STORMWATER BACTERIA SOURCE TRACING AT SEATTLE-TACOMA INTERNATIONAL AIRPORT

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ABSTRACT

As a follow up to past NPDES stormwater sampling, the Port of Seattle used the microbial source tracking (MST) technique to evaluate potential sources of fecal coliform (FC) bacteria present in runoff from Seattle-Tacoma International Airport. This genetic "fingerprinting" technique indicated that overall, more than 90% of the fecal contamination in runoff was attributable to animals. More than 60% of the "fingerprints" matched bird sources and 30% matched small mammals and domestic pets. Pigeons accounted for 20 to 25% of the bird sources for two outfalls in particular, and were most likely linked with a pigeon colony found on the terminal rooftop. Overall, less than 10% of the isolates matched human sources, and these were limited to certain sampling stations and events. Baseflow samples from the principal outfall investigated, as well as others at the airport, did not contain human isolates. Instream samples collected up gradient from the airport exhibited human isolates in storm and baseflow samples. Many of these receiving water samples had FC counts that would exceed the current state water quality standard of 50 CFU/100ml. Overall, *E. coli* represented 62% of the fecal coliforms present.

Overall, the MST study showed that human sources were present sporadically for two airport outfalls and two stream locations, but occurred in small numbers relative to animal sources. Coupled with this low incidence of human source fingerprints, the FC concentrations point to minor contributions from human sources. The highest FC concentrations found in airport runoff were several orders of magnitude less than FC counts found in local raw domestic sanitary and aircraft lavatory wastewater. Several source-specific fingerprints linked the *E. coli* strains of human origin found in the airport's storm drain system to aircraft lavatory wastewater handling. Although this study shows that this potential source is very limited, the Port is currently investigating improvements to best management practices. The Port already has an active aircraft bird-strike and rodent control program, which has been adapting to reduce nuisance populations.

KEYWORDS

NPDES, stormwater, fecal coliforms, source tracing, genetics

INTRODUCTION

The Port of Seattle conducted a microbial source tracking (MST) project that stemmed from occasionally elevated fecal coliform (FC) counts found in stormwater samples collected from one of a dozen outfalls at the airport. In the 7-year history of National Pollutant Discharge Elimination System (NPDES) sampling for this one particular outfall, fecal coliforms have ranged from near detection limits to counts over 10³/100 ml using the MPN method (Port of Seattle 2001). Though elevated levels of FC are not unusual for stormwater (NURP 1983, City of Bellevue 1995), the Port elected to perform pro-active source-tracing investigations in the area draining this outfall.

The primary outfall characterized (SDE4) drains an area of more than 57 ha (142 ac), predominantly the entire airport's "landside" including terminal and cargo building rooftops, vehicle arrival/departure roads, landscaped areas (small trees, ivy) and a limited taxiway area. The airfield outfall investigated (SDS3) drains an area of more than 185 ha (460 ac) comprising the majority of the runways and taxiways. Together, these two outfalls drain nearly two thirds of the airport south to Des Moines Creek, which flows to Puget Sound over a 3-mile length. The SDS3 station is above the point of final discharge to the Northwest ponds (which also receive non-airport runoff), which in turn form the headwaters of the West branch of Des Moines Creek.

In contrast, SDE4 runoff flows directly to the East branch of the creek along with drainage from Bow Lake and the surrounding city area. It should also be noted that the airport has a unique onsite industrial wastewater treatment plant (IWTP) collects and treats runoff (by dissolved air flotation) from the 148 ha (370 ac) area surrounding the terminal and cargo areas, including the aircraft servicing areas (gates or ramps). The IWTP was not studied in this project because it discharges to Puget Sound directly via a separate outfall, and has not exhibited FC concerns.

