Possible -

## **23 - Generation of Enterococci Bacteria in Saltwater Marsh and its impact on the surf zone water quality**

Steven B. Grant, B.F. Sanders, A.B. Boehm, A.J. Redman, J.H. Kim, R.D. Mrše, A.K. Chu, M. Gouldin, C.D. McGee, N.A. Gardiner, B.H. Jones, J. Svejkovsky, G.V. Leipzig, and A. Brown

<https://www.crops.org/publications/jeq/pdfs/31/4/1300>

Purpose - To characterize the sources and transport of Enterococcus in tidally influenced flood control channels and a saltwater marsh.

Results - We find that enterococci bacteria are present at high concentrations in urban runoff, bird feces, marsh sediments, and on marine vegetation. Surprisingly, urban runoff appears to have relatively little impact on surf zone water quality because of the long time required for this water to travel from its source to the ocean. On the other hand, enterococci bacteria generated in a tidal saltwater marsh located near the beach significantly impacts surf zone water quality.

Sources:

Probable – Marsh (non-anthropogenic; non-specific source), wildlife (marsh avian), marsh sediment, soil/sediment/sand

Potential –

Possible –

## **92 - Antibiotic Resistance Profiles to Determine Sources of Fecal Contamination in a Rural Virginia Watershed**

Alexandria K. Graves, C. Hagedorn, A. Teetor, M. Mahal, A.M. Booth, and R.B. Reneau

<https://www.crops.org/publications/jeq/pdfs/31/4/1300>

Purpose - Antibiotic resistance analysis (ARA) was used to determine if enterococci of human origin were present in a stream (Spout Run) that passes through a rural non-sewered community (Millwood, VA)

Results - A human signature was found in Spout Run as it passed through upper and middle Millwood. No evidence of a human signature was found in Page Brook in an earlier report (Hagedorn et al., 1999), and no evidence of a human signature was found in any of the tributaries that form Spout Run in this study. There are 32 homes in upper Millwood, 21 homes in middle Millwood, and 13 homes in lower Millwood, all on individual septic systems. Repair or replacement of unsatisfactory systems (or installation of a community system) should result in removal of the human signature from Spout Run.

Sources:

Probable – Septic system (sewage infrastructure; human waste), Livestock (domestic animals; anthropogenic non-human sources), wildlife (non-anthropogenic)

Potential –

Possible –

## **2 - San Diego County Enterococcus Regrowth Study; Draft Final Report, June 11, 2011**

John Griffith and D. Ferguson

Purpose - To investigate storm drains as a potential source of Enterococcus bacteria to San Diego's coastal waters during dry weather.

Results –The results of this study suggest that enterococci in these storm drain systems came from predominantly natural sources and include strains that are capable of growing on drain pipe surfaces. The results of the concrete coupon/growth study showed that enterococci were capable of attaching to and growing on concrete coupons. Testing of enterococci extracted from coupons in Cottonwood Creek revealed species and biotypes most closely related to freshwater plants and decomposed algae/vegetation. The majority (77%) of enterococci from the surfaces of coupons, pipe and cobble rock at a La Jolla storm drain were identified as an enterococcal species associated with plants.

A number of natural sources of enterococci were identified at Moonlight State Beach. In this study, up to 70% of creek water isolates were identified as a species commonly found on plants. Multivariate analysis of species and biotypes showed that enterococci in Cottonwood Creek were most similar enterococci found in decomposed algae and vegetation, freshwater plants and seawrack. At least 52% of enterococci in beach water were of a species found in plants, however 34% of isolates were either non-Enterococcus species or unidentifiable, suggesting the possibility of additional sources of enterococci that were not evaluated in this study. Some of the enterococci biotypes in beach water were the same ones found in decomposed algae and vegetation, freshwater plants and seawrack.

The low numbers of birds and predominance of *E. faecalis* in bird stools indicate that birds may not have been a major source of enterococci to creek and beach water, however the dissimilarity in enterococcal populations could also be related to different selection pressures.

All beach and storm drain/creek water samples tested for Bacteroidales indicated very low or non-detectable levels of the human marker, indicating that these samples had little or no evidence of human fecal material.

Sources:

Probable – MS4 Infrastructure (Human waste), avian (secondary wildlife), avian (non-anthropogenic)

Potential – Landscaping (irrigation and lawn clippings),

Possible – Wrackline, Plants (non-anthropogenic), seawrack, beach sand

### **121 - Escherichia coli and Enterococci at Beaches in the Grand Traverse Bay, Lake Michigan: Sources, Characteristics, and Environmental Pathways**

Sheridan K. Haack, L.R. Fogarty, and C. Wright

<http://www.glin.net/lists/beachnet/2007-07/pdf00000.pdf>

Purpose - Overall objectives were to (i) quantify EC and ENT in dominant source materials and recreational waters; (ii) characterize selected source isolates using genomic (EC) or biochemical (ENT) profiling; (iii) identify associations between numbers of these two indicator bacteria groups and ambient conditions; (iv) identify processes that influence spatiotemporal variability of indicator bacteria at these beaches; and (v) evaluate standardized monitoring approaches in light of site-specific knowledge about sources and environmental processes

Results - Bird feces are likely one significant source of bacterial contamination to these beaches. Storm drains and the Boardman River contributed large numbers of EC and ENT to the bay, even during non-runoff conditions.

Sources:

Probable – Seawrack (vegetation and other detritus)

Potential –

Possible –

### **94 - Determining Sources of Fecal Pollution in a Rural Virginia Watershed with Antibiotic Resistance Patterns in Fecal Streptococci**

C. Hagedorn, S.L. Robinson, J.R. Filtz, S.M. Grubbs, T.A. Angier, and R.B. Reneau Jr.

<http://aem.asm.org/content/65/12/5522.full.pdf+html>

Purpose - The objectives of this project were (i) to validate the method of using antibiotic resistance patterns in fecal streptococci and discriminant analysis (DA) to differentiate between human and animal sources and between certain types of animal sources with a larger database of known source isolates from a wider geographical region and (ii) to use this method in a watershed project to identify fecal pollution sources.

Results - The results presented affirm that antibiotic resistance patterns can be used with fecal streptococci to determine sources of fecal pollution in water. Results (detection of no human isolates) had a direct impact on water quality improvement in Page Brook, as local officials were able to focus restoration efforts on the actual sources (e.g., beef cattle) rather than on those that made no contribution to the water pollution.

Sources:

Probable – Cattle (domestic animals; anthropogenic non-human sources)

Potential – Waterfowl, deer unidentified (wildlife; non-anthropogenic)

Possible – Non-specific source (human waste)

### **69 - Influence of Freshwater Sediment Characteristics on Persistence of Fecal Indicator Bacteria**

Laurence Haller, E. Amedegnato, J. Pote, and W. Wildi

<http://www.springerlink.com/content/ju524662v67v4967/fulltext.pdf>

Purpose - To investigate the effect of sediment characteristics such as particle grain size and nutrient and organic matter contents on the survival of fecal indicator bacteria including total coliforms, E. Coli, and Enterococcus.

Results - FIB survival in sediments and possible re-suspension are considerable significance for understanding permanent microbial pollution. Results revealed (1) FIB survived in sediments up to 50 days, (2) higher growth and lower decay rates of FIB in sediments with high levels of organic matter and nutrients and small grain size, (3) longer survival of Enterococcus compared to E. coli and total coliforms.

Sources:

Probable – Wastewater treatment plant (based on other studies), Soil/Sediment/Sand

Potential – Cattle and horses, storm runoff (MS4 Infrastructure; human waste), Agriculture

Possible – Septic (sewage infrastructure), Wastewater treatment plant, storm runoff (MS4 Infrastructure; human waste), Agriculture, Land use

### **193 - Soil: the environmental source of Escherichia coli and Enterococci in Hawaii's streams**

C. M. Hardina, and R. Fukuda

<http://mdl.csa.com/partners/viewrecord.php?requester=gs&collection=ENV&recid=9200969&q=&uid=791338866&setcookie=yes>

Purpose - To determine the concentrations and sources of Escherichia coli and enterococci in a typical stream (Manoa) in Hawaii.

Results - Soil is considered the most likely source for the high concentrations of indicator bacteria naturally present in the freshwater streams of Hawaii.

Sources:

Probable – Wastewater treatment plant (based on other studies), Soil/Sediment/Sand

Potential – Cattle and horses, storm runoff (MS4 Infrastructure; human waste), Agriculture, Land use

Possible – Septic (sewage infrastructure), Wastewater treatment plant, storm runoff (MS4 Infrastructure; human waste), Agriculture, Land use

**61 - Combining targeted sampling and fluorometry to identify human fecal contamination in a freshwater creek**

Peter G. Hartel, K. Rodgers, G.L. Moody, S.N.J. Hemmings, J.A. Fisher, and J.L. McDonald  
<http://www.iwaponline.com/jwh/006/0105/0060105.pdf>

Purpose - The aim of this study was to conduct sampling at 2 reaches at Potato Creek, a freshwater creek in Georgia, and 1 tributary during baseflow and stormflow conditions and detect human sources of fecal contamination by using targeted sampling (finding hot spots of fecal contamination within the Creek and/or tributaries and re-sampling these spots) and fluorometry (detection of fluorescing compounds, optical brighteners, & laundry detergents)

Results - Humans, dogs, and cattle are the major suspected sources (not sampled) for fecal contamination in the Potato Creek reaches

Sources:

Probable -

Potential -

Possible – Broken home sewer line, dogs, cows, wildlife (non-anthropogenic),

**63 - Drayton Harbor Watershed Microbial Source Tracking Pilot Study Phase 2: California Creek, Dakota Creek and Cain Creek Sub-watersheds**

Hirsch Consulting Services

<http://whatcomshellfish.whatcomcounty.org/Drayton/documents/DraytonHarborSanitarySurvey2010.pdf>

Purpose - The objective of this study was to determine whether human or ruminant sources contribute to fecal contamination at selected sampling stations to inform follow-up investigations and corrective actions by Whatcom County and other agencies and to inform the Drayton Harbor Fecal Coliform TMDL Evaluation.

Results - Ruminant and human fecal sources threaten the shellfish harvest.

Sources:

Probable - Non-specific source (human waste), domestic animals,

Potential -

Possible -

**67 - Sources and Mechanisms of Delivery of E. coli (bacteria) Pollution to the Lake Huron**

Todd Howell

Purpose - To identify the potential sources of fecal pollution to the shoreline.

Results – The long-term fate of the potentially high E. coli loads delivered to the lake at these times is poorly understood. The association of E. coli with particulate material is thought to be a key mechanism by which survival and transport in the lake environment is enhanced.

Sources:

Probable – Agriculture,

Potential – Soil/Sediment/Sand

Possible - **Non-specific source (human waste), agriculture (listed under other with no degree of designation (probable, low, etc.)**

### **10 - Wrack promotes the persistence of fecal indicator bacteria in marine sands and seawater**

Gregory J. Imamura, R.S. Thompson, A.B. Boehm, and J.A. Jay

<http://onlinelibrary.wiley.com/doi/10.1111/j.1574-6941.2011.01082.x/full>

Purpose - Study examined the relationship between beach wrack, FIB, and surrounding water and sediment at marine beaches along the California coast.

Results – FIB concentrations normalized to dry weight were the highest in stranded dry wrack, followed by stranded wet and suspended ‘surf’ wrack. Laboratory microcosms were conducted to examine the effect of wrack on FIB persistence in seawater and sediment. Indigenous enterococci and Escherichia coli incubated in a seawater microcosm containing wrack showed increased persistence relative to those incubated in a microcosm without wrack. FIB concentrations in microcosms containing wrack-covered sand were significantly higher than those in uncovered sand after several days. These findings implicate beach wrack as an important FIB reservoir.

Sources:

Probable – Seawrack [1-Dry wrack (highest FIB), 2-wet wrack, 3-surf wrack]

Potential -

Possible -

### **57 - Presence and Growth of Naturalized Escherichia Coli in Temperate Soils from Lake Superior Watersheds**

Satoshi Ishii, W.B. Ksoll, R.E. Hicks, and M.J. Sadowsky

<http://aem.asm.org/content/72/1/612.full.pdf+html>

Purpose - The goal of the study was to (i) examine the survival and persistence of E. coli populations in three soils in several coastal Lake Superior watersheds (extreme environmental conditions) and to determine if these E. coli strains have become naturalized to these soils, (ii) examine the genetic relatedness of soilborne E. coli strains from different locations, and (iii) determine if soilborne E. coli could actively multiply in the soils examined.

Results - E. Coli is able to survive and grow in soil, with growth occurring when temperature and nutrients are higher and able to survive in extreme environments (low temps). Animal feces of surrounding wildlife not shown to be likely source.

Sources:

Probable – Soil/Sediment/Sand

Potential -

Possible - Wildlife

### **156 - Sources and Persistence of Fecal Coliform Bacteria in a Rural Watershed**

Rob C. Jamieson, R. J. Gordon, S. C. Tattrie, and G. W. Stratton

<http://www.cawq.ca/journal/temp/journal/7.pdf#page=32>

Purpose - Quantify the presence of fecal coliform bacteria in the surface waters of a rural watershed and to attempt to determine the primary sources of fecal pollution within rural watersheds.

Results - Fecal coliform levels frequently exceeded recreational water quality guidelines. At the watershed outlet, 94% of the collected samples exceeded the recreational water quality guideline during low flow conditions. Substantial bacterial loading was observed along stream reaches impacted by livestock operations. Bacterial loading was also observed along a stream reach that was not impacted by agricultural activities.

Sources:

Probable – Livestock

Potential -

Possible -

### **200 - The effect of cattle grazing on indicator bacteria in runoff from a Pacific Northwest watershed**

M.D. Jawson, L.F. Elliott, K.E. Saxton, and D.H. Fortier

<http://lshs.tamu.edu/docs/lshs/end->

[notes/the%20effect%20of%20cattle%20grazing%20on%20indica-1987218764/the%20effect%20of%20cattle%20grazing%20on%20indicator%20bacteria%20in%20runoff%20from%20a%20pacific%20northwest%20watershed.pdf](http://lshs.tamu.edu/docs/lshs/end-notes/the%20effect%20of%20cattle%20grazing%20on%20indica-1987218764/the%20effect%20of%20cattle%20grazing%20on%20indicator%20bacteria%20in%20runoff%20from%20a%20pacific%20northwest%20watershed.pdf)

Purpose - Total coliform (TC), fecal coliform (FC), and fecal streptococcal (FS) numbers were monitored for 3 years to determine the effect of grazing on the presence of these organisms in runoff from a cattle grazed and a non-grazed watershed in the Pacific Northwest

Results - Sampling at several locations within the grazed watershed showed that sources of indicator bacteria were well distributed, and as a result were nonpoint after the initial runoff events. Thus, present FC recommendations developed for point-sources would not apply adequately to grazed land in the Pacific Northwest. Indicator bacteria as presently analyzed would not provide a basis for developing best management practices.

Sources:

Probable – Secondary Wildlife (Cows)

Potential -

Possible –

### **12 - 2009 Investigation of Spatial and Temporal Distribution of Human-specific Bacteroidales marker in Malibu Creek, Lagoon and Surfrider Beach**

Jennifer Jay, R.F. Ambrose, V. Thulsiraj, and S. Estes

Purpose - The goal of the study is to understand the relationship between Fecal indicator bacteria (FIB) and human-specific Bacteroidales (HSB) in coastal wetland. The study examines the spatial & temporal relationship of human-specific Bacteroidales marker (HBM) & FIB in lower Malibu Creek, Lagoon, and Surfrider Beach during wet and dry weather to determine the presence of detectable concentrations of HBM in the lagoon and if concentrations of HBM correlate with FIB

Results - Of the 80 water samples analyzed within the Malibu watershed, five samples were positive for the human-specific HF183 Bacteroidales marker (HBM). The highest percent exceedance of FIB and HBM concentrations were measured during wet weather. During the study, 93.8% of the samples did not have detectable concentrations of HBM. These data do not rule out any particular potential sources of human fecal contamination.

Sources:

Probable -

Potential - storm drains

Possible - Septic systems, Tapia Wastewater Reclamation Facility disinfected discharge, wildlife and birds

### **98 - Microbial source tracking in a small southern California urban watershed indicates wild animals and growth as the source of fecal bacteria**

Sunny C. Jiang, W. Chu B.H. Olson, J. He, S. Choi, J. Zhang, J.Y. Le, and P.B. Gedalanga  
<http://www.eng.uci.edu/files/07-1MST.pdf>

Purpose - Apply three MST tools, namely, ARA, human viruses, and E. coli toxin biomarkers to aid in the cleanup of unknown pollution sources in Laguna Niguel. Laguna Niguel is a small urban watershed in southern California that experienced chronic fecal coliform and enterococci contamination, with concentrations on average of 2–4 orders of magnitude greater than State of California established type 2 recreational standards.

Results - Using three independent microbial source tracking methods, the results of this study indicate that human sewage was not a major contributor of fecal bacterial impairment in this small urban watershed. This study showed that rabbit feces contain one of the highest concentrations of Enterococcus spp. per unit weight.

Sources:

Probable – Urban land use (non-specific source), dogs (urban land use), cows and horses (rural open land use),

Potential –

Possible –

## **76 - Freshwater Beach Total Maximum Daily Load Microbial Source Tracking Study**

Dr. Stephen H. Jones

[http://des.state.nh.us/organization/divisions/water/wmb/tmdl/documents/sand\\_dam\\_appendix\\_b\\_beach.pdf](http://des.state.nh.us/organization/divisions/water/wmb/tmdl/documents/sand_dam_appendix_b_beach.pdf)

Purpose - The goal of this project was to investigate actual and potential bacterial sources at (3) public beaches. The approach reflects the latest concepts for efficient use of bacterial ribotyping for pollution source identification in New Hampshire, i.e., ribotyping of high priority samples and development of small local source species databases. This targeted approach was designed to optimize identification of the most significant contamination sources at the 3 beaches.

Results - Overall, birds were the most prevalent (37%) source species type, followed by livestock (24%), humans (5%), wild animals (4%) and pets (3%). The most commonly identified source species was geese (17 isolates), followed by cows and mixed avian (7) sheep (6), horses and ducks (3), septage, goat, wastewater effluent and dog (2), with single isolates identified as coming from deer, red foxes, wild turkeys and mixed wildlife.

Sources:

Probable – Livestock, birds (secondary wildlife)

Potential –

Possible – Non-specific source (human waste), pets, wildlife

## **99 - Tracking Bacterial Pollution Sources in Stormwater Pipes**

Dr. Stephen H. Jones

<http://www.unh.edu/users/unh/acad/colsa/marine-program/nhep/resources/pdf/trackingbacterialpollution-unh-03.pdf>

Purpose - Determine the bacteria source species from two of the highest priority storm drain pipes that discharge to Hampton Harbor

Results - Many storm water/runoff studies have attributed fecal contamination to pet wastes. Of the four types of sources identified, pets were the least common, behind birds, humans and wildlife.

