MONITORING REPORT

FOR

COUNTYWIDE DRY WEATHER BACTERIA SOURCE IDENTIFICATION STUDY

Prepared by:

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1. Introduction and Goals of the Study

Ventura Countywide Stormwater Quality Management Program recognizes that elevated fecal indicator bacteria (FIB) concentrations in municipal separate storm sewer systems (MS4) and receiving waters are among its top water quality concerns. Elevated FIB concentrations associated with human fecal sources (e.g. sewage) are correlated with increased bather illness rates, causing gastrointestinal and other diseases. While FIB derived from fresh cattle waste pose similar risk levels to humans as those from human waste, FIB derived from other warm-blooded animals (e.g. birds, dogs, wildlife) pose significantly lower risks, at equivalent FIB concentrations. Therefore, optimal protection of human health requires identification of sources of fecal pollution, so that high priority sources can be targeted for remediation, and resources are not wasted on remediating innocuous sources.

The goal of this study is to determine the importance of human, dog and birds as sources of fecal indicator bacteria to Ventura County MS4.

2. Methods

2.1. Sampling summary

As the goal of the study involves a regional assessment of fecal sources, sampling design included probabilistic sampling of MS4 locations. Probabilistic sampling avoids bias in site selection, allows representative sampling of population, and therefore allows extrapolation of monitoring results to population (i.e. Countywide MS4). Existing major outfall locations were also included as targeted locations, as these were chosen to represent co-permittee MS4's for monitoring under the 2009 Ventura County stormwater NPDES Permit, and a 5-yr record of FIB monitoring is available.

All monitoring was performed between April and October of 2014. At each locations, grab samples were collected for analysis of *E. coli* (IDEXX Quanti-Tray/2000) and host-specific genetic markers. Grab samples were immediately stored on ice, and analyzed or filtered within 6 hours of collection. For DNA analysis, 100 ml of sample was filtered on 0.45 µm polycarbonate membrane filters at the Ventura County Public Health Laboratory and stored at -80°C. Archived filters were shipped on dry ice to Weston Laboratories (Carlsbad, CA) for analysis of human (HF183 qPCR), dog (DogBact qPCR) and bird (GFD SYBRAvian qPCR) host-specific markers. Field measurements included dissolved oxygen, specific conductance, salinity, water temperature and pH.

2.2. Selection of sampling locations

Targeted locations consist of the 11 major outfall sites, each sampled twice in 2014, for a total of 22 samples. In case major outfall locations were not flowing, backup sites (as defined for 2009 Ventura County stormwater NPDES permit) were sampled.

The target design for probabilistic locations includes 22 MS4 storm drains, 22 MS4 open channels, and 10 control locations. Each probabilistic locations was sampled once in 2014, for a total of 54 samples. Probabilistic MS4 locations were stratified based on co-permittee jurisdictions, with the number of MS4 locations for each co-permittee based on population and MS4 size. Probabilistic control locations were stratified based on watershed, with number of control locations for each watershed based on watershed size (5 for Santa Clara River, 3 for Calleguas Creek, 1 for Ventura River, 1 for coastal watersheds). Final MS4 sample allocation is summarized in Table 1.

Table 1. Target number of MS4 sampling locations broken down per co-permittee and sample type. Number of samples per year is indicated in parentheses).

Jurisdiction	Probabilistic MS4 storm drain (1)	Probabilistic MS4 open channel (1)	Targeted MS4 major outfall (2)	Total no. of MS4 samples
Ojai	1	1	1	4
Moorpark	1	1	1	4
Port Hueneme	1	1	1	4
Santa Paula	1	1	1	4
Fillmore	1	1	1	4
Camarillo	2	2	1	6
Oxnard	3	3	1	8
Ventura	3	3	1	8
Thousand Oaks	3	3	1	8
Simi Valley	3	3	1	8
County Unincorporated	3	3	1	8
TOTAL NUMBER OF SAMPLES	**22**	**22**	**22**	**66**

Probabilistic sampling locations for 2014 were determined as follows:

1) Define site selection criteria to determine population of probabilistic locations for MS4 storm drains, MS4 open channels, and control locations (Table 2).
2) Map population of probabilistic locations in GIS, using cities' and county's storm drain and redline channel layers (Fig. 1).
3) Stratify populations of MS4 and control probabilistic locations based on co-permittee jurisdictions and watershed, respectively.
4) Randomly select 2014 sampling locations from population strata. Randomization was performed by generating a random number for each location using the excel RAND function, and sorting locations according to random number values, creating list of samples for each stratum in random order.
5) Samples for 2014 were selected by going down randomized location list, until desired number of samples was obtained (e.g. 3 MS4 storm drain samples and 3 MS4 open channel samples for Oxnard). Sampling locations were selected first using desktop assessment, and if locations were on private properties or had difficult access, locations were discarded and next sample on list was selected. Additionally, if field visits showed locations were inaccessible or not flowing, locations were discarded and next sample on list was selected for subsequent field visit. Sampling of adjacent locations was avoided if possible. If adjacent locations were the only ones available, sampling was performed on separate days.

Table 2. Selection criteria for defining populations of probabilistic sampling locations.

Population	Criteria
MS4 storm drains	• Storm drain manholes and outfalls only • One location every 4000 – 6500 ft section of storm drain main • Downstream of at least 1000 ft storm drain main • Receives mostly urban runoff • Receives no agriculture runoff or baseflow • Likely flow during spring/summer • Allows safe access (exclude private property, busy road intersections,…)
MS4 open channels	• Concrete and soft-bottom open channels within city boundaries or County urban infill areas (mostly redline channels) • One location every 4000 – 6500 ft of channel within city boundaries or County urban infill areas • Downstream of at least 3000 ft of open channel within city boundaries (excludes County unincorporated locations) • County unincorporated locations: downstream of at least 2000 ft of open channel within County urban infill areas • County unincorporated locations: downstream of at least 1000 ft of MS4 storm drain main • No tidal influence • Receives mostly urban runoff • Receives no agriculture runoff or baseflow • Likely flow during spring/summer • Allows safe access (exclude private property, busy road intersections,…)
Control locations	• Channels and creeks upstream of co-permittee jurisdictions • Select from redline channels • Drainage area land use only includes one or more of: o vacant undifferentiated o water storage facilities o irrigated cropland and improved pasture land o orchards and vineyard o up to 2 parcels rural residential, not adjacent to channel