The airport comprises about 27% of the entire 1500 ha (5.8 mi²) Des Moines Creek watershed, which also contains the cities of Des Moines and SeaTac. This creek is 303(d)-listed for FC and hence, eventually subject to a total maximum daily load assessment (TMDL). Others have shown FC levels increasing downstream, suggesting sources in other developed areas of this

watershed (Herrera 2001). A limited MST study performed in 1996 by King County suggested that the FC originated from unsewered areas (septage) lower in the watershed (KCDNR 1997).

Two other outfalls tested (SDN1 and SDN4) drain about 5% of the airport to Miller Creek in the North (this creek is not 303(d) listed). The airport's current drainage constitutes about 5% of the 2100 ha (8 mi²) watershed for Miller Creek. Though these two outfalls have routinely exhibited low to non-detectable FC in storm samples, they were tested for reference. Figure 1 shows fecal coliform data (and number of samples, "n") from the past 7-years for the airport's four principal outfalls that together drain more than two-thirds of the airport.

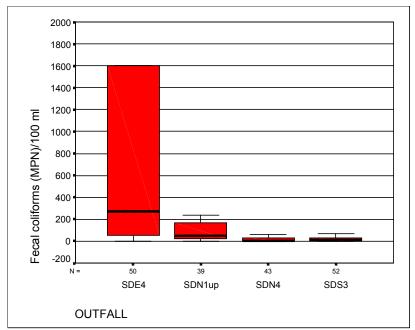


Figure 1 Seven-year sampling history for principal airport outfalls

In the Port's initial source tracing study, chemical indicators were used to determine if the SDE4 runoff was contaminated by sanitary wastewater. Concentrations of surfactants, ammonia, fluoride, and potassium were compared to reference values suggestive of sanitary wastewater contamination (Lalor et al 1993). These findings showed that wastewater was not likely present in the many baseflow and stormflow samples collected (POS 1999). To further explore other potential sources, the Port began the MST study in early 2000.

The MST technique has been used in the Pacific Northwest region and nationally in a number of other studies to identify sources of fecal contamination in surface waters (Farag et al. 2000, NVRC 2000, Herrera 1999, KCDNR 1997, Trial et al 1993). Though these studies have indicated a certain degree of human fecal contamination present, they have also shown wild and domestic animals to be significant contributors of fecal coliform bacteria. Quantifying the impact of each of the sources of fecal contamination can aid managers in stemming sources and reckoning with these sources under 303(d) listings and TMDL proceedings. However, controlling wild animal contributions to FC concentrations will be challenging, particularly where certain species are protected. Two recent issues of the journal Stormwater provided an outline of the MST and other bacteria source-tracing methods (Hager 2001).

METHODOLOGY

In MST studies, a collection of *E. coli* isolates from a large number of water samples taken from study sites are established. All *E. coli* isolates are then subjected to genetic fingerprinting by the ribosomal RNA typing (ribotyping) method using two restriction enzymes (Farag et al. 2000; KCDNR 1997). These "fingerprints" are then compared to those from known sources catalogued in an existing library as well as watershed specific sources collected during the study to identify matching signatures associated with particular types of animals, including humans. The Washington Department of Ecology recognizes this method as an effective tool (Ecology 1999).

In this study, water samples were analyzed first for fecal coliforms by membrane filtration method (Standard Method 9222D, APHA 1995) then *E. coli* colonies were isolated for ribotying. This procedure allows comparison of FC concentrations with the types of *E. coli* isolates (attributable to particular sources) matched in a particular sample. To provide the potential to add local sources to the database and lead to potentially higher matching rates, a number of local fecal matter samples were collected and ribotyped. These sources included animals (dogs, coyote, crows, geese, gulls, pigeons, starlings, and ducks) and local human sources from municipal sanitary wastewater (MWW), and aircraft lavatory wastewater (AWW).