Sources:

Probable – Non-specific source (human waste), geese (secondary wildlife), cormorants (wildlife; non-anthropogenic)

Potential –

Possible – Cats and dogs (domestic animals; anthropogenic non-human sources), seagulls and pigeons (secondary wildlife), foxes, raccoons and coyotes (wildlife; non-anthropogenic)

## **32 - USING MULTIPLE ANTIBIOTIC RESISTANCE AND LAND USE CHARACTERISTICS TO DETERMINE SOURCES OF FECAL COLIFORM BACTERIAL POLLUTION**

R. Heath Kelsey, G.I. Scott, D.E. Porter, B. Thompson, and L. Webster

<http://www.springerlink.com/content/p5p4413ku0082707/fulltext.pdf>

Purpose - Multiple Antibiotic Resistance (MAR) analysis and regression modeling techniques were used to identify surface water areas impacted by fecal pollution from human sources, and to determine the effects of land use on fecal pollution in Murrells Inlet, a small, urbanized, high-salinity estuary located between Myrtle Beach and Georgetown, South Carolina.

Results - MAR results suggest that the majority of the fecal pollution detected in the Murrells Inlet estuary may be from non-human sources, including fecal coliforms isolated from areas in close proximity to high densities of active septic tanks.

Sources:

Probable -

Potential -

Possible -

#### **144 - Bacteria Attenuation Modeling and Source Identification in Kranji Catchment and Reservoir**

Kathleen B. Kerigan, and J.M. Yeager

<http://censam.mit.edu/publications/yeager.pdf>

Purpose - Determine the bacterial loading of Kranji Catchment and Reservoir and how this will affect planned recreational use of the reservoir.

Results - Farm run-off near the reservoir was the bacterial source of greatest concern. The relatively high concentrations coupled with the short travel time, which diminishes opportunity for attenuation, resulted in high concentrations reaching the reservoir downstream levels.

#### **73 - Draft Calleguas Creek Watershed Quantitative Microbial Source Tracking Study**

Beverly Kildare, V. Rajal, S. Tiwari, D. Thompson, B. McSwain, S. Wuertz, D. Bambic, and G. Reide (Report Prepared by UC Davis in Collaboration with Larry Walker Associates)

Wuertz, S., Bambic, D., and Reide, G. (Report Prepared by UC Davis in Collaboration with Larry Walker Associates)

[http://www.calleguas.com/ccwmp/DRAFT\\_CCW\\_MST\\_061406.pdf](http://www.calleguas.com/ccwmp/DRAFT_CCW_MST_061406.pdf)

Purpose - The goal of this microbial source tracking (MST) study was to provide quantitative, host-specific fecal source data and assist in the development of a bacteria TMDL for the Calleguas Creek Watershed(CCW).

Results - Urban areas were found to be sources of human and canine bacteria to Arroyo Simi and Conejo Creek. The Tapo Canyon site, which is upstream of urban influences, exhibited the lowest concentrations and ratios of the mixed-human marker, but the highest concentrations and ratios of the cow/horse marker. Analysis of tertiary-treated wastewater samples indicates that mixed-human Bacteroidales concentrations may be relatively high in discharged effluent. However, such cells are most likely non-viable and thus not associated with water quality objective exceedances.

Sources:

Probable – Non-specific source (human waste), dogs (canine urban land use), cows and horses (rural and open space)

Potential –

Possible –

**100 - Non-point source pollution: Determination of replication versus persistence of Escherichia coli in surface water and sediments with correlation of levels to readily measurable environmental parameters**

Julie Kinzelman, S.L. McLellan, A.D. Daniels, S. Cashin, A. Singh, S. Gradus, and R. Bagley  
<http://www.iwaponline.com/jwh/002/0103/0020103.pdf>

Purpose - Racine, Wisconsin, located on Lake Michigan, experiences frequent recreational water quality advisories in the absence of any identifiable point source of pollution. This research examines the environmental distribution of Escherichia coli in conjunction with the assessment of additional parameters (rainfall, turbidity, wave height, wind direction, wind speed and algal presence) in order to determine the most probable factors that influence E. coli levels in surface waters.

Results - This study indicates that persistence, rather than environmental replication of E. coli, is responsible for the majority of microorganisms recovered from foreshore sands, submerged sands and surface waters at Racine, Wisconsin, beaches along Lake Michigan.

Sources:

Probable – Non-specific source (persistence in surface water; non-anthropogenic),

Soil/Sediment/Sand (persistence)

Potential –

Possible –

**135 - Source tracking faecal contamination in an urbanised and a rural waterway in the Nelson-Tasman region, New Zealand**

M. Kirs, V.J. Harwood, A.E. Fidler, P.A. Gillespie, W.R. Fyfe, A.D. Blackwood, and C.D. Cornelisen

<http://www.tandfonline.com/doi/pdf/10.1080/00288330.2010.535494>

Purpose - Eight MST markers, including general, ruminant and human-associated Bacteroidales markers, a duck-associated E2 marker, a gull-associated Catellicoccus marimammalium marker and three additional human markers [Enterococcus faecium esp gene, Methanobrevibacter smithii nifH gene, and human polyoma viruses (HPyVs)] were tested for host specificity and sensitivity using an array of animal faecal samples of known origin and wastewater samples.

Results - The validation and application of a suite of end-point PCR assays for MST markers enabled us to identify the presence of faecal contamination from multiple sources, including humans, in a New Zealand urbanised waterway. Outcomes demonstrate that MST markers developed overseas can be utilised in New Zealand context.

## **150 - PISMO BEACH FECAL CONTAMINATION SOURCE IDENTIFICATION STUDY**

Christopher L. Kitts, M.W. Black, M.Y. Moline, A.K. Hamrick, I.C. Robbins, A.A. Schaffner, and N.I. Boutet

[http://digitalcommons.calpoly.edu/cgi/viewcontent.cgi?article=1325&context=bio\\_fac](http://digitalcommons.calpoly.edu/cgi/viewcontent.cgi?article=1325&context=bio_fac)

Purpose - Identify the biological sources of fecal contamination as well as the physical and environmental factors that influence the levels of bacteria in the ocean waters at Pismo Beach, California.

Results - The main source of fecal contamination on the beach is bird droppings near the pier. Both wave direction and current direction worked to push high concentrations of FIB away from the pier as the main source of fecal contamination.

Sources:

Probable – Sewage Infrastructure, Domestic animals (dogs, cats and horses), Secondary wildlife (cows, pigeons and gulls)

Potential –

Possible –

## **101 - Presence and Sources of Fecal Coliform Bacteria in Epilithic Periphyton Communities of Lake Superior**

Winfried B. Ksoll, S. Ishii, M.J. Sadowsky, and R.E. Hicks

<http://aem.asm.org/content/73/12/3771.full.pdf+html>

Purpose - (i) determine if fecal coliforms and *E. coli* populations are present and persist in periphyton communities from a harbor and Lake Superior, (ii) identify the most probable sources of *E. coli* found in periphyton, (iii) use laboratory microcosms to examine colonization and survival of *E. coli* in natural periphyton communities, and (iv) estimate the contribution of periphyton borne *E. coli* to overlying waters.

Results - Although many *E. coli* strains isolated from periphyton may have originated from waterfowl and sewage effluent, other strains appeared to be unique to the periphyton studied and may have developed self-sustaining naturalized populations in these communities. *E. coli* cells attached to periphyton, whether they are unique to these periphyton communities or not, can detach and contribute to fecal coliform numbers measured in coastal waters. This confounds the use of fecal coliforms as a reliable indicator of recent fecal contamination of recreational waters.

Sources:

Probable –

Potential – Sewage effluent (wastewater treatment plant; human waste), waterfowl (wildlife; non-anthropogenic), algae (non-anthropogenic)

Possible –

### **65 - Microbial Source Tracking Study for South Cypress Creek**

Thomas B. Lawrence, P.E. (City of Memphis, Division of Public Works)

Purpose - The objective of this project was to be able to determine possible sources of fecal coliform levels found in South Cypress Creek, as well as to be able to try to quantify the impacts. By identifying the sources of the impacts, the City will work to achieve the goal of the Clean Water Act by addressing the specific sources where possible.

Results – Data indicated that there may be both diffuse sources of Avian fecal coliform (such as deposited areas that are washed into the creek at a slow rate), as well as direct discharges into the creek, providing the high numbers. The total human impact was fairly low. Thus, pet contributions may be more related to storm water runoff, rather than would be seen with the other major source types which may be related to direct contact with the creek water. For sources attributed to Wild Animals, the number of isolates was higher than all of the other sources in all fecal result groups, except for the “TNTC” group, where it was second to Avian.

Sources:

Probable – avian (secondary wildlife), wildlife (including birds),

Potential -

Possible - Non-specific source (human waste), domestic animals,

### **39 - LINKING ON-FARM DAIRY MANAGEMENT PRACTICES TO STORM-FLOW FECAL COLIFORM LOADING FOR CALIFORNIA COASTAL WATERSHEDS**

David J. Lewis, E.R. Atwill, M.S. Lennox, L. Hou, B. Karle, and K.W. Tate

[http://waterquality.ucanr.org/documents/Dairy\\_Management\\_Resources7451.pdf](http://waterquality.ucanr.org/documents/Dairy_Management_Resources7451.pdf)

Purpose - We have conducted a systems approach study of 10 coastal dairies and ranches to document fecal coliform concentration and loading to surface waters at the management decision unit scale. Water quality samples were collected on a storm event basis from loading units that included: manure management systems; gutters; storm drains; pastures; and corrals and lots.

Results – Fecal coliform load from units of concentrated animals and manure are significantly more than units such as pastures while storm flow amounts were significantly less. Fecal coliform concentrations demonstrate high variability both within and between loading units. Fecal coliform concentrations for pastures range from 206 to 2,288,888 cfu/100 ml and for lots from 1,933 to 166,105,000 cfu/100 ml.

Sources:

Probable - Manure Management Systems, Stockpiles, and lots (agriculture),

Potential – MS4 Infrastructure (human waste), pasture (land use)

Possible -

### **15 - Evaluation of Chemical, Molecular, and Traditional Markers of Fecal Contamination in an Effluent Dominated Urban Stream**

R.M. Litton, J.H. Ahn, B. Sercu, P.A. Holden, D.L. Sedlak, and S.B. Grant

<http://pubs.acs.org/doi/abs/10.1021/es101092g>

Purpose - To perform a quantitative sanitary survey of the Middle Santa Ana River, in southern California, utilizing a variety of source tracking tools, including traditional culture-dependent fecal markers, speciation of enterococci isolates, culture-independent fecal markers, and chemical markers of sewage and wastewater

Results - The results support the notion that regrowth of fecal indicator bacteria (FIB) in river sediments may lead to a decoupling between FIB and pathogen concentrations in the water column and thus limit the utility of FIB as an indicator of recreational waterborne illness in inland waters.

Sources:

Probable - in-situ growth in streambed sediments

Potential - effluent stream tributary to Santa Ana River, tributary to RW (Riverside WWTP plant stream tributary to Santa Ana River

Possible - Riverside WWTP & discharge pipe

### **128 - Snapshot investigation of likely contaminant sources in the Tilligerry Estuary catchment (Zones 5A and 5B)**

S.A. Lucas, P.M. Geary, P.J. Coombes, and R.H. Dunstan

[http://scholar.googleusercontent.com/scholar?q=cache:F75WyRF5YdUJ:scholar.google.com/&hl=en&num=100&as\\_sdt=0,5&as\\_vis=1](http://scholar.googleusercontent.com/scholar?q=cache:F75WyRF5YdUJ:scholar.google.com/&hl=en&num=100&as_sdt=0,5&as_vis=1)

Purpose - a) To provide a “snapshot” of water quality in major surface waters draining to the estuary and within the estuary after a particularly wet period. The samples were analysed for nutrients (orthophosphate and nitrate), total coliforms, faecal coliforms, E.Coli, faecal streptococci and faecal sterols and; b) To interpret the most likely sources of faecal contamination from the data obtained as elevated faecal coliform concentrations had been recorded after significant rainfall in the past.

Results - However, the high microbial concentrations observed in major surface drains on the western and eastern side of the estuary also warrant further investigation, however it is clear that the majority of faecal contamination in the estuary is from agricultural land uses. A management program to control and mitigate runoff sources from agricultural lands in the catchment is therefore seen as an integral part of any plan to reduce faecal contamination in Tilligerry estuary.

Sources:

Probable –Human Waste (Non-specific source), Herbivores (Secondary Wildlife)

Potential -

Possible -

### **62 - Bacteriological methods for distinguishing between human and animal faecal pollution of water: results of fieldwork in Nigeria and Zimbabwe**

D. Duncan Mara and J. Oragui

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2536379/pdf/bullwho00087-0144.pdf>

Purpose - Recently, methods have been developed to distinguish between human and animal faecal pollution in temperate climates. The present study assessed the applicability and practicality of these methods in tropical countries.

Results - Ruminant and human fecal sources threaten the shellfish harvest.

Sources:

Probable –domestic animals,

Potential - Non-specific source (human waste), Non-specific source (anthropogenic non-human source),

Possible -

### **207 - Identifying sources of fecal contamination inexpensively with targeted sampling and bacterial source tracking**

J.L. McDonald, P.G. Hartel, L.C. Gentit, C.N. Belcher, K.W. Gates, K. Rodgers, J.A. Fisher, K.A. Smith, and K.A. Payne

[http://www.water.rutgers.edu/Source\\_Tracking/Enterococcus/IdentifyingSourcesofFecalContaminationInexpensivelywithTargetedSamplingandBacterialSource.pdf](http://www.water.rutgers.edu/Source_Tracking/Enterococcus/IdentifyingSourcesofFecalContaminationInexpensivelywithTargetedSamplingandBacterialSource.pdf)

Purpose - Our objective was to identify the sources of fecal contamination inexpensively at St. Andrews Park and Sea Island during calm and stormy weather conditions using targeted sampling and two or more BST methods: Enterococcus speciation, the detection of the esp gene, and fluorometry.

Results - Targeted sampling, when combined with two or more of three BST methods- enterococcal speciation, detection of the esp gene, and fluorometry--was able to identify sources of fecal contamination quickly, easily, and inexpensively.

Sources:

Probable – Wildlife (Birds)

Potential -

Possible –Human Waste (Non-specific source), Sewage infrastructure (leaking sewer lines), Unspecified wildlife

### **26 - Application of Bacteroides fragilis Phage as an Alternative Indicator of Sewage Pollution in Tampa Bay, Florida**

Molly R. McLaughlin, and J.B. Rose

<http://www.springerlink.com/content/9221116k3286u5p3/fulltext.pdf>

Purpose - The use of bacteriophages were evaluated in the drainage basins of Tampa Bay

Results – In this study, the phages that infect *B. fragilis* host RYC2056 (RYC), including phage B56-3, and host ATCC 51477-HSP40 (HSP), including the human specific phage B40-8, were evaluated in the drainage basins of Tampa Bay, 7 samples (n=62), or 11%, tested positive for the presence of phages infecting the host HSP, whereas 28 samples, or 45%, tested positive using the host RYC.

Sources:

Probable – Septic (sewage infrastructure),

Potential -

Possible -

#### **4 - PB Point Bacterial Source Investigation Final Data Report**

MEC- Weston and City of San Diego

Purpose - The goal of this study was to use molecular and standard bacterial indicator techniques to assess the host origin of the bacteria found in the receiving waters at PB point.

Results - The results of the PCR analysis are also presented in Table 2. Of the ten receiving water samples collected (not including duplicates), four (75-R on 8/15, 75R on 8/18, 75-L on 8/18 and 75-R on 8/20) were positive for the general PCR marker (GB), suggesting the presence of fecal material. Among the four samples that tested positive for the general marker, two were positive for at least one of the human-specific markers (75-L on 8/18 and 75-R on 8/20), which suggests the presence of bacteria from human origin.

Although the values for the bacterial indicators from all of the storm drain samples were high, only one (not including duplicates) of the five storm drain samples was positive for the general PCR marker (SD-0 on 8/15). None of the storm drain samples were positive for either of the two human markers.

Sources:

Probable –

Potential – Non-specific source (human waste)

Possible -

#### **55 - MISSION BAY - Clean Beaches Initiative Bacterial Source Identification Study**

MEC- Weston and City of San Diego

Purpose - The overall goal of this study was to identify the sources of bacterial contamination to Mission Bay.

Results -Results from both MST methods utilized in Phase II confirmed that the large majority of the enteric bacteria in Mission Bay originates from birds and contributions from human sources are insignificant

Sources:

Probable – Avian (secondary wildlife),

Potential –Dogs, over-irrigation, MS4 Infrastructure (delta sediment at storm drain outlet)

Possible - park restrooms and RV pump stations (human waste), boats and homeless(mobile sources), groundwater (non-anthropogenic), marine mammals, bay sediment

### **105 - Temporal and Spatial Variability of Fecal Indicator Bacteria: Implications for the Application of MST Methodologies to Differentiate Sources of Fecal Contamination**

Marirosa Molina

<http://www.environmental-center.com/Files%5C7698%5CArticles%5C5788%5CMolina20600.pdf>

Purpose - Identify and compare the temporal and spatial variability of fecal indicator bacteria from a specific host in manure and water samples and evaluate the implications of such variability on microbial source tracking approaches and applications.

Results - Building an enterococci library is a time-consuming, expensive approach that has the potential to provide a great deal of information when the proper statistical analytical approach (in this case it was cluster analysis) is used to interpret the results. Application of a library-independent approach, such as the Bacteroides markers allows for a much faster and possibly less expensive results, but there remains a lack of thorough temporal, spatial and specificity analyses of the few genetic markers available so far.

Sources:

Probable – Cattle (domestic animals; anthropogenic non-human sources)

Potential –

Possible –

### **38 - Bacteria Monitoring and Source Tracking in Corpus Christi Bay at Cole and Ropes Parks**

Joanna Mott, M. Lindsey, R. Sealy, and A. Smith

<http://www.cbbe.org/publications/virtuallibrary/1010.pdf>

Purpose - In this study water samples from the six Texas Beach Watch stations at Ropes and Cole Parks were analyzed to detect the esp marker as an indicator of human contamination at these locations. Additionally, data on three other human-specific markers--Bacteroidales, Human 2 Polyoma Viruses (HPyVs), and ethanobrevibacter.smithii—from another study, are included in this report for comparison with the esp analysis results.

Results - Human source contamination was detected at Ropes and Cole Park stations under ambient weather conditions as measured by several human-specific markers. The esp gene was detected when levels of enterococci at Ropes Park were higher following rainfall and suggest a human contribution at this location presumably either from storm drain outflow or non-point source run-off. For Ropes and Cole Parks, a broader bacteria source tracking project is recommended to examine not only human, but other sources of contamination.

Sources:

Probable – Non-specific source (human waste),

Potential -

Possible – MS4 Infrastructure (human waste),

## **72 - Bacteria Source Tracking on the Mission and Aransas Rivers**

Joanna Mott, R. Lehman, Ph.D. and A. Smith

Purpose - In this study, bacteria source tracking (BST) was used to evaluate the sources of fecal contamination in the Mission and Aransas River segments and to provide additional data for assessment of sources of contamination into Copano Bay, the water body into which both segments empty.

Results - The majority of unknown source isolates collected from water samples at the five sampling stations along the Mission and Aransas tidal segments were classified as human source. Overall, 63.7-66.9% of unknown source isolate profiles from the composite (ARA+CSU) dataset were classified as treated human sources (originating from treated wastewater effluent). The remaining unknown source isolates were classified as livestock animals and wildlife, with cow, horse and duck contributions accounting for the majority of the animal sources in both the composite dataset and PFGE profiles.