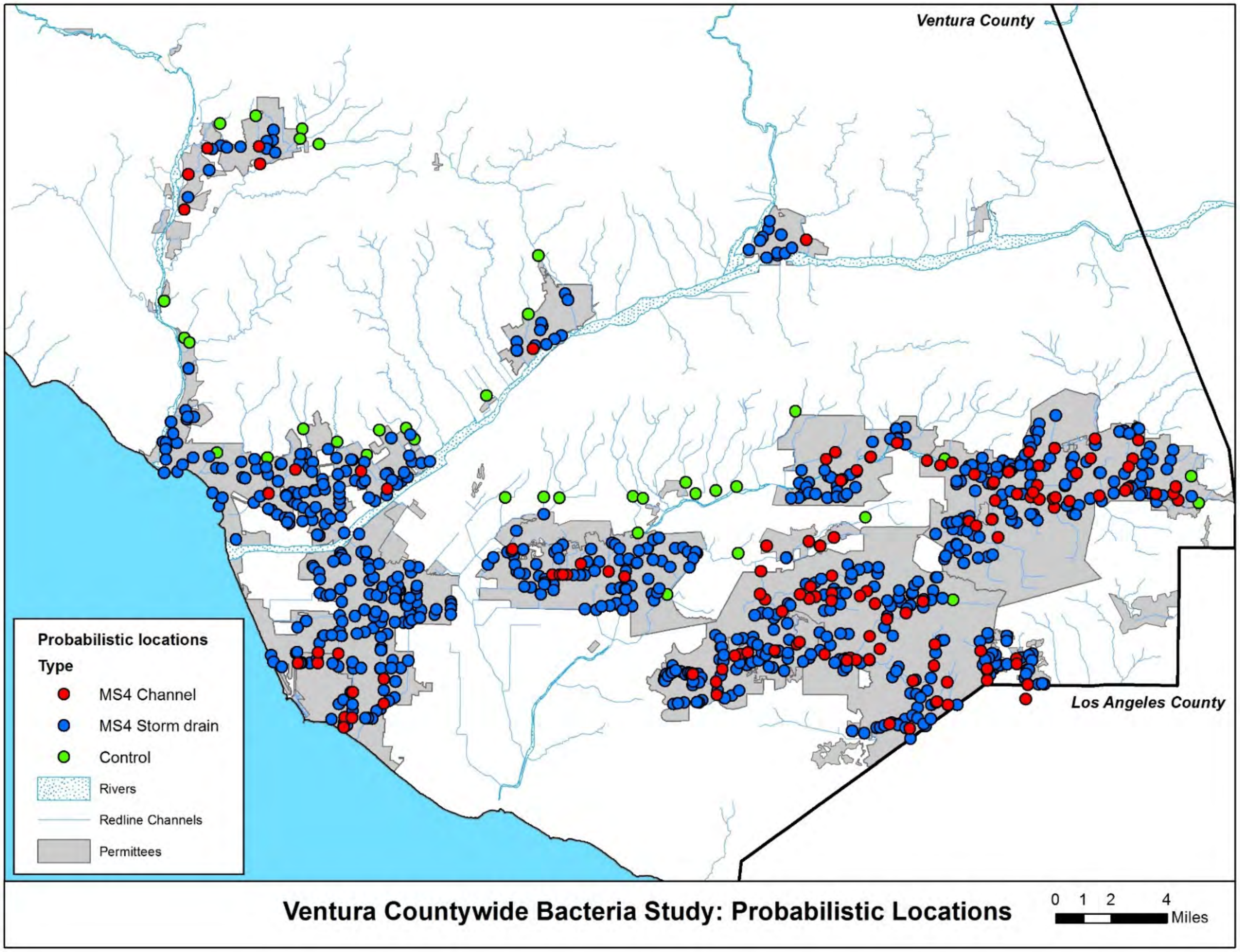

Figure 1. Population of probabilistic locations from which 2014 sampling locations were randomly selected.

3. Results

3.1. Field Sampling

The number of samples collected was very close to the target (Table 3). The lower number of non-MS4 control samples was related to dry conditions in many channels upstream of MS4s. Also, many MS4 locations were dry, especially in County unincorporated, Camarillo and Ojai. Probabilistic and targeted sampling locations for 2014 are shown in Fig. 2.

Table 3. Summary of 2014 field sampling versus targets. No. of dry locations indicates how many locations were visited and were dry before sampling was successful.

Watershed/co-permittee	Sample type	No. samples target	No. samples collected	No. dry locations
Calleguas Creek	Non-MS4 control	5	2	16
Santa Clara River	Non-MS4 control	3	4	4
Ventura River	Non-MS4 control	1	0	8
Coastal watersheds	Non-MS4 control	1	0	3
Ventura	MS4 storm drain	3	4	1
	MS4 open channel	3	3	2
	Major outfall	2	2	
County unincorporated	MS4 storm drain	3	3	5
	MS4 open channel	3	3	7
	Major outfall	2	2	
Oxnard	MS4 storm drain	3	3	0
	MS4 open channel	3	3	2
	Major outfall	2	2	
Thousand Oaks	MS4 storm drain	3	3	1
	MS4 open channel	3	3	0
	Major outfall	2	2	
Simi Valley	MS4 storm drain	3	3	0
	MS4 open channel	3	3	0
	Major outfall	2	2	
Camarillo	MS4 storm drain	2	2	0
	MS4 open channel	2	2	4
	Major outfall	2	2	
Santa Paula	MS4 storm drain	1	1	1
	MS4 open channel	1	1	0
	Major outfall	2	2	
Fillmore	MS4 storm drain	1	1	0
	MS4 open channel	1	1	0
	Major outfall	2	2	
Ojai	MS4 storm drain	1	1	2
	MS4 open channel	1	1	1
	Major outfall	2	2	
Moorpark	MS4 storm drain	1	1	0
	MS4 open channel	1	1	1
	Major outfall	2	2	
Port Hueneme	MS4 storm drain	1	1	0
	MS4 open channel	1	1	0