The two key airport outfalls, SDS3 and SDE4 described above were sampled at their routine NPDES monitoring stations. Of principal interest, the SDE4 drainage was also sampled at two upstream points in the piping to allow comparison of runoff from different land use areas. The "SDE4 up" station segregates the upper 20% of the basin associated with service roads, several cargo rooftops, and landscaped roadside areas. The SDE4 midpoint station segregates the upper 75% of the basin associated with the upper station and an additional 32 ha (80 ac) area that includes more roads, cargo rooftops and taxiway portions. Meanwhile, the SDE4 outfall station adds runoff from areas around the terminal (rooftops, arrival/bag claim drives, parking structures and considerable landscaped area). All three of these SDE4 stations are in-pipe and are from 6m to 10m below ground level.

The Des Moines creek station was sampled at the South 200th St crossing, and aggregates the airport and city runoff with stream flows. There are other drainage areas and pipes that contribute runoff and baseflows to the creek above the sampling station, though these were not sampled (roads, hotels and commercial areas within the City of SeaTac). Figure 2 depicts these other sources and the relative station locations for the Des Moines Creek watershed. Four other stations were added midway through the project for added perspective: Bow Lake outlet and NW Pond inlet, and the SDN1 and SDN4 outfalls (consequently there are fewer samples and isolates for these stations). The Bow Lake and NW Pond stations represent flows up gradient from the airport.

Water samples were collected from the stream and accessible outfall locations in 500-ml wide-mouth plastic jars that were attached to the end of a 5-foot pole. Because the SDE4 sampling locations were deep underground, samples were collected remotely using a special apparatus designed to ensure sterile sampling, while preventing personnel from having to enter confined



spaces during stormflows (see photograph 1). This apparatus was lowered on a pole to the in-pipe sampling point and used a vacuum (drawn by peristaltic pump on the surface) to collect samples in a 250-ml autoclaved jar. The unit was disinfected prior to each sample by spraying and rinsing with a one-percent chlorine bleach solution. The sample intake tubing was autoclaved before use and dedicated to each sampling location. Blank samples were collected following the same procedures above, but collected on the surface using deionized water.

Photograph 1 Special downhole sampling apparatus. The unit is suspended from the extension

pole. A peristaltic pump (not shown) draws a vacuum through the tube on the right, which in turn draws the water sample in the tube on left and deposits it in the sample container in the enclosed clear plastic housing. The second tube on the left also draws sample water, which raises the orange float to contact the switch that breaks the vacuum and stops sample collection.

RESULTS AND DISCUSSION

Overall, more than 150 stormflow and baseflow samples were collected during 15 storm events and 4 baseflow events. During the majority of these events, stations were sampled twice to represent discharges early and later on the hydrograph. These samples yielded a total of 851 isolates, where 648 (76%) matched with existing and/or new isolates. This overall matching rate is high compared with older studies and compares favorably with other recent similar work. A total of 599 isolates matched animal sources accounting for 92% of the total matched. Birds represented 376 matched isolates (58%) where seagulls and pigeons accounted for 15% and 7% of the total matched, respectively. See Figures 2-5.

Figure 2 shows pie charts for each station sampled in the Des Moines Creek drainage, and indicates relative locations of several discharge pathways not characterized in the study (adjacent city drainage and two minor airport outfalls). Table 1 summarizes fecal coliform concentrations in storm and baseflow samples.

At each station, birds represented from 48% (Bow Lake outlet) to 73% (NW Pond inlet) of the total isolates. Small mammals and domestic animals together represented from 27% (NW pond inlet) to 38% (Bow Lake outlet) of the sample isolates at each station. In sharp contrast to these animal occurrences, human isolates were not found in samples from the NW pond inlet and the upstream most station in the SDE4 (landside) drainage area. Human isolates were found in samples from two airport outfalls (SDE4 and SDS3), the Bow Lake outlet and the Des Moines Creek station, accounting for 7% to 14% of the total isolates matched at each of these stations. Importantly, human isolates were not found in airport baseflow samples. In contrast, human isolates were present in both storm and baseflow samples from the Bow Lake outlet and the Des Moines Creek station.