Sources:

Probable – Wastewater treatment plant, cows, horses, ducks

Potential –

Possible – Gulls (secondary wildlife), hogs

## **41 - Multi-scale landscape factors influencing stream water quality in the state of Oregon**

Maliha S. Nash, D.T. Heggem, D. Ebert, T.G. Wade, and R.K. Hall

<http://www.springerlink.com/content/y17u3uh60155w313/fulltext.pdf>

Purpose - This study used the State of Oregon surface water data to determine the likelihood of animal pathogen presence using enterococci and analyzed the spatial distribution and relationship of biotic (enterococci) and biotic (nitrogen and phosphorous) surface water constituents to landscape metrics and others (e.g. human use, percent riparian cover, natural covers, grazing, etc.).

Results – Landscape metrics related to amount of agriculture, wetlands and urban all contributed to increasing nutrients in surface water but at different scales. The probability of having sites with concentrations of enterococci above the threshold was much lower in areas of natural land cover and much higher in areas with higher urban land use within 60 m of stream. A 1% increase in natural land cover was associated with a 12% decrease in the predicted odds of having a site exceeding the threshold. Opposite to natural land cover, a one unit change in each of manmade barren and urban land use led to an increase of the likelihood of exceeding the threshold by 73%, and 11%, respectively. Change in urban land use had a higher influence on the likelihood of a site exceeding the threshold than that of natural land cover.

Sources:

Probable - Urbanized land use

Potential -

Possible – Agriculture

## **66 - Coastal Nonpoint Source Pollution Monitoring Program**

New Jersey Department of Environmental Protection

Purpose - To identify the causes of the degrading water quality in the upper Navesink River. Perform stormwater monitoring to delineate major sources of fecal contamination. Utilize specialized tests, including coliphage and Multiple Antibiotic Resistance (MAR) analyses, to identify the sources of contamination (i.e., human, domestic animal, and wildlife). Once identified, actions can be recommended and taken to eliminate or reduce the impact.

Results – Results for Microbial Source Tracking indicators (F+RNA coliphage and Multiple Antibiotic Resistance) suggest a human source of fecal contamination at sites. Sites were identified as 'hot spots' for further source investigations.

Sources:

Probable - Non-specific source (human waste), wildlife

Potential – Domestic animals,

Possible -

## **1 - Multi-tiered Approach Using Quantitative Polymerase Chain Reaction for Tracking Source of Fecal Pollution to Santa Monica Bay, Ca, February 2005**

Rachel T. Noble, J.F. Griffith, A.D. Blackwood, J.A. Fuhrman, J.B. Gregory, X. Hernandez, X. Liang, A.A. Bera, and K. Schiff

[ftp://ftp.sccwrp.org/pub/download/DOCUMENTS/AnnualReports/2005\\_06AnnualReport/AR0506\\_181-194.pdf](ftp://ftp.sccwrp.org/pub/download/DOCUMENTS/AnnualReports/2005_06AnnualReport/AR0506_181-194.pdf)

Purpose - The objective of this study was to identify the contribution and quantify the loading of fecal contamination to the SMB using a multi-tiered approach. No discussion on what fecal source types (agriculture, birds, dogs) are impacting Santa Monica Bay

Results - Measurements of *Bacteroides* sp. and enterovirus indicated the presence of human fecal contamination throughout the system. *Bacteroides* sp. was present in 33% of mainstem samples. Enterovirus was present in 44% of mainstem samples. The concordance among these measurements was nearly complete; almost every location that detected *Bacteroides* sp. was also positive for enterovirus.

Sources:

Probable - Non-specific Source (human waste)

Potential -

Possible-

## **108 - Use of Fecal Steroids to Infer the Sources of Fecal Indicator Bacteria in the Lower Santa Ana River Watershed, California: Sewage Is Unlikely a Significant Source**

James A. Noblet, D.L. Young, E.Y. Zeng and S. Ensari

[ftp://ftp.sccwrp.org/pub/download/DOCUMENTS/JournalArticles/444\\_fecal\\_steroids.pdf](ftp://ftp.sccwrp.org/pub/download/DOCUMENTS/JournalArticles/444_fecal_steroids.pdf)

Purpose - Utilize a suite of fecal steroids, as chemical markers to examine whether sewage was a significant source of FIB within the lower Santa Ana River watershed.

Results - The results implied that sewage was not a significant source of fecal steroids, and therefore perhaps FIB to the study area. Instead, birds may be one possible source of the intermittently high levels of FIB observed in the lower Santa Ana River watershed and the nearby surf zone.

Sources:

Probable –

Potential – Gulls (secondary wildlife; anthropogenic non-human sources)

Possible – Sewage infrastructure (human waste), dogs (domestic animals; anthropogenic non-human sources)

### **109 - Fecal source tracking by antibiotic resistance analysis on a watershed exhibiting low resistance**

Yolanda Olivas, and B.R. Faulkner

<http://www.springerlink.com/content/k02q5v6748702773/fulltext.pdf>

Purpose - To test the efficiency of the antibiotic resistance analysis (ARA) method under low resistance by tracking the fecal sources at Turkey Creek, Oklahoma exhibiting this condition.

Results - The original seasonal and annual DA of the stream sources showed no significant difference between human and livestock input rates in winter, spring and summer ( $0.56 \leq P \leq 0.76$ ). Deer was consistently lower than the other two sources ( $0.00 \leq P \leq 0.30$ ). In fall, the human source predominated over livestock and deer ( $P < 0.0001$ ). Revision of the original DA using the rates of misclassification, decreased classification into the human and deer sources by 6–7% ( $0.22 \leq P \leq 0.33$ ), and increased classification into livestock by 13–14% ( $0.04 \leq P \leq 0.06$ ), showing the significance of the original DA misclassification. In conclusion, the major effect of low antibiotic resistance to this ARA work was a significant level of negative misclassification into the livestock source.

Sources:

Probable – Non-specific source (human waste), livestock (domestic animals; anthropogenic non-human sources)

Potential – Deer (wildlife; non-anthropogenic)

Possible –

### **143 - Investigation of Faecal Pollution and Occurrence of Antibiotic Resistant Bacteria in the Mooi River System as a Function of a Changed Environment**

M.J. Pantshwa, A.M. van der Walt, S.S. Cilliers, and C.C. Bezuidenhout

[http://www.ewisa.co.za/literature/files/2008\\_137.pdf](http://www.ewisa.co.za/literature/files/2008_137.pdf)

Purpose - Water quality monitoring and assessments are of paramount importance to identify the river confluence vulnerable to the pollution impacts of urbanization. Investigate some physico-chemical parameters, levels of faecal pollution and occurrence of antibiotic resistant bacteria in the Mooi River system as a function of a changed environment.

Results - Non-human sources contributed greater towards faecal pollution. Urban gradient was recognized in terms of faecal indicator species distribution. Higher levels of antibiotic resistant bacteria were detected in urban sites when compared to lower upstream and elevated downstream levels.

### **75 - Middle Rio Grande Microbial Source Tracking Assessment Report**

Parsons Water & Infrastructure Inc.

Purpose - The objective of this project was to identify specific sources of fecal coliform causing high levels of bacteria in the Middle Rio Grande.

Results - Overall, ribotyping results show, the largest fraction of *E. coli* matched those found in avian sources, followed by canine, human/sewage, rodents, bovine, and equine. The source of approximately 9 percent of the *E. coli* could not be identified. With the exception of rodents, only a few species of wild mammals were identified as sources of fecal coliform found in water: deer or elk, raccoon, coyote, bear, and opossum. It should be noted that an unknown fraction of the canine isolates may be from coyotes and foxes, as many *E. coli* strains are resident both in domestic dogs and wild canines.

Sources:

Probable – Cats, dogs, birds (wildlife)

Potential – Non-specific source (human waste), livestock, rodents (secondary wildlife), Wildlife (deer or elk, raccoon, coyote, bear, and opossum)

Possible –

### **125 - Bacterial Contamination and Antibiotic Resistance in Fecal Coliforms from Glacial Water Runoff**

S.P. Pathak, and K. Gopal

<http://www.springerlink.com/content/fup31h3742514123/fulltext.pdf>

Purpose - Assess the bacteriological contamination in glacial water runoff from the Gangotri glacier and Gangetic river system (Gaumukh to Rishikesh) by enumerating aerobic heterotrophs, coliforms, fecal coliforms and fecal streptococci. Antibiotic resistance among the fecal coliforms, identified as *E. coli*, was also studied.

Results - Contamination of coliform was observed in all samples, while fecal coliform and fecal streptococci were detected in 17 and 18 samples, respectively (Fig. 2). Thus, bacteriological analysis exhibited maximum contamination in most of the water samples from post-Gangotri and Gangetic stations. The observed increase in the proportion of coliforms and fecal coliforms was statistically significant ( $p < 0.001$ ). The counts of fecal streptococci in all study stretches were too low for statistical comparison.

## **129 - Fecal BMAP Implementation: Identification of Probable Sources in the Butcher Pen Creek Watershed**

PBS&J

[http://publicfiles.dep.state.fl.us/dear/BMAP/LowerStJohns/Tributaries%20Fecal%20Coliform%20BMAPs/Technical\\_Reports/ButcherPen/Final%20Draft%20Butcher%20Pen%20WBID%202322%20Tech%20Report%20041008.pdf](http://publicfiles.dep.state.fl.us/dear/BMAP/LowerStJohns/Tributaries%20Fecal%20Coliform%20BMAPs/Technical_Reports/ButcherPen/Final%20Draft%20Butcher%20Pen%20WBID%202322%20Tech%20Report%20041008.pdf)

Purpose - FDEP has verified 54 tributaries of the Lower St. Johns River—located throughout Duval County and in small portions of Clay and St. Johns Counties—as impaired for fecal coliform, and TMDLs must be developed for these waterbodies. Local stakeholders in the Lower St. Johns Basin, in conjunction with FDEP, are currently working to develop a Basin Management Action Plan (BMAP) to implement the TMDLs for fecal coliform.

Results - Elevated levels of fecal coliforms following rainfall may be an indication that unidentified pollution sources (e.g., leaking wastewater conveyance systems) are being transported by stormwater into Butcher Pen Creek. This evaluation indicates that the probable sources of fecal contamination in the Butcher Pen Creek WBID are human-related. Although Butcher Pen Creek does not have a designated septic tank phase-out area, some areas of the basin have likely had OSTDS failures, as indicated by the existence of septic tank repair permit applications, especially in the northeast corners of the watershed. Therefore, it is likely that there still remain isolated and problematic septic systems that are contaminating the neighboring surface waters.

Sources:

Probable – Sewage infrastructure (SSO events),

Potential – Wastewater discharge

Possible –

## **34 - Origin and spatial–temporal distribution of faecal bacteria in a bay of Lake Geneva, Switzerland**

John Poté, N. Goldscheider, L. Haller, J. Zopfi, F. Khajehnouri, and W. Wildi

[http://doc.rero.ch/lm.php?url=1000,43,4,20100511154847-XI/Pot\\_John\\_-\\_Origin\\_and\\_spatial-temporal\\_distribution\\_of\\_faecal\\_bacteria\\_20100511.pdf](http://doc.rero.ch/lm.php?url=1000,43,4,20100511154847-XI/Pot_John_-_Origin_and_spatial-temporal_distribution_of_faecal_bacteria_20100511.pdf)

Purpose - To quantify the input flux rates of faecal bacteria from the main contamination sources and to assess their spatial and temporal distribution in the bay, in order to estimate the human health risk related to recreational activities and drinking water use.

Results - The highest FIB concentrations in the near-surface water of the bay consequently occur during floods and mixed lake conditions. Although the thermocline protects the epilimnion from contamination in summer, effluent water may spread in the hypolimnion and reach the drinking-water pumping station 3.8 km further to the west.

Sources:

Probable – Wastewater Treatment Plant

Potential –

Possible –

### **110 - Classification Tree Method for Bacterial Source Tracking with Antibiotic Resistance Analysis Data**

Bertram Price, E.A. Venso, M.F. Frana, J. Greenberg, A. Ware, and L. Currey

<http://aem.asm.org/content/72/5/3468.full.pdf+html>

Purpose - Apply the statistical method known as classification trees to build a model for BST for the Anacostia Watershed in Maryland.

Results - Applying the tree classification model to the 1,565 Anacostia River water isolates yielded the following distribution of sources: 468 (29.9%) pet, 222 (14.2%) human, 437 (27.9%) livestock, and 438 (28.0%) wildlife. These results were determined from analysis of all the water isolates, which represent six monitoring stations with samples collected monthly for 1 year. Therefore, the source distribution presented here does not account for the distribution of high-flow and low-flow periods, which may contribute different sources to the streams. Also, note that bacterial sources can be site specific in a watershed, given the non-conservative nature of bacterial transport. For the purpose of this analysis, all the water isolates from the six monitoring stations were used to estimate the overall watershed relative source contributions. The results based on this averaging method indicate that humans contribute the least bacterial contamination to the Anacostia River. The other sources of bacterial contamination are evenly distributed among pet animals, livestock, and wildlife.

Sources:

Probable – Pets and livestock (domestic animals; anthropogenic non-human sources), wildlife (non-anthropogenic)

Potential – Non-specific sources (human waste)

Possible –

### **113 - Quantitative microbial faecal source tracking with sampling guided by hydrological catchment dynamics**

G. H. Reischer, J.M. Haider, R. Sommer, H. Stadler, K.M. Keiblinger, R. Hornek, W. Zerobin, R.L. Mach, and A.H. Farnleitner

<http://onlinelibrary.wiley.com/doi/10.1111/j.1462-2920.2008.01682.x/pdf>

Purpose - Apply modern quantitative microbial source tracking methods on a large and complex karstic spring catchment in context with hydrology and other water quality parameters over a prolonged period of time in order to comprehensively, qualitatively and quantitatively characterize the pollution sources.

Results - 1) Established and evaluated a new sampling concept with consideration for the whole seasonal hydrological catchment variability and special emphasis on strong pollution events. 2) Demonstrated the ability of quantitative microbial source tracking studies to quantitatively link source-specific marker levels to general faecal pollution indicators in order to estimate the contribution of one source group to total faecal pollution as measured in conventional faecal monitoring.

3) Showed that the thorough investigation of catchment hydrology and pollution dynamics is a prerequisite for successful quantitative microbial source tracking study design.

Sources:

Probable – Ruminant (wildlife; non-anthropogenic)

Potential – Non-specific sources (human waste)

Possible – Soil/Sediment/Sand

### **133 - Assessment of Sources of Bacterial Contamination At Santa Cruz County Beaches**

John Ricker and S. Peters

[ftp://ftpdpla.water.ca.gov/users/prop50/10045\\_SantaCruz/Work%20Plan%20CD%2004/reference%20plans%20and%20background%20information/Sources%20of%20Contamination%20at%20OSCC%20Beaches%202005.pdf](ftp://ftpdpla.water.ca.gov/users/prop50/10045_SantaCruz/Work%20Plan%20CD%2004/reference%20plans%20and%20background%20information/Sources%20of%20Contamination%20at%20OSCC%20Beaches%202005.pdf)

Purpose - Determine the source and health threat of elevated bacteria levels at Santa Cruz County beaches

Results - The most significant source of beach contamination in Santa Cruz County is discharge from the creeks, with a high urban runoff component during both wet and dry weather. 22 point plan to be implemented to improve water quality

Sources:

Probable – Non-specific sources (human waste), Sewage infrastructure (storm drains), Domestic animals (dogs), Secondary wildlife (birds), Wildlife (rats)

Potential –

Possible –

### **42 - Bacterial Source Tracking Pilot Study DNA Fingerprinting, Human Bacteroidetes ID and Human Enterococci ID**

Rogue Valley Council of Governments

Natural Resources Department

Purpose - The purpose of the pilot study was 1) to determine whether bacteria found in local streams is from human or animal sources and 2) to evaluate different BST methodology for future use within the Rogue Valley.

Results - DNA Fingerprinting results show that animal fecal matter is present, but were inconclusive in identifying whether human contamination was present. Many of the analyzed colonies could not be matched to animal or human sources. However, based on the isolates identified, animals are the primary contributor of bacteria to Ashland Creek, Baby Bear, and Griffin Creek (31 of 50).

Sources:

Probable - Domestic animals, wildlife,

Potential -

Possible – Non-specific source (human waste)

## **7 - Microbiological Water Quality at Reference Beaches in Southern California During Wet Weather**

Kenneth Schiff, J. Griffith, and G. Lyon

[http://www.sccwrp.org:8060/pub/download/DOCUMENTS/TechnicalReports/448\\_reference\\_beach.pdf](http://www.sccwrp.org:8060/pub/download/DOCUMENTS/TechnicalReports/448_reference_beach.pdf)

Purpose - The contribution of non-human sources of bacteria was quantified at coastal reference beaches in southern California. Provides an overview of sampling methods and analytical results for reference beaches are discussed. Bacteria sources were not identified

Results – Based on the results from this study, natural contributions of nonhuman fecal indicator bacteria were sufficient to generate exceedances of the State of California water quality thresholds during wet weather. Total coliform, E. coli, and enterococcus samples collected during wet weather exceeded water quality thresholds greater than 10 times more frequently during wet weather than during recent dry weather in summer or winter, although the frequency differed by beach. San Onofre State Beach had the greatest concentrations of bacteria and the greatest frequency of water quality threshold exceedances. This may have been the result of several factors that we cannot disentangle. First, San Onofre Creek was the largest watershed we sampled, which may have led to a greater number of nonhuman sources of fecal indicator bacteria upstream. Second, San Onofre Creek had the largest and most mature lagoon of any site sampled, which was located at the beach interface and may have attracted nonhuman fecal sources (i.e. birds). Third, San Onofre Creek was the only discharge where we found human enteric virus. The San Onofre Creek watershed had the greatest fraction of developed land use (3%) of any of the other watershed systems and human activities are known to occur in the lower part of this watershed.

Sources:

Probable – Non-specific source (anthropogenic)

Potential – Non-specific source (human waste)

Possible –

## **221 - Presence of Bacteroidales as a Predictor of Pathogens in Surface Waters of the Central California Coast**

A. Schriever, W.A. Miller, B.A. Byrne, M.A. Miller, S. Oates, P.A. Conrad, D. Hardin, H.H. Yang, N. Chouicha, A. Melli, D. Jessup, C. Dominik, and S. Wuertz

<http://ukpmc.ac.uk/articles/PMC2935056>

Purpose - Evaluate the value of Bacteroidales genetic markers and fecal indicator bacteria (FIB) to predict the occurrence of waterborne pathogens in ambient waters along the central California coast.

Results - The ability to predict pathogen occurrence in relation to indicator threshold cutoff levels was evaluated using a weighted measure that showed the universal Bacteroidales genetic marker to have a comparable or higher mean predictive potential than standard FIB. This

predictive ability, in addition to the Bacteroidales assays providing information on contributing host fecal sources, supports using Bacteroidales assays in water quality monitoring programs.