	Major outfall	2	2	

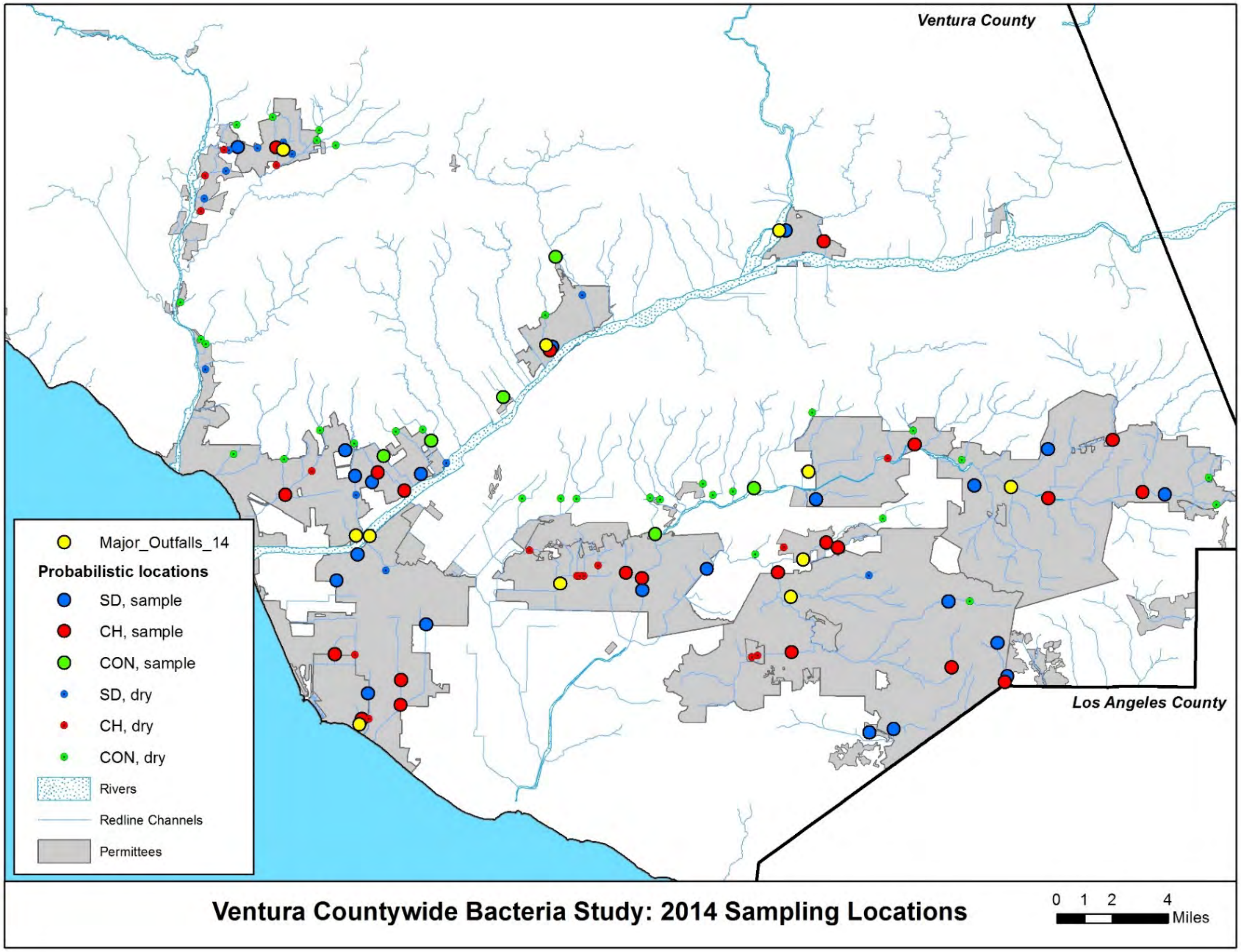

Figure 2. Probabilistic and targeted (major outfalls) sampling locations for 2014. Locations that were visited but were dry are shown using smaller symbols.

3.1. *E. coli* concentrations

Results for *E. coli* are included as Appendix A. *E. coli* concentrations are summarized here using charts. When grouping probabilistic and targeted samples per sample type (Fig. 3), it can be observed that *E. coli* concentrations are higher in MS4 storm drains compared to MS4 open channels (Kruskall-Wallis, p = 0.024), potentially because *E. coli* concentrations decay downstream from the storm drain source. *E. coli* concentrations are not significantly different in MS4 samples and non-MS4 control samples (Kruskal-Wallis, p = 0.24). Note that only six non-MS4 samples were collected, and increased sample size may show significant differences as median value of non-MS4 samples is (193 mpn/100 ml) is about 3 times lower compared to MS4 samples (609 mpn/100 ml).

Grouping samples per jurisdiction (Fig. 4) shows that significant differences in *E. coli* concentrations occur (samples are shown in decreasing order of median concentrations). For example, *E. coli* concentrations in samples from Camarillo were much higher compared to other jurisdictions, while concentrations in Moorpark samples were much lower.

Outfall *E. coli* concentrations collected during this study were very similar to historic outfall concentrations (2009-2014) (Fig. 5), showing this study's monitoring was representative of historic bacteria water quality. Comparing *E. coli* concentrations from this study's probabilistic locations to this year's outfall locations shows more exceedances in the former (80% vs. 60%), suggesting overall outfall exceedance rates are slightly low biased compared to Countywide MS4 exceedance rates.