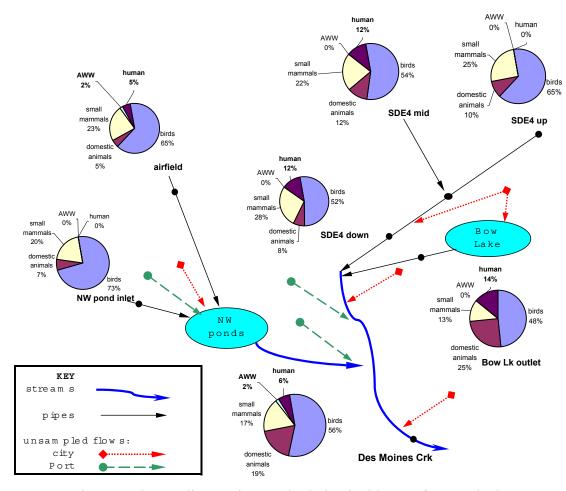
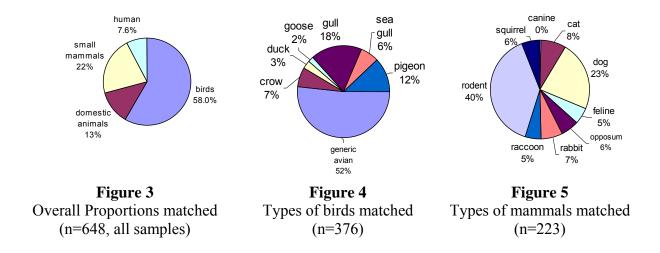


Figure 2 Des Moines Creek sampling stations and relative incidence of source isolates



A total of 49 isolates matched human sources, or 7.6% of the overall total matched. Again, there were several stations where human isolates were not found (SDE4 up, NW pond inlet, and the SDN1 and SDN4 outfalls). Of the total, 44 matched generic human isolates, while only 3 were

unique matches to aircraft wastewater (AWW) isolates obtained from source samples at the airport. All three of these AWW isolates were found in SDS3 and Des Moines Creek samples during the May 9, 2000 storm event. An additional two isolates for these two stations during other storm events each matched both the AWW and MWW human isolates obtained locally. Note however that it is possible that the AWW isolates could be from any human source and the generic human isolates found could have come from the AWW source. Nonetheless, compared to the animal sources found, these human source indications revealed a very low incidence of human fecal contamination. See Figures 2-5.

There were 31 unique samples with 1 or more human isolates found (17 of the 48 isolates were replicate human matches in certain samples). But overall, this incidence of human sources was low considering that more than 100 samples did not exhibit human isolates. Human isolates were not found in any of the many samples taken at the SDE4 up station that segregates runoff from the upstream portion of the principal drainage area of interest (SDE4).

Table 1. Fecal coliform bacteria summary for storm and base flow samples.

Location	Number of Samples	Geometric Mean (CFU ¹ /100 ml)	Minimum (CFU ¹ /100 mL)	Maximum (CFU¹/100 mL)	Percent E. coli ²
Storm Flow Samples					
SDE4 upstream	20	165	2	1,400	55
SDE4 midstream	20	538	104	10,000	55
SDE4 outfall	20	945	100	10,200	70
SDS3 outfall	20	83	39	180	54
SDN1 outfall	4	12	<2	200	40
SDN4 outfall	4	3	<2	7	20
Des Moines Creek at S. 200 th St.	20	527	66	4,600	77
Bow Lake outlet	9	67	20	320	64
NW Ponds inflow	9	593	102	2,000	55
Base Flow Samples					
SDE4 upstream	2	<2	<2	<2	
SDE4 midstream	0	Baseflow was absent			
SDE4 outfall	2	4	<2	8	
SDS3 outfall	8	3	<2	225	
Des Moines Creek at S. 200 th St.	8	19	6	70	
Bow Lake outlet	4	7	3	16	
NW Ponds inflow	4	13	4	32	

¹CFU/100 mL = colony forming units per 100 milliliters by the membrane filter method ² for all samples, ratio of number of positive E. coli colonies to number of fecal coliform colonies isolated from all samples at each station.