### **77 - Tracking Sources of Fecal Pollution in a South Carolina Watershed by Ribotyping *Escherichia coli*: A Case Study**

Troy M. Scott, J. Caren, G.R. Nelson, T.M. Jenkins, and J. Lukasik

<http://sourcemolecular.com/pdfs/scott3.pdf>

Purpose - To describe the effective use of the ribotyping microbial source tracking procedure to determine the source(s) of *Escherichia coli* within a South Carolina watershed.

Results - Prior to investigating potential fecal inputs into this watershed, a significant human source was suspected as the primary input; however, of the 515 *E. coli* isolated from water samples collected during the course of this study, 88% were typed as being of animal fecal origin. Thus, this study was integral in the realization that animals may be a significant source of contamination and that remediation efforts should be redirected to accommodate these findings. Of the 454 animal isolates analyzed, 51 RT profiles were directly matched from a specific animal source. Of these, 22 (43%) were classified as coming from deer feces and 9 (18%) directly matched those generated from dog feces.

Sources:

Probable – Wildlife (deer, raccoons, birds and pelicans),

Potential – Non-specific source (human waste), cats and dogs, gulls (secondary wildlife)

Possible –

### **19 - Sewage Exfiltration As a Source of Storm Drain Contamination during Dry Weather in Urban Watersheds**

Bram Sercu

<http://pubs.acs.org/doi/abs/10.1021/es200981k>

Purpose - To determine whether transmission of sewage is occurring from leaking sanitary sewers directly to leaking separated storm drains, field experiments were performed in three watersheds in Santa Barbara, CA.

Results – Above-background RWT peaks were detected in storm drains in high-risk areas, and multiple locations of sewage contamination were found. Sewage contamination during the field studies was confirmed using the human-specific Bacteroidales HF183 and *Methanobrevibacter smithii* nifH DNA markers. This study is the first to provide direct evidence that leaking sanitary sewers can directly contaminate nearby leaking storm drains with untreated sewage during dry weather and suggests that chronic sanitary sewer leakage contributes to downstream fecal contamination of coastal beaches.

Sources:

Probable -

Potential -

Possible -

## **6 - Storm Drains are Sources of Human Fecal Pollution during Dry Weather in Three Urban Southern California Watersheds**

Bram Sercu, L.C. Van de Werehorst, J. Murray, and P.A. Holden

[http://www.santabarbaraca.gov/NR/rdonlyres/C3B1ADAE-37E8-4F89-8F2D-1A24FBAB8D6A/0/Sercuetal\\_ESnT\\_2009\\_v43p2938SI.pdf](http://www.santabarbaraca.gov/NR/rdonlyres/C3B1ADAE-37E8-4F89-8F2D-1A24FBAB8D6A/0/Sercuetal_ESnT_2009_v43p2938SI.pdf)

Purpose - Dry weather bacteria monitoring in urbanized Santa Barbara, CA watersheds

Results - Of the 80 water samples analyzed within the Malibu watershed, five samples were positive for the human-specific HF183 Bacteroidales marker (HBM). The highest percent exceedance of FIB and HBM concentrations were measured during wet weather. During the study, 93.8% of the samples did not have detectable concentrations of HBM. These data do not rule out any particular potential sources of human fecal contamination.

Sources:

Probable -

Potential - Sewage infrastructure, non-stormwater discharges, MS4 infrastructure (less likely – human waste), MS4 infrastructure (anthropogenic non-human sources)

Possible -

## **116 - Identification of human fecal pollution sources in a coastal area: a case study at Oostende (Belgium)**

Sylvie Seurinck, M. Verdievel, W. Verstraete, and S.D. Siciliano

<http://www.iwaponline.com/jwh/004/0167/0040167.pdf>

Purpose - Identify fecal pollution sources in the North Sea and produce a model required to predict fecal pollution

Results - The canal Gent-Oostende, the Dode Kreek and Gauwelozeekreek, the Voorhaven, and the Montgommerydok contained high levels of the indicator bacteria. The European E. coli standard (5 £ 10<sup>2</sup>/ 100 ml) suggested in the revised draft Bathing Water Directive (Council of the European Communities 2000) was exceeded most of the time at these sites. The human specific Bacteroides marker was detected in almost all water samples from these sites, which indicates that they are regularly contaminated with human fecal pollution. The river Noordede, the Visserijdok and the beach water at 2 sites were only lightly contaminated based on the European E. coli standard. At these sampling sites the human-specific Bacteroides marker was less frequently detected and in lower amounts, except at one locations where high concentrations of 10<sup>7</sup> human-specific Bacteroides marker per l were recorded at the beginning of the sampling survey and at the end. The detection of indicator organisms and the human specific Bacteroides marker was strongly related to rainfall for this coastal area.

Sources:

Probable – Non-specific sources (human waste)

Potential – Wildlife (non-anthropogenic)

Possible –

## **11 - Regrowth of Enterococci & Fecal Coliform in Biofilm. Printed in The Journal for Surface Water**

John F. Skinner, J. Guzman, and J. Kappeler

Purpose - The goal of the study was to determine the sources of high numbers of enterococci and fecal coliform found in street gutter runoff flowing from residential areas to the Dover Drive storm drain in Newport Beach, Orange County

Results – Bacteria counts in runoff from washing the sidewalk using bacteria-free hose water were 220 enterococci/100 ml and 180 fecal coliform/100 ml. Washoff water from the driveway by manually flooding a residential front lawn was 160 enterococci/100 ml and 9 fecal coliform/100 ml. Runoff from flooding the grass contained 1,250 enterococci/100 ml and 2,000 fecal coliform/100 ml. Water draining directly into the gutter through a hole cut through the curb grew out 70 enterococci/100 ml and 100 fecal coliform/100 ml.

Bacteria-free hose water was introduced into a dry street gutter and tested for enterococci and fecal coliform at 10 meters, 45 meters, and 100 meters downstream when the flow from the hose water reached those locations. There was a progressive rise of both enterococci and fecal coliform bacteria with the increased distance of flow. The levels of fecal indicator bacteria were 26,000 enterococci/100 ml and 14,000 fecal coliform/100 ml when the water reached the 100-meter test site, the last testing station. The source of these high numbers of bacteria is suspected to be coming from regrowth in the street gutters.

The findings of these studies provide evidence that regrowth of both enterococci and fecal coliform bacteria are occurring in biofilm located in residential street gutters and storm drains in Newport Beach.

Sources:

Probable - Street gutter biofilm regrowth (MS4 infrastructure)

Potential – Dog excrement (not tested), lawn irrigation runoff, sidewalk and driveway runoff (Solid/liquid waste), residential washwater, residential lawn runoff

Possible - Residential backyard and side yard patios, roof gutter drains but not tested

## **49 - F+ RNA Coliphages as Source Tracking Viral Indicators of Fecal Contamination**

Dr. Mark D. Sobsey, D.C. Love, and G.L. Lovelace

<http://webmail.ciceet.unh.edu/news/releases/springReports07/pdf/sobsey.pdf>

Purpose - To evaluate and apply novel, cost-effective technologies and methods for the detection, quantification and identification of sources of microbial contaminants and the characterization of those sources as human or nonhuman.

Results - Microbial indicator concentrations in water and shellfish were higher at sites with greater wastewater treatment plant discharges. Of the 9 estuaries in the study, 4 were impacted by point source discharges of waste water treatment plant (WWTP) effluent. Human point source pollution in this study was primarily from waste water treatment plant (WWTP) treated effluent

and possibly raw sewage leaks, while likely human non-point sources included urban runoff, seepage from septic tanks, and boat dumping. Sites with non-human non-point fecal waste contained populations of wildfowl (goose, duck, gull), wild horses, other feral animals, agricultural animals, a dog park and urban pet waste. At 4 estuaries the impacted sites included human point and non-point sources, while the non-impacted sites were pristine sites with wildlife refuges or were geographically separated from human populations. In the Tijuana River Reserve in Southern CA human impacts were documented at all study sites, so in the absence of a truly pristine or non-impacted site, a site with only non-point source runoff from human development was compared to a more contaminated site at the mouth of the Tijuana River containing untreated sewage from Mexico.

Sources:

Probable -

Potential – Sewage infrastructure, Urban runoff (MS4 infrastructure - human waste; suspected to potential)

Possible -

#### **45 - Faecal sterols analysis for the identification of human faecal pollution in a non-sewered catchment.**

D. Sullivan, P. Brooks, N. Tindale, S. Chapman, and Ahmed, W.

[http://publicationslist.org/data/w.ahmed/ref-14/Daryle\\_s%20article\\_%20WST\\_revised%20version.pdf](http://publicationslist.org/data/w.ahmed/ref-14/Daryle_s%20article_%20WST_revised%20version.pdf)

Purpose - To identify human faecal pollution in a non-sewered catchment using faecal sterols.

Results - In this study, faecal sterol analysis was used to identify the presence of human sourced faecal pollution or others (non-point sources) in two adjacent creeks of North Maroochy Catchment. It appears that stanols concentrations generally increased with increased catchment runoff. After moderate rainfall, high coprostanols levels found in water samples indicated human faecal pollution and defective septic systems are the most likely sources of pollution. The human signal was traced on one occasion to a defective septic system. In contrast, it appears that during dry weather human faecal pollution is not occurring in the study catchment.

Sources:

Probable – Septic (sewage infrastructure),

Potential –

Possible -

#### **124 - Ecological Control of Fecal Indicator Bacteria in an Urban Stream**

Cristiane Q. Surbeck, S.C. Jiang, and S.B. Grant

<http://lshs.tamu.edu/docs/lshs/end-notes/ecological%20control%20of%20fecal%20indicator%20bacteria%20in%20an%20urban%20stream-1429959691/ecological%20control%20of%20fecal%20indicator%20bacteria%20in%20an%20urban%20stream.pdf>

Purpose - Determine the source(s) of elevated FIB concentrations in Cucamonga Creek, a concrete-lined urban stream in southern California. Flow in the creek consists primarily of treated and disinfected wastewater effluent, mixed with relatively smaller but variable flow of runoff from the surrounding urban landscape.

Results - Mass and volume balance calculations indicate that treated wastewater is not a significant source of FIB to Cucamonga Creek. Runoff from the urban landscape appears to be the primary source of FIB loading to Cucamonga Creek during both dry weather and wet weather periods. Observations from the study imply that DOC and FIB concentrations in runoff should co-vary, which is indeed the case both at Cucamonga Creek and in many agricultural and urban streams along the California coast. These results are not consistent with the hypothesis that FIB are static contaminants (like sediments or nutrients) with well-defined and land-use-specific export coefficients, as has been suggested for catchments in the United Kingdom. Rather, our data suggest that nonpoint source FIB impairments in southern California are best viewed as an ecological phenomenon, in which a dynamic balance between FIB sources, nutrient availability, competition with other heterotrophic bacteria, and predator prevalence determines the magnitude and extent of FIB pollution and its human health implications.

Sources:

Probable – Non-specific Source (Human Waste), Domestic animals (dogs), Secondary Wildlife (birds)

Potential –

Possible -

### **50 - B Street/Broadway Piers, Downtown Anchorage, and Switzer Creek Storm Drain Characterization Study**

Tetra Tech, City of San Diego

Purpose - To further characterize the City's storm drain system discharges during both wet and dry weather. This monitoring program evaluated the potential sources of the pollutants-of-concern (POCs) throughout the MS4 system and collected data to calibrate and validate preliminary wet weather runoff modeling efforts for the San Diego Bay TMDLs.

Results - Bacteria concentrations from residential land use site DBR01 are higher than commercial land use site DBC02. The differences in bacteria concentrations across land use sampling sites were compared using t-test or Mann-Whitney Rank Sum test if data do not meet normality test. The results suggested significant difference in concentrations between the two sampling sites for both events and for all three microbiological parameters. Higher concentrations were found at the residential site (DBR01) than the commercial land use site (DBC02).

Sources:

Probable – Residential (Land use)

Potential – Commercial (Land use)

Possible -

### **53 - Chollas Storm Drain Characterization Study**

Tetra Tech, City of San Diego

Purpose - To further characterize the City's storm drain system discharges during both wet and dry weather. This monitoring program evaluated the potential sources of the pollutants-of-concern (POCs) throughout the MS4 system and collected data to calibrate and validate preliminary wet weather runoff modeling efforts for the San Diego Bay TMDLs.

Results - The measured enterococcus and coliform concentrations generally showed large variations. The enterococcus concentrations showed a number of exceedances of the basin action level at a number of sites including several commercial and industrial sites and two residential sites. Fecal coliform concentrations were generally below action levels, with a few industrial and residential sites showing some exceedances. Total coliform concentrations showed a large number of exceedances at seven out of the ten sampling sites. The difference in bacteria concentrations across land use sampling sites was compared based on median concentrations and using the Mann-Whitney Rank Sum test (Table 7-4). The results suggested significant difference in concentrations among the sampling sites for both events and for all three microbiological parameters. Higher concentrations were found at two commercial (CHC07 and CHC12), industrial (CHI08) and two residential sites (CHR03 and CHR04).

Sources:

Probable – Commercial/Industrial (anthropogenic non-human sources; potential to probable), Commercial and industrial (land use)

Potential – Residential (land use)

Possible -

### **9 - Using Microbial Source Tracking to Support TMDL Development and Implementation**

Tetra Tech, Inc. and Herrera Environmental Consultants

Purpose - Provides an overview of Microbial Source Tracking (MST) and how it can be used to support TMDL development and implementation. The document covers potential uses of MST, descriptions of common MST methods, factors for selecting an MST method and designing an MST study, and examples of MST studies used to support TMDL development or implementation.

Results – ID Study: The Bacteroides PCR results generally supported the PFGE results that wildlife was the predominant source of fecal bacteria in the sampled streams. The genetic fingerprinting showed that greater than 10 percent of the total E. coli colonies isolated were from dogs, and cats were almost 20 percent. In addition, there were two days on lower Hauser Creek when Idaho's primary contact water quality criterion for E. coli was exceeded, during which dogs were the source of over 40 percent of the isolates. Horses and cattle each did not exceed 10 percent of the total E. coli isolates; however, horses were greater than 15 percent of the E. coli isolates. Although humans made up 11 percent of the total E. coli colonies isolated on Right Fork Hauser Creek, only one E. coli colony was isolated from water samples collected on days when the water quality criterion was exceeded.

OR: Results indicated widespread contamination from ruminants (non-elk) and, in certain river segments of the Trask, Miami, and Tillamook Rivers and Holden Creek, significant contamination from humans.

NM: Overall, ribotyping results show the largest fraction of *E. coli* matched those found in avian sources, followed by canine, human/sewage, rodents, bovine, and equine. The source of approximately 9 percent of the *E. coli* could not be identified.

VA: MST Results indicate majority of sources derive from wildlife and livestock, followed by humans, and then pets.

NH: Ribotyping identified source species for 76% (19/25) of the *E. coli* isolates in the water samples. The remaining isolates (24%) could not be matched with certainty to patterns in the ribopattern database. Of the identified isolates, geese constituted the largest portion (52%) followed by livestock [sheep (12%) and cows (4%) for a total of 16%] and dogs (8%).

MI: During dry conditions, the human biomarker was present at all sites, except one site. The results were always negative for the human biomarker, giving a strong indication that *E. coli* from human sources was not impacting this site during dry conditions. Positive results for the other sites suggest that there are dry-weather sources of *E. coli* of human origin. These human sources of *E. coli* could include cross-connections between the sanitary and storm sewer systems, illicit discharges to storm sewers, failed on-site sewage disposal systems, and leaking sanitary sewers.

SD: Among the isolates for which the source could be identified, 26% were equine (horse) and 30% were ovine (sheep). Other identified animal sources include porcine (pig), bovine (cow), canine (dog), feline (cat) and human. Based on review of available information and communication with state and local authorities, the primary nonpoint sources of fecal coliform within the Beaver Creek watershed include agricultural runoff, as well as wildlife and human sources. Septic systems are assumed to be the primary human source of bacteria loads to Beaver Creek. The HSPF model was used to determine the contribution of fecal coliform bacteria from identified sources in the Beaver Creek watershed and evaluate the implementation of BMPs to control these sources.

Sources:

Probable – Geese (NH), avian (NM)

Potential – Non-specific source (human waste – NM, OR), sewage infrastructure (MI), illegal connections, domestic animals (NH, ID, NM), agriculture (OR), secondary wildlife (ID)

Possible -

### **37 - Monitoring Report for Bacterial Source Tracking Segments 0806, 0841, and 0805 of the Trinity River Bacteria TMDL**

Texas Institute for Applied Environmental Research (TIAER)

[http://repositories1.lib.utexas.edu/bitstream/handle/2152/7038/crwr\\_onlinereport08-08.pdf?sequence=2](http://repositories1.lib.utexas.edu/bitstream/handle/2152/7038/crwr_onlinereport08-08.pdf?sequence=2)

Purpose - This report includes information on study area, characteristics, materials and methods of bacterial source tracking, and results and findings of the source tracking study.

Results – Overall, each of the source contributors showed a definite trend, whether positive or negative, as one moves downstream from Segment 0806, through Segment 0841, and into Segment 0805. The categories did show consistencies in source species. The avian category was consistently dominated by non waterfowl species, while the livestock category's contribution was shared by bovine and horses. Mammalian wildlife was found to be high in rodent species and raccoons, while the pet category was found to be consistently led by dogs.

Sources:

Probable – Non-specific source (human waste – potential to probable)

Potential - Pets and livestock, avian and mammals (wildlife)

Possible -

### **149 - Assessment of the Origins of Microbiological Contamination of Groundwater at a Rural Watershed in Chile**

Mariela Valenzuela, M.A. Mondaca, M. Claret, C. Perez, B. Lagos, and O. Parra

<http://www.scielo.org.mx/pdf/agro/v43n4/v43n4a10.pdf>

Purpose - To improve the state of knowledge on the microbiological quality of groundwater at a rural watershed. Characterize the microbiological quality of the groundwater and to identify sources of contamination.

Results - The main source of fecal contamination is of animal origin, a diffuse one. Concentrations of bacterial indicators have a temporal basis showing variable levels among seasons, with a higher concentration in the rainy one. All 42 wells analyzed contained opportunistic pathogens.

### **167 - Bacterial pathogens in Hawaiian coastal streams-Associations with fecal indicators, land cover, and water quality**

E.J. Viau, K.D. Goodwin, K.M. Yamahara, B.A. Layton, L.M. Sassoubre, S.L. Burns, H.I. Tong, S.H. Wong, and A.B. Boehm

<http://www.sciencedirect.com/science/article/pii/S0043135411001448>

Purpose - To understand the distribution of five bacterial pathogens in O'ahu coastal streams and relate their presence to microbial indicator concentrations, land cover of the surrounding watersheds, and physical-chemical measures of stream water quality.

Results - Results implicate streams as a source of pathogens to coastal waters. Future work is recommended to determine infectious risks of recreational waterborne illness related to O'ahu stream exposures and to mitigate these risks through control of land-based runoff sources.

### **146 - EFFECTS OF RUNOFF CONTROLS ON THE QUANTITY AND QUALITY OF URBAN RUNOFF AT TWO LOCATIONS IN AUSTIN, TEXAS**

Clarence T. Welborn, and J.E. Veenhuis

<http://pubs.usgs.gov/wri/1987/4004/report.pdf>

Purpose - Determine if the rapid urban development in the Austin metropolitan area is causing an increase in the peak discharges from storm runoff and the degradation of the quality in receiving waters.