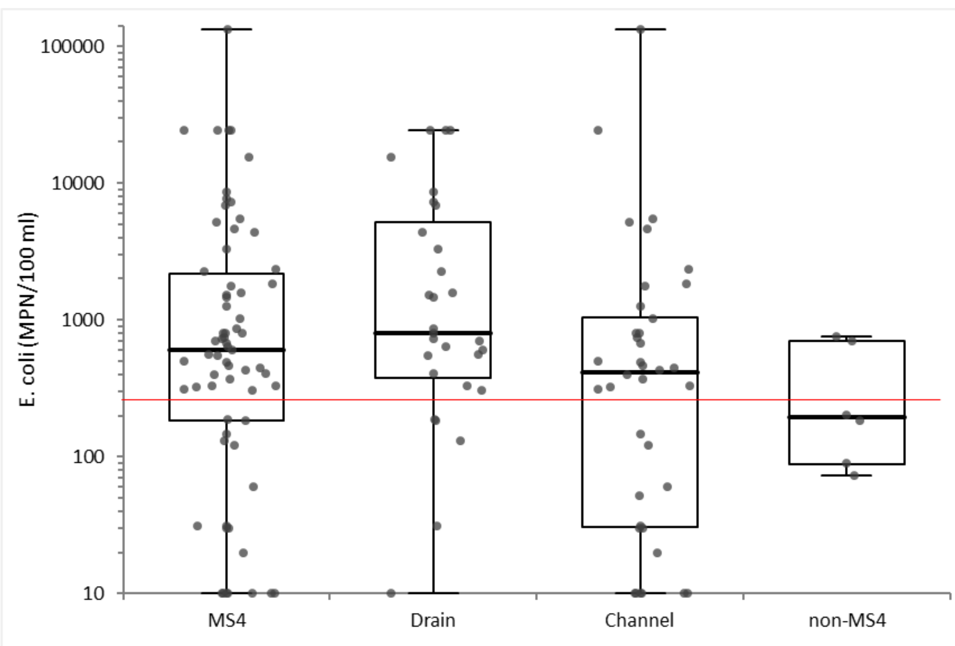

Figure 3. ***E coli*** **concentrations grouped per sample type: all MS4 samples (MS4), MS4 storm drain samples (Drain), MS4 open channel samples (Channel) and non-MS4 control samples (non-MS4). Single sample maximum concentration objective is indicated by red line.**

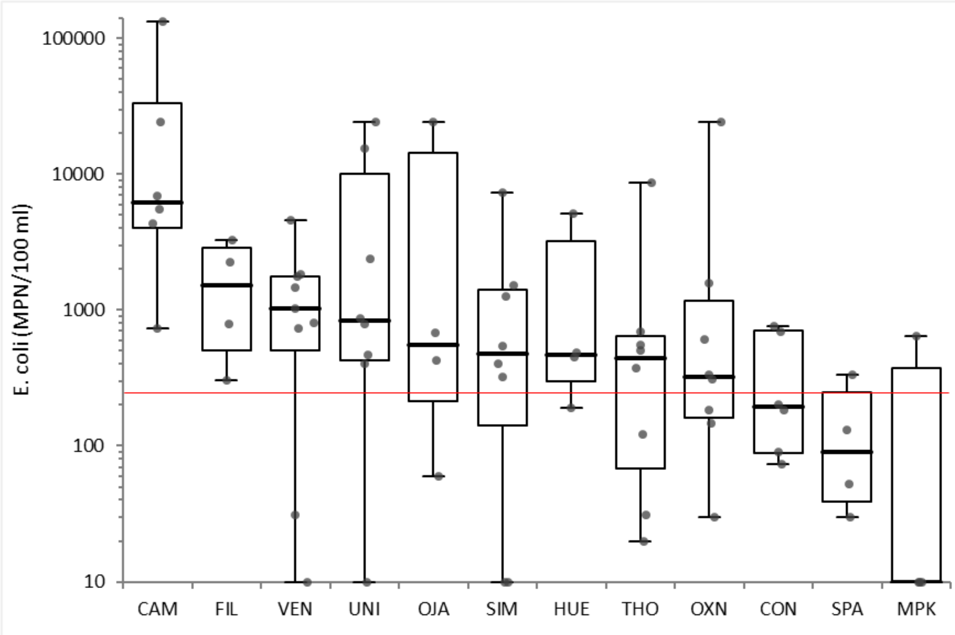

Figure 4. ***E coli*** **concentrations grouped per jurisdiction. Single sample maximum concentration objective is indicated by red line.**

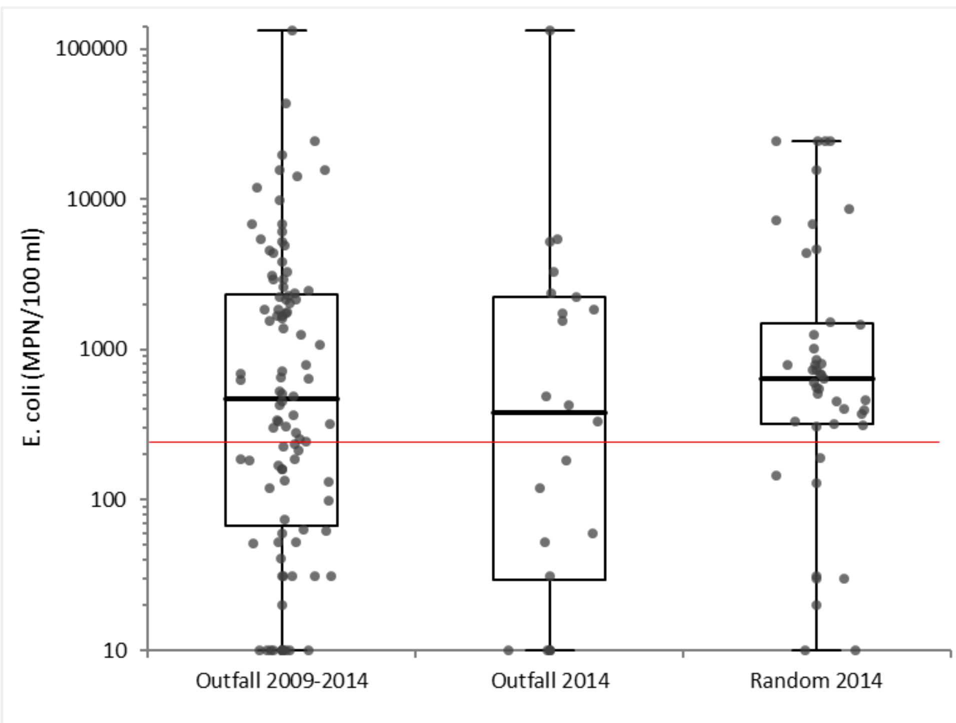

Figure 5. ***E coli*** **concentrations in major outfall samples collected during 2009-2014 compared to outfall samples collected in this study (Outfall 2014) and probabilistic samples collected in this study (Random 2014). Single sample maximum concentration objective is indicated by red line.**

3.2. Host-specific markers

Results for host specific markers are included as Appendix A, and summarized in Table 4.