Human isolates were found during most sampling events at one or more locations. However, the incidence of human isolates did not correlate well with FC concentrations. Four of the seven samples with highest FC concentrations, including the sample with the single highest value, had

just a single human match (and many animal matches). Meanwhile, nearly two thirds of the 31 samples exhibiting human isolates had FC concentrations of less than 500 CFU/100 ml (well within the range of typical urban stormwater). The single sample with the highest degree of human presence (6 of 9 isolates matched humans) had an FC concentration of 1440 CFU/100 ml. In contrast, there were a number of samples with comparatively high FC concentrations that did not have human isolates.

Physical evidence of human sources (fecal matter) found during the study was very limited. Human fecal matter was observed near the downstream creek location. The transfer of the lavatory wastewater from aircraft (AWW) may allow small leaks, but it only takes place within the IWTP drainage areas. However, vehicles transporting the AWW to the onsite sanitary disposal station travel near, or on the border between the IWTP drainage area and the SDS3 drainage area. Perhaps the limited number of human isolates found in the SDS3 outfall samples could be associated with leaks or drips occurring during AWW transport in this vicinity. There are no AWW handling or transport activities known to occur in the mapped SDE4 storm drainage area.

This study yielded a total of 171 new *E. coli* isolates from the human and animal fecal source samples collected in the vicinity. These unique isolates were added to the existing national database and included 60 from municipal wastewater, 90 from aircraft wastewater, 17 from bird feces and 4 from mammal (dog and coyote) feces. A fraction of these new isolates may represent duplications (isolates with identical ribotypes).

Of the 851 *E. coli* isolates obtained from the water samples, a total of 43 (5 percent) matched only those obtained from source-specific samples collected for this study. Of these 43 local-source matches, 36 represented pigeons, 6 related to local municipal and aircraft wastewater, and one was from a dog. Therefore, the source sampling effort is estimated to have increased the overall matching percentage by approximately 5 percent.

Fecal coliform concentrations found in the municipal wastewater source samples ranged from 6,000 to 1,900,000 CFU/100 ml. The range of these values was below the 10⁶ to 10⁷ CFU/100 ml concentration range typically found in untreated domestic wastewater (Metcalf and Eddy 1991). Concentrations found in the aircraft wastewater source samples were at least an order of magnitude higher than those found in the municipal wastewater samples, and were comparable to the typical domestic wastewater ranges. Higher fecal coliform concentrations in the aircraft wastewater samples are likely due to the lower volume of water used in an aircraft lavatory. These results also indicate that toilet chemicals added to aircraft wastewaters have little, if any, disinfecting properties.

CONCLUSIONS

The results of the quantitative MST study showed that various species of animals (avian, and urban wildlife) constituted the major sources of fecal coliform bacteria of the airport's storm drain system and in Des Moines Creek. Because animals were significant sources, particularly birds, this study indicates they were principally responsible for the sporadic elevated FC counts found in airport runoff. This indication was particularly true for the landside area (outfall SDE4)

where the pigeon colony and guano was found on a terminal rooftop (since removed). The data and observations suggest an inherent reason why landside runoff had higher FC concentrations than the airfield: roosting and nesting sites such as the trees, parking structures, elevated roadways, and bridges prevalent in the landside areas are largely absent on the airfield.

Combined with previous studies' results, the low incidence of human sources coupled with relatively low FC concentrations found in runoff in this study supports an absence of direct cross connections with sanitary wastewater at the airport. Instead, the data indicate infrequent and minor contributions of contamination are present from diffuse wastewater sources, most likely attributable to the occasional small drips and leaks from aircraft wastewater handling and transfer. Nonetheless, these potential human sources will be addressed with an appropriate BMP. This study also showed that sources of human fecal contamination for the streams existed unrelated to (and up gradient from) the airport.

The use of the MST methodology has allowed determination of the relative impacts of each known source of microbial pollution in the area of interest. This knowledge can serve the development of appropriate source control measures, and should aid future TMDL work in the area.

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