Results - Loads of most constituents and total densities of bacteria at the mall site were substantially larger in the inflow than in the outflow. The total densities of bacteria at the outflow were less by about 80 percent. Discharge weighted concentration data for Alta Vista indicate that the grass-covered swales and the grass-covered detention area had little or no effects on reducing concentrations or densities of most water-quality constituents.

Sources:

Probable – Residential, Industrial and Commercial Land Use(street, lawn and parking lot runoff)

Potential -

Possible -

#### **14 - Tecolote Creek Microbial Source Tracking Summary Phases I, II, and III**

Weston Solutions

Purpose - To investigate the bacterial sources, origins, and loads in the Tecolote Creek watershed and to assess and characterize specific priority activity contributions.

Results – Wet weather bacteria loads from individual land uses indicated that there were no significant differences between different land uses with flows merging and combining throughout drainage areas. There was some indication that higher loads were attributable to transportation corridors, commercial areas, and industrial land uses. Dry weather loads were higher in residential and commercial areas with specific activities identified as including poorly maintained dumpsters leaking high concentrations of indicator bacteria. A key transport mechanism found especially in commercial and industrial areas was over-irrigation. Residential areas were found to be abiding by water conservation recommendations, but this was not seen in commercial and industrial areas.

During dry weather, five positive *Bacteroides* samples were obtained. Each follow-up investigation failed to locate a point source; however, in every instance there was evidence of transient human activity. During wet weather, only 1 sample from a total of 37 samples collected over 9 storms was found to be positive for *Bacteroides*. This sample was collected during the early phase of the storm flows in an area known to be a transient area.

Biofilms on the walls of the MS4 system in particular were found to grow rapidly and contain high numbers of enterococci. Speciation of these enterococci determined that the origins were most likely environmental rather than fecal. Further investigation determined that the storm water, with high numbers of enterococci of fecal origin, was the primary inoculation mechanism but that biofilms matured rapidly into complex communities with a variety of species present. The high flows generated during wet weather were found to cause significant biofilm sloughing. The impact of biofilms on wet weather loads of indicator bacteria into receiving waters would

appear to be significant. Sediments and biofilms within the creek and MS4 system were found to be significant reservoirs.

Sources:

Probable - Biofilm (MS4 Infrastructure), Sediment and biofilms in Tecolote Creek, Sediment and biofilms in MS4 Infrastructure

Potential - MS4 Infrastructure (anthropogenic non-human sources) Land use (residential, commercial, schools, restaurants, nurseries, golf course, livestock & domestic animal, industrial, Open space/Parks/Recreation, transportation corridors)

Possible -

## **52 - Dry Weather Bacterial Source Identification Study in the Mouth of Chollas Creek**

Weston Solutions and the City of San Diego

Purpose - 1. What are the sources and magnitudes of dry weather urban runoff and associated indicator bacteria that influence water quality at the mouth of Chollas Creek?

2. What BMPs may be put in place to reduce or eliminate the influence of dry weather urban runoff at the mouth of Chollas Creek?

Results - During dry weather, there is no hydrologic connection between the mouth of Chollas Creek (the area influenced by tidal action) and the upstream drainage. Thus, bacteria found in the receiving waters of the creek mouth originate from sources that discharge directly to the mouth (i.e., storm drains). The highest bacterial concentrations were associated with the two storm drains near the National Avenue Bridge. Concentrations of indicator bacteria associated with the other identified storm drains were lower, but still contributed to elevated concentrations in the receiving water in the south fork and main stem, respectively. Two sources of flow that contributed to the high bacterial concentrations were identified as (1) over-irrigation of landscaping at the strip mall located at National Avenue and 35th Street and (2) a freshwater slough adjacent to a freeway off ramp that periodically discharges to a storm drain in the south fork of the creek.

Sources:

Probable - Storm drains and scour ponds at storm drain outlet; MS4 infrastructure; human waste), over-irrigation (landscaping)

Potential – Non-specific source (Freshwater slough; non-anthropogenic)

Possible -

## **54 - Regional Harbor Monitoring Program Pilot Project 2005-08 Summary Final Report**

Weston Solutions and the City of San Diego

Purpose - The core monitoring program assesses the conditions found in the harbors based on comparisons to historical reference values for the four harbors and comparisons of contaminant concentrations to known surface water and sediment thresholds using chemistry, bacterial, toxicology, and benthic infaunal community indicators.

Results - Based on the results of the Pilot Project, the following statements can be made: 1) All bacterial concentrations were well below AB 411 levels, 2) The majorities of the marina and

freshwater-influenced strata contained sediments that were not toxic, 3) Benthic infaunal communities in both strata occurred at intermediate levels of disturbance, 4) Toxicity levels in the marina sediments generally were better than harbor-wide historical conditions, 5) Toxicity levels and benthic infaunal communities did not differ between the two strata, and 6) From 2005-2007, no negative short-term trends were evident for any indicator that would be indicative of a degrading condition.

#### **70 - 2009-2010 Coastal Storm Drain Monitoring Annual Report**

Weston Solutions, Inc. and County of San Diego Copermittees

Purpose - To determine the impacts that storm drains have on coastal receiving waters.

Results - There were a total of 28 exceedances of the total coliform storm drain action level. Twelve sites had at least one exceedance for total coliform, of which 3 had a total coliform exceedance on multiple dates.

Sources:

Probable – Cats

Potential –Cows, horses, fox, cormorants,

Possible – Non-specific source (human waste), gulls (secondary wildlife), Wildlife (muskrats, raccoons, coyotes, rabbits, turkeys and geese)

#### **74 - MICROBIAL SOURCE TRACKING IN TWO SOUTHERN MAINE WATERSHEDS Report Number: MSG-TR-04-03 March 2004 Merriland River, Branch Brook and Little River (MBLR) Watershed Report**

Kristen Whiting-Grant, F. Dillon, C. Dalton, Dr. M. Dionne, and Dr. S. Jones

Purpose - This study focuses on the Merriland River, Branch Brook and Little River (MBLR) watershed in Wells, Kennebunk and Sanford Maine, where chronic and persistent bacterial contamination from unidentified sources has restricted shellfish harvesting.

Results - Cats were the most frequently identified single source of bacterial contamination (21%); followed by cow (11%); fox (7%); cormorant (5%); human, rabbit, muskrat, horse and gull (all at 3%); turkey (2%); and goose, raccoon, coyote and dog (all at 1%). Also note that ribotypes for 35% of the bacteria samples analyzed by JEL could not be identified, which is to say that no clear matches could be established between ribotypes of known source species and ribotypes from unknown water samples.

Sources:

Probable – Cats

Potential –Cows, horses, fox, cormorants,

Possible – Non-specific source (human waste), gulls (secondary wildlife), Wildlife (muskrats, raccoons, coyotes, rabbits, turkeys and geese)

#### **64 - Microbial Source Tracking in the Dungeness Watershed, Washington**

D.L. Woodruff, N.K. Sather, V.I. Cullinan, and S.L. Sargeant

Purpose - To determine the sources of fecal coliform pollution that have been impacting the water quality and shellfish harvesting activities for more than a decade.

Results – The predominant sources of fecal coliform contamination in the Dungeness from all matrix types (e.g. water, sediment, wrack) in the freshwater and marine environments were, in rank order, avian (19.6%), gull (12.5%), waterfowl (9.7%), raccoon (9.2%), unknown (7.3%), human-derived (7.1%), rodent (6.3%) and dog (4.3%). When bird groups were combined, they represented in total about 42% of samples collected and analyzed throughout the study.

Sources:

Probable – Wildlife,

Potential - Non-specific source (human waste), domestic animals,

Possible -

#### **44 - Quantitative Pathogen Detection and MST Combined with modeling of fate and transport of Bacteroidales in San Pablo Bay.**

Stefan Wuertz, F. Bombardelli, K. Sirikanchana, A. Schriewer, and Z. Kaveh

Purpose - To develop a decision-making tool in the form of a 3-D model to benefit coastal managers both in terms of pinpointing major sources of fecal pollution and maximizing the usefulness of any monitoring activity.

Results – Monitoring results indicated low-level general and human-derived fecal contamination in the bay, while cow- and dog-derived contamination was not detected, except for one sample which contained dog-specific genetic marker. Human viruses were also below the sample detection limit. The pollution was more likely to come from surrounding urban areas or wastewater treatment facilities than from agricultural farm land or wildlife areas.

Sources:

Probable – Non-specific source (human waste),

Potential -

Possible – Dogs and cows

#### **232 - Indicator organism sources and coastal water quality: a catchment study on the island of Jersey**

M.D. Wyer, D. Kay, G.F. Jackson, H.M. Dawson, J. Yeo, and L. Tanguy

<http://www.ncbi.nlm.nih.gov/pubmed/7730205>

Purpose - Compliance monitoring of bathing waters at La Grève de Lecq on the North coast of Jersey revealed a significant deterioration in water quality between 1992 and 1993, as indexed by presumptive coliform, presumptive *Escherichia coli* and streptococci concentrations. During the 1993 bathing season the beach failed to attain the compliance with the EC Guideline criteria for presumptive *E. coli* and streptococci.

Results - A bacteriological survey of the stream catchment draining to the beach revealed that: (i) concentrations of faecal indicator organisms were enhanced at high discharge after rainfall; and (ii) a captive water fowl population, which expanded between 1990 and 1993, was a potential source of faecal pollution.

### **233 - Beach sands along the California coast are diffuse sources of fecal bacteria to coastal waters**

K.M. Yamahara, B.A. Layton, A.E. Santoro, and A.B. Boehm

<http://pubs.acs.org/doi/abs/10.1021/es062822n>

Purpose - The potential for FIB to be transported from the sand to sea was investigated at a single wave-sheltered beach with high densities of ENT in beach sand

Results - We collected samples of exposed and submerged sands as well as water over a 24 h period in order to compare the disappearance or appearance of ENT in sand and the water column. Exposed sands had significantly higher densities of ENT than submerged sands with the highest densities located near the high tide line. Water column ENT densities began low, increased sharply during the first flood tide and slowly decreased over the remainder of the study. During the first flood tide, the number of ENT that entered the water column was nearly equivalent to the number of ENT lost from exposed sands when they were submerged by seawater. The decrease in nearshore ENT concentrations after the initial influx can be explained by ENT die-off and dilution with clean ocean water. While some ENT in the water and sand at LP might be of human origin because they were positive for the esp gene, others lacked the esp gene and were therefore equivocal with respect to their origin.

### **58 - High-Throughput and Quantitative Procedure for Determining Sources of Escherichia coli in Waterways by Using Host-Specific DNA Marker Genes**

Tao Yan, M.J. Hamilton, and M.J. Sadowsky

<http://aem.asm.org/content/73/3/890.full.pdf+html>

Purpose - The objective of the study was to evaluate a high-throughput, semi-automated, quantitative procedure for determining sources of *E. coli* in waterways by using host-specific DNA marker genes of geese and ducks and robot-assisted high-throughput technology. Although the objective was to evaluate the method, the seasonal goose/duck population as a bacteria source was evaluated at 2 lakes frequented with migratory goose/duck populations and an additional lake that is not frequented by migratory goose

Results - The relative contributions of fecal *E. coli* from the geese/ducks were estimated to be 34% and 51% in Lake Superior and Lake Calhoun, respectively and 0.28% at Lake Hartwell (which has no migratory goose population)

Sources:

Probable – Wildlife (Lake Calhoun, Lake Superior),

Potential -

Possible–Wildlife (Lake Hartwell which has no migratory goose populations)

## **NSC (Not Source Characterization) Studies**

### **137 - Relationship between rainfall and beach bacterial concentrations on Santa Monica Bay beaches**

Drew Ackerman and S. B. Weisberg

[http://www.sccwrp.org:8060/pub/download/DOCUMENTS/AnnualReports/2001\\_02AnnualReport/18\\_ar37-drew.pdf](http://www.sccwrp.org:8060/pub/download/DOCUMENTS/AnnualReports/2001_02AnnualReport/18_ar37-drew.pdf)

Purpose - To enhance the scientific foundation for preemptive public health warnings, examine the relationship between rainfall and beach indicator bacteria concentrations using five years of fecal coliform data taken daily at 20 sites in southern California.

Results - There was a clear relationship between the incidence of rainfall and reduction in beach bacterial water quality in Los Angeles County. Bacterial concentrations remained elevated for five days following a storm, although they generally returned to levels below state water quality standards within three days. The length of the antecedent dry period had a minimal effect on this relationship, probably reflecting a quickly developing equilibrium between the decay of older fecal material and the introduction of new fecal material to the landscape.

### **175 - Persistence and potential growth of the fecal indicator bacteria, *Escherichia coli* in shoreline sand at Lake Huron**

E.W. Alm, J. Burke, and E. Hagan

<http://www.bioone.org/doi/abs/10.3394/0380-1330%282006%2932%5B401:PAPGOT%5D2.0.CO;2>

Purpose - This study was initiated to test the hypothesis that high abundances of the fecal indicator *Escherichia coli* in shoreline sand at freshwater beaches can be explained, at least in part, by the ability of *E. coli* to persist and grow in beach sand.

Results - In controlled laboratory microcosm studies using autoclaved beach sand inoculated with *E. coli* strains previously isolated from ambient beach sand, *E. coli* densities increased from 2 CFU/g to more than  $2 \times 10^5$  CFU/g sand after 2 days of incubation at 19°C, and remained above  $2 \times 10^5$  CFU/g for at least 35 days. In field studies utilizing similarly inoculated beach sand in diffusion chambers incubated at a Lake Huron beach, *E. coli* also grew rapidly, reaching high densities (approximately  $7.5 \times 10^5$  CFU/g), and persisting in a cultivable state at high density for at least 48 days. In comparison, *E. coli* levels in ambient beach sand adjacent to the chambers always had densities <100 CFU/g. Lake Huron beach sand clearly provides nutrients, temperatures, and other conditions needed to support growth of *E. coli*. The growth of *E. coli* in sterile sand diffusion chambers to higher levels than occurs in ambient beach sand may indicate the presence in ambient sand of biological controls on bacterial growth, such as predation or competition.

### **59 - Host Species-Specific Metabolic Fingerprint Database for Enterococci and *Escherichia coli* and Its Application to Identify Sources of Fecal Contamination in Surface Waters**

Warish Ahmed, R. Neller, and M. Katoulli

<http://aem.asm.org/content/71/8/4461.full.pdf+html>

Purpose - To characterize two fecal indicator bacteria, enterococci and *E. coli*, from different host groups (i.e., animal species) to develop a metabolic fingerprint database to identify the source(s) of fecal contamination in a creek in Australia.

Results - Out of 27 water samples: 10% of the biochemical phenotypes (BPT) found for enterococci belonged to human origin, 61% belonged to animals tested. 13% of the BPTs found for *E. coli* belonged to human origin and 54% belonged to animals tested. The remaining BPT found for Enterococci and *E. coli* belonged to BPTs shared between humans and animals or did not match database

Sources:

Probable –Septic (human waste), animal farms (domestic animals), animal farms (agriculture),

Potential -

Possible -

## **80 - Persistence and Differential Survival of Fecal Indicator Bacteria in Subtropical Waters and Sediments**

K.L. Anderson, J.E. Whitlock, and V.J. Harwood

<http://aem.asm.org/content/71/6/3041.full.pdf+html>

Purpose - Fecal coliforms and enterococci are indicator organisms used worldwide to monitor water quality. These bacteria are used in microbial source tracking (MST) studies, which attempt to assess the contribution of various host species to fecal pollution in water. Ideally, all strains of a given indicator organism (IO) would experience equal persistence (maintenance of culturable populations) in water; however, some strains may have comparatively extended persistence outside the host, while others may persist very poorly in environmental waters. Assessment of the relative contribution of host species to fecal pollution would be confounded by differential persistence of strains.

Results - IO persistence according to mesocosm treatment followed the trend: contaminated soil > wastewater > dog feces. *E. coli* ribotyping demonstrated that certain strains were more persistent than others in freshwater mesocosms, and the distribution of ribotypes sampled from mesocosm waters was dissimilar from the distribution in fecal material. These results have implications for the accuracy of MST methods, modeling of microbial populations in water, and efficacy of regulatory standards for protection of water quality. Saltwater had a negative effect on FC persistence, as the decay rates of FC (all inoculum sources combined) in saltwater sediments and water column were greater than those in freshwater. Saltwater also significantly increased enterococcal decay rates compared to freshwater. IO persistence tended to be greater in sediments than in the water column. The average decay rate of FC in sediments of freshwater mesocosms was significantly less than those in the water column, and the difference was nearly significantly at the  $\alpha = 0.05$  level in saltwater ( $P = 0.083$ ). Although decay rates of enterococci tended to be greater in the water column than in sediments, the difference was not significant in freshwater or saltwater mesocosms.

### **176 - Persistence and differential survival of fecal indicator bacteria in subtropical waters and sediments**

K.L. Anderson, J.E. Whitlock, and V.J. Harwood

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC1151827/>

Purpose - This study utilized mesocosms designed to simulate natural conditions, which were inoculated with fecal material, to test the hypothesis that certain *E. coli* phylotypes exhibit greater persistence than others in aquatic environments.

Results - This study demonstrated a high degree of variability in the response of fecal indicator organisms to stresses in aquatic environments on all levels investigated. Responses to water type (saline versus fresh), location (sediment versus water column), and inoculum type all varied within and between indicator bacterial groups (FC and ENT). The discrepant results emphasize the difficulties encountered in attempting to regulate diverse types of water bodies by one regulatory standard. Also cautionary is the persistence of indicator organisms in sediments, which leads to elevation of their densities and a false indication of recent pollution in the water column after events such as rain storms, construction, or recreational use.

### **130 - LEVELS OF FECAL INDICATOR BACTERIA AT DOG BEACH AND NEARBY COASTAL BEACHES OF THE CITY OF SAN DIEGO, CA**

Amir Baum

[http://www.sandiegoriver.org/documents/baum\\_final\\_thesis.pdf](http://www.sandiegoriver.org/documents/baum_final_thesis.pdf)

Purpose - An analysis of historical County of San Diego microbial marine water quality was conducted to quantitatively compare the levels of fecal indicator bacteria (FIB) levels at Dog Beach, located at the San Diego River Outlet, and nearby coastal beaches. Additionally, this study aimed to determine if relationships existed between daily average river flow/daily precipitation and FIB densities at Dog Beach and nearby coastal beach stations and if significant associations existed between daily precipitation and FIB single sample exceedances.

Results - The study found the strongest association between river flow, precipitation, and TC levels to be at river discharge points during wet months, but no significant association was found during dry weather. The study demonstrated that using a stratified-random sampling design, urban runoff outlets are a primary source of contaminated runoff with 90% of sites near urban runoff outlets failing water quality standards.

### **81 - Integrated Analysis of Established and Novel Microbial and Chemical Methods for Microbial Source Tracking**

Anicet R. Blanch, L. Belanche-Muñoz, X. Bonjoch, J. Ebdon, C. Gantzer, F. Lucena, J. Ottoson, C. Kourtis, A. Iversen, I. Kühn, L. Mocé, M. Muniesa, J. Schwartzbrod, S. Skrabber, G.T.