Table 4. Summary of number of samples with detectable and quantifiable concentrations of host-specific markers

Sample Type	No. of samples	No. of detects/quantified Human	No. of detects/quantified Dog	No. of detects/quantified Bird
Random MS4 storm drains	23	0/0	2/2	8/5
Random MS4 open channels	22	0/0	3/1	9/6
Targeted MS4 outfalls	22	0/0	2/0	6/5
Non-MS4 control	6	0/0	0/0	3/2
Field blank	4	0/0	1/0	1/1

3.2.1 Human markers

Human marker concentrations were below detection limit in all 2014 samples, including MS4 samples, control samples and field blanks.

3.2.2 Dog markers

Dog markers were detected in 7 of the 67 MS4 samples, or approximately 10% of samples. Only 3 of the detected MS4 samples were within the quantifiable concentration range:

- THO-CH-15 (Lower Skeleton Canyon): 1,537 dog markers/100 ml
- UNI-SD-39 (Oak Park Lindero outfall): 1,647 dog markers/100 ml
- VEN-SD-50 (S. Saticoy Ave storm drain manhole): 83,546 dog markers/100 ml

3.2.3 Bird markers

Bird markers were frequently detected in all types of samples: 34% of MS4 samples, 50% of non-MS4 control samples and 25% of field blank samples (1 of the 4 blanks). Most of the bird marker concentrations were in the quantifiable range (Fig. 6). While bird markers concentrations were relatively high, they did not correlate with *E. coli* concentrations (Fig. 7), suggesting bird waste is not the predominant source of *E. coli*.

Based on discussions with analytical lab (Weston Solutions), the most logical explanation for the high bird marker concentration in one field blank sample was sample mix-up. There is no known source of bird markers in the lab environment (as opposed to human markers), contamination with bird marker genes had never been observed before by the analytical lab, and the lab noted that field blank extract was colored, while blank samples should be clear. Additional negative control samples should be analyzed to verify absence of bird marker.

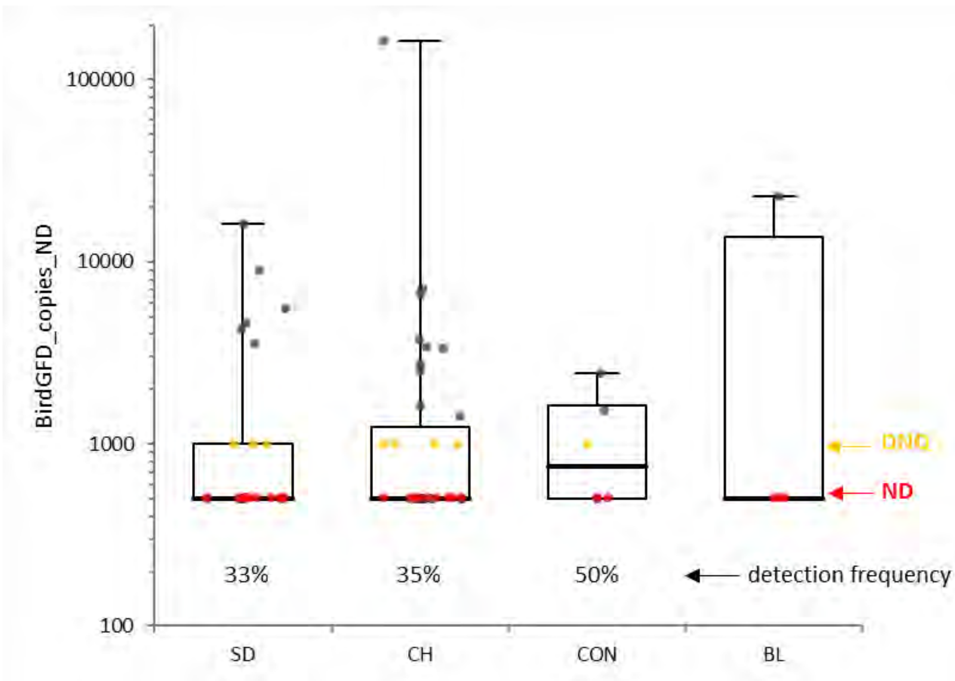

Figure 6. Bird marker concentrations in MS4 storm drain (SD), MS4 open channel (CH), non-MS4 control (CON) and field blank (BL) samples. Levels substituted for non-detects (ND) and detectable but non-quantifiable (DNQ) results are indicated.