Papageorgiou, H. Taylor, J. Wallis, and J. Jofre

<http://aem.asm.org/content/72/9/5915.full.pdf+html>

Purpose - The objectives of the present study were (i) to determine the most discriminant tracers showing wide and consistent geographical stability between all locations, (ii) to identify subsets of variables derived from tracers with the highest discriminant capacity, and (iii) to evaluate and

compare statistical or machine learning methods to develop predictive models for source tracking using the minimum number of these variables. In this multilaboratory study, different microbial and chemical indicators were analyzed in order to distinguish human fecal sources from nonhuman fecal sources using wastewaters and slurries from diverse geographical areas within Europe.

Results - Fecal coliforms, enterococci, clostridia, somatic coliphages, and total bifidobacteria were detected in almost all samples (other than a single sample in the case of total bifidobacteria) of both human and animal origin. They were more abundant in the animal samples than in the human samples, but this seems to be due to the higher fecal load of these samples, since relative densities were similar in both groups of samples.

## **21 - Enterococci Concentrations in Diverse Coastal Environments Exhibit Extreme Variability**

A.R. Boehm

<http://pubs.acs.org/doi/abs/10.1021/es071807v>

Purpose - The study examines extreme temporal variations (periods between 1 min and 24 h) in FIB concentrations in diverse marine coastal environments ranging from wave-sheltered to wave-exposed open ocean beaches.

Results - The high frequency variability indicates that regardless of sampling time, a single sample of water tells one little about the true water quality, so multiple samples need to be collected. If it is not feasible to collect multiple samples, then a spatially or temporally composited sample will improve the estimate of the true water quality.

## **157 - Methicillin-resistant Staphylococcus aureus (MRSA) in municipal wastewater: an uncharted threat?**

S. Börjesson, A. Matussek, S. Melin, S. Löfgren, and P.E. Lindgren

<http://www.mendeley.com/research/methicillinresistant-staphylococcus-aureus-mrsa-in-municipal-wastewater-an-uncharted-threat/#page-1>

Purpose - (i) To cultivate methicillin-resistant Staphylococcus aureus (MRSA) from a full-scale wastewater treatment plant (WWTP), (ii) To characterize the indigenous MRSA-flora, (iii) To investigate how the treatment process affects clonal distribution and (iv) to examine the genetic relation between MRSA from wastewater and clinical MRSA.

Results - MRSA could be isolated on all sampling occasions, but only from inlet and activated sludge. The number of isolates and diversity of MRSA were reduced by the treatment process, but there are indications that the process was selected for strains with more extensive antibiotic resistance and PVL+ strains. The wastewater MRSA-flora had a close genetic relationship to clinical isolates, most likely reflecting carriage in the community.

### **158 - A seasonal study of the mecA gene and Staphylococcus aureus including methicillin-resistant S. aureus in a municipal wastewater treatment plant**

S. Börjesson, S. Melin, A. Matussek, and P.E. Lindgren

<http://www.loudounnats.org/pdf/09WRASEASONALSTUDYOFMECAStAUREUSANDMRSAinafull-scaleWWTP.pdf>

Purpose - Determine the effect of wastewater treatment processes on mecA gene concentrations, and the prevalence of S. aureus and MRSA over time. To achieve this a municipal wastewater treatment plant was investigated for the mecA gene, S. aureus and MRSA, using real-time PCR assays

Results - Using molecular methods and cultivation, MRSA was for the first time detected in a municipal activated sludge and trickling filter WWTP, but mainly in the early treatment steps, IN, PS and AS. The mecA gene and S. aureus could be detected throughout the year at all sampling sites. The wastewater treatment process reduces mecA gene concentrations, which can partly be explained by removal of biomass.

### **140 - Particle Associated Microorganisms in Stormwater Runoff**

Michael Borst, and A. Selvakumar

<http://www.epa.gov/ORD/NRMRL/pubs/600j03262/600j03262.pdf>

Purpose - Investigate the effects of blending and chemical addition before analysis of the concentration of microorganisms in stormwater runoff play a significant role.

Results - Particle-associated microorganisms play an important, if often unmeasured, portion of the total organism count in stormwater. All organisms, except for E. coli, showed an increase in the measured concentration after blending samples at 22,000 rpm with or without the chemical mixture. Other than fecal streptococci, the organism concentrations decreased with the addition of the Camper's solution in both blended and unblended samples before analyses. There was a statistically significant interaction between the effects of Camper's solution and the effects of blending for all the organisms tested, except for total coliform. Blending did not alter the mean particle size significantly. The results show no correlation between increased total coliform, fecal coliform, and fecal streptococcus concentrations and the mean particle size.

### **87 - Direct comparison of four bacterial source tracking methods and use of composite data sets**

E.A. Casarez, S.D. Pillai, J.B. Mott, M. Vargas, K.E. Dean and G.D. Di Giovanni

<http://onlinelibrary.wiley.com/doi/10.1111/j.1365-2672.2006.03246.x/pdf>

Purpose - (i) To compare the identification ability of the four BST methods individually and in combination through the use of composite data sets and (ii) to evaluate the use of the developed data sets for the identification of faecal contamination sources in two Central Texas lakes suspected of being impacted by agricultural operations and dairy cattle.

Results - Best matching identification using the composite data set correctly identified 100% of the replicate QC cultures (precision), and had 100% accuracy for E. coli strain and source class

identification of the isolates. Therefore, the four-method composite performed better than any single method.

#### **154 - Removal of bacterial indicators of fecal contamination in urban stormwater using a natural riparian buffer**

M.J. Casteel, G. Bartow, S.R. Taylor, and P. Sweetland

[http://www.lmtf.org/FoLM/Plans/Water/VistaGrande/Casteetal\\_10icud\\_paper.PDF](http://www.lmtf.org/FoLM/Plans/Water/VistaGrande/Casteetal_10icud_paper.PDF)

Purpose - Determine if riparian buffers are able to remove bacterial indicators of fecal contamination and other microbial contaminants from intermittent, high-volume flows such as those encountered during storm events in heavily urbanized areas.

Results - Analysis of lake water showed that levels of *Escherichia coli* and total coliforms increased significantly during storm events, indicating the presence of nonpoint sources of fecal contamination in the area surrounding the lake.

#### **134 - Population structure and persistence of *Escherichia coli* in ditch sediments and water in the Seven Mile Creek Watershed**

Ramyavardhane Chandrasekaran

[http://conservancy.umn.edu/bitstream/108879/1/Chandrasekaran\\_Ramyavardhane\\_May2011.pdf](http://conservancy.umn.edu/bitstream/108879/1/Chandrasekaran_Ramyavardhane_May2011.pdf)

Purpose - Examined the population structure of *E. coli* and determined whether ditch sediments can serve as reservoirs of environmental *E. coli* in the Seven Mile Creek (SMC) watershed, a minor watershed located in south central Minnesota

Results - Further analysis of the count data revealed a strong correlation between *E. coli* concentrations and temperature profile at the SMC. *E. coli* densities in SMC water samples exceeded the permissible Minnesota standard (126 CFU/100 ml) predominantly during summer and fall seasons. In addition to temperature, rainfall also drastically influenced the dynamics and distribution of *E. coli* populations at the SMC. Results suggest that the seasonal variation in *E. coli* counts observed in water and sediments are most likely related to temperature, rainfall, and the patchy distribution of *E. coli* within sampling locations

#### **88 - Relative Decay of Bacteroidales Microbial Source Tracking Markers and Cultivated *Escherichia coli* in Freshwater Microcosms**

Linda K. Dick, Erin A. Stelzer, Erin E. Bertke, Denise L. Fong, and Donald M. Stoeckel

<http://aem.asm.org/content/76/10/3255.full.pdf+html>

Purpose - Fecal indicator bacteria (FIB), commonly used to regulate sanitary water quality, cannot discriminate among sources of contamination. The use of alternative quantitative PCR (qPCR) methods for monitoring fecal contamination or microbial source tracking requires an understanding of relationships with cultivate FIB, as contamination ages under various conditions in the environment. In this study, the decay rates of three Bacteroidales 16S rRNA gene markers (AllBac for general contamination and qHF183 and BacHum for human-associated contamination) were compared with the decay rate of cultivated *Escherichia coli* in river water microcosms spiked with human wastewater.

Results - A major finding of this study was that HF marker decay was consistent with, or significantly faster than, that of E. coli under all treatments. This indicates that the HF markers might be useful as conservative estimators of human origin E. coli even as fecal contamination ages in the environment.

### **118 - Bacteriological Quality of Runoff Water from Pastureland**

J.W. Doran, and D.M. Linn

<http://aem.asm.org/content/37/5/985.abstract>

Purpose - Determine the bacteriological characteristics of pasture runoff and to compare them with runoff from an ungrazed area.

Results - We found no relationship between FC and FS counts in rainfall runoff and either rainfall or total runoff for most events. Bacteriological quality of snowmelt runoff. During the 3-year study, there were 10 snowmelt runoff events-two in 1976 and 8 in 1978. The levels of TC in snowmelt runoff from both grazed and ungrazed pasture areas exceeded recommended water quality standards. FC counts, often considered a better index of fecal contamination, were within recommended standards.

### **89 - Microbial source tracking using host specific FAME profiles of fecal coliforms**

Metin Duran, Berat Z. Haznedaroglu, and Daniel H. Zitomer

<http://www.prairieswine.com/pdf/3397.pdf>

Purpose - The objective of this study was to investigate the host-specific differences in fatty acid methyl ester (FAME) profiles of fecal coliforms (FC).

Results - The results presented here provide further evidence that FAME profiles of indicator organisms have statistically significant host specificity and suggest that these differences may be useful in predicting sources of microbial pollution in water environments. However, more research is needed to determine the mechanisms causing the host specificity and to assess the possible temporal and spatial variations in FAME profiles before FAME can be applied in the field.

### **183 - Quantitative evaluation of enterococci and Bacteroidales released by adults and toddlers in marine water**

S.M. Elmir, T. Shibata, H.M. Solo-Gabriele, C.D. Sinigalliano, M.L. Gidley, G. Miller, L.R.W. Plano, J. Kish, K. Withum, and L.E. Fleming

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2761526/>

Purpose - The main objectives of the this study were to measure shedding of enterococci and Bacteroidales using traditional and emerging laboratory methods, and to evaluate shedding from toddlers and adults. The added value of the current study was the evaluation of shedding from toddlers (all prior studies used adult volunteers), and the use of additional methods of fecal indicator bacteria analyses (i.e. enterococci by CS and qPCR, and Bacteroidales by qPCR) as no data are available which directly measure fecal indicator bacteria shedding using these alternate methods.

Results - Human bathers have the potential to release significant amounts of fecal indicator bacteria into the water column via direct shedding off their body and via sand transported by their skin. Direct shedding from the body can include releases from fecally contaminated body areas and skin, and releases from fecally contaminated diapers. In this study, the quantity of enterococci released was a function of bathing cycle, sand exposure, beach sand contamination levels, and microbial flora variations between swimmers.

### **182 - Quantitative evaluation of bacteria released by bathers in a marine water**

S.M Elmir, M.E. Wright, A. Abdelzaher, H.M. Solo-Gabriele, L.E. Fleming, G. Miller, M. Rybolowik, M.T. Peter Shih, S.P. Pillai, J.A. Cooper and E.A. Quayle  
<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2633726/>

Purpose - This study focused on estimating the amounts of enterococci and *S. aureus* shed by bathers directly off their skin and indirectly via sand adhered to skin.

Results - This study demonstrated that bathers shed significant concentrations of enterococci and *S. aureus* into the water column and that *S. aureus* was shed at concentrations at least one order of magnitude greater than enterococci. This study also showed that total enterococci and *S. aureus* released by bathers decreased significantly between bathing episodes, in particular after the first wash cycle. This conclusion agrees with the long standing universal requirement that bathers should shower before entering recreational waters to reduce the microbial load in particular at swimming pools since the water volume is limited. It is concluded from this study that the enterococci contribution from sand adhered to skin, was small relative to the amount shed directly from the skin and represented less than 5% of the total enterococci shed by bathers.

### **159 - Staphylococcus aureus and fecal indicators in Egyptian coastal waters of Aqaba Gulf, Suez Gulf, and Red Sea**

M.A. El-Shenawy

[http://www.nodc-egypt.org/contacts\\_files/vol-31-2/Volume%2031%20%282%29%202005.PDF/9/Text.pdf](http://www.nodc-egypt.org/contacts_files/vol-31-2/Volume%2031%20%282%29%202005.PDF/9/Text.pdf)

Purpose - Study the hygienic status of Egyptian coastal waters of Aqaba Gulf, Suez Gulf and Red Sea. The possibility of using *S.aureus* as supplementary indicator to the conventional bacterial indicators was another goal.

Results - 107 samples (53.5 %) of the 200 total examined samples were found to harbour *S aureus* exceeding the aforementioned guide standards. The present results concluded that addition of *S. aureus* as supplementary indicator to the conventional fecal indications may be useful for judging the marine water quality in Red Sea region.

### **138 - Sediment Bacterial Indicators in an Urban Shellfishing Subestuary of the Lower Chesapeake Bay**

Carl W. Erkenbrecher Jr.

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC244041/pdf/aem00190-0106.pdf>

Purpose - Historically, the Lynnhaven, an urban shellfishing estuary of the lower Chesapeake Bay region, has been opened and closed periodically to shellfishing during the past 40 years due to high fecal coliform counts. Document the spatial and temporal distributions and compositions of bacteria in the sediments and overlying waters of an important urban shellfishing area in the lower Chesapeake Bay region, the Lynnhaven Estuary.

Results - Densities of all indicator bacteria were always significantly higher in the sediments than in the overlying subsurface waters. The major problems inherent in this system are nonpoint in their origin. The primary sources of the Lynnhaven's bacterial pollution appeared to be typical of urban and agricultural runoff, although failure of septic tank systems was suspected as a problem in the Lynnhaven's western branch. These results illustrated that sediments in shellfishing areas could serve as a reservoir for high densities of indicator bacteria and that, potentially, pathogens could pose a health hazard.

#### **184 - Enumeration and speciation of enterococci found in marine and intertidal sediments and coastal water in southern California**

D.M. Ferguson, D.F. Moore, M.A. Getrich, and M.H. Zhouandai

<http://www.ochealthinfo.com/docs/public/h2o/Enumeration-speciation.pdf>

Purpose - To determine the levels and species distribution of enterococci in intertidal and marine sediments and coastal waters at two beaches frequently in violation of bacterial water standards.

Results - High levels of *Enterococcus* in intertidal sediments indicate retention and possible regrowth in this environment. Significance and Impact of the Study: Re-suspension of enterococci that are persistent in sediments may cause beach water quality failures and calls into question the specificity of this indicator for determining recent faecal contamination.

#### **90 - Comparison of Bacteroides-Prevotella 16S rRNA Genetic Markers for Fecal Samples from Different Animal Species**

Lisa R. Fogarty and Mary A. Voytek

<http://aem.asm.org/content/71/10/5999.full.pdf+html>

Purpose - The goals of this study were to compare *Bacteroides-Prevotella* populations from nine host species collected at multiple geographical locations and to determine if unique populations could be identified for each host species that could be used to develop markers for fecal source tracking.

Results - Results support the use of molecular techniques to characterize *Bacteroides-Prevotella* populations as a means to improve the ability to track sources of fecal contamination, but also show the need for more development of these methods.

#### **186 - Abundance and characteristics of the recreational water quality indicator bacteria *Escherichia coli* and enterococci in gull faeces**

L.R. Fogarty, S.K. Haack, M.J. Wolcott, and R.L. Whitman

<http://cws.msu.edu/documents/FogartyetalJAM2003.pdf>

Purpose - To evaluate the numbers and selected phenotypic and genotypic characteristics of the faecal indicator bacteria *Escherichia coli* and enterococci in gull faeces at representative Great Lakes swimming beaches in the United States.

Results - Gull faeces could be a major contributor of *E. coli* (105–109 CFU g<sup>-1</sup>) and enterococci (104– 108 CFU g<sup>-1</sup>) to Great Lakes recreational waters. *E. coli* and enterococci in gull faeces are highly variable with respect to their genotypic and phenotypic characteristics and may exhibit temporal or geographic trends in these features.

### **162 - A preliminary investigation of fecal indicator bacteria, human pathogens, and source tracking markers in beach water and sand**

K.D. Goodwin, L. Matragrano, D. Wanless, C. Sinigalliano, and M.J. LaGier

[http://yyy.rsmas.miami.edu/groups/ohh/projects/microbesresearch/GoodwinERK2\\_4.pdf](http://yyy.rsmas.miami.edu/groups/ohh/projects/microbesresearch/GoodwinERK2_4.pdf)

Purpose - Data suggesting that fecal indicating bacteria may persist and/or regrow in sand has raised concerns that fecal indicators may become uncoupled from sources of human fecal pollution. To investigate this possibility, wet and dry beach sand, beach water, riverine water, canal water, and raw sewage samples were screened by PCR for certain pathogenic microbes and molecular markers of human fecal pollution.

Results - Overall, this analysis pointed to the need to find better methods of extracting nucleic acids from environmental samples in order to reduce the possibility of false negative results. High quality nucleic acids need to be consistently and efficiently delivered to the detector system if the relationship between fecal indicators and human pathogens and human source tracking markers is to be elucidated.

### **93 - Comparing Wastewater Chemicals, Indicator Bacteria Concentrations, and Bacterial Pathogen Genes as Fecal Pollution Indicators**

Sheridan K. Haack, Joseph W. Duris, Lisa R. Fogarty, Dana W. Kolpin, Michael J. Focazio, Edward T. Furlong, and Michael T. Meyer

<https://www.crops.org/publications/jeq/pdfs/38/1/248>

Purpose - Compare fecal indicator bacteria (FIB) (fecal coliforms, *Escherichia coli* [EC], and enterococci [ENT]) concentrations with a wide array of typical organic wastewater chemicals and selected bacterial genes as indicators of fecal pollution in water samples collected at or near 18 surface water drinking water intakes.

Results - In our study, which examined ambient waters in various land use environments with a wide range of FIB concentrations, fecal pollution was indicated by gene-based and/or chemical-based markers for 14 of the 18 tested samples, with little relation to FIB standards.

### **95 - Development of Goose- and Duck-Specific DNA Markers To Determine Sources of *Escherichia coli* in Waterways**

Matthew J. Hamilton, Tao Yan, and Michael J. Sadowsky

<http://aem.asm.org/content/72/6/4012.full.pdf+html>

Purpose - The development and validation of host source-specific genetic markers for *E. coli* strains originating from Canada geese (*Branta canadensis*).

Results - SSH was successfully used to identify seven DNA markers with high levels of hybridization specificity for *E. coli* strains originating from geese. Combined, the marker DNAs were capable of identifying about 76% of the goose *E. coli* strains examined and 73% of the duck *E. coli* strains examined.

### **192 - Waterfowl Abundance Does Not Predict the Dominant Avian Source of Beach *Escherichia coli***

D.L. Hansen, S. Ishii, M.J. Sadowsky, and R.E. Hicks

<https://www.soils.org/publications/jeq/abstracts/40/6/1924?access=0&view=pdf>

Purpose - The horizontal, fluorophore enhanced, rep-PCR (HFERP) DNA fingerprinting technique was used to identify potential sources of *Escherichia coli* in water, nearshore sand, and sediment at two beaches in the Duluth-Superior Harbor, near Duluth, MN, and Superior, WI, during May, July, and September 2006.

Results - Waterfowl, including Canada geese, ring-billed gulls, and mallard ducks, were the largest source of *E. coli* that could be identified in water (55–100%), sand (59–100%), and sediment (92–100%) at both beaches. Although ring-billed gulls were more abundant in this harbor, Canada geese were usually the dominant source of waterfowl *E. coli* found at these beaches.

### **96 - Validation and field testing of library-independent microbial source tracking methods in the Gulf of Mexico**

Valerie J. Harwood, Miriam Brownell, Shiao Wang, Joe Lepo, R.D. Ellender, Abidemi Ajidahun, Kristen N. Hellein, Elizabeth Kennedy, Xunyan Ye, and Christopher Flood

<http://www.usm.edu/bst/pdf/Water%20Res%202009.pdf>

Purpose - Standardize and validate MST methods across laboratories in coastal Gulf of Mexico states.

Results - An SOP was developed that allowed simultaneous purification of DNA for viral and bacterial markers, and gave comparable results among three laboratories. The method performance was generally similar whether it was conducted in buffer, fresh water or salt water; however, the human Bacteroidales method had a lower limit of detection in buffer and in salt water compared to fresh water.

### **97 - Fidelity of bacterial source tracking: *Escherichia coli* vs. *Enterococcus* spp. and minimizing assignment of isolates from non-library sources**

W.M. Hassan, R.D. Ellender and S.Y. Wang

<http://onlinelibrary.wiley.com/doi/10.1111/j.1365-2672.2006.03077.x/pdf>

Purpose - Improve the fidelity of library-dependent bacterial source tracking efforts in determining sources of faecal pollution.

Results - The use of enterococci provides higher rates of correct source assignment compared with E. coli. The use of similarity thresholds to decide whether to accept source assignments made by computer programmes reduces the rate of mis-assignment of non-library isolates.

### **197 - Contact with beach sand among beachgoers and risk of illness**

C. D. Heaney, E. Sams, S. Wing, S. Marshall, K. Brenner, A.P. Dufour, and T.J. Wade

<http://aje.oxfordjournals.org/content/170/2/164.full.pdf>

Purpose - The purpose of this study is to better understand the illness risk associated with beach sand that can harbor high concentrations of fecal indicator organisms, as well as fecal pathogens.

Results - The results of our study suggest that, among beachgoers participating in a large prospective cohort study at beaches nearby sewage treatment discharges, reported contact with beach sand (defined as either digging in the sand or having one's body buried in the sand) was associated with an elevated risk of enteric illnesses (gastrointestinal illness and diarrhea). Being buried in the sand was more strongly associated with enteric illness than was digging in the sand. We also observed a higher proportion of people who got sand in their mouth among those buried in the sand (40%) compared with those who dug in the sand (20%).

### **155 - The Impact of Rainfall on Fecal Coliform Bacteria in Bayou Dorcheat (North Louisiana)**

Dagne D. Hill, W.E. Owens, and P.B. Tchounwou

[www.mdpi.com/1660-4601/3/1/114/pdf](http://www.mdpi.com/1660-4601/3/1/114/pdf)

Purpose - Assess the effect of surface runoff amounts and rainfall amount parameters on fecal coliform bacterial densities in Bayou Dorcheat in Louisiana.

Results - Nonpoint source pollution that is carried by surface runoff has a significant effect on bacterial levels in water resources.

### **199 - Beach sand and sediments are temporal sinks and sources of Escherichia coli in Lake Superior**

Satoshi Ishii, D.L. Hansen, R.E. Hicks, and M.J. Sadowsky

<http://pubs.acs.org/doi/pdf/10.1021/es0623156>

Purpose - Report on a 2-year investigation of the seasonal variation of E. coli concentrations in water, sand, and sediment at the DBC Beach in the Duluth-Superior Harbor of Lake Superior.

Results - Waterfowl in addition to humans can be a significant source of fecal indicator bacteria like E. coli at Great Lakes beaches. Although waterfowl have been reported to carry a limited number of pathogenic E. coli (36), which was also found our study, they may harbor other potential pathogens such as Salmonella and Campylobacter (37). The potential health risks associated with waterfowl-borne bacteria found at beaches needs to be investigated in the future.

### **122 - Fecal bacteria and sex hormones in soil and runoff from cropped watersheds amended with poultry litter**

Michael B. Jenkins, D.M. Endale, H.H. Schomberg, and R.R. Sharpe

<http://phoenix.nal.usda.gov/bitstream/10113/15527/1/IND44044786.pdf>

Purpose - Determine if applications of poultry litter to small watersheds would contribute to the load of fecal bacteria and sex hormones to soil and runoff

Results - Under the conditions of drought and conservation tillage, the rates at which we applied poultry litter to the four cropped watersheds appeared to have little or no significant effect on (a) soil community of fecal indicator bacteria, (b) concentrations of estradiol and testosterone in surface soil, and (c) quantities of estradiol and testosterone coming off the watersheds with runoff.

### **202 - Bacteroidales Diversity in Ring-Billed Gulls (*Larus delawarensis*) Residing at Lake Michigan Beaches**

S.N. Jeter, C.M. McDermott, P.A. Bower, J.L. Kinzelman, M. J. Bootsma, G.W. Goetz, and S.L. McLellan

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2655448/pdf/2261-08.pdf>

Purpose - This study investigated the occurrence and diversity of Bacteroidales fecal bacteria in gulls residing in the Great Lakes region.

Results - A total of 467 gull fecal samples from five coastal beaches spanning Lake Michigan's western shore and one inland beach on Lake Winnebago were screened for the presence of Bacteroidales by PCR. There was a low but consistent occurrence of Bacteroidales in the gull populations at these beaches.

### **151 - The Impact of Annual Average Daily Traffic on Highway Runoff Pollutant Concentrations**

Masoud Kayhanian, A. Singh, C. Suverkropp, and S. Borroum

<http://escholarship.org/uc/item/86f8c8n8>

Purpose - Evaluate correlations between annual average daily traffic and storm water runoff pollutant concentrations generated from California Department of Transportation highway sites.

Results - No direct linear correlation was found between highway runoff pollutant mean concentrations and AADT. However, through multiple regression analyses, it was shown that AADT has an influence on most highway runoff constituent concentrations, in conjunction with factors associated with watershed characteristics and pollutant build-up and wash off.

### **102 - Development of Bacteroides 16S rRNA Gene TaqMan-Based Real-Time PCR Assays for Estimation of Total, Human, and Bovine Fecal Pollution in Water**

Alice Layton, Larry McKay, Dan Williams, Victoria Garrett, Randall Gentry, and Gary Saylor

<http://aem.asm.org/content/72/6/4214.full.pdf+html>

Purpose - Design real-time PC assay to target *Bacteroides* species (AllBac) present in human, cattle, and equine feces.

Results - This assay was shown empirically to be proportional to the concentration of human, bovine, and equine feces in water and thus can be used to estimate fecal concentrations without calculating the number of *Bacteroides* cells in the sample. The simplicity of performing these assays by direct PCR of water samples suggests that these assays may be field deployable and thus would aid data collection in watersheds with inherently high spatial and temporal variabilities.

### **203 - Persistence of fecal indicator bacteria in Santa Monica Bay beach sediments**

C.M. Lee, T.Y. Lin, C.C. Lin, G.A. Kohbodi, A. Bhatt, R. Lee, and J.A. Jay

<http://www.sciencedirect.com/science/article/pii/S004313540600220X>

Purpose - This study involved monitoring the fecal indicator bacteria (FIB) levels in water and sediment at three ocean beaches (two exposed and one enclosed) during a storm event, conducting laboratory microcosm experiments with sediment from these beaches, and surveying sediment FIB levels at 13 beaches (some exposed and some enclosed).

Results - Results from microcosm experiments showing similar, dramatic growth of FIB in both overlying water and sediment from all beaches, as well as results from the beach survey, support the hypothesis that the quiescent environment rather than sediment characteristics can explain the elevated sediment FIB levels observed at enclosed beaches. This work has implications for the predictive value of FIB measurements, and points to the importance of the sediment reservoir.

### **205 - Phylogenetic Diversity and Molecular Detection of Bacteria in Gull Feces**

J. Lu, J.W. Santo Domingo, R. Lamendella, T. Edge, and S. Hill

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2446513/>

Purpose - To determine the occurrence of *C. marimammalium* in waterfowl, species-specific 16S rRNA gene PCR and real-time assays were developed and used to test fecal DNA extracts from different bird (n = 13) and mammal (n = 26) species.

Results - To determine the occurrence of *C. marimammalium* in waterfowl, species-specific 16S rRNA gene PCR and real-time assays were developed and used to test fecal DNA extracts from different bird (n = 13) and mammal (n = 26) species.

### **103 - Genetic Diversity of *Escherichia coli* Isolated from Urban Rivers and Beach Water**

Sandra L. McLellan

<http://aem.asm.org/content/70/8/4658.full.pdf+html>

Purpose - Evaluate the genetic profiles of *E. coli* strains found in stormwater, where fecal pollution is derived from multiple uncharacterized host sources, and compare these profiles to known host sources of pollution.

Results - There does not appear to be a proportional relationship between fecal indicator bacteria from a host and what is actually detected in the environment, which will be an important consideration when developing methods for fecal pollution source tracking. Matching of isolates to the entire data set demonstrated that strains from a type of sample (e.g., gull, sewage, stormwater, river water, beach water) were most similar to other strains from the same host or environmental source. These findings may be a function of geographic distribution rather than host source specificity.

### **126 - Identification and Quantification of Bacterial Pollution At Milwaukee County Beaches**

Sandra L. McLellan, and E.T. Jensen

<http://www.glwi.freshwater.uwm.edu/research/genomics/ecoli/media/Technical%20document%2009-12-05.pdf>

Purpose - Assess the bacterial contaminant load in the waters and sand at beaches within Milwaukee County.

Results - Bacterial water data collected during the summer 2005 beach surveys suggests a positive relationship between rainfall and increased E. coli levels at these particular beach sites. Sewage contamination could potentially reach the beach during combined sewage overflows, or from nearby sewer infrastructure failures.

### **104 - Evaluation of Repetitive Extragenic Palindromic-PCR for Discrimination of Fecal Escherichia coli from Humans, and Different Domestic and Wild Animals**

Bidyut Mohapatra, Klaas Broersma, Rick Nordin and Asit Mazumder

<http://web.uvic.ca/~h2o/publications/Mohapatra%20et%20al.%20MI07pdf.pdf>

Purpose - Investigate the potential of rep-PCR in differentiating e. coli isolates of human, domestic and wild animal origin that might be used as a molecular tool to identify the possible source(s) of fecal pollution of source water.

Results - Rep-PCR DNA fingerprinting results provide evidence about the robustness of this method, and it's simple and cost-effective screening tool to isolate and track non-point sources of fecal contamination.

### **106 - Evaluation of antibiotic resistance analysis and ribotyping for identification of faecal pollution sources in an urban watershed**

D.F. Moore, V.J. Harwood, D.M. Ferguson, J. Lukasik, P. Hannah<sup>1</sup>, M. Getrich and M. Brownell

<http://onlinelibrary.wiley.com/doi/10.1111/j.1365-2672.2005.02612.x/pdf>

Purpose - The accuracy of ribotyping and antibiotic resistance analysis (ARA) for prediction of sources of faecal bacterial pollution in an urban Southern California watershed was determined using blinded proficiency samples. Low rates of correct classification for E. coli proficiency isolates compared with the ARCCs of the libraries indicate that testing of bacteria from samples that are not represented in the library, such as blinded proficiency samples, is necessary to

accurately measure predictive ability. The library-based MST methods used in this study may not be suited for determination of the source(s) of faecal pollution in large, urban watersheds.

Results - None of the methods performed well enough on the proficiency panel to be judged ready for application to environmental samples.

### **210 - Species distribution and antimicrobial resistance of enterococci isolated from surface and ocean water**

D.F. Moore, J.A. Guzman, and C. McGee

<http://www.glin.net/lists/beachnet/2008-05/pdf00000.pdf>

Purpose - The species identification and antimicrobial resistance profiles were determined for enterococci isolated from Southern California surface and ocean waters.

Results - *Enterococcus faecalis*, *E. faecium*, *E. casseliflavus* and *E. mundti* are the most commonly isolated Enterococcus species from urban runoff and receiving waters in Southern California.

### **107 - A review of technologies for rapid detection of bacteria in recreational waters**

Rachel T. Noble and Stephen B. Weisberg

[http://www.environmental-expert.com/Files%5C19961%5Carticles%5C6674%5C479\\_rapid\\_detection\\_recreational\\_waters.pdf](http://www.environmental-expert.com/Files%5C19961%5Carticles%5C6674%5C479_rapid_detection_recreational_waters.pdf)

Purpose - Review new methods that have the potential to reduce measurement period for fecal indicator bacteria from more than a day to less than an hour to reduce risk of swimmers to fecal bacteria.

Results - Enzyme substrate methods are most likely to be the first rapid methods adopted for recreational water quality. Enzymatic substrate methods are based on the same capture technology as currently-approved EPA methods, with greater speed attained through enhanced detection technology. As such, the relationship to health risk can be established by demonstrating that the new detection capability produces equivalent results to existing procedures.

### **214 - Comparison of total coliform, fecal coliform, and enterococcus bacterial indicator response for ocean recreational water quality testing**

Rachel T. Noble, D.F. Moore M.K. Leecaster, C.D. McGee, and S.B. Weisberg

<http://www.ochealthinfo.com/docs/public/epi/h2o/Water-Research-Publication-2003.pdf>

Purpose - To compare the relationship between the bacterial indicators, and the effect that changing the standards would have on recreational water regulatory actions, three regional studies were conducted along the southern California shoreline from Santa Barbara to San Diego, California.

Results - Cumulatively, our results suggest that replacement of a TC standard with an EC standard will lead to a five-fold increase in failures during dry weather and a doubling of failures

during wet weather. Replacing a TC standard with one based on all three indicators will lead to an eight-fold increase in failures. Changes in the requirements for water quality testing have strong implications for increases in beach closures and restrictions.

### **217 - Relationships between sand and water quality at recreational beaches**

M.C. Phillips, H.M. Solo-Gabriele, A.M. Piggot, J.S. Klaus and Y. Zhang

<http://www.sciencedirect.com/science/article/pii/S0043135411006269>

Purpose - Enterococci are used to assess the risk of negative human health impacts from recreational waters. Studies have shown sustained populations of enterococci within sediments of beaches but comprehensive surveys of multiple tidal zones on beaches in a regional area and their relationship to beach management decisions are limited.

Results - We sampled three tidal zones on eight South Florida beaches in Miami-Dade and Broward counties and found that enterococci were ubiquitous within South Florida beach sands although their levels varied greatly both among the beaches and between the supratidal, intertidal and subtidal zones.

### **218 - Shedding of Staphylococcus aureus and methicillin-resistant Staphylococcus aureus from adult and pediatric bathers in marine waters**

L.R.W. Plano, A.C. Garza, T. Shibata, S.M. Elmier, J. Kish, C.D. Sinigalliano, M.L. Gidley, G. Miller, K. Withum, L.E. Fleming, and H.M. Solo-Gabriele

<http://www.biomedsearch.com/attachments/00/21/21/10/21211014/1471-2180-11-5.pdf>

Purpose - The primary aim of this study was to evaluate the amount and characteristics of the shedding of methicillin sensitive S. aureus, MSSA and MRSA by human bathers in marine waters.

Results - Twelve of 15 MRSA isolates collected from the water had identical genetic characteristics as the organisms isolated from the participants exposed to that water while the remaining 3 MRSA were without matching nasal isolates from participants. The amount of S. aureus shed per person corresponded to 105 to 106 CFU per person per 15-minute bathing period, with 15 to 20% of this quantity testing positive for MRSA. These findings clearly demonstrate that adults and toddlers shed their colonizing organisms into marine waters and therefore can be sources of potentially pathogenic S. aureus and MRSA in recreational marine waters. Additional research is needed to evaluate recreational beaches and marine waters as potential exposure and transmission pathways for MRSA.

### **111 - A comparison of ARA and DNA data for microbial source tracking based on source-classification models developed using classification trees**

Bertram Price, Elichia Venso, Mark Frana, Joshua Greenberg, and Adam Ware

<http://faculty.salisbury.edu/~mffrana/Cell%20Bio1%20Spring%2008/Frana%20paper,%20after.pdf>

Purpose - Determine whether increased reliability, if any, of library-based MST developed with DNA data is sufficient to justify its higher cost, where source predictions are used in TMDL surface water management programs.

Results - While the overall rates of correct classification are higher for the DNA data than for the ARA data, the resulting source predictions for both data indicate similar TMDL surface water bacterial contamination reduction strategies. Questioning the value of DNA data relative to ARA data for MST intended for application in a TMDL program is justified, and the answer may favor ARA data for this application.

### **112 - Quantitative PCR Method for Sensitive Detection of Ruminant Fecal Pollution in Freshwater and Evaluation of This Method in Alpine Karstic Regions**

Georg H. Reischer, David C. Kasper, Ralf Steinborn, Robert L. Mach, and Andreas H. Farnleitner

<http://aem.asm.org/content/72/8/5610.full.pdf+html>

Purpose - Establish a method for the sensitive quantification of ruminant fecal pollution in spring water and groundwater from alpine karstic regions important for public water supplies. Identify a ruminant-specific genetic marker in fecal members of the phylum Bacteroidetes.

Results - The marker could be found at concentrations ranging from not detectable in 4.5 liters (KPAS) to 106 marker equivalents per liter (LKAS2 flood). Strong differences in occurrence were obvious and in accordance with the expected different levels of ruminant fecal.

Preliminary experiments testing the stability of the marker in highly diluted fecal suspensions in spring water at ambient temperatures (4°C) found no strong reduction of detectable marker levels during an incubation period of 2 months.

After additional evaluation, the assay might allow the specific allocation of fecal pollution in alpine water sources, enabling target oriented measures in the catchment area and thus facilitating watershed management. Furthermore, it could also provide additional information for quantitative microbial risk assessment studies as part of water safety plans recommended by the WHO (35), allowing the relative estimation of ruminant fecal input compared to other sources.

### **164 - Pathogenic fungi: an unacknowledged risk at coastal resorts? New insights on microbiological sand quality in Portugal**

R. Sabino, C. Verissimo, M.A. Cunha, B. Wergikoski, F.C. Ferreira, R. Rodrigues, H. Parada, L. Falcão, L. Rosado, C. Pinheiro, E. Paixão, and J. Brandão

<http://www.sciencedirect.com/science/article/pii/S0025326X11001962>

Purpose - Determine the presence of yeasts, pathogenic fungi, dermatophytes, total coliforms, *Escherichia coli* and intestinal enterococci in sand at thirty-three beaches across Portugal.

Results - Results showed that 60.4% of the samples were positive for fungi and that 25.2% were positive for the bacterial parameters. The most frequent fungal species found were *Candida* sp. and *Aspergillus* sp., whereas intestinal enterococci were the most frequently isolated bacteria.