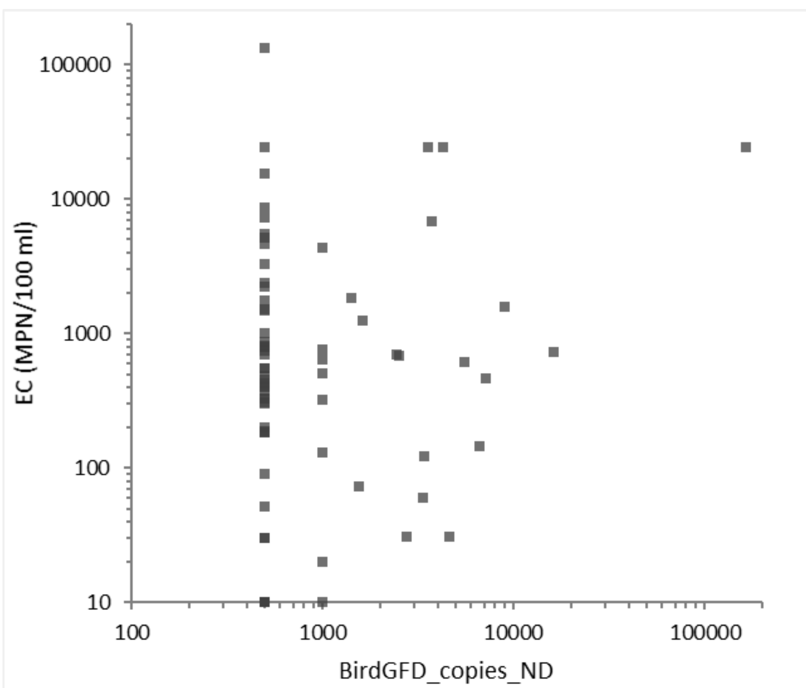

Figure 7. Correlation of *E. coli* and bird marker concentrations for all MS4 and non-MS4 control samples. Bird marker concentrations at detection limit and in the detectable but non-quantifiable range were plotted at 500 copies/100 ml and 1000 copies/100 ml, respectively.

3.2.4 Identification of sources of *E. coli*

MS4 and non-MS4 control samples were analyzed for human, dog and bird host-specific markers, all of which were expected to be sources of *E. coli* to dry weather runoff in storm drains, albeit of varying magnitudes. However, human markers were not detected, and dog markers only in 10% of samples. Bird markers were more prevalent, but still did not correlate with *E. coli* concentrations.

In 60% of samples, none of the markers tested for were detected, while *E. coli* concentrations were as high in those samples compared to samples where one or more markers were detected (Fig. 8). This suggests sources of *E. coli* remain mostly unidentified, but are not associated with humans, dogs or birds.

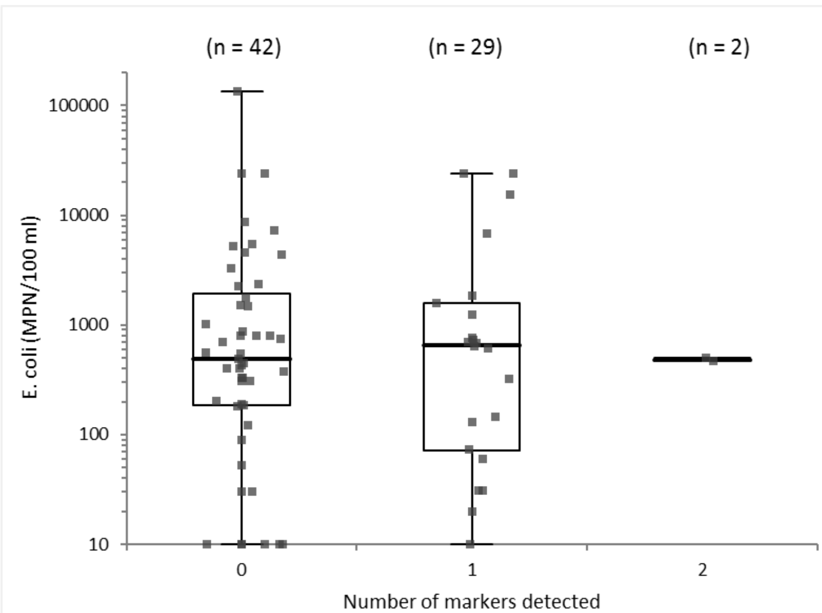

Figure 8. *E. coli* concentrations for all samples grouped according to number of markers detected in the sample.

3.2.4 Additional quality control samples

Given that none of the samples were positive for human markers, which was unexpected, and only few for dog markers, additional positive control samples were prepared and analyzed for these markers. In addition, extra field blank samples were prepared, to test presence of dog and bird markers, because currently available field blank samples included some positives for these markers. These samples are summarized in Table 5.

Expected results are:

1) All human positive control samples are positive for human HF183 marker. If only the highest concentration sample is positive, that is still acceptable. Such outcome will show that HF183 is sensitive enough to detect human waste, and the fact that none of the 2014 samples was positive is a valid result.

2) Both or only highest concentration dog positive control samples are positive for dog DogBact marker. Such outcome will show that DogBact is sensitive enough to detect dog waste, and the fact that few 2014 samples were positive is a valid result. Measured *E. coli* concentrations in these control samples were lower than expected, and it is possible none of the dog positive control samples are positive for dog markers. In that case, preparation and analysis of more concentrated samples should be considered to better determine detection limit. In any case, samples positive for dog markers in 2014 samples are valid.
3) Field blank samples are negative for dog DogBact and bird BirdGFD markers. This would imply that the high concentration of bird markers found in one 2014 field blank is due to sample mix-up. If one or two DNQ results are observed, that's acceptable, but it implies DNQ results in real samples should not be considered positives. If quantifiable bird marker concentrations are found, field and/or lab procedures should be assessed.

Table 5. Summary of additional quality control samples, including amount of fecal material added (wet weight), measured *E. coli* concentrations, and planned additional marker analysis.

<table>
<tr><th>Sample ID</th><th>Description</th><th>Fecal concentration</th><th>E. coli (mpn/100 ml)</th><th>Additional marker analysis</th></tr>
<tr><td>HC1000</td><td rowspan="2">Human pos. control (OVSD raw influent) in Ventura River water (ME-VR2)</td><td>0.3 ml sewage/l sample</td><td>1607</td><td>Human HF183</td></tr>
<tr><td>HC100</td><td>0.03 ml sewage/l sample</td><td>315</td><td>Human HF183</td></tr>
<tr><td>HP1000</td><td rowspan="2">Human pos. control (OVSD raw influent) in sterile phosphate buffered saline</td><td>0.3 ml sewage/l sample</td><td>3654</td><td>Human HF183</td></tr>
<tr><td>HP100</td><td>0.03 ml sewage/l sample</td><td>309</td><td>Human HF183</td></tr>
<tr><td>DC1000</td><td rowspan="2">Dog pos. control (composite of 3 individuals) in Ventura River water (ME-VR2)</td><td>30 µg dog waste/l sample</td><td>146</td><td>DogBact</td></tr>
<tr><td>DC100</td><td>3 µg dog waste/l sample</td><td>86</td><td>DogBact</td></tr>
<tr><td>DP1000</td><td rowspan="2">Dog pos. control (composite of 3 individuals) in sterile phosphate buffered saline</td><td>30 µg dog waste/l sample</td><td>108</td><td>DogBact</td></tr>
<tr><td>DP100</td><td>3 µg dog waste/l sample</td><td>0</td><td>DogBact</td></tr>
<tr><td>FB-1</td><td rowspan="4">Field blank</td><td rowspan="4">n/a</td><td rowspan="4">n/a</td><td>DogBact, BirdGFD</td></tr>
<tr><td>FB-2</td><td>DogBact, BirdGFD</td></tr>
<tr><td>FB-3</td><td>DogBact, BirdGFD</td></tr>
<tr><td>FB-4</td><td>DogBact, BirdGFD</td></tr>
</table>