Positive associations were detected among analyzed parameters and country-regions but none among those parameters and sampling period. Regarding threshold values, we propose 15 cfu/g for yeasts, 17 cfu/g for potential pathogenic fungi, 8 cfu/g for dermatophytes. Eighty four cfu/g for coliforms, 250 cfu/g for E. coli, and 100 cfu/g for intestinal enterococci.

#### **114 - The use of ribotyping and antibiotic resistance patterns for identification of host sources of Escherichia coli strains**

M. Samadpour, M.C. Roberts, C. Kitts, W. Mulugeta and D. Alfi

<http://onlinelibrary.wiley.com/doi/10.1111/j.1472-765X.2004.01630.x/pdf>

Purpose - To compare antibiotic resistance and ribotyping patterns ability to identify triplicate isolates sent from a group of 40 Escherichia coli taken from seven host sources.

Results - Of the 120 isolates, 22 isolates were resistant to ampicillin, streptomycin, tetracycline and trimethoprim and 98 isolates were susceptible. Antibiotic patterns identified 33 of the triplicates and three of the six groups had isolates from multiple hosts. Ribotyping divided the isolates into 27 ribotype groups with all triplicates grouped into the same ribotype group with one host per group.

#### **219 - The effects of rainfall on Escherichia coli and total coliform levels at 15 Lake Superior recreational beaches**

R. Sampson, S. Swiatnicki, C. McDermott, and G. Kleinheinz

<http://www.environmental-expert.com/Files%5C6063%5Carticles%5C9235%5C11-12-6.pdf>

Purpose - Fifteen beaches along Lake Superior were monitored over the course of the 2003 and 2004 summer swimming seasons from mid-May through mid-September. Water samples were collected at these 15 beaches less than 24-h after a rainfall event of at least 6 mm. The effect of rainfall on bacterial concentrations along the Wisconsin shores of Lake Superior was investigated.

Results - No relationship between rainfall amount and bacterial concentrations at any of the 15 beaches tested was found. Although other researchers have observed a direct positive relationship between rainfall and E. coli levels in beach water, we found no significant relationship for Lake Superior beaches. This is an important finding given the fact that beach closures are often based upon rainfall alone rather than on actual E. coli concentration measurements. This study reinforces the fact that the data obtained at one location should not necessarily be extrapolated to beach closure decisions at other locations.

#### **141 - Modeling the dry-weather tidal cycling of fecal indicator bacteria in surface waters of an intertidal wetland**

Brett F. Sanders, F. Arega, and M. Sutula

[ftp://www.sccwrp.org/pub/download/DOCUMENTS/AnnualReports/2005\\_06AnnualReport/AR0506\\_051-66.pdf](ftp://www.sccwrp.org/pub/download/DOCUMENTS/AnnualReports/2005_06AnnualReport/AR0506_051-66.pdf)

Purpose - Utilize a developed model and apply it to predict the dry-weather tidal cycling of FIB in Talbert Marsh, in response to loads from urban runoff, bird feces and resuspended sediments.

Results - Model predictions show that surface water concentrations of TC, EC, and ENT in the wetland are driven by loads from urban runoff and resuspended wetland sediments. The model more accurately predicts TC than EC or ENT. The crucial role that sediments play in the cycling of FIB is highlighted by this study. Sediments function as a reservoir of FIB that may accumulate FIB due to regrowth or settling, or shed FIB when tidal currents or storm flows scour away or even just disturb surficial particles.

### **115 - Patterns of Antimicrobial Resistance Observed in Escherichia coli Isolates Obtained from Domestic- and Wild-Animal Fecal Samples, Human Septage, and Surface Water**

Raida S. Sayah, J.B. Kaneene, Y. Johnson, and R. Miller

<http://aem.asm.org/content/71/3/1394.full.pdf+html>

Purpose - (i) To identify patterns of antimicrobial agent resistance of E. coli strains obtained from human septage, domestic animals, and wildlife living in the Red Cedar watershed in Michigan, and (ii) to compare these antimicrobial agent resistance patterns with those of E. coli strains obtained from surface water in the same watershed.

Results - Antimicrobial agent resistance was detected in all types of samples collected (Table 4). The most frequently encountered form of resistance in all samples was resistance to tetracycline (27.3%), followed by resistance to cephalothin (22.7%), resistance to sulfisoxazole (13.3%), and resistance to streptomycin (13.1%). Animal fecal samples exhibited resistance to all agents tested, while human septage and river water samples showed resistance to three agents and one agent, respectively.

Resistance to cephalothin was present in all types of samples, while tetracycline resistance and streptomycin resistance were found in all types of samples except river water. Resistance to tetracycline was present in both fecal and farm environment samples from all livestock species, while resistance to trimethoprim-sulfamethoxazole was present in both types of samples from only dairy cattle and equids.

### **142 - Tracking sources of bacterial contamination in stormwater discharges from Mission Bay, California**

Kenneth C. Schiff, and P. Kinney

[ftp://www.sccwrp.org/pub/download/DOCUMENTS/AnnualReports/1999AnnualReport/07\\_ar06.pdf](ftp://www.sccwrp.org/pub/download/DOCUMENTS/AnnualReports/1999AnnualReport/07_ar06.pdf)

Purpose - Identify whether wet-weather discharges were the predominant source of bacterial contamination to receiving waters.

Results - Seasonal cycles were evident, with the highest levels of total coliform, fecal coliform and enterococcus occurring during the wettest months.

### **220 - Microbiological Water Quality at Reference Beaches in Southern California During Wet Weather. Technical Report #448**

Kenneth C. Schiff, J. Griffith, and G. Lyon

[http://www.sccwrp.org:8060/pub/download/DOCUMENTS/TechnicalReports/448\\_reference\\_beach.pdf](http://www.sccwrp.org:8060/pub/download/DOCUMENTS/TechnicalReports/448_reference_beach.pdf)

Purpose - Assess the microbial water quality at reference beaches following wet weather events in southern California.

Results - Based on the results from this study, natural contributions of nonhuman fecal indicator bacteria were sufficient to generate exceedances of the State of California water quality thresholds during wet weather.

### **145 - Water Quality Indicators and the Risk of Illness in Non-Point Source Impacted Recreational Waters**

Kenneth C. Schiff, S.B. Weisberg and J.M. Colford Jr.

<ftp://swrcb2a.waterboards.ca.gov/pub/rwqcb2/TMDL-WEF/5d.pdf>

Purpose - Determine if: 1) water contact increased the risk of illness in the two weeks following exposure to water in Mission Bay? and 2) did the risk of illness increase with increasing levels of microbial indicators of water quality?

Results - Outside of skin rash and diarrhea, there was no statistically increased risk of 12 other symptoms, including highly credible gastrointestinal illness (HCGI). These results contrast with most other recreational bathing studies, most likely because of the lack of human sources of fecal pollution.

### **165 - Variation of microorganism concentrations in urban stormwater runoff with land use and seasons**

A. Selvakumar, and M. Borst

<http://www.iwaponline.com/jwh/004/0109/0040109.pdf>

Purpose - This study investigates if variations in concentrations of microorganisms by at least 1/3-log at the 95% level of confidence are potentially attributable to land use and seasons. Differences less than 1/3-log have little practical importance even if there is statistical significance as the sensitivity of the analyses procedure is less than these.

Results - Statistically significant differences were found between land uses for all microorganisms studied except for E. coli. Other than E. coli, the microbial concentrations in stormwater runoff consistently vary within and between land uses. Generally, the concentrations in runoff from high-density residential areas are higher than the concentrations in other tested land uses.

### **222 - Indicator microbes correlate with pathogenic bacteria, yeasts and helminthes in sand at a subtropical recreational beach site**

A.H. Shah, A.M. Abdelzaher, M. Phillips, R. Hernandez, H.M. Solo-Gabriele, J. Kish, G. Scorzetti, J.W. Fell, M.R. Diaz, T.M. Scott, J. Lukasik, V.J. Harwood, S. McQuaig, C.D. Sinigalliano, M.L. Gidley, D. Wanless, A. Ager, J. Lui, J.R. Stewart, L.R. Plano, and L.E. Fleming

<http://www.ncbi.nlm.nih.gov/pubmed/21447014>

Purpose - The objectives of this study were to evaluate the presence and distribution of pathogens in various zones of beach sand (subtidal, intertidal and supratidal) and to assess their relationship with environmental parameters and indicator microbes at a non-point source subtropical marine beach.

Results - Results indicate that indicator microbes may predict the presence of some of the pathogens, in particular helminthes, yeasts and the bacterial pathogen *Staphylococcus aureus* including methicillin-resistant forms. Indicator microbes may thus be useful for monitoring beach sand and water quality at non-point source beaches.

### **132 - Evaluation of conventional and alternative monitoring methods for a recreational marine beach with non-point source of fecal contamination**

Tomoyuki Shibata, H.M. Solo-Gabriele, C.D. Sinigalliano, M.L. Gidley, L.R.W. Plano, J.M. Fleisher, J.D. Wang, S.M. Elmir, G. He, M.E. Wright, A.M. Abdelzاهر, C. Ortega, D. Wanless, A.C. Garza, J. Kish, T. Scott, J. Hollenbeck, L.C. Backer, and L.E. Fleming

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2966524/>

Purpose - Compare enterococci (ENT) measurements based on the membrane filter, ENT(MF) with alternatives that can provide faster results including alternative enterococci methods (e.g. chromogenic substrate (CS), and quantitative polymerase chain reaction (qPCR)), and results from regression models based upon environmental parameters that can be measured in real-time.

Results - In addition to physico-chemical and hydrometeorological parameters, results also suggested that bacterial indicator levels were affected by the numbers of animals on the beach which may also have seasonal patterns associated with their numbers and fecal inputs. Thus, levels of enterococci at non-point source beaches are affected by a myriad of environmental factors and input loadings which are very difficult to capture within simple regression models.

### **223 - Adhesion of *Enterococcus faecalis* in the nonculturable state to plankton is the main mechanisms responsible for persistence of this bacterium in both lake and seawater**

C. Signoretto, G. Burlacchini, M. del Mar Lleò, C. Pruzzo, M. Zampini, L. Pane, G. Franzini, and P. Canepari

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC525140/>

Purpose - In this study we describe the results of the monitoring of the microbiological quality of both freshwater and marine water by applying an approach consisting of detecting both culturable and nonculturable enterococci which are present in water and adherent to the plankton in order to evaluate to what extent the adhesion to plankton and the VBNC state may represent survival strategies and contribute to the formation of environmental reservoirs of these microorganisms.

Results - We show that molecular methods for the detection of enterococci resulted in a higher number of positive samples than the culture method. The most interesting result of this study was the observation that in Lake Garda *E. faecalis* is almost exclusively found either adhering to plankton or in water, and not both. This result was also confirmed by the results in seawater, although not to such an evident extent.

### **123 - TRANSPORT OF FECAL BACTERIA FROM POULTRY LITTER AND CATTLE MANURES APPLIED TO PASTURELAND**

M.L. Soupir, S. Mostaghimi, E.R. Yagow, C. Hagedorn, and D.H. Vaughan

<http://www.environmental-center.com/Files%5C0%5Carticles%5C9338%5CTransportOfFecalBacteria.pdf>

Purpose - An understanding of the overland transport mechanisms from land applied waste is needed to improve design of best management practices (BMPs) and modeling of nonpoint source (NPS) pollution.

Results - Results of this comparative study clearly indicate that cowpies have a greater potential to contribute high fecal bacteria concentrations into streams than the land application of liquid dairy manure or turkey litter, although bacteria concentrations in runoff from all treatments exceeded Federal standards for primary contact in the United States. The relationship between runoff rates and concentrations of the indicator species was dependent upon the animal waste application, the indicator species and antecedent soil moisture conditions.

### **152 - Variability of Indicator Bacteria at Different Time Scales in the Upper Hoosic River Watershed**

Elena Traister, and S.C. Anisfeld

<http://www.forestry.yale.edu/uploads/publications/Anisfeld-pub03.pdf>

Purpose - Evaluate whether the Upper Hoosic River Basin is meeting water quality criteria for indicator bacteria.

Results - Bacterial levels were higher in more developed watersheds; in summer rather than winter; in storms rather than baseflow; and in the early morning rather than afternoon.

### **227- Prevalence of yeasts in beach sand at three bathing beaches in South Florida**

C. Vogel, A. Rogerson, S. Schatz, H. Laubach, A. Tallman, and J. Fell

<http://www.sciencedirect.com/science/article/pii/S004313540700108X>

Purpose - Determine the abundance and types of yeasts in the wet and dry sand of three recreational beaches in South Florida.

Results - While definitive statements cannot be made, high levels of yeasts may have a deleterious bearing on human health and the presence of such a diverse aggregation of species suggests that yeasts could have a role as indicators of beach health.

### **224 - Effect of waterfowl (*Anas platyrhynchos*) on indicator bacteria populations in a recreational lake in Madison, Wisconsin**

J.H. Standridge, J.J. Delfino, L.B. Kleppe, and R. Butler

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC243530/pdf/aem00202-0205.pdf>

Purpose - Determine the level of effect that waterfowl has on the water quality of a Madison, WI lake.

Results - The most common human health hazard associated with ducks is swimmer's itch, or echinostoma revolutum (12). The duck tapeworm can also occasionally infect humans (4). Ducks have often been implicated as carriers and disseminators of Salmonella (1, 3, 11, 12, 16, 17). The occurrence of these zoonoses indicates that fecal contamination from ducks is a human health hazard and that beach closings based on the presence of high counts of fecal coliform indicator bacteria are warranted. Future surveys aimed at detecting the possible presence of Salmonella in the Vilas Park beach area are indicated.

### **228 - Estimation of enterococci input from bathers and animals on a recreational beach using camera images**

J.D. Wang, H.M. Solo-Gabriele, Am. M. Abdelzher, and L.E. Fleming

<http://www.sciencedirect.com/science/article/pii/S0025326X10001062>

Purpose - Develop a counting methodology to better understand non-point source load impacts. Enterococci inputs to the study beach site (located in Miami, FL) are dominated by non-point sources (including humans and animals).

Results - Enterococci source functions were computed from the observed number of unique individuals for average days of each month of the year, and from average load contributions for humans and for animals. Results indicate that dogs represent the larger source of enterococci relative to humans and birds.

### **229 - Hand-mouth transfer and potential for exposure to E. coli and F+ coliphage in beach sand, Chicago, Illinois**

R.L. Whitman, K. Przybyla-Kelly, D.A. Shively, M.B. Nevers, and M.N. Byappanahalli

<http://www.ncbi.nlm.nih.gov/pubmed/19590129>

Purpose - Examine the transferability of Escherichia coli and F+ coliphage (MS2) from beach sand to hands in order to estimate the potential subsequent health risk.

Results - Using dose-response estimates developed for swimming water, it was determined that the number of individuals per thousand that would develop gastrointestinal symptoms would be 11 if all E. coli on the fingertip were ingested or 33 if all E. coli on the hand were ingested. These results suggest that beach sand may be an important medium for microbial exposure; bacteria transfer is related to initial concentration in the sand; and rinsing may be effective in limiting oral exposure to sand-borne microbes of human concern.

### **169 - Microbial load from animal feces at a recreational beach**

M.E. Wright, H.M. Solo-Gabriele, S. Elmir, and L.E. Fleming

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2771205/pdf/nihms138348.pdf>

Purpose - The goal of this study was to quantify the microbial load (enterococci) contributed by the different animals that frequent a beach site.

Results - The highest enterococci concentrations were observed in dog feces with average levels of  $3.9 \times 10^7$  CFU/g; the next highest enterococci levels were observed in birds averaging  $3.3 \times 10^5$  CFU/g. The lowest measured levels of enterococci were observed in material collected from shrimp fecal mounds (2.0 CFU/g). A comparison of the microbial loads showed that 1 dog fecal event was equivalent to 6940 bird fecal events or  $3.2 \times 10^8$  shrimp fecal mounds. Comparing animal contributions to previously published numbers for human bather shedding indicates that one adult human swimmer contributes approximately the same microbial load as one bird fecal event. Given the abundance of animals observed on the beach, this study suggests that dogs are the largest contributing animal source of enterococci to the beach site.

### **231 - Microbial load from animal feces at a recreational beach**

M.E. Wright, H.M. Solo-Gabriele, S. Elmir, and L.E. Fleming

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2771205/>

Purpose - Quantify the microbial load (enterococci) contributed by the different animals that frequent a beach site.

Results - Results from this study provide evidence that dog feces represent the largest animal source to the study site. Improved management of dog feces at the beach could potentially reduce enterococci inputs to the beach, thereby decreasing the number of advisories for beach sites which are frequented by significant numbers of dogs.

### **8 - Are microbial indicators and pathogens correlated? A statistical analysis of 40 years of research**

J. Wu, S. C. Long, D. Das and S. M. Dorner

<http://www.iwaponline.com/jwh/up/wh2011117.htm>

Purpose - The data were analyzed to assess factors affecting correlations using a logistic regression model considering indicator classes, pathogen classes, water types, pathogen sources, sample size, the number of samples with pathogens, the detection method, year of publication and statistical methods.

### **136 - Monitoring and Modeling Non-Point Source Contributions of Host-Specific Fecal Contamination in San Pablo Bay**

Stefan Wuertz, F.A. Bombardelli, K. Sirikanchana, and D. Wang

<http://escholarship.org/uc/item/8tk0z6p0.pdf>

Purpose - This study employed mathematical and numerical transport models in concert with new molecular techniques to (i) characterize the sources of fecal contamination of water bodies and (ii) quantify the loads and distributions of *Bacteroidales* marker DNA sequences originating from different animal hosts in San Pablo Bay.

Results - Microbial source tracking using fecal *Bacteroidales* is an effective way to monitor fecal pollution of coastal waters. Low levels of the universal genetic marker are ubiquitous throughout

San Pablo Bay. The human marker BacHum-UCD was found in 75% of all samples but no cow- and almost no dog-specific marker was detected.

**234 - Growth of enterococci in unaltered, unseeded beach sands subjected to tidal wetting**

K.M. Yamahara, S.P. Walters, and A.B. Boehm

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2655449/>

Purpose - To establish if naturally occurring enterococci can replicate in beach sands under environmentally relevant conditions.

Results - The results provide evidence that enterococci may not be an appropriate indicator of enteric disease risk at recreational beaches subject to nonpoint sources of pollution.

**170 - A water quality modeling study of non-point sources at recreational marine beaches**

X. Zhu, J.D. Wang, H.M. Solo-Gabriele, L.E. Fleming

<http://www.sciencedirect.com/science/article/pii/S0043135411001266>

Purpose - A model study was conducted to understand the influence of non-point sources including bather shedding, animal fecal sources, and near shore sand, as well as the impact of the environmental conditions, on the fate and transport of the indicator microbe, enterococci, at a subtropical recreational marine beach in South Florida.

Results - Enterococci released from beach sand during high tide caused mildly elevated concentration for a short period of time (ten to twenty of CFU/100 ml initially, reduced to 2 CFU/100 ml within 4 h during sunny weather) similar to the average baseline numbers observed at the beach. Bather shedding resulted in minimal impacts (less than 1 CFU/100 ml), even during crowded holiday weekends. In addition, weak current velocity near the beach shoreline was found to cause longer dwelling times for the elevated concentrations of enterococci, while solar deactivation was found to be a strong factor in reducing these microbial concentrations.