3.2.5 Horse PCR assay testing

Co-permittees expressed interest in testing for horse waste in dry weather runoff samples. However, analytical lab (Weston Solutions) had concerns that current horse PCR method is not sufficiently sensitive to detect environmentally relevant concentrations. Therefore, dilution series of horse waste were prepared in three different matrixes: Ventura River water at ME-VR2 location (VR samples), storm drain water at location upstream of MO-VEN just downstream of railroad culvert (VEN samples), and sterile phosphate buffered saline as a control matrix (P samples). Horse waste was collected from 5 individual horses at the California Coastal Horse Rescue facility near Ojai, CA, and added in equal proportions to control samples. Table 6 summarized sample IDs, horse waste concentrations (sum of 5 individuals) and measured *E. coli* concentrations. All samples will be analyzed for horse PCR in duplicate.

E. coli concentrations in prepared samples were much lower than expected, even for samples where presence of horse waste was clearly visible (Fig. 9). For example, horse waste was easily observed visually for sample VR-4, while *E. coli* concentrations associated with that dilution was only 554 mpn/100 ml, and 545 mpn/100 ml in the control matrix sample P4 with same amount of horse waste (in which case the matrix water did not add additional *E. coli*). Therefore, the horse assay needs to be positive for the VR4, VR3, VEN4, VEN3 samples in order to be useful for field applications.

Table 6. Summary of horse PCR method testing samples, including amount of fecal material added (wet weight), and measured *E. coli* concentrations. All samples will be analyzed in duplicate

Sample ID	Fecal concentration	*E. coli* (mpn/100 ml)
VR4	2 g horse waste/l sample	554
VR3	200 mg horse waste/l sample	122
VR2	20 mg horse waste/l sample	74
VEN4	2 g horse waste/l sample	1785
VEN3	200 mg horse waste/l sample	2489
VEN2	20 mg horse waste/l sample	1793
P4	2 g horse waste/l sample	545
P3	200 mg horse waste/l sample	52
P2	20 mg horse waste/l sample	0

Figure 7. Dilution series of horse positive control samples in VR matrix sample.

4. Conclusions

The absence of human markers countywide suggests the risk to human health associated with elevated *E. coli* levels in storm drains and is lower than currently assumed, and current water quality criteria may be overprotective. The results should be verified by analyzing positive control samples for human markers.

Dog markers were detected in about 10% of samples, usually in low quantities, suggesting dog waste is only a minor source of *E. coli* in MS4 and non-MS4 control samples countywide. The results should still be verified by analyzing positive control samples and field blanks for dog markers.

Bird markers were detected in samples countywide, making birds the most significant source of *E. coli* positively identified in Ventura County so far. Still, birds did not appear a dominant source of *E. coli*, given the absence of any correlation between *E. coli* and marker concentrations. Results should be verified by analyzing additional field blanks for bird markers.

Dominant sources of *E. coli* remain unclear, despite countywide analysis of human, dog and bird markers. Potential other sources include wildlife, biofilm growth, and locally perhaps horse and cattle. Source control for wildlife and biofilm-derived *E. coli* would be very challenging. All of these potential sources, except cattle, pose much lower risks to human health compared to human waste.

Results from this study, once finalized, can be used to:

- Inform public and other stakeholders on countywide MS4 bacterial water quality and potential public health risks
- Set regional benchmark for bacterial water quality
- Inform local source identification studies
- Support need for site-specific objectives and Quantitative Microbial Risk Assessment
- Identify science gaps, for example new methods for analyzing wildlife genetic markers or testing biofilm growth.

				E coli		Human HF183	DogBact		BirdGFD		
Date	Jurisdiction	Type	Loc_ID	sign	MPN/100 ml	copies/100 ml	copies/100 ml	stdev	copies/100 ml	stdev	field_comments
4/25/2014	CAM	CH	MO-CAM	=	5476	ND	ND		ND		
8/6/2014	CAM	CH	MO-CAM	=	133400	ND	ND		BDL		
8/7/2014	CAM	CH	CAM-CH-5	>	24196	ND	ND		163207	8214	
8/7/2014	CAM	SD	CAM-SD-46	=	728	ND	ND		16257	11619	
8/7/2014	CAM	SD	CAM-SD-71	=	4352	ND	BDL		DNQ		
10/2/2014	CAM	CH	CAM-CH-6	=	6867	ND	ND		3707	225	Some algae
4/23/2014	FIL	SD	MO-FIL	=	3298	ND	ND		BDL		
8/5/2014	FIL	SD	MO-FIL	=	2247	ND	ND		BDL		
10/1/2014	FIL	SD	FIL-SD-0	=	305	ND	ND		BDL		Sediment, trash
10/1/2014	FIL	CH	FIL-CH-0	=	794	ND	ND		ND		
4/30/2014	HUE	CH	MO-HUE	=	5172	ND	ND		ND		
8/6/2014	HUE	CH	Hueneme-3	=	488	ND	DNQ		BDL		
8/26/2014	HUE	CH	HUE-CH-2	=	450	ND	ND		BDL		Stagnant, trash
8/28/2014	HUE	SD	HUE-SD-5	=	189	ND	ND		BDL		
8/5/2014	MPK	CH	Moorpark-2	<	10	ND	ND		DNQ		
9/4/2014	MPK	CH	MPK-CH-1	=	10	ND	ND		BDL		
9/4/2014	MPK	CH	Moorpark-2	=	10	ND	ND		BDL		Trash
9/30/2014	MPK	SD	MPK-SD-19	=	637	ND	ND		DNQ		
8/4/2014	OJA	CH	OJA-CH-0	=	677	ND	BDL		2528	1899	
8/4/2014	OJA	SD	OJA-SD-3	>	24196	ND	ND		3555	47	
8/5/2014	OJA	CH	Ojai-6	=	60	ND	BDL		3354	3261	
8/13/2014	OJA	CH	Ojai-6	=	426	ND	ND		ND		
8/26/2014	OXN	CH	OXN-CH-5	=	146	ND	BDL		6590	768	
8/28/2014	OXN	CH	OXN-CH-2	=	30	ND	ND		ND		Algae
9/9/2014	OXN	SD	Oxnard-2	=	1565	ND	BDL		9004	4444	Algae, trash
9/9/2014	OXN	SD	OXN-SD-41	=	609	ND	BDL		5540	3136	
9/9/2014	OXN	CH	OXN-CH-4	=	311	ND	DNQ		ND		Algae, trash
9/11/2014	OXN	SD	Oxnard-2	=	183	ND	DNQ		ND		Algae, trash
9/11/2014	OXN	SD	OXN-SD-7	>	24196	ND	ND		4276	1801	Human feces (sampled just upstream), trash
10/2/2014	OXN	SD	OXN-SD-99	=	331	ND	ND		BDL		
4/25/2014	SIM	CH	MO-SIM	<	10	ND	ND		ND		
8/6/2014	SIM	CH	MO-SIM	<	10	ND	BDL		BDL		
8/27/2014	SIM	SD	SIM-SD-46	=	546	ND	ND		ND		
8/27/2014	SIM	CH	SIM-CH-5	=	1250	ND	ND		1614	1522	
8/27/2014	SIM	SD	SIM-SD-121	=	1529	ND	ND		BDL		
8/27/2014	SIM	CH	SIM-CH-38	=	323	ND	ND		DNQ		
8/27/2014	SIM	CH	SIM-CH-17	=	399	ND	ND		ND		
8/27/2014	SIM	SD	SIM-SD-103	=	7270	ND	ND		BDL		
8/5/2014	SPA	CH	Santa Paula-2	=	52	ND	ND		ND		
8/13/2014	SPA	CH	Santa Paula-2	=	332	ND	ND		ND		
8/21/2014	SPA	CH	SPA-CH-0	=	30	ND	ND		ND		
8/21/2014	SPA	SD	SPA-SD-5	=	130	ND	ND		DNQ		
4/25/2014	THO	CH	MO-THO	=	121	ND	ND		3412	146	
8/6/2014	THO	CH	MO-THO	=	31	ND	BDL		2751	420	
8/26/2014	THO	CH	THO-CH-41	=	20	ND	BDL		DNQ		
8/26/2014	THO	CH	THO-CH-15	=	504	ND	1537	267	DNQ		
8/26/2014	THO	SD	THO-SD-134	=	556	ND	ND		BDL		
8/26/2014	THO	CH	THO-CH-5	=	373	ND	ND		BDL		Green algae, lots
9/4/2014	THO	SD	THO-SD-150	=	8664	ND	ND		BDL		Irrigation testing flowing to one catch basin, likely other sources of flow
9/4/2014	THO	SD	THO-SD-158	=	697	ND	ND		ND		
8/6/2014	UNI	CH	Unincorporated-4	<	10	ND	ND		ND		
8/13/2014	UNI	SD	Uni-SD-20	=	862	ND	ND		ND		
8/26/2014	UNI	CH	Unincorporated-4	=	2359	ND	BDL		BDL		
8/27/2014	UNI	CH	UNI-CH-14	=	464	ND	DNQ		7185	4044	
9/4/2014	UNI	SD	UNI-SD-39	=	15531	ND	1647	1184	ND		
9/4/2014	UNI	CH	UNI-CH-8	=	794	ND	ND		BDL		
9/30/2014	UNI	SD	UNI-SD-3	>	24196	ND	ND		ND		~30 bats in manhole, smelly
10/2/2014	UNI	CH	UNI-CH-3	=	404	ND	ND		BDL		

Date	Jurisdiction	Type	Loc_ID	E coli		Human HF183	DogBact		BirdGFD		field_comments
				sign	MPN/100 ml	copies/100 ml	copies/100 ml	stdev	copies/100 ml	stdev	
4/23/2014	VEN	CH	MO-VEN	=	1754	ND	ND		BDL		
8/6/2014	VEN	CH	MO-VEN	=	1829	ND	BDL		1421	837	
8/21/2014	VEN	SD	VEN-SD-20	=	1467	ND	ND		ND		
8/21/2014	VEN	CH	VEN-CH-4	=	738	ND	ND		BDL		
8/21/2014	VEN	CH	VEN-CH-2	=	1017	ND	ND		ND		
9/9/2014	VEN	CH	VEN-CH-3	=	4611	ND	ND		ND		Trash, leaves
10/1/2014	VEN	SD	VEN-SD-50	<	10	ND	83546	13047	ND		
10/1/2014	VEN	SD	VEN-SD-72	=	31	ND	ND		4619	2173	Sediment
10/1/2014	VEN	SD	VEN-SD-90	=	805	ND	ND		BDL		
8/7/2014		CON	CON-CC-West-17	=	697	ND	BDL		2436	204	
8/13/2014		CON	CON-SCR-5	=	185	ND	ND		ND		
8/13/2014		CON	CON-SCR-7	=	73	ND	ND		1539	2014	
8/21/2014		CON	CON-SCR-0	=	90	ND	ND		ND		
9/30/2014		CON	CON-CC-West-14	=	763	ND	ND		DNQ		Smell horses, stables nearby, turbid brown water
10/1/2014		CON	CON-SCR-3	=	201	ND	ND		BDL		Algae